Full wwPDB X-ray Structure Validation Report (i)

Sep 25, 2023 – 10:06 am BST

PDB ID	:	8AN8
Title	:	Crystal structure of wild-type c-MET bound by compound 7.
Authors	:	Collie, G.W.
Deposited on	:	2022-08-04
Resolution	:	2.39 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:

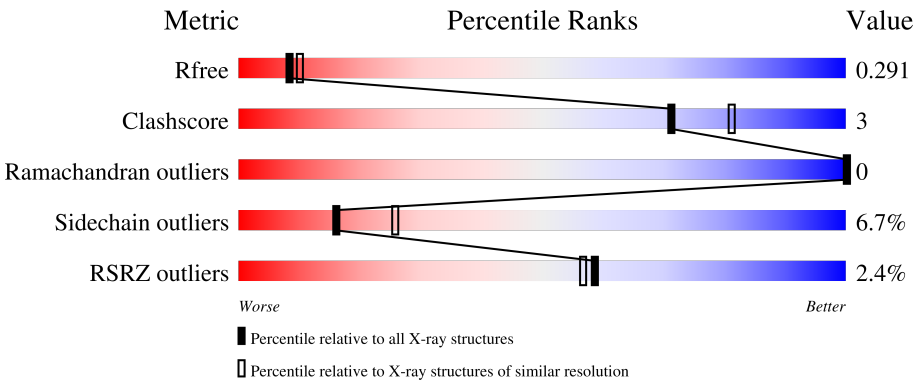
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	296	2% 74% 8% • 18%
1	B	296	2% 76% 10% • 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4176 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.

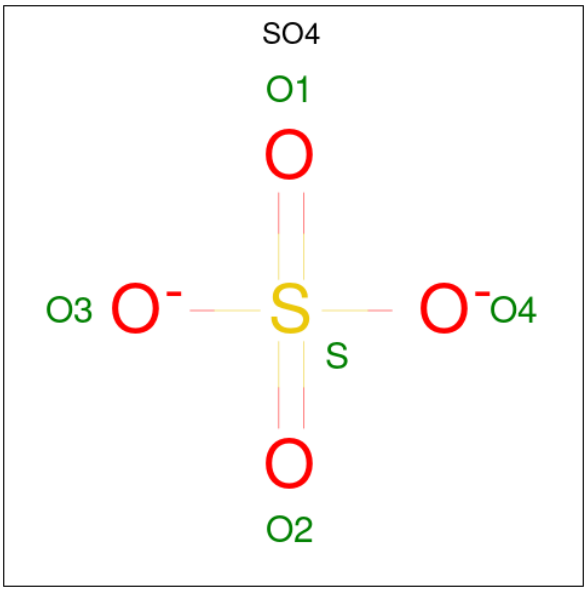
- Molecule 1 is a protein called Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	244	1943	1268	322	338	15	0	0	0
1	B	263	2057	1338	344	361	14	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1051	GLY	-	expression tag	UNP P08581
B	1051	GLY	-	expression tag	UNP P08581

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

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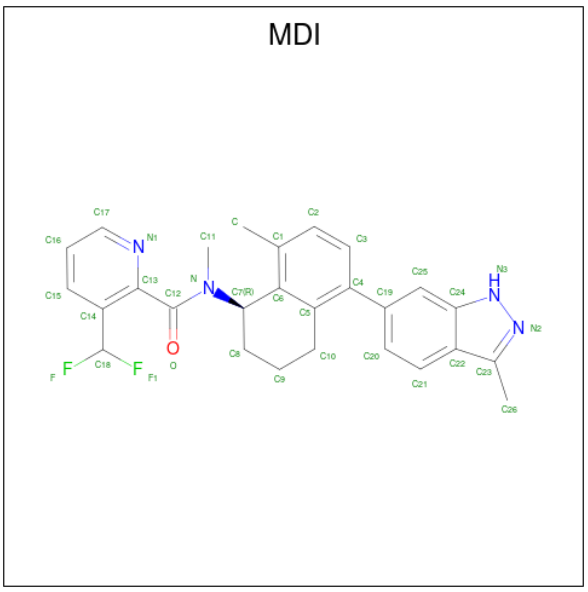
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is 3-[bis(fluoranyl)methyl]- {N}-methyl- {N}-[(1 {R})-8-methyl-5-(3-methyl-1 {H}-indazol-6-yl)-1,2,3,4-tetrahydronaphthalen-1-yl]pyridine-2-carboxamide (three-letter code: MDI) (formula: $C_{27}H_{26}F_2N_4O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C F N O 34 27 2 4 1	0	0
3	B	1	Total C F N O 34 27 2 4 1	0	0

- Molecule 4 is water.

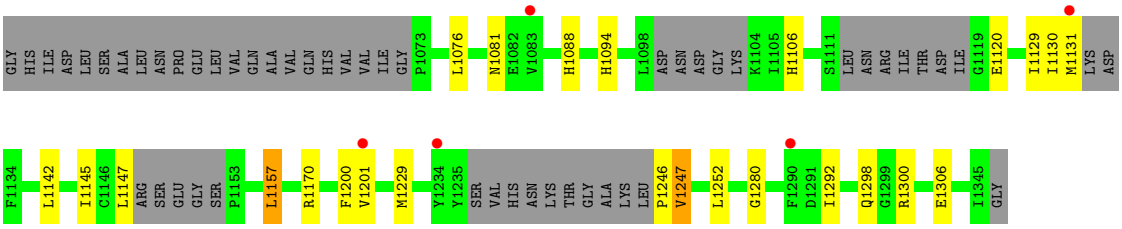
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	47	Total O 47 47	0	0
4	B	36	Total O 36 36	0	0

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.

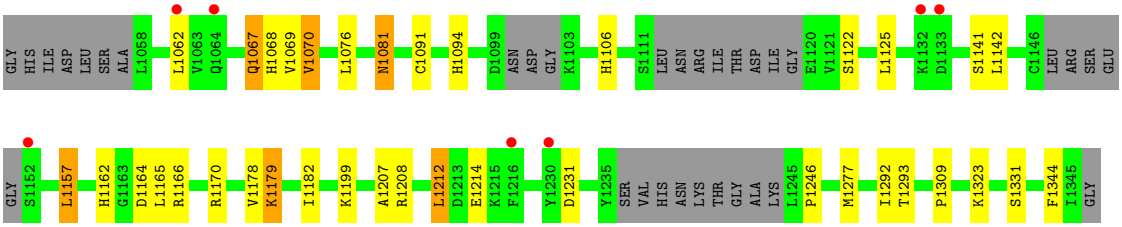
• Molecule 1: Hepatocyte growth factor receptor

Chain A:



• Molecule 1: Hepatocyte growth factor receptor

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	42.84Å 52.18Å 84.07Å 74.26° 77.64° 70.55°	Depositor
Resolution (Å)	48.03 – 2.39 48.03 – 2.39	Depositor EDS
% Data completeness (in resolution range)	96.4 (48.03-2.39) 96.4 (48.03-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.11.8 (24-FEB-2021)	Depositor
R, R_{free}	0.241 , 0.298 0.232 , 0.291	Depositor DCC
R_{free} test set	1256 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	30.5	Xtriage
Anisotropy	1.108	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 52.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4176	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.87% 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: MDI, SO4

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	0.44	0/1993	0.60	0/2695
1	B	0.42	0/2109	0.59	0/2864
All	All	0.43	0/4102	0.59	0/5559

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	1943	0	1933	12	0
1	B	2057	0	2023	16	0
2	A	20	0	0	0	0
2	B	5	0	0	0	0
3	A	34	0	0	0	0
3	B	34	0	0	0	0
4	A	47	0	0	0	0
4	B	36	0	0	0	0
All	All	4176	0	3956	28	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 (28) 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:1298:GLN:NE2	1:A:1300:ARG:HH11	1.75	0.85
1:B:1094:HIS:HD2	1:B:1106:HIS:NE2	1.78	0.82
1:A:1298:GLN:NE2	1:A:1300:ARG:NH1	2.29	0.79
1:A:1094:HIS:HD2	1:A:1106:HIS:NE2	1.86	0.73
1:A:1298:GLN:HE21	1:A:1300:ARG:HH11	1.49	0.61
1:B:1068:HIS:CE1	1:B:1069:VAL:HG13	2.36	0.60
1:A:1298:GLN:HE21	1:A:1300:ARG:NH1	2.00	0.59
1:B:1179:LYS:HG3	1:B:1344:PHE:HB2	1.85	0.59
1:B:1094:HIS:CD2	1:B:1106:HIS:NE2	2.67	0.58
1:B:1081:ASN:HD22	1:B:1081:ASN:H	1.54	0.56
1:B:1162:HIS:HB2	1:B:1212:LEU:HG	1.87	0.55
1:A:1170:ARG:HG3	1:A:1280:GLY:HA3	1.89	0.54
1:B:1122:SER:HB3	1:B:1125:LEU:HD13	1.90	0.54
1:B:1208:ARG:HH12	1:B:1246:PRO:HG3	1.75	0.52
1:A:1142:LEU:HA	1:A:1157:LEU:HD22	1.92	0.52
1:B:1142:LEU:HA	1:B:1157:LEU:HD22	1.94	0.50
1:A:1298:GLN:HE22	1:A:1300:ARG:NH1	2.10	0.48
1:B:1165:LEU:HB3	1:B:1207:ALA:O	2.14	0.46
1:B:1178:VAL:O	1:B:1182:ILE:HG13	2.16	0.46
1:B:1067:GLN:HA	1:B:1070:VAL:HB	1.97	0.46
1:A:1247:VAL:HG13	1:A:1292:ILE:HG21	1.98	0.44
1:A:1201:VAL:HG23	1:A:1229:MET:SD	2.58	0.44
1:A:1120:GLU:O	1:A:1120:GLU:HG2	2.18	0.43
1:B:1199:LYS:HB3	1:B:1199:LYS:HE2	1.85	0.43
1:A:1129:ILE:HG22	1:A:1130:ILE:HD12	2.00	0.42
1:B:1166:ARG:CZ	1:B:1170:ARG:HD2	2.50	0.42
1:B:1068:HIS:CE1	1:B:1069:VAL:CG1	3.02	0.42
1:B:1277:MET:HE2	1:B:1309:PRO:HD3	2.02	0.42

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	232/296 (78%)	224 (97%)	8 (3%)	0	100	100
1	B	253/296 (86%)	240 (95%)	13 (5%)	0	100	100
All	All	485/592 (82%)	464 (96%)	21 (4%)	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	213/261 (82%)	201 (94%)	12 (6%)	21	34
1	B	222/261 (85%)	205 (92%)	17 (8%)	13	20
All	All	435/522 (83%)	406 (93%)	29 (7%)	16	26

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1076	LEU
1	A	1081	ASN
1	A	1088	HIS
1	A	1131	MET
1	A	1145	ILE
1	A	1147	LEU
1	A	1157	LEU
1	A	1200	PHE
1	A	1246	PRO
1	A	1247	VAL
1	A	1252	LEU
1	A	1306	GLU
1	B	1062	LEU
1	B	1067	GLN
1	B	1070	VAL

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Mol	Chain	Res	Type
1	B	1076	LEU
1	B	1081	ASN
1	B	1091	CYS
1	B	1141	SER
1	B	1157	LEU
1	B	1164	ASP
1	B	1179	LYS
1	B	1212	LEU
1	B	1214	GLU
1	B	1231	ASP
1	B	1292	ILE
1	B	1293	THR
1	B	1323	LYS
1	B	1331	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1081	ASN
1	A	1094	HIS
1	A	1256	GLN
1	A	1298	GLN
1	B	1081	ASN
1	B	1094	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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)

7 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	SO4	B	1401	-	4,4,4	0.29	0	6,6,6	0.32	0
2	SO4	A	1404	-	4,4,4	0.22	0	6,6,6	0.10	0
2	SO4	A	1402	-	4,4,4	0.17	0	6,6,6	0.23	0
2	SO4	A	1403	-	4,4,4	0.12	0	6,6,6	0.10	0
3	MDI	A	1405	-	34,38,38	0.65	1 (2%)	36,56,56	1.47	6 (16%)
3	MDI	B	1402	-	34,38,38	0.68	1 (2%)	36,56,56	1.37	6 (16%)
2	SO4	A	1401	-	4,4,4	0.29	0	6,6,6	0.14	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
3	MDI	A	1405	-	-	2/18/30/30	0/5/5/5
3	MDI	B	1402	-	-	2/18/30/30	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1405	MDI	C9-C10	2.28	1.59	1.51
3	B	1402	MDI	C9-C10	2.21	1.59	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1402	MDI	C9-C8-C7	-3.99	100.52	111.57
3	A	1405	MDI	F-C18-C14	-3.95	107.02	110.41
3	A	1405	MDI	C9-C8-C7	-3.76	101.16	111.57
3	A	1405	MDI	C11-N-C7	-3.28	111.93	117.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1402	MDI	C11-N-C7	-3.17	112.12	117.73
3	B	1402	MDI	C6-C7-N	2.87	115.75	112.21
3	A	1405	MDI	C11-N-C12	-2.73	114.25	121.85
3	B	1402	MDI	C10-C5-C6	-2.52	115.12	120.18
3	B	1402	MDI	C19-C25-C24	-2.50	119.25	121.44
3	A	1405	MDI	C19-C25-C24	-2.47	119.28	121.44
3	A	1405	MDI	C10-C5-C6	-2.43	115.30	120.18
3	B	1402	MDI	C11-N-C12	-2.30	115.45	121.85

There are no chirality outliers.

All (4) torsion outliers are listed below:

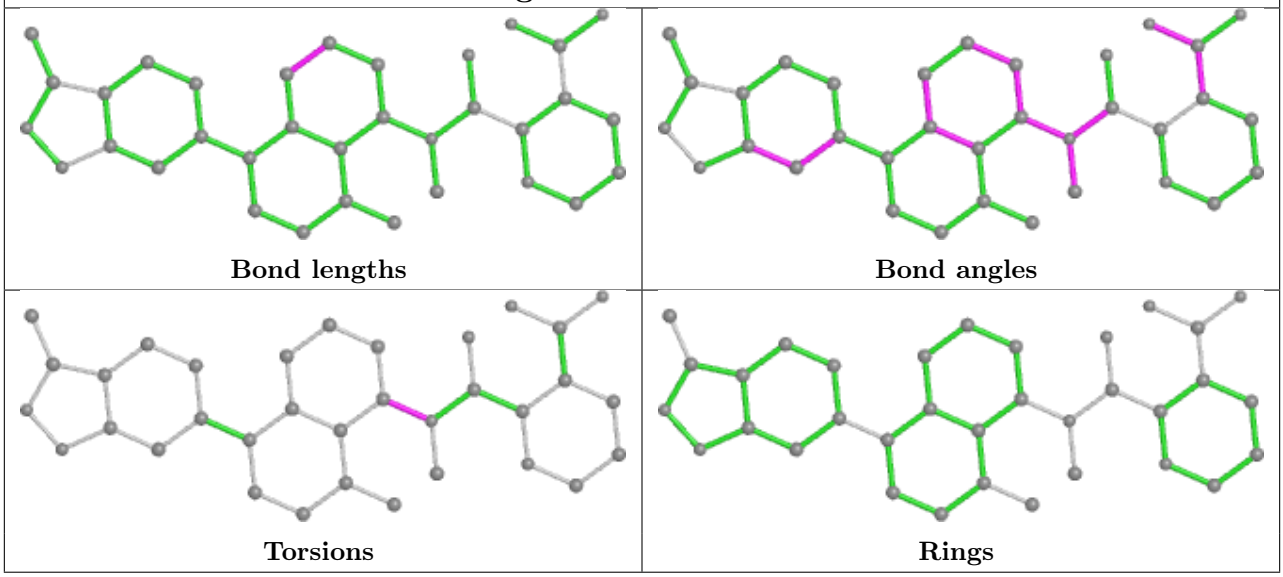
Mol	Chain	Res	Type	Atoms
3	A	1405	MDI	C8-C7-N-C11
3	A	1405	MDI	C8-C7-N-C12
3	B	1402	MDI	C8-C7-N-C12
3	B	1402	MDI	C8-C7-N-C11

There are no ring outliers.

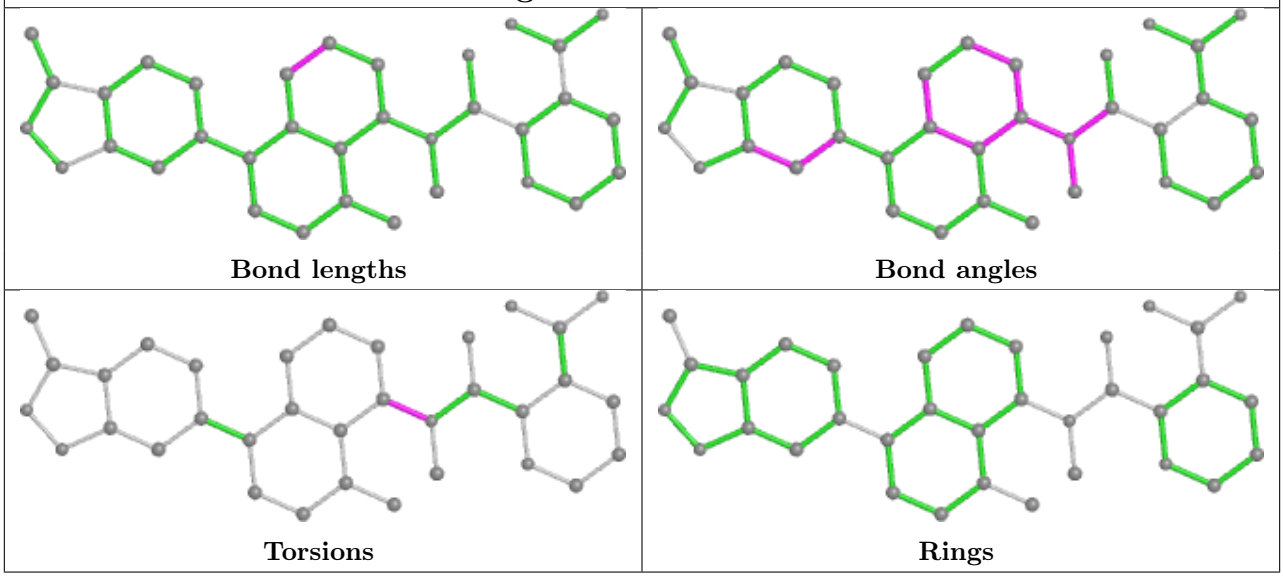
No monomer is involved in short contacts.

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 MDI A 1405



Ligand MDI B 1402



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	244/296 (82%)	0.23	5 (2%)	65	63	23, 40, 55, 67	0
1	B	263/296 (88%)	0.33	7 (2%)	54	52	22, 42, 59, 65	0
All	All	507/592 (85%)	0.28	12 (2%)	59	57	22, 41, 58, 67	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1152	SER	3.9
1	A	1290	PHE	3.7
1	A	1234	TYR	2.4
1	B	1133	ASP	2.4
1	B	1132	LYS	2.4
1	A	1201	VAL	2.4
1	B	1230	TYR	2.3
1	B	1064	GLN	2.1
1	B	1216	PHE	2.1
1	B	1062	LEU	2.1
1	A	1131	MET	2.1
1	A	1083	VAL	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)

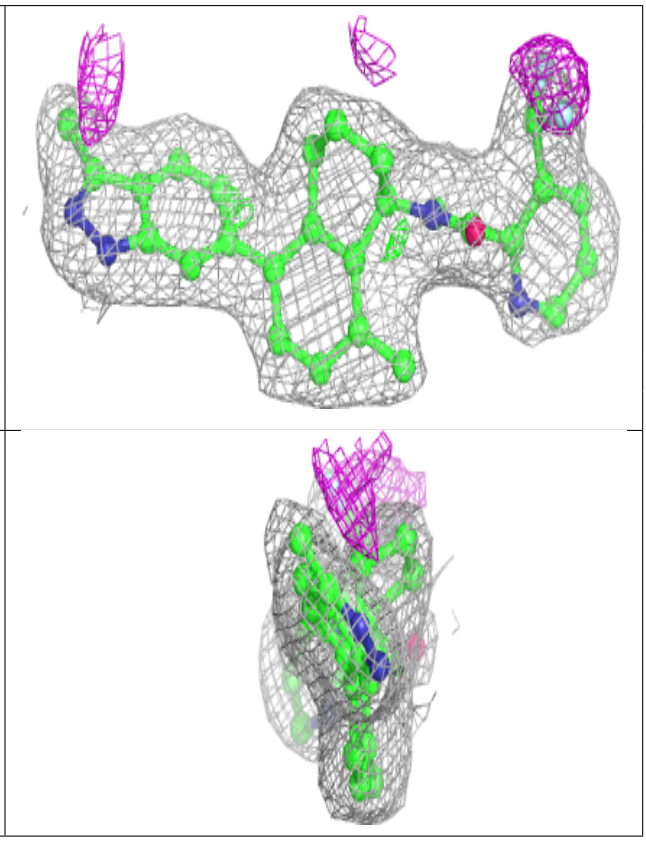
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MDI	A	1405	34/34	0.89	0.19	30,34,48,49	0
3	MDI	B	1402	34/34	0.90	0.17	34,37,46,47	0
2	SO4	A	1402	5/5	0.92	0.15	68,68,68,68	0
2	SO4	B	1401	5/5	0.94	0.11	59,60,60,60	0
2	SO4	A	1403	5/5	0.95	0.10	89,89,89,89	0
2	SO4	A	1404	5/5	0.96	0.13	79,79,80,80	0
2	SO4	A	1401	5/5	0.98	0.10	54,54,54,54	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.

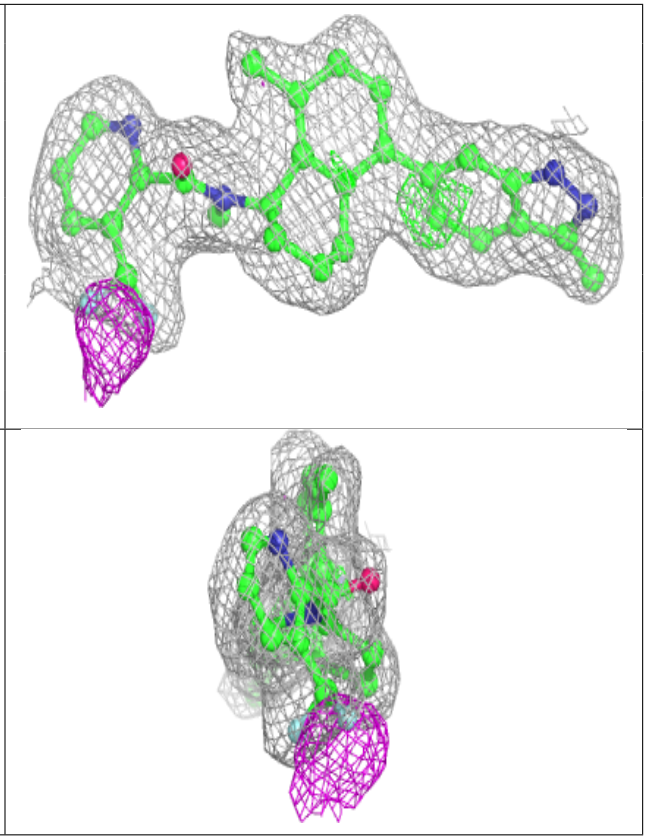
Electron density around MDI A 1405:

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 MDI B 1402:

$2mF_o$-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.