

Full wwPDB X-ray Structure Validation Report (i)

May 17, 2020 – 01:30 pm BST

PDB ID : 6N7A

Title : Structure of the human JAK1 kinase domain with compound 39

Authors : Lupardus, P.J.; Brown, D.

Deposited on : 2018-11-27

Resolution : 1.33 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.11

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)

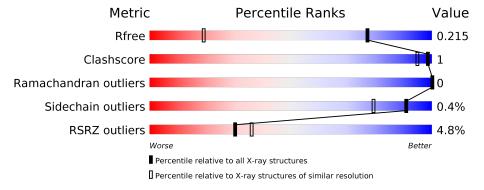
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.33 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	1385 (1.36-1.32)
Clashscore	141614	1417 (1.36-1.32)
Ramachandran outliers	138981	1397 (1.36-1.32)
Sidechain outliers	138945	1397 (1.36-1.32)
RSRZ outliers	127900	1369 (1.36-1.32)

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 on 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 <=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	304	89%	•	9%
1	В	304	95%		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5309 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.

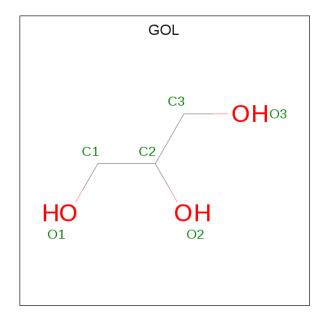
• Molecule 1 is a protein called Tyrosine-protein kinase JAK1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	278	Total 2284	C 1459	N 387	O 421	P 2	S 15	0	4	0
1	В	294	Total 2363	C 1507	N 397	O 442	P 2	S 15	0	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	851	GLY	-	expression tag	UNP P23458
A	852	SER	-	expression tag	UNP P23458
A	853	GLY	_	expression tag	UNP P23458
В	851	GLY	_	expression tag	UNP P23458
В	852	SER	-	expression tag	UNP P23458
В	853	GLY	-	expression tag	UNP P23458

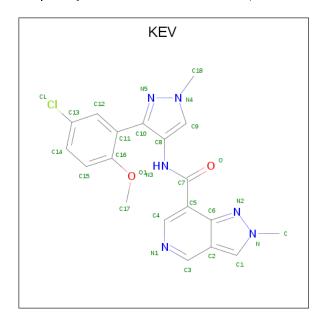
• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	В	1	Total C O 6 3 3	0	0

• Molecule 3 is N-[3-(5-chloro-2-methoxyphenyl)-1-methyl-1H-pyrazol-4-yl]-2-methyl-2H-pyrazolo[4,3-c]pyridine-7-carboxamide (three-letter code: KEV) (formula: $C_{19}H_{17}ClN_6O_2$).



Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	
3	A	1	Total 28				0	0
3	В	1	Total 28		Cl 1		0	0

• Molecule 4 is water.

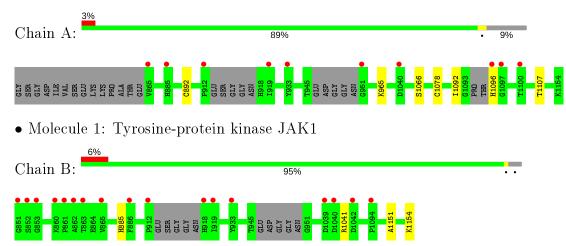
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	${f AltConf}$
4	A	308	Total O 308 308	0	0
4	В	280	Total O 280 280	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Tyrosine-protein kinase JAK1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	42.72Å 173.23Å 45.06Å	Depositor
a, b, c, α , β , γ	90.00° 94.17° 90.00°	Depositor
Resolution (Å)	86.62 - 1.33	Depositor
Resolution (A)	86.61 - 1.33	EDS
% Data completeness	98.2 (86.62-1.33)	Depositor
(in resolution range)	98.2 (86.61-1.33)	EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.44 (at 1.33Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
P. P.	0.192 , 0.207	Depositor
R, R_{free}	0.197 , 0.215	DCC
R_{free} test set	7315 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor (\mathring{A}^2)	11.8	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 45.4	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5309	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: GOL, PTR, KEV

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		
MIOI		RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.58	0/2307	0.66	0/3103	
1	В	0.54	0/2385	0.62	0/3215	
All	All	0.56	0/4692	0.64	0/6318	

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	$\mathbf{H}(\mathbf{model})$	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2284	0	2278	4	0
1	В	2363	0	2343	2	0
2	A	12	0	16	1	0
2	В	6	0	8	0	0
3	A	28	0	0	0	0
3	В	28	0	0	0	0
4	A	308	0	0	0	0
4	В	280	0	0	0	0
All	All	5309	0	4645	5	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 (5) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{c} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:1096:HIS:HB2	1:B:1041:ARG:HA	1.64	0.77
1:A:965:LYS:HD2	1:A:1078:CYS:HB3	1.86	0.56
1:A:1092:ILE:HG22	1:A:1107:THR:OG1	2.20	0.41
1:A:892:CYS:SG	2:A:1201:GOL:H12	2.60	0.41
1:B:1151:ALA:O	1:B:1154:LYS:HG2	2.20	0.41

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	Perce	${f ntiles}$
1	A	272/304~(90%)	270 (99%)	2 (1%)	0	100	100
1	В	288/304~(95%)	287 (100%)	1 (0%)	0	100	100
All	All	560/608 (92%)	557 (100%)	3 (0%)	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	$251/268 \; (94\%)$	249 (99%)	2 (1%)	81 57		

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
1	В	258/268 (96%)	257 (100%)	1 (0%)	91	79
All	All	509/536 (95%)	506 (99%)	3 (1%)	91	67

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

Mol	Chain	Res	Type
1	A	1066[A]	SER
1	A	1066[B]	SER
1	В	885	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	Tuno	Chain	Res	Link	Во	ond leng	ths	Bond angles		
MIGI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	$\mid \# Z > 2$
1	PTR	В	1034	1	15,16,17	0.50	0	19,22,24	0.87	0
1	PTR	A	1035	1	15,16,17	0.67	0	19,22,24	0.71	0
1	PTR	В	1035	1	15,16,17	0.74	1 (6%)	19,22,24	0.88	1 (5%)
1	PTR	A	1034	1	15,16,17	0.58	0	19,22,24	0.74	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	PTR	В	1034	1	-	0/10/11/13	0/1/1/1
1	PTR	A	1035	1	-	0/10/11/13	0/1/1/1
1	PTR	В	1035	1	=	0/10/11/13	0/1/1/1
1	PTR	A	1034	1	=	0/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	${ m Observed}({ m \AA})$	$\mathbf{Ideal}(\mathbf{\AA})$
1	В	1035	PTR	P-O1P	2.08	1.57	1.50

All (1) bond angle outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	${f Atoms}$	Z	$\operatorname{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	В	1035	PTR	O3P-P-OH	2.12	111.88	105.24

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

5 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	Dog Link		Res Link Bond lengths			Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	1202	-	5,5,5	0.24	0	5,5,5	0.54	0
2	GOL	A	1201	-	5,5,5	0.07	0	5,5,5	0.14	0
3	KEV	A	1203	-	25,31,31	0.85	0	27,45,45	0.67	0



Mol	Tuno	Chain	Res Link		Во	ond leng	ths	В	ond ang	les
10101	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	В	1201	-	5,5,5	0.17	0	5,5,5	0.56	0
3	KEV	В	1202	_	25,31,31	0.86	1 (4%)	27,45,45	0.63	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	GOL	A	1202	-	-	0/4/4/4	-
2	GOL	A	1201	-	-	0/4/4/4	-
3	KEV	A	1203	-	-	0/10/14/14	0/4/4/4
2	GOL	В	1201	-	-	0/4/4/4	-
3	KEV	В	1202	-	-	0/10/14/14	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	${f Observed(\AA)}$	$oxed{Ideal(\AA)}$
3	В	1202	KEV	C10-N5	-2.23	1.33	1.35

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

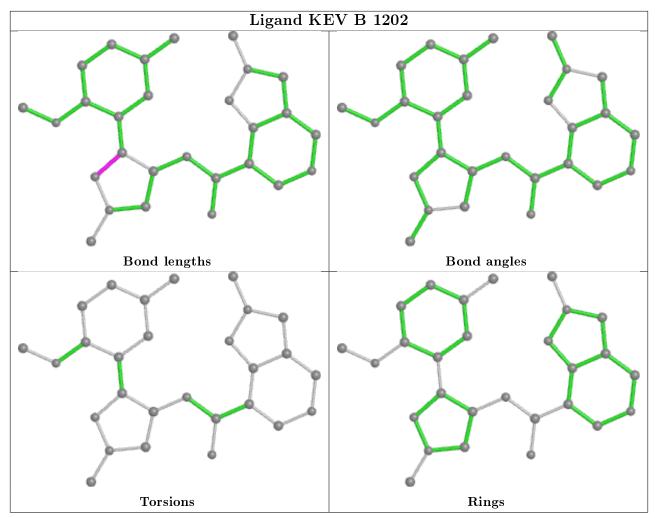
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	GOL	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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

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^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$		$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	A	$276/304 \ (90\%)$	-0.14	10 (3%) 42	49	7, 14, 38, 50	0
1	В	292/304~(96%)	-0.02	17 (5%) 23	25	9, 17, 39, 67	0
All	All	568/608 (93%)	-0.08	27 (4%) 30	36	7, 15, 38, 67	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ
1	В	852		
1	В	851	GLY	6.9
1	В	912	PRO	6.0
1	В	863	THR	5.7
1	В	861	PRO	5.3
1	A	865	VAL	5.1
1	A	933	TYR	4.9
1	В	886	PHE	4.2
1	A	951	GLY	4.1
1	В	933	TYR	3.9
1			VAL	3.7
1			PRO	3.6
1	В	919	ILE	3.5
1	В	1042	ASP	3.5
1	A	1096	HIS	3.5
1	A	1097 GLY		3.4
1	В	1040 ASP		3.3
1	В	862 AI		3.3
1	В	860	LYS	3.1
1	В	853	GLY	2.9
1	A	919	ILE	2.7
1	В	1039	ASP	2.5
1	A	885	HIS	2.4
1	1 B		HIS	2.3

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Mol	Chain	Res	Type	RSRZ	
1	A	912	PRO	2.3	
1	A	1100	THR	2.0	
1	A	1040	ASP	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, 95^{th} 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	${f Res}$	Atoms	RSCC	RSR	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
1	PTR	В	1035	16/17	0.87	0.12	13,23,43,43	0
1	PTR	A	1035	16/17	0.89	0.10	12,19,43,43	0
1	PTR	A	1034	16/17	0.91	0.09	12,17,41,41	0
1	PTR	В	1034	16/17	0.94	0.08	13,20,40,40	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

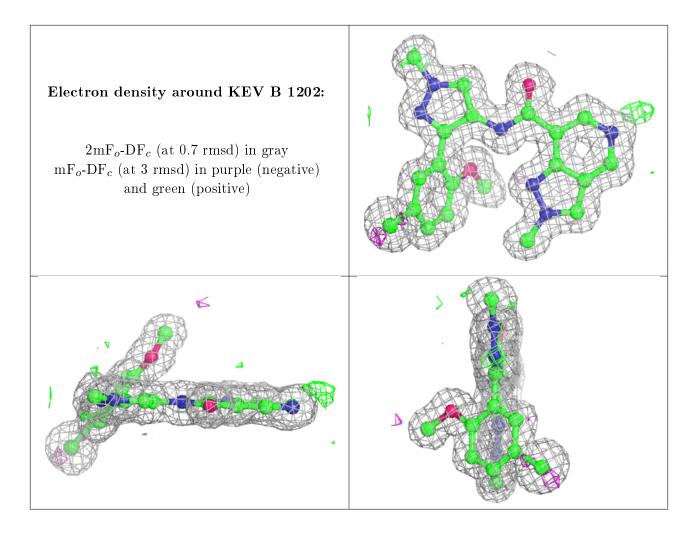
6.4 Ligands (i)

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^{th} 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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
2	GOL	A	1201	6/6	0.81	0.15	32,38,41,42	0
2	GOL	В	1201	6/6	0.88	0.13	23,24,25,27	0
2	GOL	A	1202	6/6	0.91	0.12	19,21,22,24	0
3	KEV	A	1203	28/28	0.98	0.06	7,9,11,13	0
3	KEV	В	1202	28/28	0.98	0.05	10,12,15,17	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.

