Full wwPDB X-ray Structure Validation Report (i)

May 25, 2020 – 02:42 pm BST

PDB ID	:	6PFM
Title	:	Crystal structure of GDC-0927 bound to estrogen receptor alpha
Authors	:	Kiefer, J.R.; Vinogradova, M.; Liang, J.; Zhang, B.; Wang, X.; Zbieg, J.R.; Labadie, S.S.; Li, J.; Ray, N.C.; Ortwine, D.
Deposited on	:	2019-06-21
Resolution	:	2.84 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

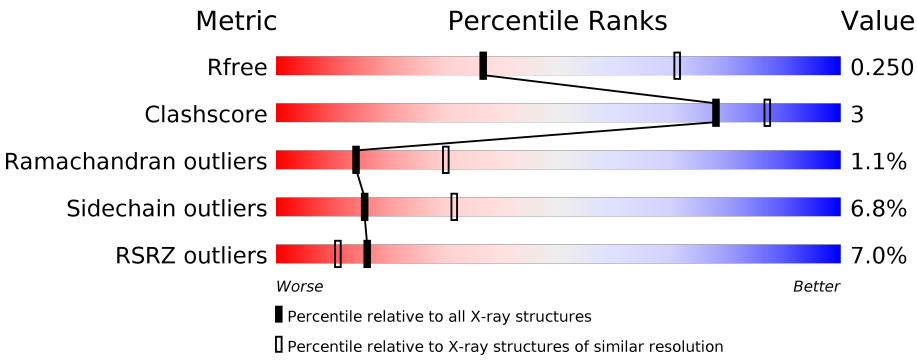
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.84 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}	130704	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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	280	6% 69% 10% • 20%
1	D	280	5% 74% 9% • 16%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7260 atoms, of which 3556 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 Estrogen receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	D	235	3649	1180	1797	316	337	19	0	2	0
1	A	224	3469	1129	1707	297	319	17	0	2	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	274	MET	-	expression tag	UNP P03372
D	275	HIS	-	expression tag	UNP P03372
D	276	HIS	-	expression tag	UNP P03372
D	277	HIS	-	expression tag	UNP P03372
D	278	HIS	-	expression tag	UNP P03372
D	279	HIS	-	expression tag	UNP P03372
D	280	HIS	-	expression tag	UNP P03372
D	281	SER	-	expression tag	UNP P03372
D	282	SER	-	expression tag	UNP P03372
D	283	GLY	-	expression tag	UNP P03372
D	284	VAL	-	expression tag	UNP P03372
D	285	ASP	-	expression tag	UNP P03372
D	286	LEU	-	expression tag	UNP P03372
D	287	GLY	-	expression tag	UNP P03372
D	288	THR	-	expression tag	UNP P03372
D	289	GLU	-	expression tag	UNP P03372
D	290	ASN	-	expression tag	UNP P03372
D	291	LEU	-	expression tag	UNP P03372
D	292	TYR	-	expression tag	UNP P03372
D	293	PHE	-	expression tag	UNP P03372
D	294	GLN	-	expression tag	UNP P03372
D	295	SER	-	expression tag	UNP P03372
D	296	ASN	-	expression tag	UNP P03372
D	297	ALA	-	expression tag	UNP P03372
D	372	SER	LEU	engineered mutation	UNP P03372

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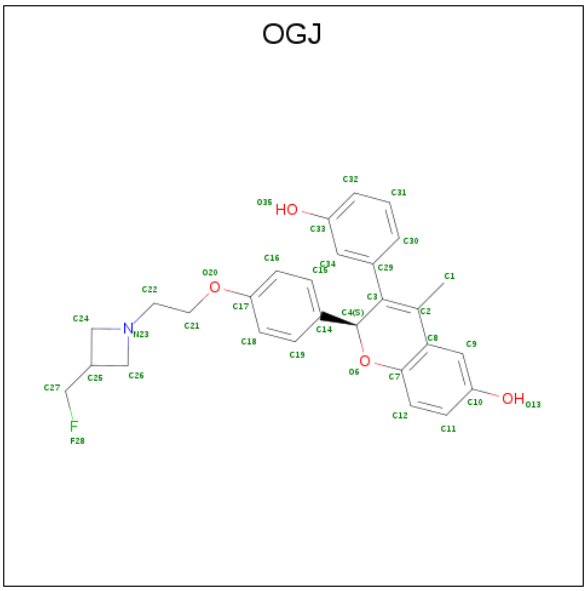
Chain	Residue	Modelled	Actual	Comment	Reference
D	536	SER	LEU	engineered mutation	UNP P03372
A	274	MET	-	expression tag	UNP P03372
A	275	HIS	-	expression tag	UNP P03372
A	276	HIS	-	expression tag	UNP P03372
A	277	HIS	-	expression tag	UNP P03372
A	278	HIS	-	expression tag	UNP P03372
A	279	HIS	-	expression tag	UNP P03372
A	280	HIS	-	expression tag	UNP P03372
A	281	SER	-	expression tag	UNP P03372
A	282	SER	-	expression tag	UNP P03372
A	283	GLY	-	expression tag	UNP P03372
A	284	VAL	-	expression tag	UNP P03372
A	285	ASP	-	expression tag	UNP P03372
A	286	LEU	-	expression tag	UNP P03372
A	287	GLY	-	expression tag	UNP P03372
A	288	THR	-	expression tag	UNP P03372
A	289	GLU	-	expression tag	UNP P03372
A	290	ASN	-	expression tag	UNP P03372
A	291	LEU	-	expression tag	UNP P03372
A	292	TYR	-	expression tag	UNP P03372
A	293	PHE	-	expression tag	UNP P03372
A	294	GLN	-	expression tag	UNP P03372
A	295	SER	-	expression tag	UNP P03372
A	296	ASN	-	expression tag	UNP P03372
A	297	ALA	-	expression tag	UNP P03372
A	372	SER	LEU	engineered mutation	UNP P03372
A	536	SER	LEU	engineered mutation	UNP P03372

- Molecule 2 is (2S)-2-(4-{2-[3-(fluoromethyl)azetidin-1-yl]ethoxy}phenyl)-3-(3-hydroxyphenyl)-4-methyl-2H-1-benzopyran-6-ol (three-letter code: OGJ) (formula: $C_{28}H_{28}FNO_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	F	H	N	O		
2	D	1	60	28	1	26	1	4	0	0
			Total	C	F	H	N	O		
2	A	1	60	28	1	26	1	4	0	0

- Molecule 3 is water.

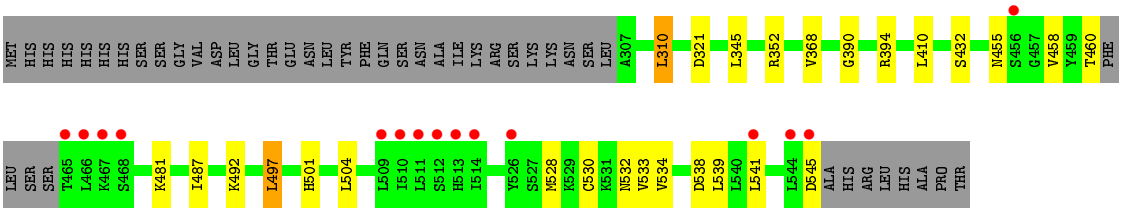
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	D	18	19	19	0	1
			Total	O		
3	A	3	3	3	0	0

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.

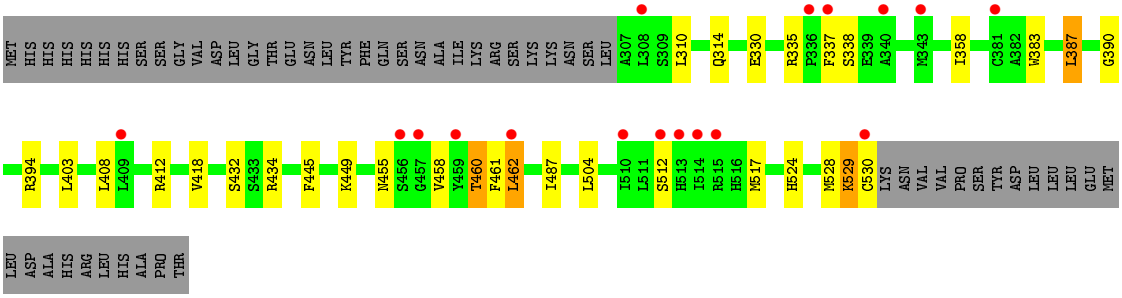
- Molecule 1: Estrogen receptor

Chain D:



- Molecule 1: Estrogen receptor

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	144.11Å 144.11Å 171.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.95 – 2.84 33.93 – 2.84	Depositor EDS
% Data completeness (in resolution range)	99.7 (33.95-2.84) 99.8 (33.93-2.84)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.58 (at 2.85Å)	Xtriage
Refinement program	REFMAC 5.8.0232	Depositor
R, R_{free}	0.209 , 0.249 0.208 , 0.250	Depositor DCC
R_{free} test set	814 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	62.5	Xtriage
Anisotropy	0.267	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 71.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.040 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l 0.029 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l 0.020 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7260	wwPDB-VP
Average B, all atoms (Å^2)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

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: OGJ

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	0/1796	0.74	0/2431
1	D	0.66	0/1885	0.77	0/2548
All	All	0.65	0/3681	0.75	0/4979

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	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1762	1707	1773	12	0
1	D	1852	1797	1865	9	0
2	A	34	26	0	0	0
2	D	34	26	0	0	0
3	A	3	0	0	0	0
3	D	19	0	0	0	0
All	All	3704	3556	3638	21	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 3.

All (21) 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:418:VAL:HG11	1:A:528:MET:HE1	1.87	0.56
1:D:352[B]:ARG:HG3	1:D:352[B]:ARG:HH21	1.71	0.56
1:A:310:LEU:HD23	1:A:314:GLN:HE21	1.73	0.53
1:D:497:LEU:HD22	1:D:501:HIS:CE1	2.44	0.53
1:A:390:GLY:O	1:A:394:ARG:HG3	2.13	0.48
1:A:460:THR:O	1:A:462:LEU:N	2.46	0.48
1:A:418:VAL:CG1	1:A:528:MET:HE1	2.44	0.47
1:A:418:VAL:HG11	1:A:528:MET:CE	2.45	0.47
1:D:390:GLY:O	1:D:394:ARG:HG3	2.14	0.46
1:A:445:PHE:CZ	1:A:449:LYS:HD2	2.51	0.45
1:D:310:LEU:O	1:D:481:LYS:HE3	2.18	0.44
1:D:352[B]:ARG:HG3	1:D:352[B]:ARG:NH2	2.33	0.44
1:A:383:TRP:HE3	1:A:387:LEU:HD13	1.82	0.44
1:D:455:ASN:O	1:D:458:VAL:HG12	2.17	0.43
1:A:524:HIS:O	1:A:528:MET:HG2	2.19	0.43
1:D:487:ILE:HD11	1:D:504:LEU:HD22	2.02	0.42
1:A:455:ASN:O	1:A:458:VAL:HG12	2.19	0.42
1:D:410:LEU:N	1:D:410:LEU:HD22	2.34	0.42
1:A:487:ILE:HD11	1:A:504:LEU:HD22	2.03	0.41
1:A:529:LYS:O	1:A:530:CYS:SG	2.75	0.41
1:D:532:ASN:C	1:D:534:VAL:H	2.24	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	223/280 (80%)	209 (94%)	10 (4%)	4 (2%)	8 19
1	D	232/280 (83%)	224 (97%)	7 (3%)	1 (0%)	34 56
All	All	455/560 (81%)	433 (95%)	17 (4%)	5 (1%)	14 30

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	461	PHE
1	A	462	LEU
1	A	529	LYS
1	D	533	VAL
1	A	335	ARG

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	194/252 (77%)	180 (93%)	14 (7%)	14	29
1	D	205/252 (81%)	191 (93%)	14 (7%)	16	31
All	All	399/504 (79%)	371 (93%)	28 (7%)	16	30

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	310	LEU
1	D	321	ASP
1	D	345	LEU
1	D	368	VAL
1	D	432	SER
1	D	460	THR
1	D	492	LYS
1	D	497	LEU
1	D	528	MET
1	D	530	CYS
1	D	538	ASP
1	D	539	LEU
1	D	541	LEU
1	D	545	ASP
1	A	330[A]	GLU
1	A	330[B]	GLU
1	A	337	PHE
1	A	338	SER

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Mol	Chain	Res	Type
1	A	358	ILE
1	A	387	LEU
1	A	403	LEU
1	A	408	LEU
1	A	412	ARG
1	A	432	SER
1	A	434	ARG
1	A	460	THR
1	A	512	SER
1	A	517	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	356	HIS
1	D	375	GLN
1	D	413	ASN
1	D	501	HIS
1	D	532	ASN
1	A	314	GLN
1	A	413	ASN
1	A	441	GLN
1	A	502	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
2	OGJ	A	601	-	37,38,38	4.23	11 (29%)	43,54,54	1.06	3 (6%)
2	OGJ	D	601	-	37,38,38	4.24	12 (32%)	43,54,54	1.20	4 (9%)

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	OGJ	A	601	-	-	4/12/40/40	0/5/5/5
2	OGJ	D	601	-	-	3/12/40/40	0/5/5/5

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	OGJ	C22-N23	-15.52	1.11	1.47
2	A	601	OGJ	C22-N23	-15.40	1.12	1.47
2	A	601	OGJ	C24-C25	-9.35	1.42	1.54
2	D	601	OGJ	C24-C25	-9.31	1.42	1.54
2	D	601	OGJ	C26-C25	-9.09	1.42	1.54
2	A	601	OGJ	C26-C25	-8.63	1.43	1.54
2	A	601	OGJ	O6-C7	7.88	1.48	1.38
2	A	601	OGJ	C3-C2	7.79	1.46	1.35
2	D	601	OGJ	C3-C2	7.63	1.46	1.35
2	D	601	OGJ	O6-C7	7.20	1.47	1.38
2	D	601	OGJ	C26-N23	-6.78	1.43	1.49
2	A	601	OGJ	C26-N23	-6.51	1.43	1.49
2	D	601	OGJ	C24-N23	-6.35	1.43	1.49
2	A	601	OGJ	C24-N23	-6.30	1.43	1.49
2	A	601	OGJ	O6-C4	4.25	1.51	1.45
2	D	601	OGJ	O6-C4	3.82	1.51	1.45
2	D	601	OGJ	C29-C3	2.97	1.54	1.48
2	D	601	OGJ	C9-C8	2.49	1.43	1.39
2	A	601	OGJ	C29-C3	2.42	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	OGJ	C8-C7	-2.37	1.36	1.40
2	D	601	OGJ	O20-C17	2.35	1.43	1.37
2	A	601	OGJ	C9-C8	2.35	1.43	1.39
2	A	601	OGJ	C8-C7	-2.12	1.36	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	601	OGJ	C1-C2-C3	-4.18	118.96	124.49
2	A	601	OGJ	C1-C2-C3	-3.63	119.68	124.49
2	A	601	OGJ	C1-C2-C8	3.32	122.29	118.57
2	D	601	OGJ	O6-C4-C14	3.27	114.44	109.53
2	D	601	OGJ	C1-C2-C8	2.99	121.91	118.57
2	D	601	OGJ	C14-C4-C3	-2.68	109.65	114.48
2	A	601	OGJ	C14-C4-C3	-2.39	110.16	114.48

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	OGJ	O20-C21-C22-N23
2	D	601	OGJ	C16-C17-O20-C21
2	D	601	OGJ	C18-C17-O20-C21
2	A	601	OGJ	C30-C29-C3-C2
2	A	601	OGJ	C34-C29-C3-C2
2	A	601	OGJ	C15-C14-C4-C3
2	D	601	OGJ	C30-C29-C3-C2

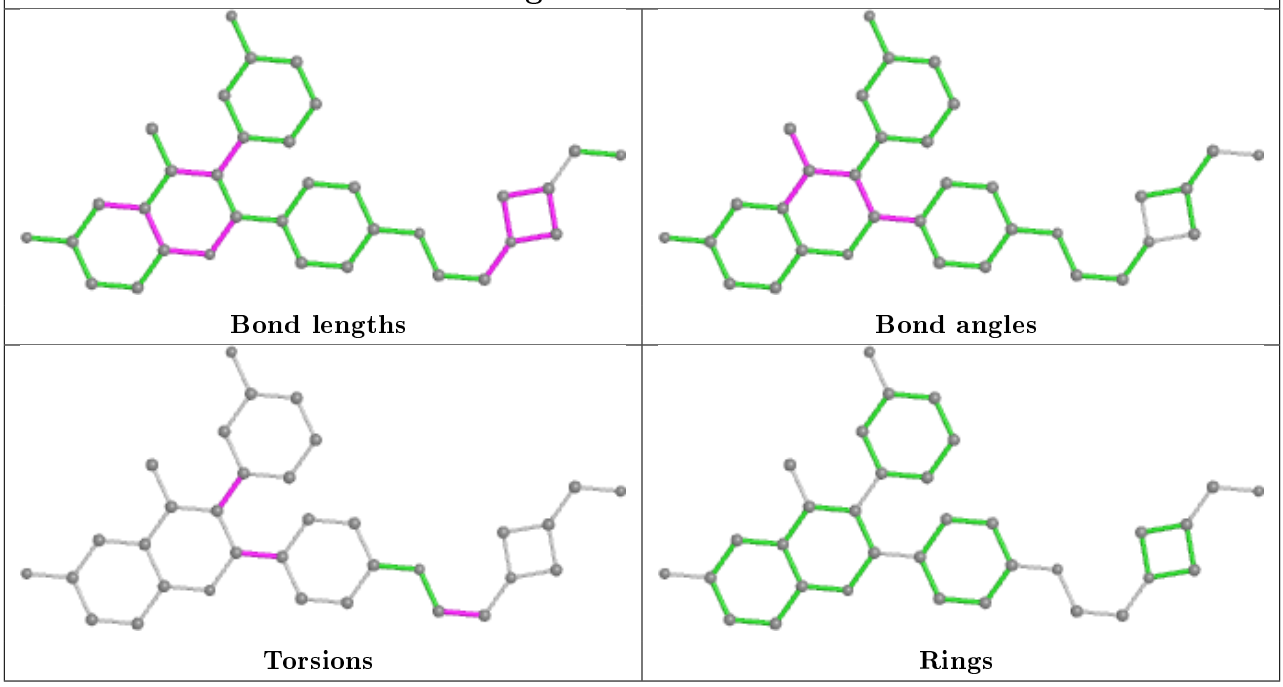
There are no ring outliers.

No monomer is involved in short contacts.

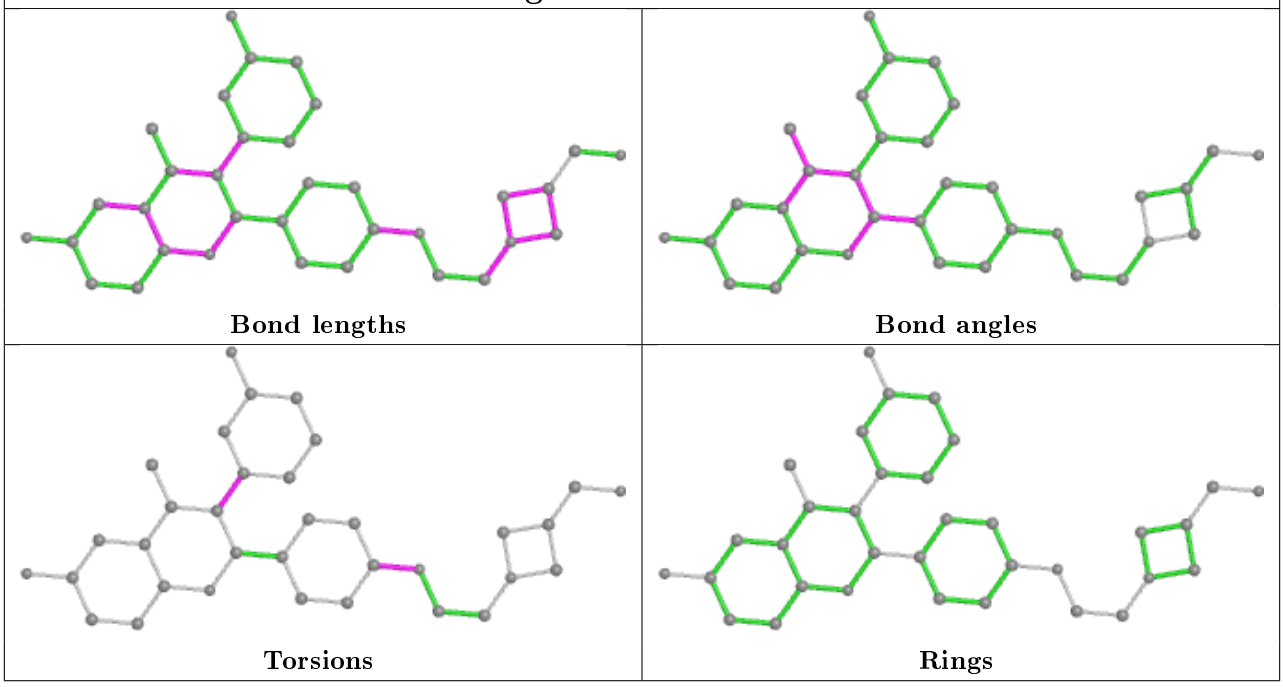
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand OGJ A 601



Ligand OGJ D 601



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	224/280 (80%)	0.55	17 (7%)	13	8	56, 89, 120, 150	0
1	D	235/280 (83%)	0.27	15 (6%)	19	13	46, 63, 123, 152	0
All	All	459/560 (81%)	0.41	32 (6%)	16	11	46, 76, 121, 152	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	512	SER	4.1
1	D	466	LEU	4.0
1	A	308	LEU	3.8
1	A	462	LEU	3.6
1	A	336	PRO	3.4
1	A	456	SER	3.1
1	A	512	SER	3.0
1	A	340	ALA	3.0
1	A	337	PHE	2.9
1	D	465	THR	2.8
1	D	513	HIS	2.8
1	A	343	MET	2.7
1	A	513	HIS	2.7
1	D	526	TYR	2.6
1	D	467	LYS	2.6
1	A	514	ILE	2.6
1	A	515	ARG	2.5
1	A	459	TYR	2.5
1	A	510	ILE	2.4
1	A	530	CYS	2.3
1	D	545	ASP	2.3
1	D	456	SER	2.3
1	D	511	LEU	2.3
1	A	409	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	544	LEU	2.3
1	D	468	SER	2.3
1	A	381	CYS	2.2
1	D	509	LEU	2.1
1	D	541	LEU	2.1
1	D	514	ILE	2.1
1	D	510	ILE	2.1
1	A	457	GLY	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 carbohydrates in this entry.

6.4 Ligands (i)

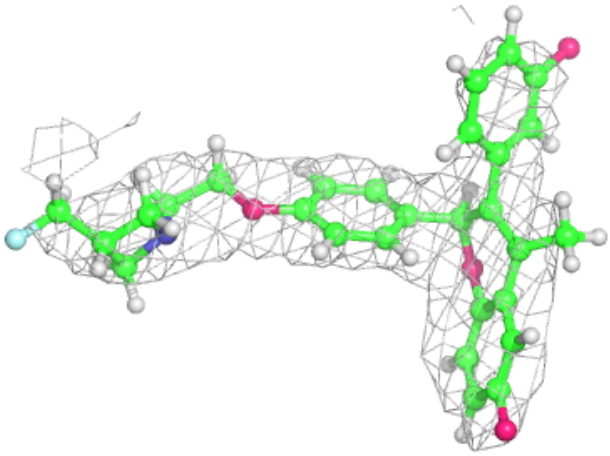
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

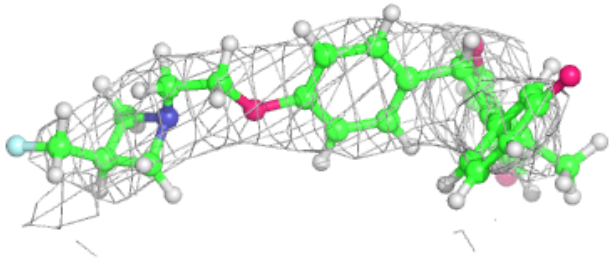
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	OGJ	A	601	34/34	0.89	0.29	64,92,111,114	0
2	OGJ	D	601	34/34	0.93	0.21	48,59,83,97	0

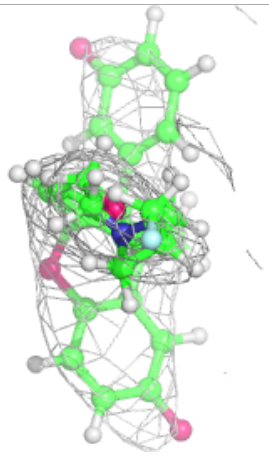
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around OGJ A 601:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

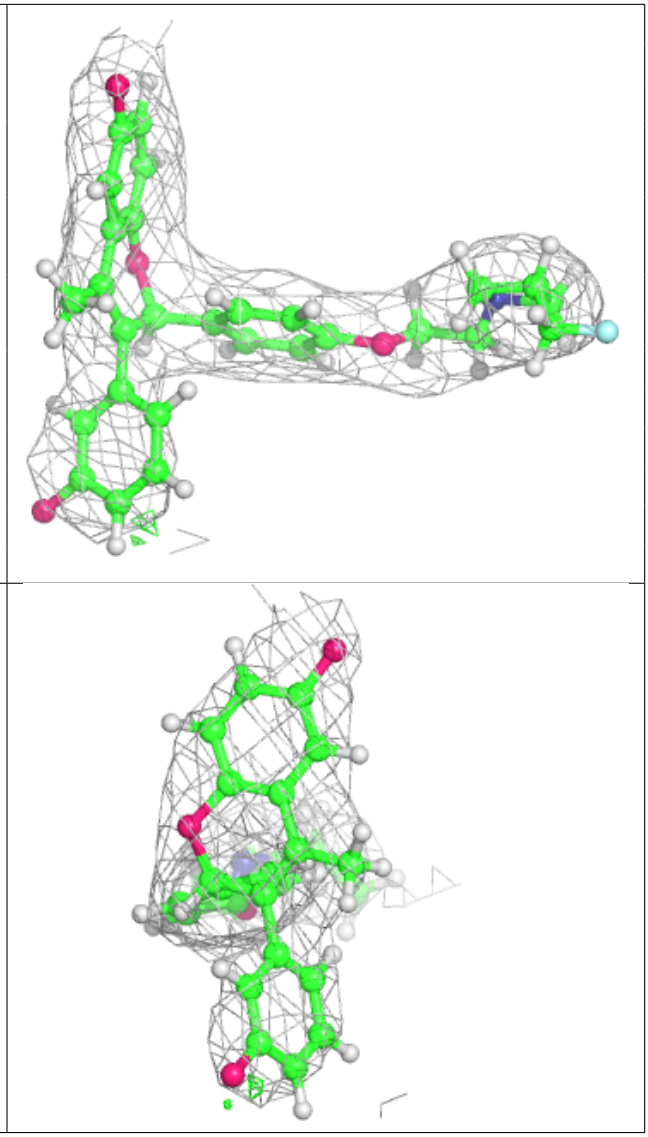






Electron density around OGJ D 601:

$2mF_o$-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.