Full wwPDB X-ray Structure Validation Report (i)

Sep 3, 2023 – 07:34 PM EDT

PDB ID	:	3SAY
Title	:	Crystal structure of human glycogen synthase kinase 3 beta (GSK3b) in complex with inhibitor 142
Authors	:	Mazanetz, M.P.; Cheng, R.K.Y.; Rowan, F.; Laughton, C.A.; Barker, J.J.; Fischer, P.M.
Deposited on	:	2011-06-03
Resolution	:	2.23 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

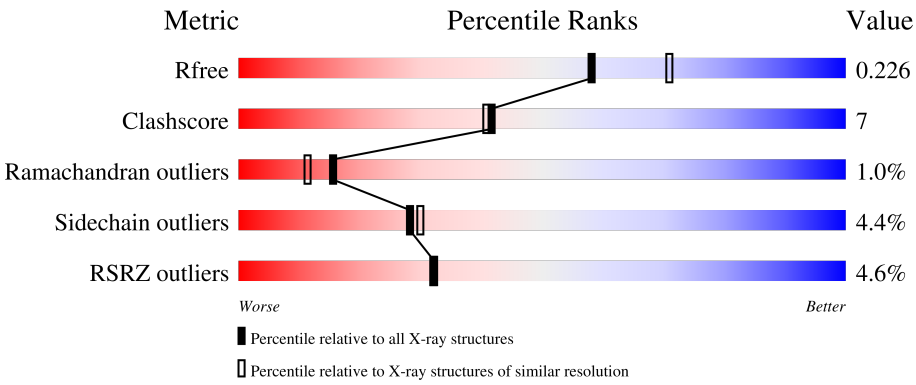
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.23 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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 <=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	430	4% 70% 10% • 19%
1	B	430	4% 67% 13% • 19%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MLA	B	432	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5858 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.

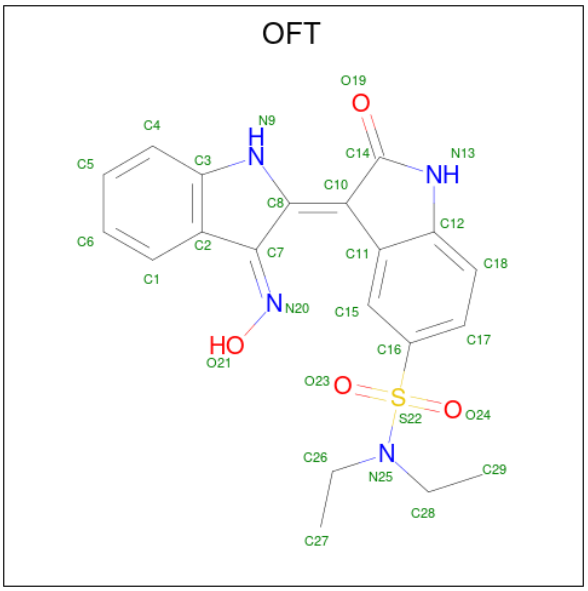
- Molecule 1 is a protein called Glycogen synthase kinase-3 beta.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	348	2775	1789	469	504	1	12	0	9	0
1	B	348	2779	1791	466	508	1	13	0	9	0

There are 20 discrepancies between the modelled and reference sequences:

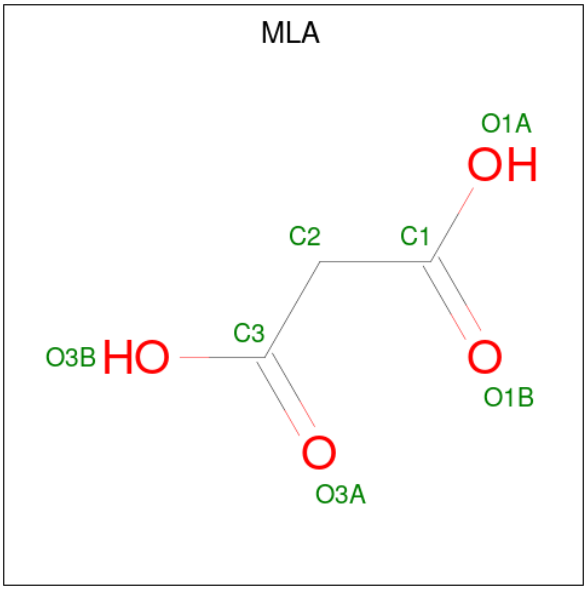
Chain	Residue	Modelled	Actual	Comment	Reference
A	421	LEU	-	expression tag	UNP P49841
A	422	GLU	-	expression tag	UNP P49841
A	423	HIS	-	expression tag	UNP P49841
A	424	HIS	-	expression tag	UNP P49841
A	425	HIS	-	expression tag	UNP P49841
A	426	HIS	-	expression tag	UNP P49841
A	427	HIS	-	expression tag	UNP P49841
A	428	HIS	-	expression tag	UNP P49841
A	429	HIS	-	expression tag	UNP P49841
A	430	HIS	-	expression tag	UNP P49841
B	421	LEU	-	expression tag	UNP P49841
B	422	GLU	-	expression tag	UNP P49841
B	423	HIS	-	expression tag	UNP P49841
B	424	HIS	-	expression tag	UNP P49841
B	425	HIS	-	expression tag	UNP P49841
B	426	HIS	-	expression tag	UNP P49841
B	427	HIS	-	expression tag	UNP P49841
B	428	HIS	-	expression tag	UNP P49841
B	429	HIS	-	expression tag	UNP P49841
B	430	HIS	-	expression tag	UNP P49841

- Molecule 2 is (3Z)-N,N-diethyl-3-[(3E)-3-(hydroxyimino)-1,3-dihydro-2H-indol-2-ylidene]-2-oxo-2,3-dihydro-1H-indole-5-sulfonamide (three-letter code: OFT) (formula: $C_{20}H_{20}N_4O_4S$).



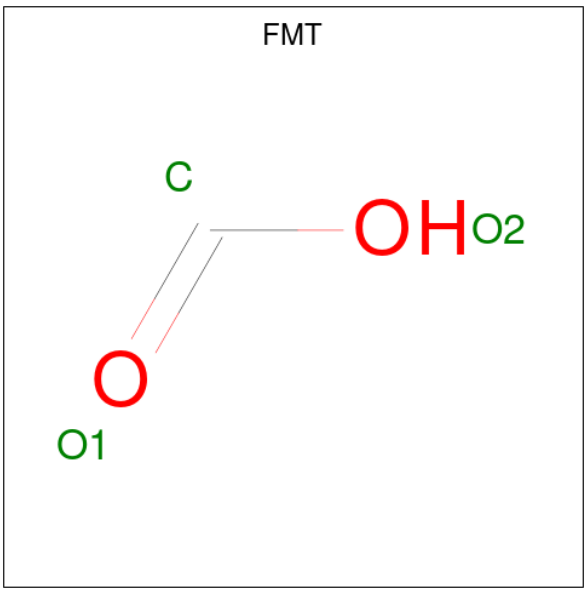
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	29	20	4	4	1	0	0
			Total	C	N	O	S		
2	B	1	29	20	4	4	1	0	0

- Molecule 3 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



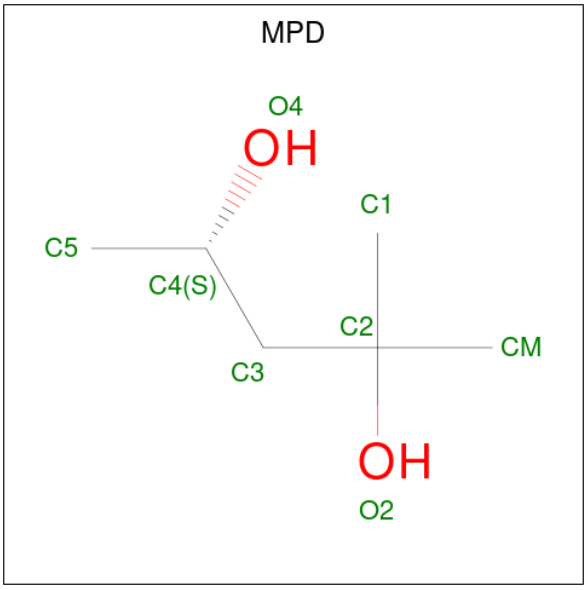
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	7	3	4	0	0
			Total	C	O		
3	B	1	7	3	4	0	0

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	8	6	2	0	0

- Molecule 6 is water.

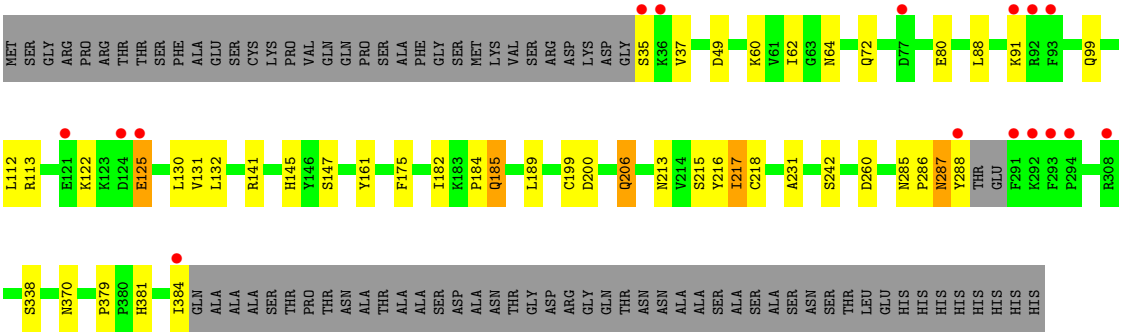
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	129	129	129	0	0
			Total	O		
6	B	92	92	92	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

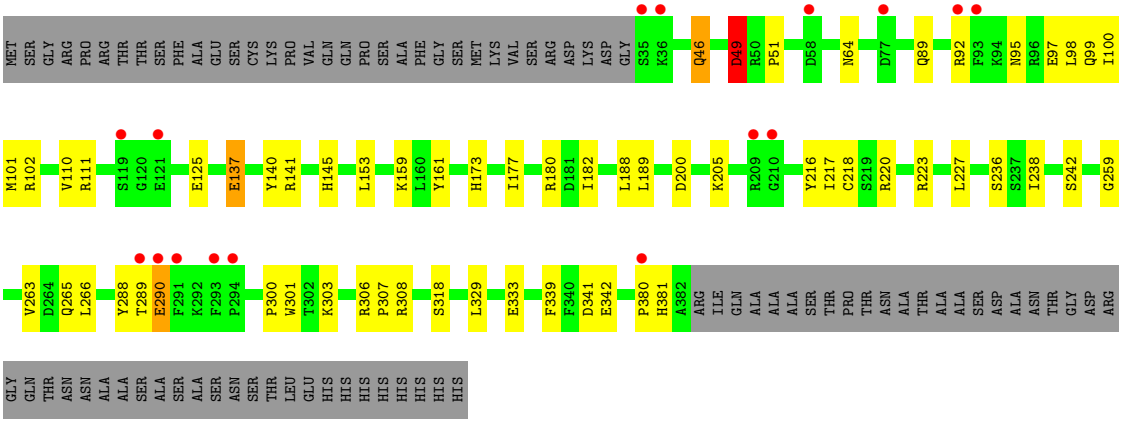
• Molecule 1: Glycogen synthase kinase-3 beta

Chain A:



• Molecule 1: Glycogen synthase kinase-3 beta

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	67.52Å 110.78Å 67.91Å 90.00° 97.08° 90.00°	Depositor
Resolution (Å)	46.14 – 2.23 46.14 – 2.23	Depositor EDS
% Data completeness (in resolution range)	97.2 (46.14-2.23) 98.2 (46.14-2.23)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.72 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.200 , 0.230 0.200 , 0.226	Depositor DCC
R_{free} test set	2408 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	39.2	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.075 for l,-k,h	Xtriage
Reported twinning fraction	0.864 for H, K, L 0.136 for L, -K, H	Depositor
Outliers	0 of 47470 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5858	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 5.14% 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: MPD, PTR, OFT, FMT, MLA

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	0.62	0/2853	0.66	0/3887
1	B	0.58	0/2861	0.65	1/3902 (0.0%)
All	All	0.60	0/5714	0.66	1/7789 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	153	LEU	CA-CB-CG	5.60	128.18	115.30

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	2775	0	2782	35	0
1	B	2779	0	2762	43	0
2	A	29	0	20	7	0
2	B	29	0	20	5	0
3	A	7	0	2	0	0
3	B	7	0	2	4	0
4	A	3	0	1	0	0
5	B	8	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	129	0	0	3	0
6	B	92	0	0	3	0
All	All	5858	0	5603	79	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 (79) 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:145[B]:HIS:ND1	6:A:558:HOH:O	1.65	1.22
1:A:145[B]:HIS:CE1	6:A:558:HOH:O	1.95	1.15
1:A:185:GLN:H	1:A:185:GLN:HE21	0.97	0.97
1:B:145[B]:HIS:NE2	6:B:520:HOH:O	2.05	0.88
1:A:185:GLN:H	1:A:185:GLN:NE2	1.76	0.82
1:A:185:GLN:HE21	1:A:185:GLN:N	1.77	0.82
1:B:145[B]:HIS:CD2	6:B:520:HOH:O	2.34	0.80
1:B:259:GLY:H	1:B:265:GLN:NE2	1.80	0.78
1:B:159:LYS:NZ	1:B:342:GLU:OE1	2.17	0.77
1:B:341:ASP:OD1	6:B:511:HOH:O	2.03	0.76
1:B:200:ASP:HB2	2:B:431:OFT:H28	1.66	0.75
1:A:141:ARG:HE	2:A:431:OFT:H6	1.51	0.73
2:B:431:OFT:N20	2:B:431:OFT:H15	2.05	0.72
1:B:110:VAL:HG11	1:B:188:LEU:HD12	1.74	0.69
1:B:205:LYS:HE2	3:B:432:MLA:HC21	1.77	0.67
2:A:431:OFT:N20	2:A:431:OFT:H15	2.15	0.62
1:B:137:GLU:HA	1:B:137:GLU:OE1	1.98	0.62
1:B:205:LYS:CE	3:B:432:MLA:HC21	2.30	0.61
1:B:46:GLN:HE22	1:B:111:ARG:HD2	1.66	0.61
1:A:141:ARG:NE	2:A:431:OFT:H6	2.14	0.61
1:B:290:GLU:O	1:B:290:GLU:HG3	2.01	0.60
1:A:88:LEU:HD11	1:A:125:GLU:HG2	1.85	0.59
1:A:141:ARG:HE	2:A:431:OFT:C6	2.16	0.59
1:B:259:GLY:H	1:B:265:GLN:HE21	1.49	0.59
1:B:46:GLN:NE2	1:B:111:ARG:HD2	2.18	0.57
1:B:220:ARG:HG2	1:B:265:GLN:HG3	1.86	0.57
1:B:300:PRO:HG2	1:B:303:LYS:HD2	1.87	0.56
1:B:89:GLN:OE1	1:B:95:ASN:HB2	2.06	0.56
1:A:62:ILE:HD13	1:A:72:GLN:HB2	1.88	0.55
1:A:132:LEU:HD13	2:A:431:OFT:H18	1.89	0.55
1:A:199:CYS:SG	2:A:431:OFT:H28A	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ASP:OD1	1:B:141[B]:ARG:NH1	2.42	0.52
1:B:110:VAL:CG1	1:B:188:LEU:HD12	2.39	0.52
1:A:80:GLU:CD	1:A:113:ARG:HH12	2.13	0.52
1:A:287:ASN:HD22	1:A:287:ASN:N	2.07	0.52
1:A:200:ASP:HB2	2:A:431:OFT:H28	1.92	0.51
1:A:49:ASP:CG	1:A:49:ASP:O	2.49	0.51
1:A:217:ILE:O	1:A:218[B]:CYS:HB2	2.11	0.51
1:A:285:ASN:O	1:A:287:ASN:N	2.43	0.50
1:A:285:ASN:C	1:A:287:ASN:H	2.14	0.49
1:A:122:LYS:O	1:A:125:GLU:HB2	2.11	0.49
1:B:205:LYS:HE3	3:B:432:MLA:C2	2.42	0.49
1:B:97:GLU:O	1:B:101:MET:HG2	2.12	0.49
1:B:259:GLY:N	1:B:265:GLN:HE21	2.12	0.48
1:B:301:TRP:CD1	1:B:318:SER:HB3	2.50	0.47
1:B:307:PRO:O	1:B:308:ARG:HB2	2.16	0.46
1:A:161:TYR:CZ	1:A:189:LEU:HD21	2.50	0.46
1:A:260:ASP:HB3	1:B:140:TYR:CE2	2.51	0.46
1:A:287:ASN:N	1:A:287:ASN:ND2	2.64	0.45
1:B:137:GLU:OE1	1:B:137:GLU:CA	2.62	0.45
1:A:379:PRO:HB2	1:A:381:HIS:CD2	2.52	0.45
1:B:329:LEU:HB3	1:B:333:GLU:HG3	1.97	0.45
1:A:175:PHE:O	1:A:206:GLN:NE2	2.48	0.45
1:B:288:TYR:O	1:B:290:GLU:N	2.41	0.45
1:B:159:LYS:HE2	1:B:339:PHE:O	2.17	0.45
1:B:141[B]:ARG:CZ	2:B:431:OFT:H6	2.47	0.45
1:A:80:GLU:OE2	1:A:113:ARG:NH2	2.41	0.45
1:B:173:HIS:CE1	1:B:236[A]:SER:HB3	2.52	0.44
1:A:215[B]:SER:OG	1:A:231:ALA:O	2.31	0.44
1:B:98:LEU:O	1:B:102:ARG:HG3	2.17	0.44
1:B:205:LYS:CE	3:B:432:MLA:C2	2.94	0.43
1:A:184:PRO:HD2	1:A:185:GLN:HE22	1.84	0.43
1:A:145[A]:HIS:HD2	6:A:558:HOH:O	2.01	0.43
2:B:431:OFT:O21	2:B:431:OFT:H29A	2.19	0.43
1:B:100:ILE:HG23	1:B:177:ILE:HD13	2.01	0.42
1:B:161:TYR:CZ	1:B:189:LEU:HD21	2.54	0.42
1:A:99[B]:GLN:NE2	1:A:99[B]:GLN:HA	2.34	0.42
1:B:288:TYR:C	1:B:290:GLU:H	2.20	0.42
1:B:182:ILE:HB	1:B:242:SER:CB	2.50	0.42
1:A:161:TYR:CE1	1:A:189:LEU:HD11	2.55	0.42
1:B:141[B]:ARG:NH2	2:B:431:OFT:H6	2.35	0.41
1:B:223:ARG:HG3	1:B:227:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:263:VAL:HG13	5:B:433:MPD:H53	2.03	0.41
1:A:384:ILE:H	1:A:384:ILE:HD12	1.85	0.41
1:A:182:ILE:HB	1:A:242:SER:CB	2.50	0.41
1:B:49:ASP:O	1:B:51:PRO:HD3	2.19	0.41
1:A:112:LEU:HA	1:A:132:LEU:HD23	2.03	0.40
1:B:180:ARG:HG2	1:B:238:ILE:HD11	2.02	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	352/430 (82%)	334 (95%)	17 (5%)	1 (0%)	41 44
1	B	354/430 (82%)	332 (94%)	16 (4%)	6 (2%)	9 4
All	All	706/860 (82%)	666 (94%)	33 (5%)	7 (1%)	15 11

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	289	THR
1	B	290	GLU
1	B	381	HIS
1	A	286	PRO
1	B	49	ASP
1	B	92	ARG
1	B	380	PRO

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	306/373 (82%)	288 (94%)	18 (6%)	19	17
1	B	306/373 (82%)	296 (97%)	10 (3%)	38	43
All	All	612/746 (82%)	584 (95%)	28 (5%)	28	28

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

Mol	Chain	Res	Type
1	A	35	SER
1	A	37	VAL
1	A	60	LYS
1	A	64	ASN
1	A	91	LYS
1	A	125	GLU
1	A	130	LEU
1	A	131	VAL
1	A	147	SER
1	A	185	GLN
1	A	206	GLN
1	A	213	ASN
1	A	217	ILE
1	A	287	ASN
1	A	288	TYR
1	A	338[A]	SER
1	A	338[B]	SER
1	A	370	ASN
1	B	46	GLN
1	B	49	ASP
1	B	64	ASN
1	B	99	GLN
1	B	125	GLU
1	B	137	GLU
1	B	217[A]	ILE
1	B	217[B]	ILE
1	B	266	LEU

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Mol	Chain	Res	Type
1	B	306	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	64	ASN
1	A	185	GLN
1	A	287	ASN
1	A	370	ASN
1	A	381	HIS
1	B	129	ASN
1	B	265	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)

2 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PTR	B	216	1	15,16,17	1.86	2 (13%)	19,22,24	0.65	0
1	PTR	A	216	1	15,16,17	1.96	2 (13%)	19,22,24	0.65	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	B	216	1	-	1/10/11/13	0/1/1/1
1	PTR	A	216	1	-	0/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	PTR	OH-CZ	-6.98	1.24	1.40
1	B	216	PTR	OH-CZ	-6.60	1.25	1.40
1	A	216	PTR	P-OH	2.47	1.63	1.59
1	B	216	PTR	P-OH	2.05	1.62	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	216	PTR	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	OFT	B	431	-	32,32,32	3.08	7 (21%)	46,48,48	2.86	21 (45%)
4	FMT	A	433	-	2,2,2	0.67	0	1,1,1	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	OFT	A	431	-	32,32,32	3.01	8 (25%)	46,48,48	2.91	21 (45%)
3	MLA	B	432	-	6,6,6	1.13	0	7,7,7	1.26	0
5	MPD	B	433	-	7,7,7	0.23	0	9,10,10	0.52	0
3	MLA	A	432	-	6,6,6	1.04	0	7,7,7	0.99	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	OFT	B	431	-	-	10/21/46/46	0/4/4/4
2	OFT	A	431	-	-	8/21/46/46	0/4/4/4
3	MLA	B	432	-	-	4/4/4/4	-
5	MPD	B	433	-	-	2/5/5/5	-
3	MLA	A	432	-	-	2/4/4/4	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	431	OFT	C16-S22	-11.27	1.60	1.76
2	A	431	OFT	C16-S22	-10.74	1.61	1.76
2	A	431	OFT	C11-C12	7.45	1.51	1.41
2	B	431	OFT	C11-C12	7.07	1.50	1.41
2	B	431	OFT	C2-C3	6.71	1.50	1.41
2	A	431	OFT	C2-C3	6.59	1.49	1.41
2	B	431	OFT	S22-N25	-6.23	1.54	1.63
2	A	431	OFT	S22-N25	-5.54	1.55	1.63
2	B	431	OFT	C10-C8	3.52	1.49	1.40
2	A	431	OFT	C10-C8	3.36	1.49	1.40
2	A	431	OFT	C7-N20	3.14	1.37	1.29
2	B	431	OFT	C7-N20	3.07	1.36	1.29
2	B	431	OFT	O19-C14	2.56	1.28	1.23
2	A	431	OFT	O19-C14	2.52	1.28	1.23
2	A	431	OFT	C8-N9	-2.37	1.34	1.38

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	431	OFT	C10-C14-N13	8.16	112.32	106.91
2	A	431	OFT	C10-C14-N13	7.96	112.19	106.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	431	OFT	O24-S22-O23	-7.42	107.50	119.52
2	B	431	OFT	O24-S22-O23	-7.11	108.00	119.52
2	B	431	OFT	C16-S22-N25	6.11	114.58	107.30
2	A	431	OFT	C16-S22-N25	5.80	114.21	107.30
2	A	431	OFT	C4-C3-C2	-5.28	116.89	122.19
2	B	431	OFT	C18-C12-C11	-5.23	116.94	122.19
2	A	431	OFT	C18-C12-C11	-5.17	117.00	122.19
2	A	431	OFT	C12-N13-C14	-5.08	108.19	111.38
2	B	431	OFT	C4-C3-C2	-5.04	117.13	122.19
2	B	431	OFT	C12-N13-C14	-4.94	108.28	111.38
2	A	431	OFT	C12-C11-C10	-4.70	102.69	106.56
2	B	431	OFT	C12-C11-C10	-4.21	103.09	106.56
2	A	431	OFT	C18-C17-C16	3.82	123.40	119.45
2	B	431	OFT	O19-C14-C10	-3.75	123.07	128.17
2	B	431	OFT	O23-S22-N25	3.61	109.98	106.69
2	A	431	OFT	C1-C2-C3	3.55	122.63	118.83
2	A	431	OFT	O19-C14-C10	-3.42	123.52	128.17
2	B	431	OFT	O21-N20-C7	3.40	121.80	113.65
2	A	431	OFT	C15-C16-S22	3.30	123.01	119.34
2	B	431	OFT	C1-C2-C3	3.26	122.33	118.83
2	B	431	OFT	C18-C17-C16	3.11	122.67	119.45
2	A	431	OFT	O23-S22-N25	3.06	109.48	106.69
2	A	431	OFT	C2-C7-N20	-3.02	126.04	132.59
2	A	431	OFT	C11-C12-N13	2.95	111.60	108.22
2	A	431	OFT	O21-N20-C7	2.82	120.41	113.65
2	B	431	OFT	C7-C8-N9	2.68	111.20	106.87
2	B	431	OFT	C11-C12-N13	2.67	111.28	108.22
2	A	431	OFT	C3-C2-C7	-2.66	103.58	106.25
2	A	431	OFT	C7-C8-N9	2.65	111.16	106.87
2	B	431	OFT	C15-C16-S22	2.64	122.28	119.34
2	A	431	OFT	C15-C11-C12	2.63	121.94	119.42
2	A	431	OFT	C17-C16-S22	-2.63	116.99	119.76
2	B	431	OFT	C3-C2-C7	-2.59	103.66	106.25
2	B	431	OFT	C15-C11-C12	2.53	121.84	119.42
2	B	431	OFT	C17-C16-S22	-2.47	117.16	119.76
2	B	431	OFT	C2-C7-N20	-2.40	127.37	132.59
2	A	431	OFT	C2-C3-N9	2.12	110.65	108.22
2	A	431	OFT	O24-S22-N25	2.11	108.61	106.69
2	B	431	OFT	C2-C3-N9	2.10	110.63	108.22
2	B	431	OFT	O24-S22-N25	2.04	108.55	106.69

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	431	OFT	C29-C28-N25-C26
2	B	431	OFT	C28-N25-S22-O23
2	B	431	OFT	C15-C16-S22-N25
2	A	431	OFT	C15-C16-S22-N25
2	B	431	OFT	C17-C16-S22-N25
2	A	431	OFT	C17-C16-S22-N25
2	B	431	OFT	C26-N25-S22-O23
2	A	431	OFT	C26-N25-S22-O23
2	A	431	OFT	C28-N25-S22-O23
2	A	431	OFT	C17-C16-S22-O24
2	B	431	OFT	C17-C16-S22-O24
2	A	431	OFT	C15-C16-S22-O24
2	B	431	OFT	C15-C16-S22-O24
3	B	432	MLA	C1-C2-C3-O3B
2	B	431	OFT	C26-N25-S22-C16
2	A	431	OFT	C26-N25-S22-C16
3	B	432	MLA	O1B-C1-C2-C3
3	B	432	MLA	C1-C2-C3-O3A
5	B	433	MPD	C2-C3-C4-C5
3	B	432	MLA	O1A-C1-C2-C3
5	B	433	MPD	C2-C3-C4-O4
3	A	432	MLA	C1-C2-C3-O3B
2	A	431	OFT	C26-N25-S22-O24
2	B	431	OFT	C28-N25-S22-C16
3	A	432	MLA	C1-C2-C3-O3A
2	B	431	OFT	C26-N25-S22-O24

There are no ring outliers.

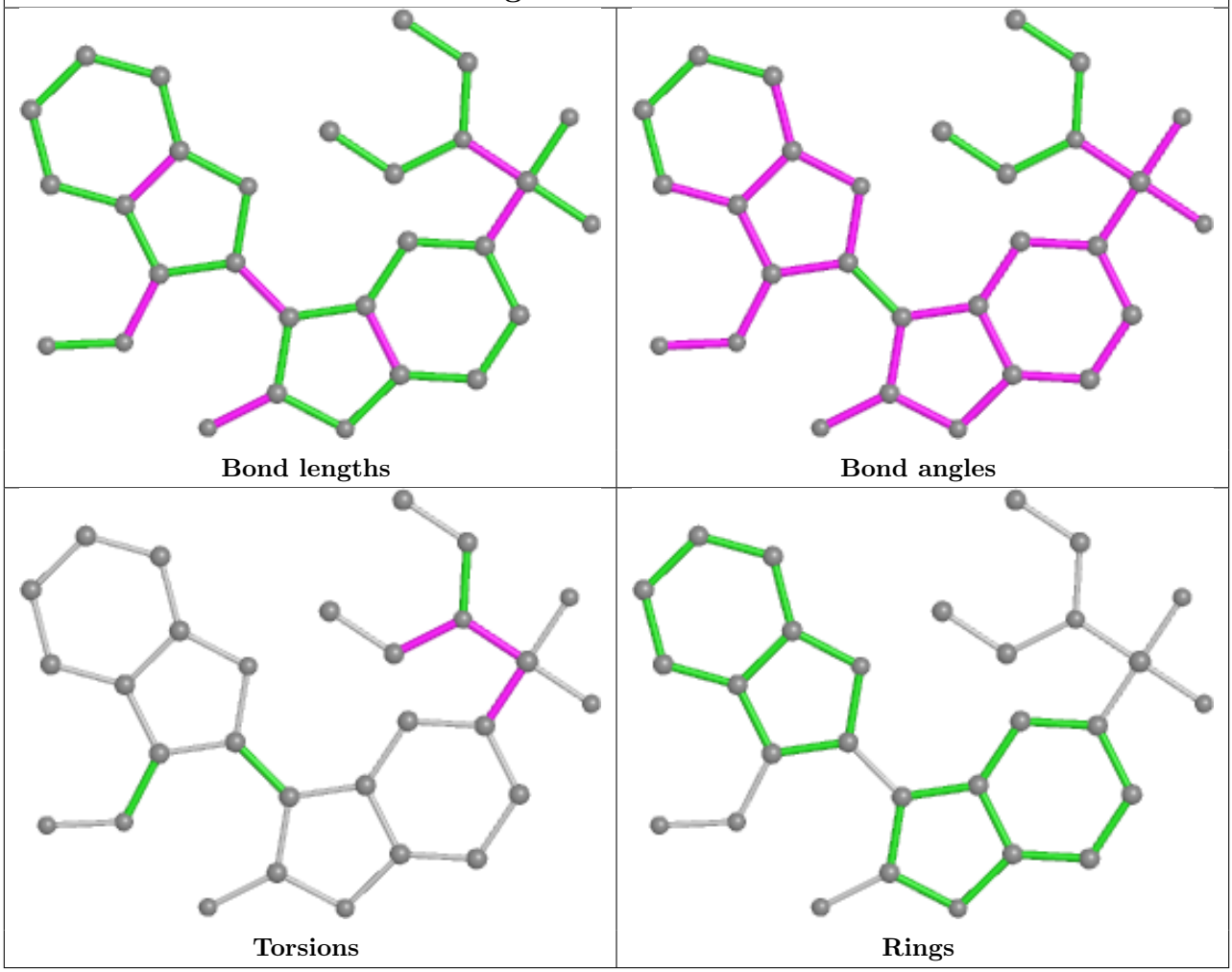
4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	431	OFT	5	0
2	A	431	OFT	7	0
3	B	432	MLA	4	0
5	B	433	MPD	1	0

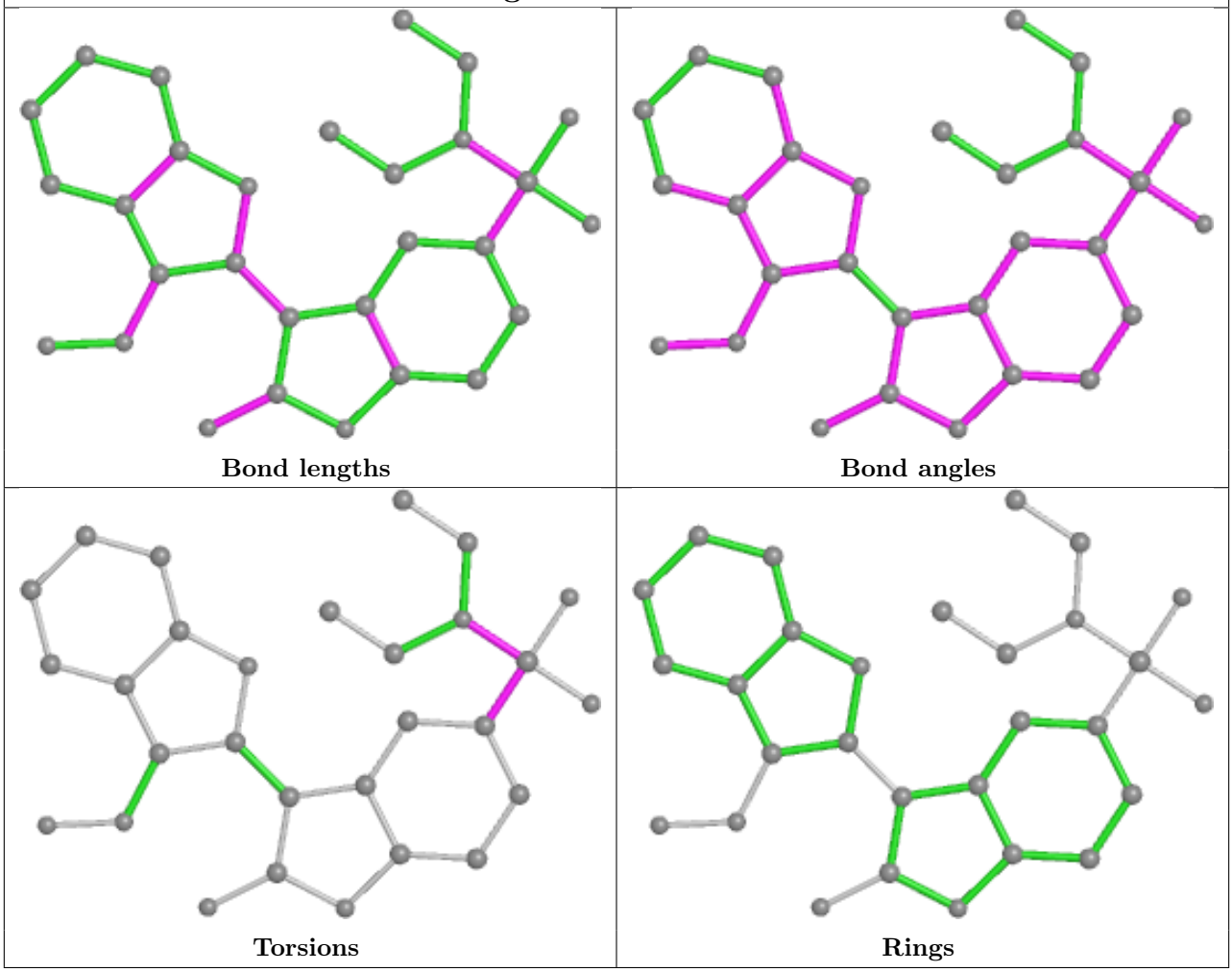
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand OFT B 431



Ligand OFT A 431



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	347/430 (80%)	0.11	16 (4%)	32	32	17, 36, 61, 77	0
1	B	347/430 (80%)	0.29	16 (4%)	32	32	21, 40, 67, 76	0
All	All	694/860 (80%)	0.20	32 (4%)	32	32	17, 39, 66, 77	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	93	PHE	6.6
1	B	289	THR	6.1
1	A	35	SER	5.9
1	A	293	PHE	5.5
1	B	293[A]	PHE	5.1
1	A	294	PRO	4.7
1	A	93	PHE	4.5
1	A	288	TYR	4.4
1	B	35	SER	4.4
1	A	92	ARG	4.1
1	A	291	PHE	3.4
1	A	292	LYS	3.4
1	A	124	ASP	3.4
1	A	384	ILE	3.3
1	B	36	LYS	3.2
1	B	209	ARG	3.2
1	B	290	GLU	3.1
1	A	125	GLU	3.0
1	A	308	ARG	2.9
1	B	380	PRO	2.9
1	A	36	LYS	2.6
1	A	77	ASP	2.6
1	B	92	ARG	2.5
1	B	291	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	121	GLU	2.3
1	B	294	PRO	2.3
1	B	77	ASP	2.2
1	B	58	ASP	2.2
1	B	210	GLY	2.2
1	B	119[A]	SER	2.1
1	A	121	GLU	2.0
1	A	91	LYS	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, 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
1	PTR	B	216	16/17	0.96	0.15	33,34,36,36	0
1	PTR	A	216	16/17	0.97	0.14	31,34,35,37	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

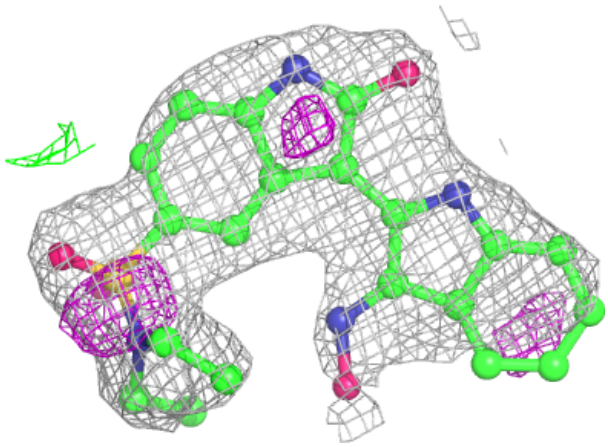
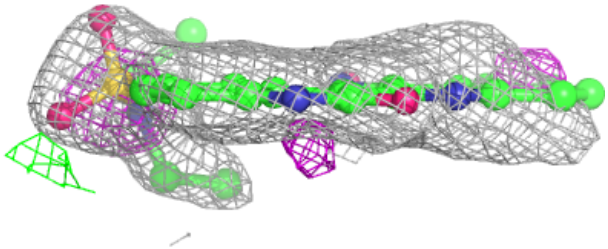
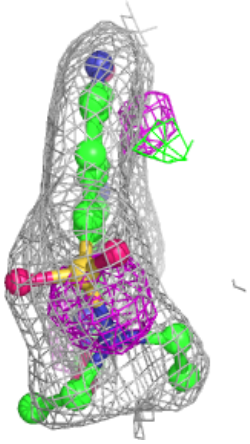
6.4 Ligands (i)

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(Å^2)	Q<0.9
2	OFT	A	431	29/29	0.85	0.25	66,70,72,72	0
4	FMT	A	433	3/3	0.85	0.17	67,67,67,67	0
2	OFT	B	431	29/29	0.86	0.28	71,72,76,79	0
5	MPD	B	433	8/8	0.89	0.24	55,56,57,57	0
3	MLA	A	432	7/7	0.90	0.15	48,50,54,56	0
3	MLA	B	432	7/7	0.93	0.32	52,54,56,56	0

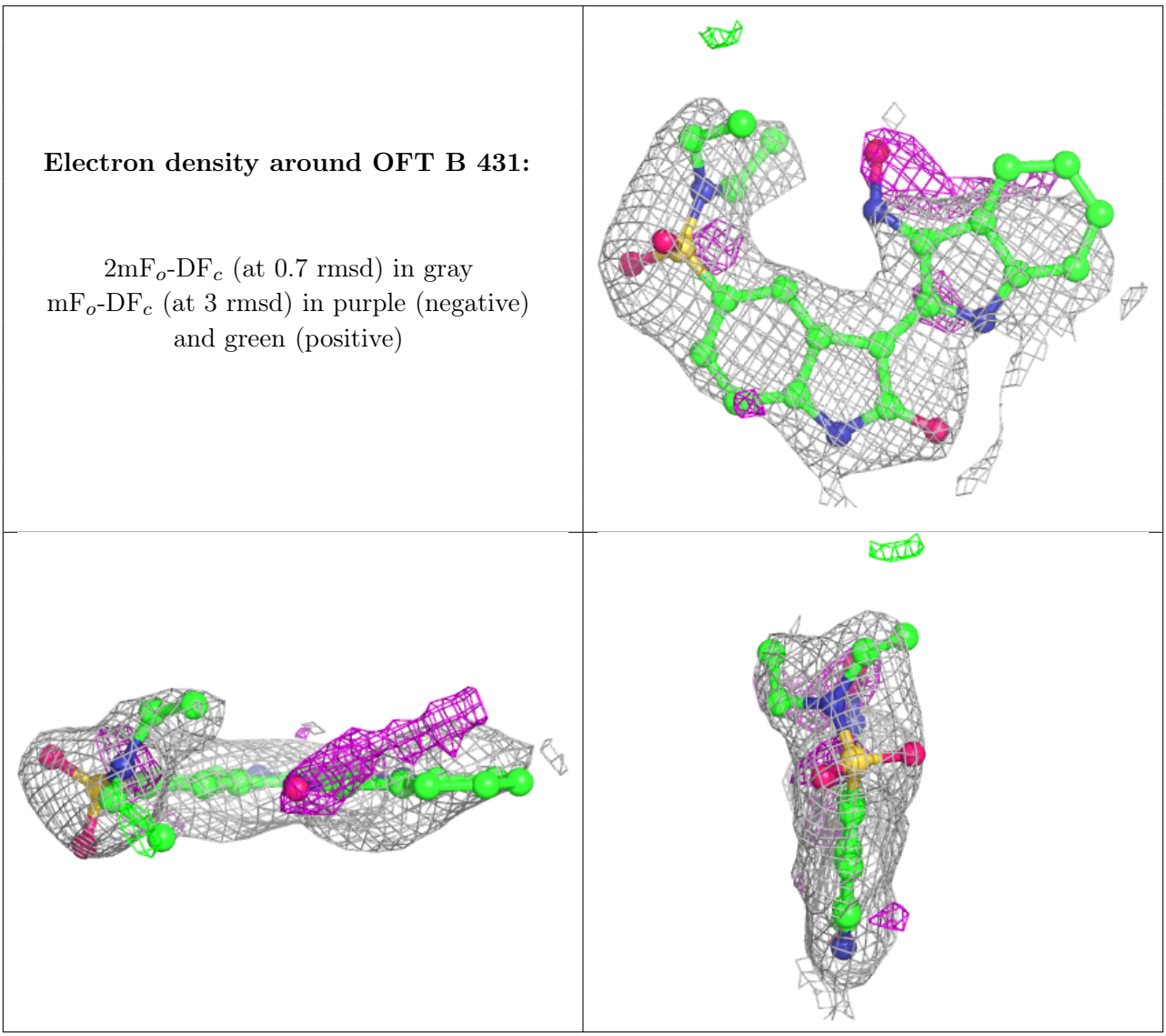
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

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 OFT A 431: 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 OFT B 431:

$2mF_o$-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.