



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 03:24 am BST

PDB ID : 5XDK
Title : Crystal structure of EGFR 696-1022 T790M in complex with CO-1686
Authors : Yan, X.E.; Yun, C.H.
Deposited on : 2017-03-28
Resolution : 2.35 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 following versions of software and data (see [references ⓘ](#)) 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

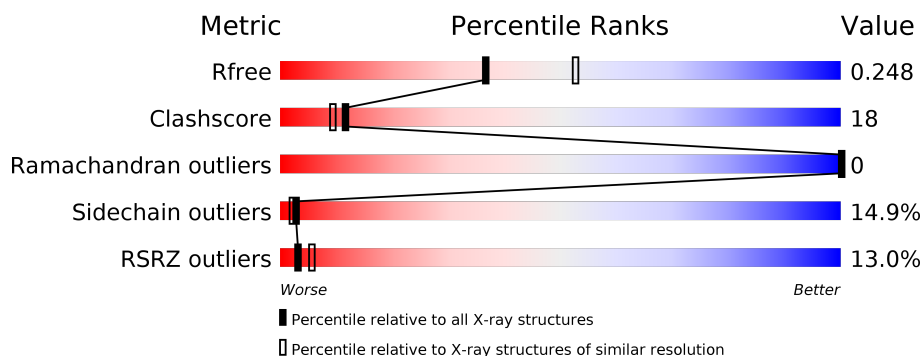
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 $\leq 5\%$. 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	331	

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.

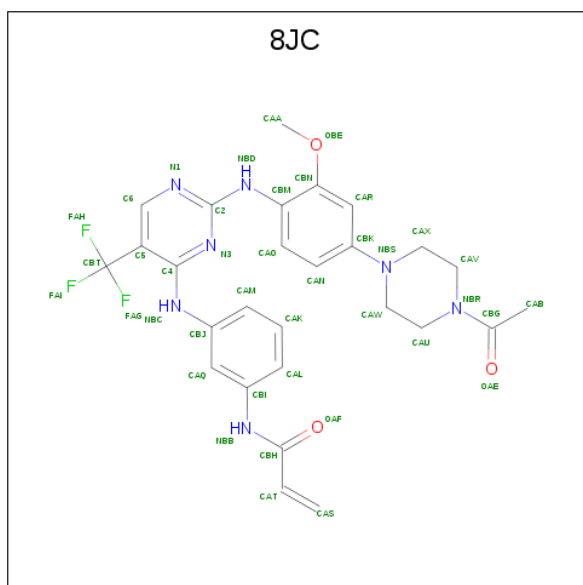
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2397	1551	401	428	17			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLY	-	expression tag	UNP P00533
A	693	ALA	-	expression tag	UNP P00533
A	694	MET	-	expression tag	UNP P00533
A	695	GLY	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533

- Molecule 2 is N-[3-[[2-[[4-(4-ethanoylpiperazin-1-yl)-2-methoxy-phenyl]amino]-5-(trifluoromethyl)pyrimidin-4-yl]amino]phenyl]prop-2-enamide (three-letter code: 8JC) (formula: C₂₇H₂₈F₃N₇O₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			40	27	3	7	3		

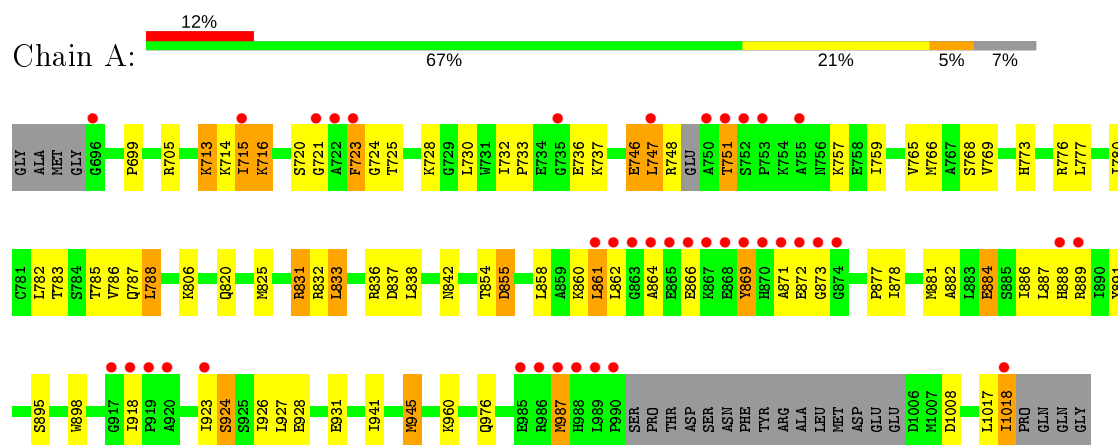
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total	O	0	0
			107	107		

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: Epidermal growth factor receptor



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	145.47Å 145.47Å 145.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.99 – 2.35 41.99 – 2.35	Depositor EDS
% Data completeness (in resolution range)	96.9 (41.99-2.35) 96.9 (41.99-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.34Å)	Xtriage
Refinement program	PHENIX (dev_2400)	Depositor
R, R_{free}	0.217 , 0.248 0.217 , 0.248	Depositor DCC
R_{free} test set	1080 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2544	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 8JC

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	0.58	0/2447	0.56	0/3311

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

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	2397	0	2420	83	0
2	A	40	0	0	2	0
3	A	107	0	0	4	0
All	All	2544	0	2420	85	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 18.

All (85) 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:721:GLY:HA3	1:A:723:PHE:CE2	1.77	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1018:ILE:HG13	1:A:1018:ILE:O	1.42	1.12
1:A:747:LEU:CD1	1:A:747:LEU:H	1.66	1.07
1:A:747:LEU:N	1:A:747:LEU:HD12	1.65	1.05
1:A:721:GLY:HA3	1:A:723:PHE:HE2	0.90	1.04
1:A:882:ALA:HB1	1:A:884:GLU:OE1	1.59	1.00
1:A:832:ARG:CZ	1:A:864:ALA:HA	1.92	1.00
1:A:721:GLY:CA	1:A:723:PHE:HE2	1.76	0.99
1:A:871:ALA:O	1:A:889:ARG:HD3	1.61	0.98
1:A:747:LEU:H	1:A:747:LEU:HD12	1.23	0.94
1:A:746:GLU:HB2	1:A:787:GLN:HG2	1.50	0.93
1:A:747:LEU:HD11	1:A:759:ILE:HD12	1.49	0.92
1:A:747:LEU:HD11	1:A:759:ILE:CD1	2.02	0.90
1:A:723:PHE:N	1:A:723:PHE:CD2	2.42	0.85
1:A:960:LYS:HE2	3:A:1218:HOH:O	1.77	0.82
1:A:831:ARG:NH2	3:A:1201:HOH:O	2.18	0.77
1:A:748:ARG:O	1:A:751:THR:CG2	2.35	0.74
1:A:715:ILE:HD13	1:A:715:ILE:N	2.02	0.74
1:A:924:SER:O	1:A:928:GLU:HG3	1.86	0.74
1:A:746:GLU:OE2	1:A:785:THR:HG21	1.88	0.73
1:A:721:GLY:CA	1:A:723:PHE:CE2	2.59	0.73
1:A:889:ARG:HH11	1:A:889:ARG:HG2	1.55	0.72
1:A:747:LEU:HD13	1:A:747:LEU:H	1.57	0.66
2:A:1101:8JC:N3	2:A:1101:8JC:CAO	2.52	0.66
1:A:1018:ILE:CG1	1:A:1018:ILE:O	2.30	0.66
1:A:773:HIS:CE1	1:A:820:GLN:HG2	2.31	0.66
1:A:723:PHE:HD2	1:A:724:GLY:H	1.42	0.65
1:A:882:ALA:CB	1:A:884:GLU:OE1	2.42	0.63
1:A:869:TYR:CE1	1:A:871:ALA:HB2	2.34	0.63
1:A:714:LYS:C	1:A:715:ILE:HD13	2.20	0.62
1:A:836:ARG:HG3	1:A:891:TYR:CD1	2.35	0.62
1:A:926:ILE:HG23	1:A:931:GLU:HB3	1.83	0.60
1:A:769:VAL:O	1:A:776:ARG:HG3	2.00	0.60
1:A:747:LEU:HD13	1:A:786:VAL:O	2.02	0.59
1:A:780:ILE:HG22	1:A:788:LEU:HD22	1.83	0.59
1:A:715:ILE:N	1:A:715:ILE:CD1	2.68	0.56
1:A:748:ARG:O	1:A:751:THR:HG23	2.06	0.55
1:A:861:LEU:HD23	3:A:1292:HOH:O	2.07	0.55
1:A:877:PRO:O	1:A:881:MET:HG3	2.08	0.54
1:A:887:LEU:HB3	1:A:888:HIS:CE1	2.42	0.54
1:A:854:THR:HG23	1:A:855:ASP:N	2.22	0.53
1:A:837:ASP:HB2	1:A:858:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:MET:HE1	3:A:1206:HOH:O	2.10	0.52
1:A:926:ILE:CG2	1:A:931:GLU:HB3	2.40	0.51
1:A:716:LYS:HD2	1:A:728:LYS:HE3	1.92	0.51
1:A:747:LEU:CD1	1:A:759:ILE:HD12	2.32	0.51
1:A:766:MET:HB3	1:A:777:LEU:HB2	1.91	0.51
1:A:746:GLU:CB	1:A:787:GLN:HG2	2.33	0.51
1:A:836:ARG:CG	1:A:891:TYR:CD1	2.93	0.51
1:A:861:LEU:HD13	1:A:862:LEU:N	2.27	0.50
1:A:832:ARG:NH1	1:A:864:ALA:HA	2.27	0.49
1:A:746:GLU:HB2	1:A:787:GLN:CG	2.33	0.49
1:A:861:LEU:C	1:A:861:LEU:HD13	2.33	0.49
2:A:1101:8JC:CAQ	2:A:1101:8JC:OAF	2.60	0.49
1:A:765:VAL:HG13	1:A:833:LEU:HD21	1.94	0.49
1:A:748:ARG:O	1:A:751:THR:HG22	2.11	0.49
1:A:723:PHE:N	1:A:723:PHE:HD2	2.02	0.49
1:A:886:ILE:HG21	1:A:924:SER:HB2	1.95	0.48
1:A:747:LEU:CD1	1:A:786:VAL:O	2.62	0.48
1:A:733:PRO:HB2	1:A:736:GLU:HB2	1.94	0.47
1:A:941:ILE:HD11	1:A:945:MET:HE1	1.96	0.47
1:A:889:ARG:NH1	1:A:889:ARG:HG2	2.26	0.46
1:A:716:LYS:HE2	1:A:716:LYS:HB3	1.36	0.46
1:A:888:HIS:N	1:A:888:HIS:ND1	2.65	0.45
1:A:887:LEU:C	1:A:888:HIS:ND1	2.69	0.45
1:A:941:ILE:CG1	1:A:945:MET:HE3	2.46	0.45
1:A:861:LEU:C	1:A:861:LEU:CD1	2.85	0.45
1:A:941:ILE:HG13	1:A:945:MET:HE3	1.99	0.45
1:A:832:ARG:NH1	1:A:864:ALA:O	2.50	0.44
1:A:730:LEU:HD23	1:A:730:LEU:HA	1.83	0.44
1:A:825:MET:SD	1:A:838:LEU:HD22	2.58	0.44
1:A:898:TRP:CD1	1:A:898:TRP:C	2.92	0.43
1:A:782:LEU:HD23	1:A:786:VAL:HG22	1.99	0.43
1:A:747:LEU:O	1:A:748:ARG:C	2.56	0.43
1:A:941:ILE:HG13	1:A:945:MET:CE	2.49	0.42
1:A:842:ASN:O	1:A:854:THR:HG22	2.19	0.42
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.55	0.42
1:A:836:ARG:HD2	1:A:891:TYR:CG	2.54	0.42
1:A:878:ILE:HG23	1:A:886:ILE:CD1	2.50	0.41
1:A:887:LEU:HB3	1:A:888:HIS:ND1	2.36	0.41
1:A:746:GLU:OE2	1:A:785:THR:CG2	2.65	0.41
1:A:873:GLY:HA2	1:A:889:ARG:NH1	2.36	0.41
1:A:831:ARG:HD2	1:A:831:ARG:HA	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:945:MET:HE3	1:A:945:MET:HB2	1.89	0.40
1:A:713:LYS:HE3	1:A:713:LYS:HB2	1.76	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	301/331 (91%)	298 (99%)	3 (1%)	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	255/288 (88%)	217 (85%)	38 (15%)	3	2

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	699	PRO
1	A	705	ARG
1	A	713	LYS
1	A	715	ILE

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Mol	Chain	Res	Type
1	A	716	LYS
1	A	720	SER
1	A	723	PHE
1	A	725	THR
1	A	732	ILE
1	A	737	LYS
1	A	746	GLU
1	A	747	LEU
1	A	751	THR
1	A	757	LYS
1	A	768	SER
1	A	783	THR
1	A	788	LEU
1	A	806	LYS
1	A	831	ARG
1	A	833	LEU
1	A	855	ASP
1	A	860	LYS
1	A	861	LEU
1	A	866	GLU
1	A	869	TYR
1	A	872	GLU
1	A	884	GLU
1	A	895	SER
1	A	918	ILE
1	A	923	ILE
1	A	924	SER
1	A	927	LEU
1	A	945	MET
1	A	976	GLN
1	A	987	MET
1	A	1008	ASP
1	A	1017	LEU
1	A	1018	ILE

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

Mol	Chain	Res	Type
1	A	773	HIS

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 carbohydrates 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	8JC	A	1101	1	43,43,43	1.93	12 (27%)	59,61,61	2.30	14 (23%)

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	8JC	A	1101	1	-	2/30/40/40	0/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	8JC	CBT-C5	-5.23	1.39	1.50
2	A	1101	8JC	FAG-CBT	-4.78	1.15	1.32
2	A	1101	8JC	CAS-CAT	4.67	1.53	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	8JC	CBI-NBB	-3.96	1.33	1.41
2	A	1101	8JC	CBJ-NBC	-3.35	1.33	1.40
2	A	1101	8JC	CAT-CBH	3.19	1.53	1.48
2	A	1101	8JC	FAI-CBT	-2.88	1.22	1.32
2	A	1101	8JC	CBM-NBD	-2.70	1.32	1.39
2	A	1101	8JC	FAH-CBT	-2.69	1.23	1.32
2	A	1101	8JC	C4-NBC	-2.22	1.33	1.36
2	A	1101	8JC	C6-N1	2.19	1.39	1.34
2	A	1101	8JC	C2-NBD	-2.05	1.32	1.36

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	8JC	CAS-CAT-CBH	-9.16	111.79	122.27
2	A	1101	8JC	N1-C2-N3	-5.70	121.15	126.55
2	A	1101	8JC	CBJ-NBC-C4	-5.34	115.97	129.39
2	A	1101	8JC	CAA-OBE-CBN	-4.95	110.06	117.53
2	A	1101	8JC	CBI-NBB-CBH	-4.22	121.88	128.26
2	A	1101	8JC	CAX-NBS-CAW	3.94	120.20	111.52
2	A	1101	8JC	C5-C6-N1	-3.93	118.76	123.95
2	A	1101	8JC	CAV-NBR-CAU	3.78	119.89	112.62
2	A	1101	8JC	C6-N1-C2	3.08	120.52	115.88
2	A	1101	8JC	CBM-NBD-C2	-3.04	120.44	129.60
2	A	1101	8JC	CAB-CBG-NBR	-2.56	115.28	118.26
2	A	1101	8JC	OAE-CBG-NBR	2.36	123.92	121.02
2	A	1101	8JC	CAR-CBK-NBS	-2.29	118.87	121.33
2	A	1101	8JC	FAI-CBT-C5	-2.13	109.00	112.70

There are no chirality outliers.

All (2) torsion outliers are listed below:

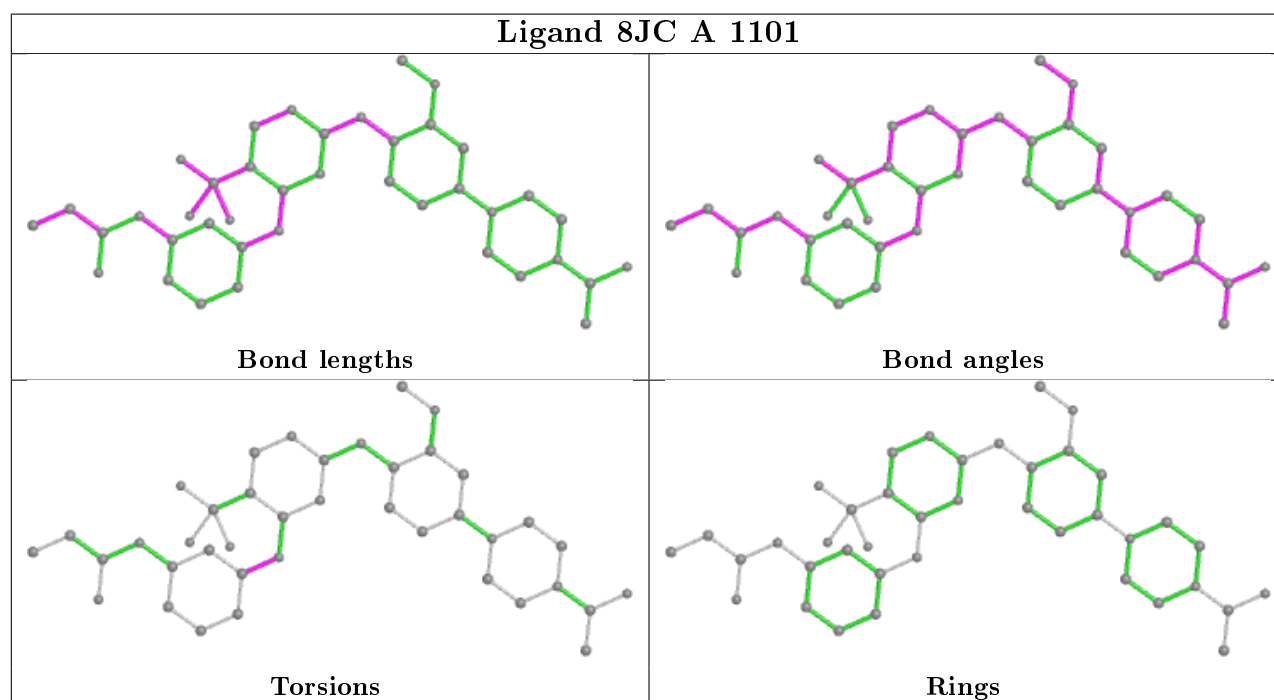
Mol	Chain	Res	Type	Atoms
2	A	1101	8JC	CAQ-CBJ-NBC-C4
2	A	1101	8JC	CAM-CBJ-NBC-C4

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	8JC	2	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	307/331 (92%)	0.78	40 (13%) 3 6	19, 36, 81, 103	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	722	ALA	8.5
1	A	750	ALA	7.8
1	A	870	HIS	7.0
1	A	864	ALA	6.8
1	A	863	GLY	6.8
1	A	721	GLY	5.9
1	A	874	GLY	5.7
1	A	917	GLY	5.2
1	A	873	GLY	5.0
1	A	988	HIS	4.8
1	A	751	THR	4.7
1	A	747	LEU	4.4
1	A	753	PRO	4.2
1	A	989	LEU	4.1
1	A	862	LEU	4.0
1	A	752	SER	4.0
1	A	723	PHE	4.0
1	A	696	GLY	3.9
1	A	866	GLU	3.8
1	A	865	GLU	3.6
1	A	861	LEU	3.6
1	A	872	GLU	3.6
1	A	986	ARG	3.5
1	A	715	ILE	3.3
1	A	889	ARG	3.1
1	A	990	PRO	3.1
1	A	987	MET	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	869	TYR	3.0
1	A	985	GLU	3.0
1	A	867	LYS	2.9
1	A	923	ILE	2.8
1	A	919	PRO	2.7
1	A	918	ILE	2.5
1	A	888	HIS	2.5
1	A	920	ALA	2.5
1	A	868	GLU	2.4
1	A	871	ALA	2.3
1	A	755	ALA	2.2
1	A	735	GLY	2.1
1	A	1018	ILE	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

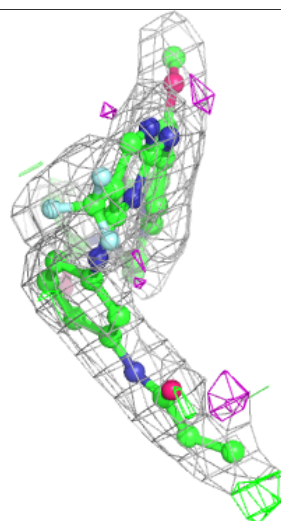
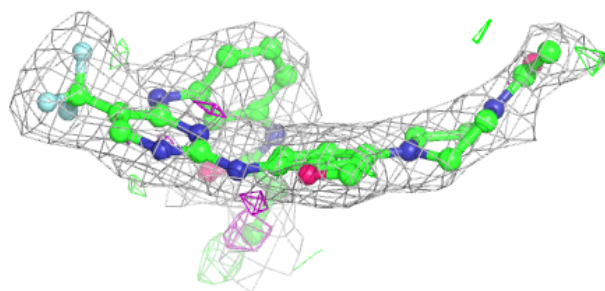
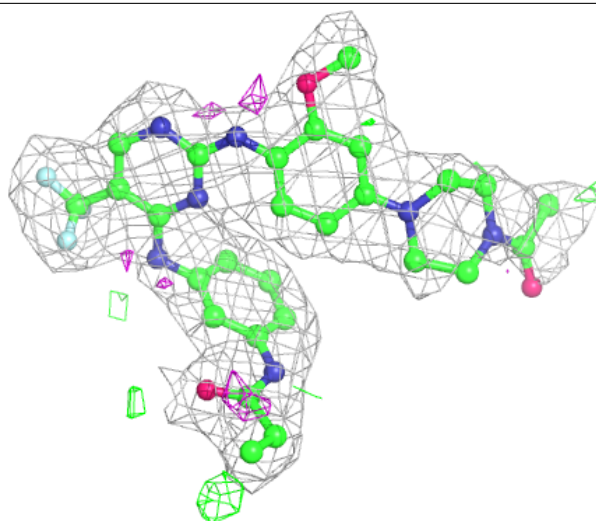
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	8JC	A	1101	40/40	0.92	0.17	26,36,69,75	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.

Electron density around 8JC A 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.