



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2022 – 10:33 pm BST

PDB ID : 8A2D
Title : EGFR kinase domain (L858R/V948R) in complex with 2-[4-(difluoromethyl)-6-[2-[4-[[4-(hydroxymethyl)-1-piperidyl]methyl]phenyl]ethynyl]-7-methyl-indazol-2-yl]-2-spiro[6,7-dihydropyrrolo[1,2-c]imidazole-5,1'-cyclopropane]-1-yl-N-tiazol-2-yl-acetamide
Authors : Kuglstatter, A.; Ehler, A.
Deposited on : 2022-06-03
Resolution : 1.11 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (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

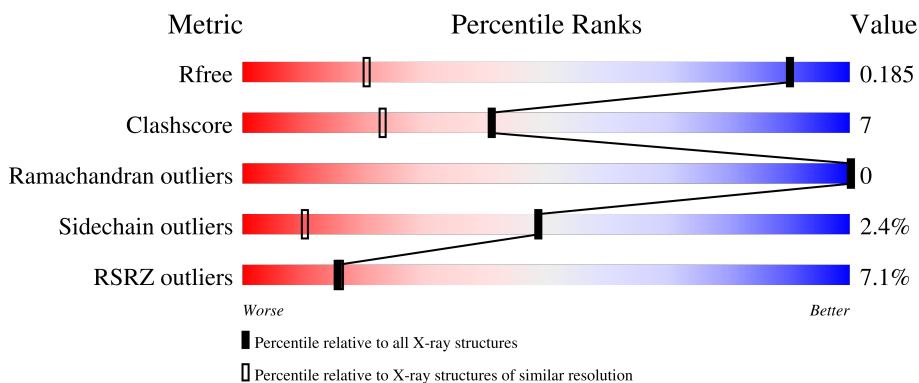
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.11 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}	130704	1168 (1.14-1.10)
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)
RSRZ outliers	127900	1146 (1.14-1.10)

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	326	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2770 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.

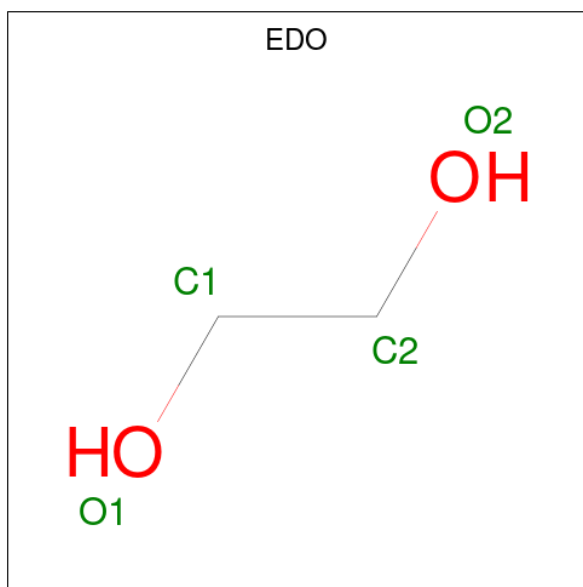
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	2318	1495	392	413	18	0	9	0

There are 5 discrepancies between the modelled and reference sequences:

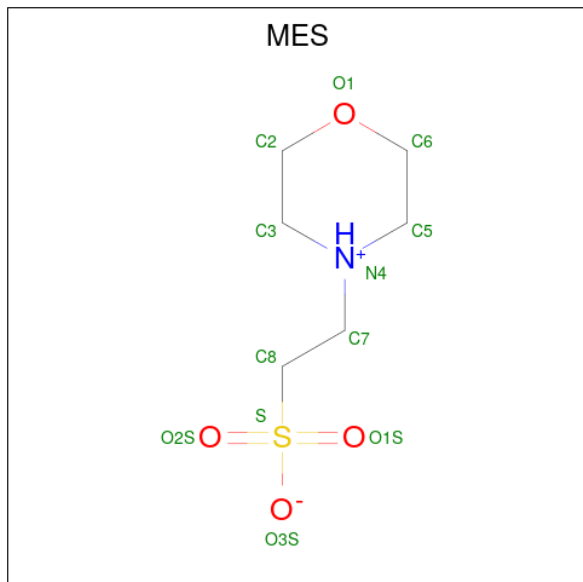
Chain	Residue	Modelled	Actual	Comment	Reference
A	697	GLY	-	expression tag	UNP P00533
A	698	SER	-	expression tag	UNP P00533
A	699	MET	-	expression tag	UNP P00533
A	858	ARG	LEU	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



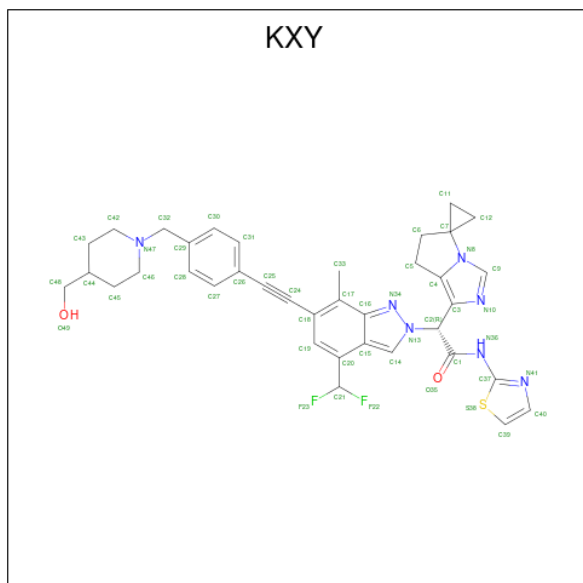
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	12	6	1	4	1	0	0

- Molecule 4 is (2R)-2-[4-[bis(fluoranyl)methyl]-6-[2-[4-[[4-(hydroxymethyl)piperidin-1-yl]methyl]phenyl]ethynyl]-7-methyl-indazol-2-yl]-2-spiro[6,7-dihydropyrrolo[1,2-c]imidazole-5,1'-cyclopropane]-1-yl-N-(1,3-thiazol-2-yl)ethanamide (three-letter code: KXY) (formula: C₃₇H₃₇F₂N₇O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
4	A	1	49	37	2	7	2	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	387	Total	O	0	0
			387	387		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.62Å 34.95Å 83.93Å 90.00° 128.81° 90.00°	Depositor
Resolution (Å)	65.40 – 1.11 65.40 – 1.11	Depositor EDS
% Data completeness (in resolution range)	89.7 (65.40-1.11) 89.7 (65.40-1.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.11Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.163 , 0.179 0.170 , 0.185	Depositor DCC
R_{free} test set	4722 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	11.8	Xtrriage
Anisotropy	0.170	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2770	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.19% 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: EDO, MES, KXY

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	0.99	2/2393 (0.1%)	1.16	12/3231 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	865	GLU	CD-OE1	6.56	1.32	1.25
1	A	711	GLU	CD-OE2	6.47	1.32	1.25

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	947	MET	CG-SD-CE	-19.42	69.13	100.20
1	A	836	ARG	NE-CZ-NH2	9.92	125.26	120.30
1	A	915	TYR	CB-CG-CD1	8.68	126.21	121.00
1	A	945[A]	MET	CG-SD-CE	-8.52	86.57	100.20
1	A	945[B]	MET	CG-SD-CE	-8.52	86.57	100.20
1	A	915	TYR	CB-CG-CD2	-8.16	116.11	121.00
1	A	952	MET	CG-SD-CE	-7.84	87.66	100.20
1	A	952	MET	CB-CG-SD	6.06	130.57	112.40
1	A	776	ARG	NE-CZ-NH1	-5.49	117.55	120.30
1	A	841	ARG	NE-CZ-NH2	5.25	122.92	120.30
1	A	856	PHE	CB-CG-CD2	5.09	124.36	120.80
1	A	776	ARG	NE-CZ-NH2	5.02	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2318	0	2392	33	0
2	A	4	0	6	0	0
3	A	12	0	13	0	0
4	A	49	0	0	1	0
5	A	387	0	0	13	0
All	All	2770	0	2411	34	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 (34) 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:816[B]:ASN:HD22	1:A:1017:LEU:HD22	1.02	1.06
1:A:816[B]:ASN:HD22	1:A:1017:LEU:CD2	1.74	0.99
1:A:816[B]:ASN:ND2	1:A:1017:LEU:HD22	1.86	0.89
1:A:986:ARG:CZ	5:A:1206:HOH:O	2.22	0.87
1:A:730:LEU:HD11	1:A:739:LYS:HB3	1.63	0.80
1:A:713:LYS:HE3	1:A:715:ILE:HD11	1.70	0.72
1:A:974:ASP:HB2	1:A:1021:GLN:HE21	1.54	0.70
1:A:785[A]:THR:HG21	5:A:1263:HOH:O	1.93	0.68
1:A:941:ILE:O	1:A:945[B]:MET:HG2	1.95	0.67
1:A:762[A]:GLU:OE1	1:A:858:ARG:NE	2.31	0.64
1:A:730:LEU:HD11	1:A:739:LYS:CB	2.30	0.61
1:A:949:LYS:HE2	5:A:1201:HOH:O	2.01	0.59
1:A:889:ARG:NH2	5:A:1205:HOH:O	2.36	0.59
1:A:949:LYS:CE	5:A:1201:HOH:O	2.51	0.59
1:A:816[B]:ASN:ND2	1:A:1017:LEU:CD2	2.57	0.58
1:A:986:ARG:NE	5:A:1206:HOH:O	2.37	0.56
1:A:745:LYS:CE	5:A:1207:HOH:O	2.55	0.55
1:A:762[A]:GLU:OE1	1:A:858:ARG:NH1	2.40	0.54
4:A:1103:KXY:S38	4:A:1103:KXY:O35	2.70	0.49
1:A:730:LEU:HD13	1:A:731:TRP:N	2.28	0.48
1:A:974:ASP:HB2	1:A:1021:GLN:NE2	2.25	0.48
1:A:762[A]:GLU:CD	1:A:858:ARG:HE	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:946:ILE:CD1	1:A:967:GLU:HG2	2.44	0.47
1:A:985:GLU:OE2	1:A:985:GLU:HA	2.15	0.47
1:A:945[B]:MET:HG3	5:A:1348:HOH:O	2.15	0.47
1:A:785[A]:THR:HG23	5:A:1273:HOH:O	2.15	0.47
1:A:852:LYS:NZ	5:A:1209:HOH:O	2.40	0.46
1:A:960:LYS:HE2	5:A:1462:HOH:O	2.16	0.45
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.51	0.45
1:A:806:LYS:HE3	5:A:1283:HOH:O	2.18	0.43
1:A:952:MET:HE3	1:A:957[B]:SER:OG	2.20	0.42
1:A:945[A]:MET:HB3	1:A:945[A]:MET:HE3	1.78	0.41
1:A:762[A]:GLU:OE1	1:A:858:ARG:CZ	2.68	0.41
1:A:960:LYS:CE	5:A:1462:HOH:O	2.68	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	Percentiles
1	A	282/326 (86%)	277 (98%)	5 (2%)	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	260/287 (91%)	254 (98%)	6 (2%)	50 11

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	730	LEU
1	A	734	GLU
1	A	849	GLN
1	A	889	ARG
1	A	942	ASP
1	A	977	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	849	GLN
1	A	1020	GLN
1	A	1021	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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$
4	KXY	A	1103	-	45,56,56	1.45	6 (13%)	45,83,83	1.94	12 (26%)
3	MES	A	1102	-	12,12,12	1.13	1 (8%)	14,16,16	1.47	1 (7%)
2	EDO	A	1101	-	3,3,3	0.39	0	2,2,2	0.53	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
4	KXY	A	1103	-	-	3/21/57/57	0/8/8/8
3	MES	A	1102	-	-	0/6/14/14	0/1/1/1
2	EDO	A	1101	-	-	0/1/1/1	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1103	KXY	C2-C1	-5.00	1.49	1.54
4	A	1103	KXY	C17-C16	-3.40	1.37	1.43
4	A	1103	KXY	C5-C4	2.90	1.54	1.49
4	A	1103	KXY	C28-C27	2.72	1.43	1.38
3	A	1102	MES	C8-S	2.46	1.81	1.77
4	A	1103	KXY	C12-C11	2.26	1.55	1.50
4	A	1103	KXY	F22-C21	2.00	1.39	1.35

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1102	MES	O2S-S-C8	-4.54	101.45	106.92
4	A	1103	KXY	C14-N13-N34	4.51	114.39	111.70
4	A	1103	KXY	C19-C20-C15	-4.47	115.53	118.37
4	A	1103	KXY	C30-C29-C28	3.85	124.22	118.17
4	A	1103	KXY	C20-C15-C16	-3.72	119.90	122.89
4	A	1103	KXY	C29-C32-N47	-3.36	106.60	113.12
4	A	1103	KXY	C46-N47-C42	3.23	116.10	108.83
4	A	1103	KXY	C37-N36-C1	-2.62	123.19	129.02
4	A	1103	KXY	C31-C26-C27	2.57	123.60	118.96
4	A	1103	KXY	C31-C30-C29	-2.41	117.71	121.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1103	KXY	C27-C28-C29	-2.34	117.80	121.03
4	A	1103	KXY	C27-C26-C25	-2.27	116.78	120.78
4	A	1103	KXY	C32-C29-C28	-2.16	116.71	120.77

There are no chirality outliers.

All (3) torsion outliers are listed below:

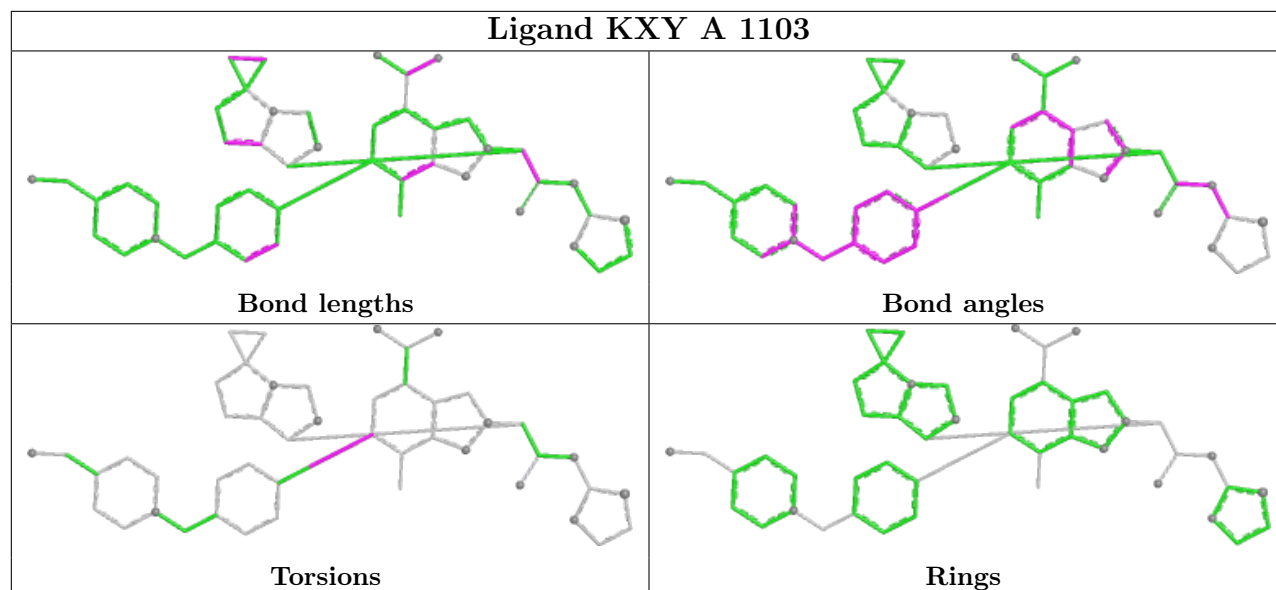
Mol	Chain	Res	Type	Atoms
4	A	1103	KXY	C18-C24-C25-C26
4	A	1103	KXY	C17-C18-C24-C25
4	A	1103	KXY	C19-C18-C24-C25

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1103	KXY	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 [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	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	281/326 (86%)	0.38	20 (7%) 16 16	7, 13, 32, 64	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1018	ILE	6.8
1	A	1019	PRO	6.8
1	A	869	TYR	6.4
1	A	1017	LEU	6.0
1	A	870	HIS	5.0
1	A	867	LYS	4.8
1	A	866	GLU	4.6
1	A	859	ALA	4.6
1	A	1021	GLN	4.6
1	A	701	GLN	4.2
1	A	1020	GLN	3.7
1	A	723	PHE	3.6
1	A	865	GLU	3.1
1	A	985	GLU	2.5
1	A	748	ARG	2.4
1	A	986	ARG	2.3
1	A	876	VAL	2.1
1	A	889	ARG	2.1
1	A	939[A]	CYS	2.1
1	A	749	GLU	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](#)

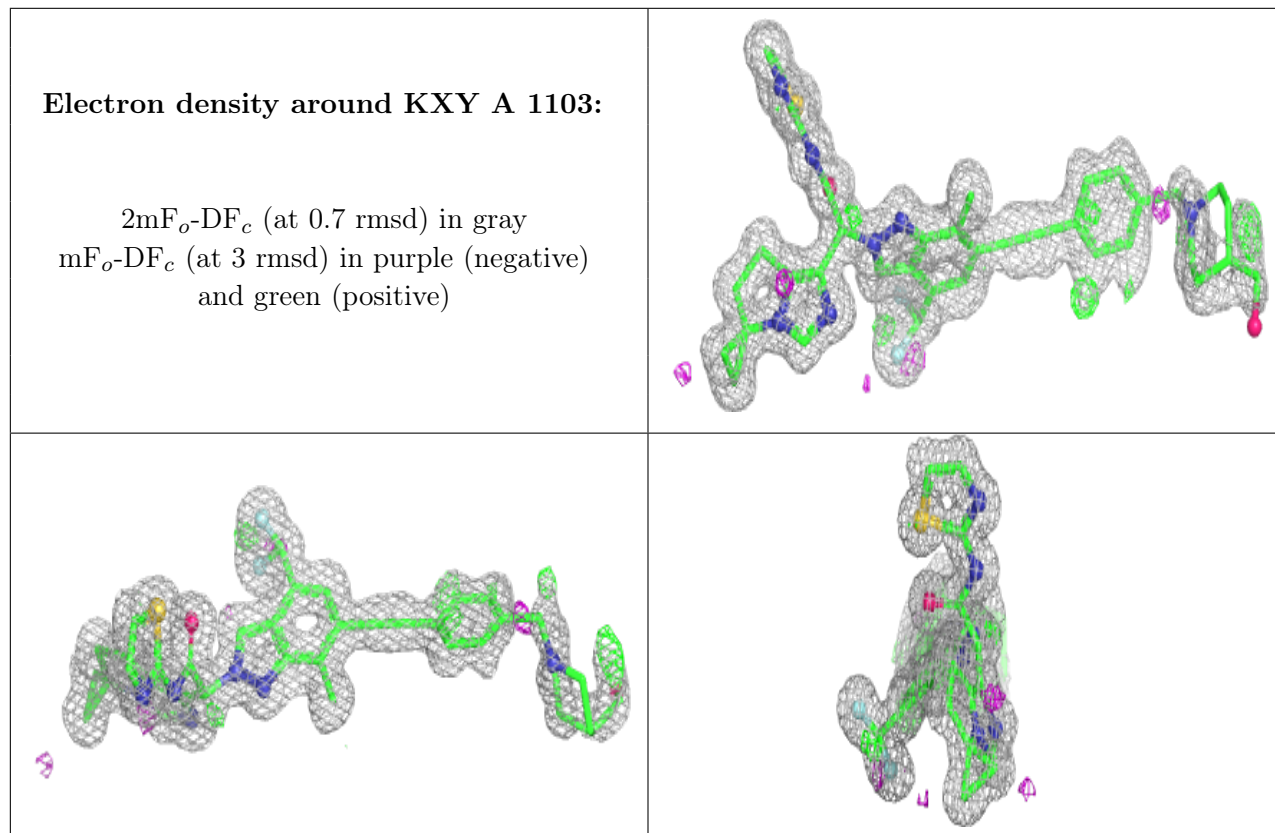
There are no monosaccharides in this entry.

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, 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(\AA^2)	Q<0.9
3	MES	A	1102	12/12	0.91	0.24	17,26,36,40	0
2	EDO	A	1101	4/4	0.92	0.07	18,19,19,24	0
4	KXY	A	1103	49/49	0.98	0.08	8,10,45,59	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.