

Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 01:07 pm BST

PDB ID	:	6PMA
Title	:	TRK-A IN COMPLEX WITH LIGAND
Authors	:	Subramanian, G.; Brown, D.G.
Deposited on	:	2019-07-01
Resolution	:	2.53 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:

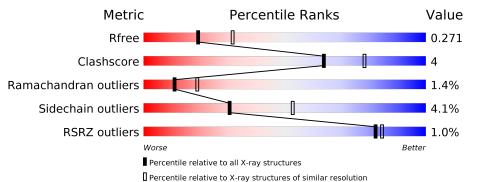
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins)	:::::::::::::::::::::::::::::::::::::::	1.8.5 (274361), CSD as541be (2020) 1.13 2.11 1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (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 2.53 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	$5743 \ (2.54-2.50)$
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335(2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630(2.54-2.50)

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	311	76%	14%	•• 7%	_



2 Entry composition (i)

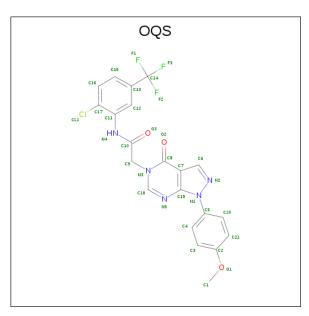
There are 3 unique types of molecules in this entry. The entry contains 2381 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 High affinity nerve growth factor receptor.

Mol	Chain	Residues		ŀ	Atom	5			ZeroOcc	AltConf	Trace
1	A	290	Total 2323	C 1482	N 417	O 407	Р 1	S 16	77	0	0

• Molecule 2 is N-[2-chloro-5-(trifluoromethyl)phenyl]-2-[1-(4-methoxyphenyl)-4-oxo-1,4 -dihydro-5H-pyrazolo[3,4-d]pyrimidin-5-yl]acetamide (three-letter code: OQS) (formula: $C_{21}H_{15}ClF_3N_5O_3$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
2	А	1	Total 33		Cl 1				0	0

• Molecule 3 is water.

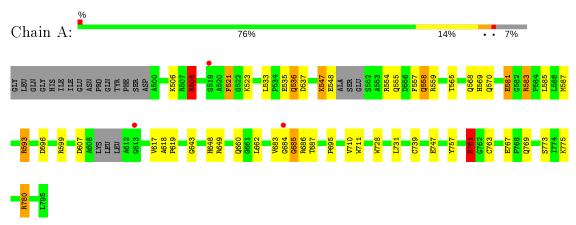
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	25	TotalO2525	0	0



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: High affinity nerve growth factor receptor





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants	52.09Å 52.09 Å 227.16 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	-
Resolution (Å)	45.16 - 2.53	Depositor
	45.11 - 2.53	EDS
% Data completeness	99.2 (45.16-2.53)	Depositor
(in resolution range)	99.2(45.11 - 2.53)	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.99 ({\rm at}2.54{ m \AA})$	Xtriage
Refinement program	REFMAC $5.8.0238$	Depositor
D D	0.204 , 0.266	Depositor
R, R_{free}	0.209 , 0.271	DCC
R_{free} test set	906 reflections (7.47%)	wwPDB-VP
Wilson B-factor $(Å^2)$	52.0	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34 , 35.2	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.075 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2381	wwPDB-VP
Average B, all atoms $(Å^2)$	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.59% of the height of the origin peak. No significant pseudotranslation is detected.

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.



 $^{^1 {\}rm Intensities}$ 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: OQS, SEP

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	Bo	nd lengths	Bond angles		
IVIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	2.07	19/2369~(0.8%)	1.94	28/3204~(0.9%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	4

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	761	ARG	NE-CZ	60.65	2.11	1.33
1	А	508	ARG	NE-CZ	-31.70	0.91	1.33
1	А	607	ASP	CB-CG	-27.24	0.94	1.51
1	А	521	PHE	CG-CD2	-24.37	1.02	1.38
1	А	780	ARG	CD-NE	-22.19	1.08	1.46
1	А	767	GLU	CG-CD	19.83	1.81	1.51
1	А	523	LYS	CE-NZ	-19.44	1.00	1.49
1	А	521	PHE	CG-CD1	19.32	1.67	1.38
1	А	686	ARG	CB-CG	17.46	1.99	1.52
1	А	570	GLN	CG-CD	-15.09	1.16	1.51
1	А	747	GLU	CG-CD	-12.51	1.33	1.51
1	А	559	ARG	CB-CG	-9.96	1.25	1.52
1	А	547	LYS	CG-CD	-8.50	1.23	1.52
1	А	554	ARG	CB-CG	-5.73	1.37	1.52
1	А	555	GLN	CB-CG	5.68	1.67	1.52
1	А	775	LYS	CD-CE	5.34	1.64	1.51
1	А	585	LEU	CG-CD1	-5.34	1.32	1.51
1	A	585	LEU	CG-CD2	5.25	1.71	1.51

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Mol	Chain	\mathbf{Res}	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(Å)
1	А	537	ASP	CB-CG	-5.20	1.40	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	583	ARG	NE-CZ-NH1	-46.07	97.27	120.30
1	А	583	ARG	NE-CZ-NH2	45.39	143.00	120.30
1	А	521	PHE	CB-CG-CD1	-27.53	101.53	120.80
1	А	761	ARG	NE-CZ-NH1	-26.17	107.22	120.30
1	А	761	ARG	CD-NE-CZ	-23.88	90.17	123.60
1	А	548	GLU	CG-CD-OE2	17.52	153.35	118.30
1	А	548	GLU	CG-CD-OE1	-17.33	83.64	118.30
1	А	686	ARG	CA-CB-CG	-16.59	76.90	113.40
1	А	583	ARG	CD-NE-CZ	15.86	145.80	123.60
1	А	523	LYS	CD-CE-NZ	13.95	143.79	111.70
1	А	780	ARG	CD-NE-CZ	12.91	141.68	123.60
1	А	508	ARG	NE-CZ-NH1	-12.81	113.89	120.30
1	А	521	PHE	CG-CD1-CE1	-11.57	108.07	120.80
1	А	570	GLN	CB-CG-CD	10.04	137.69	111.60
1	А	686	ARG	CB-CG-CD	-8.54	89.40	111.60
1	А	585	LEU	CB-CG-CD2	-8.52	96.52	111.00
1	А	521	PHE	CB-CG-CD2	8.34	126.64	120.80
1	А	570	GLN	CG-CD-OE1	-8.15	105.30	121.60
1	А	554	ARG	CA-CB-CG	7.60	130.11	113.40
1	А	747	GLU	CB-CG-CD	7.41	134.21	114.20
1	А	535	GLU	CA-CB-CG	-7.41	97.10	113.40
1	А	607	ASP	CA-CB-CG	6.65	128.02	113.40
1	А	570	GLN	CG-CD-NE2	6.41	132.07	116.70
1	А	607	ASP	CB-CG-OD2	6.10	123.79	118.30
1	А	558	GLN	CG-CD-OE1	-6.06	109.48	121.60
1	А	767	GLU	CB-CG-CD	-5.38	99.67	114.20
1	А	607	ASP	CB-CG-OD1	-5.36	113.48	118.30
1	А	761	ARG	NE-CZ-NH2	5.31	122.95	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	508	ARG	Sidechain
1	А	521	PHE	Sidechain
1	А	583	ARG	Sidechain
1	А	761	ARG	Sidechain



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	А	2323	0	2304	19	0
2	А	33	0	0	0	0
3	А	25	0	0	0	0
All	All	2381	0	2304	19	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 4.

All (19) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:A:769:GLN:HA	1:A:769:GLN:OE1	1.83	0.78
1:A:617:VAL:HG22	1:A:662:LEU:HD11	1.90	0.53
1:A:506:LYS:HD3	1:A:508:ARG:HE	1.75	0.51
1:A:757:TYR:CE2	1:A:761:ARG:HD2	2.46	0.49
1:A:568:GLN:O	1:A:569:HIS:HB2	2.12	0.49
1:A:683:VAL:HG13	1:A:687:THR:HB	1.95	0.49
1:A:533:LEU:O	1:A:536:GLN:O	2.33	0.47
1:A:581:GLU:HG3	1:A:581:GLU:O	2.14	0.47
1:A:618:ALA:HB1	1:A:619:PRO:HD2	1.97	0.47
1:A:617:VAL:HG12	1:A:618:ALA:O	2.16	0.46
1:A:695:PRO:HB3	1:A:711:TRP:CD2	2.51	0.46
1:A:581:GLU:CG	1:A:581:GLU:O	2.66	0.44
1:A:557:PHE:CD2	1:A:587:MET:HE3	2.52	0.44
1:A:648:HIS:O	1:A:649:ARG:HB2	2.18	0.43
1:A:710:VAL:O	1:A:763:CYS:HB3	2.19	0.43
1:A:683:VAL:O	1:A:685:GLY:N	2.53	0.41
1:A:728:TRP:HB3	1:A:731:LEU:HD12	2.01	0.41
1:A:565:THR:HA	1:A:568:GLN:NE2	2.35	0.41
1:A:593:ARG:NH1	1:A:660:GLN:HG3	2.36	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	А	283/311~(91%)	267 (94%)	12 (4%)	4 (1%)	11 19

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	643	GLY
1	А	684	GLY
1	А	547	LYS
1	А	685	GLY

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	А	242/260~(93%)	232~(96%)	10 (4%)	30 53	

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	508	ARG
1	А	536	GLN
1	А	558	GLN
1	А	581	GLU
1	А	593	ARG
1	А	596	ASP
1	А	599	ARG

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Mol	Chain	Res	Type
1	А	739	CYS
1	А	773	SER
1	А	780	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	\mathbf{Type}	
1	А	504	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)

1 non-standard protein/DNA/RNA residue 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	B	ond leng	gths	В	ond ang	gles
WIOI	туре	Ullalli	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
1	SEP	А	677	1	$8,\!9,\!10$	0.70	0	8,12,14	1.00	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	SEP	А	677	1	-	3/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
1	А	677	SEP	CB-OG-P-O3P
1	А	677	SEP	CB-OG-P-O1P
1	А	677	SEP	CB-OG-P-O2P

All (3) torsion outliers are listed below:

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)

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 Typ		Chain	Chain	Chain	Chain	Chain	Chain	Chain	Dec	Tink	Bo	ond leng	ths	В	ond ang	les
	Type	nes		Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2						
2	OQS	А	801	-	34,36,36	0.60	0	$41,\!53,\!53$	0.95	2 (4%)						

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	OQS	А	801	-	-	2/20/20/20	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	801	OQS	C6-N2-N1	3.13	108.03	103.93
2	А	801	OQS	C7-C8-N3	-2.91	114.17	116.15

There are no chirality outliers.

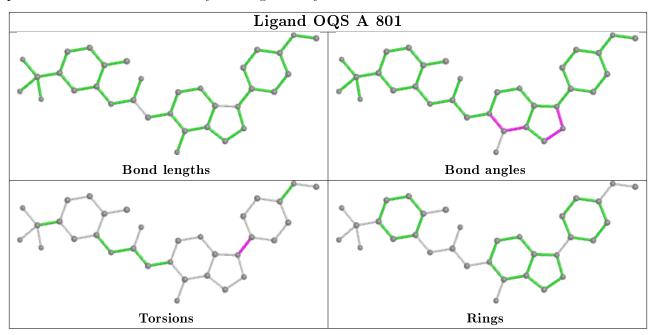
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	801	OQS	C4-C5-N1-C19
2	А	801	OQS	C20-C5-N1-C19

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 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, 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	$ $ $<$ $\mathbf{RSRZ}>$	#RSRZ >2	$OWAB(Å^2)$	Q<0.9
1	А	289/311~(92%)	-0.15	3 (1%) 82 84	26, 44, 76, 93	24 (8%)

All (3) RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
1	А	684	GLY	4.8
1	А	613	GLY	4.3
1	А	519	GLY	2.8

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	Res	Atoms	RSCC	\mathbf{RSR}	${f B} ext{-factors}({ m \AA}^2)$	$Q{<}0.9$
1	SEP	А	677	10/11	0.89	0.12	$37,\!46,\!73,\!80$	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

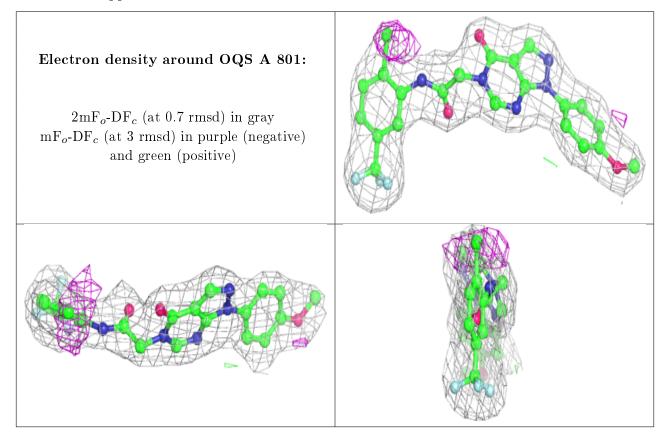
6.4 Ligands (i)

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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	OQS	А	801	33/33	0.97	0.14	$31,\!33,\!47,\!72$	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.

