



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 03:48 pm BST

PDB ID : 4MHA
Title : Crystal structure of the catalytic domain of the proto-oncogene tyrosine-protein kinase MER in complex with inhibitor UNC1817
Authors : Zhang, W.; Mciver, A.; Stashko, M.A.; Deryckere, D.; Branchford, B.R.; Hunter, D.; Kireev, D.B.; Miley, D.B.M.; Norris-Drouin, J.; Stewart, W.M.; Lee, M.; Sather, S.; Zhou, Y.; Dipaola, J.A.; Machius, M.; Janzen, W.P.; Earp, H.S.; Graham, D.K.; Frye, S.; Wang, X.
Deposited on : 2013-08-29
Resolution : 2.59 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

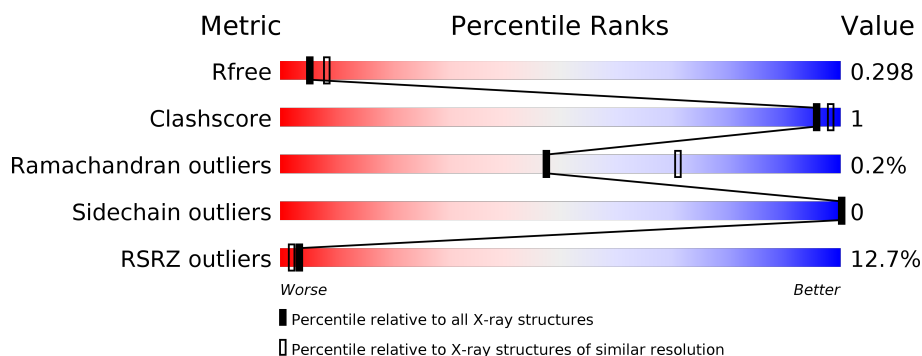
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	313	
1	B	313	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8263 atoms, of which 4121 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 Tyrosine-protein kinase Mer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	256	Total	C	H	N	O	S	0	2	0
			4137	1322	2070	346	380	19			
1	B	246	Total	C	H	N	O	S	0	0	0
			3966	1272	1987	329	360	18			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	552	MET	-	EXPRESSION TAG	UNP Q12866
A	553	GLY	-	EXPRESSION TAG	UNP Q12866
A	554	SER	-	EXPRESSION TAG	UNP Q12866
A	555	SER	-	EXPRESSION TAG	UNP Q12866
A	556	HIS	-	EXPRESSION TAG	UNP Q12866
A	557	HIS	-	EXPRESSION TAG	UNP Q12866
A	558	HIS	-	EXPRESSION TAG	UNP Q12866
A	559	HIS	-	EXPRESSION TAG	UNP Q12866
A	560	HIS	-	EXPRESSION TAG	UNP Q12866
A	561	HIS	-	EXPRESSION TAG	UNP Q12866
A	562	SER	-	EXPRESSION TAG	UNP Q12866
A	563	SER	-	EXPRESSION TAG	UNP Q12866
A	564	GLY	-	EXPRESSION TAG	UNP Q12866
A	565	LEU	-	EXPRESSION TAG	UNP Q12866
A	566	VAL	-	EXPRESSION TAG	UNP Q12866
A	567	PRO	-	EXPRESSION TAG	UNP Q12866
A	568	ARG	-	EXPRESSION TAG	UNP Q12866
A	569	GLY	-	EXPRESSION TAG	UNP Q12866
B	552	MET	-	EXPRESSION TAG	UNP Q12866
B	553	GLY	-	EXPRESSION TAG	UNP Q12866
B	554	SER	-	EXPRESSION TAG	UNP Q12866
B	555	SER	-	EXPRESSION TAG	UNP Q12866
B	556	HIS	-	EXPRESSION TAG	UNP Q12866
B	557	HIS	-	EXPRESSION TAG	UNP Q12866
B	558	HIS	-	EXPRESSION TAG	UNP Q12866

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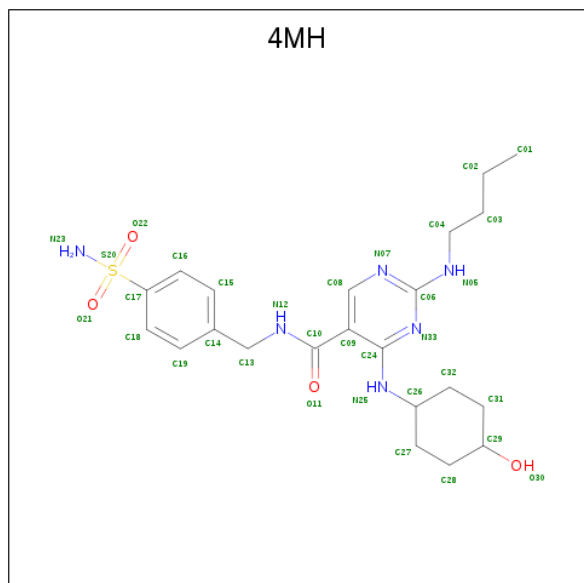
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Chain	Residue	Modelled	Actual	Comment	Reference
B	559	HIS	-	EXPRESSION TAG	UNP Q12866
B	560	HIS	-	EXPRESSION TAG	UNP Q12866
B	561	HIS	-	EXPRESSION TAG	UNP Q12866
B	562	SER	-	EXPRESSION TAG	UNP Q12866
B	563	SER	-	EXPRESSION TAG	UNP Q12866
B	564	GLY	-	EXPRESSION TAG	UNP Q12866
B	565	LEU	-	EXPRESSION TAG	UNP Q12866
B	566	VAL	-	EXPRESSION TAG	UNP Q12866
B	567	PRO	-	EXPRESSION TAG	UNP Q12866
B	568	ARG	-	EXPRESSION TAG	UNP Q12866
B	569	GLY	-	EXPRESSION TAG	UNP Q12866

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Cl 3 3	0	0
2	A	3	Total Cl 3 3	0	0

- Molecule 3 is 2-(butylamino)-4-[(trans-4-hydroxycyclohexyl)amino]-N-(4-sulfamoylbenzyl)pyrimidine-5-carboxamide (three-letter code: 4MH) (formula: C₂₂H₃₂N₆O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	S	
			65	22	32	6	4	1	

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	S	
			65	22	32	6	4	1	
								0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg		
			1	1	0	0

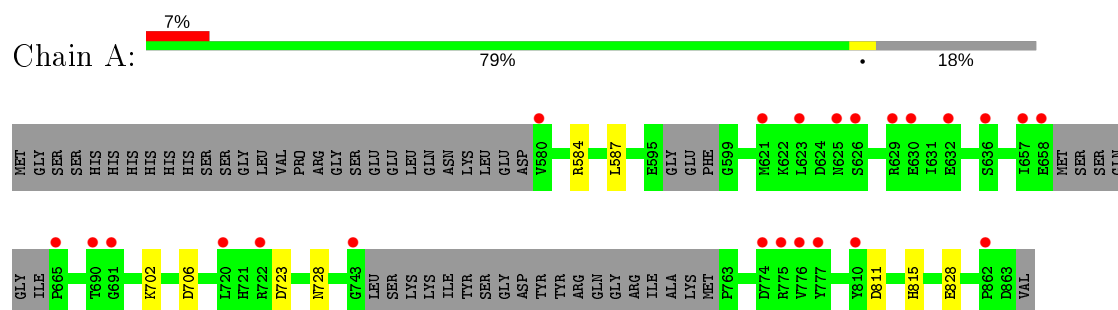
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total	O		
			7	7	0	0
5	B	16	Total	O		
			16	16	0	0

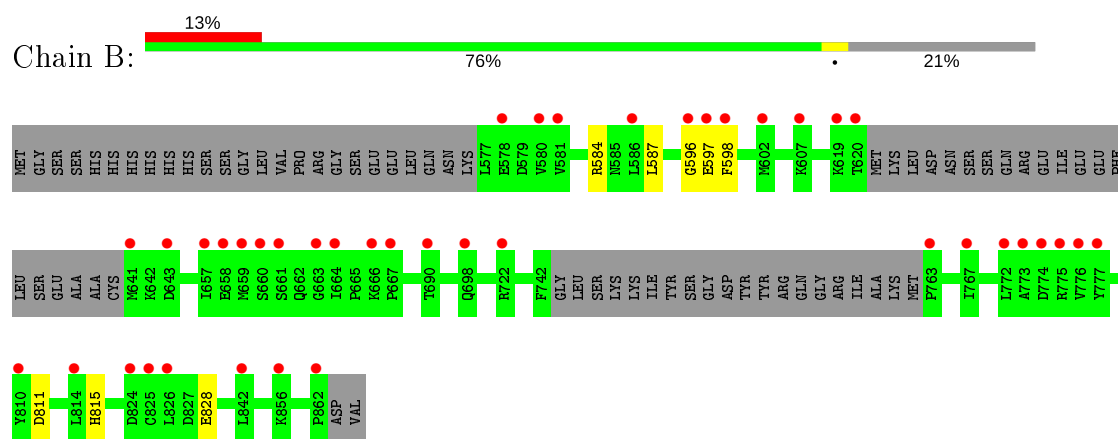
3 Residue-property plots [i](#)

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: Tyrosine-protein kinase Mer



• Molecule 1: Tyrosine-protein kinase Mer



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.14Å 91.46Å 69.93Å 90.00° 100.23° 90.00°	Depositor
Resolution (Å)	40.07 – 2.59 40.07 – 2.59	Depositor EDS
% Data completeness (in resolution range)	84.9 (40.07-2.59) 82.3 (40.07-2.59)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1468)	Depositor
R, R_{free}	0.241 , 0.294 0.244 , 0.298	Depositor DCC
R_{free} test set	1686 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8263	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.92% 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: 4MH, MG, CL

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	0.20	0/2117	0.33	0/2859
1	B	0.20	0/2022	0.33	0/2734
All	All	0.20	0/4139	0.33	0/5593

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	2067	2070	2065	5	0
1	B	1979	1987	1994	4	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	33	32	32	0	0
3	B	33	32	32	0	0
4	B	1	0	0	0	0
5	A	7	0	0	0	0
5	B	16	0	0	0	0
All	All	4142	4121	4123	9	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 1.

All (9) 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:723:ASP:O	1:A:728:ASN:ND2	2.23	0.70
1:A:811:ASP:O	1:A:815:HIS:ND1	2.32	0.63
1:A:584:ARG:NH1	1:A:587:LEU:O	2.35	0.60
1:B:811:ASP:O	1:B:815:HIS:ND1	2.37	0.58
1:A:828:GLU:N	1:A:828:GLU:OE2	2.43	0.49
1:B:584:ARG:NH1	1:B:587:LEU:O	2.47	0.47
1:A:702:LYS:NZ	1:A:706:ASP:OD1	2.47	0.47
1:B:828:GLU:N	1:B:828:GLU:OE2	2.46	0.45
1:B:596:GLY:O	1:B:598:PHE:N	2.54	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	250/313 (80%)	241 (96%)	9 (4%)	0	100	100
1	B	240/313 (77%)	232 (97%)	7 (3%)	1 (0%)	34	57
All	All	490/626 (78%)	473 (96%)	16 (3%)	1 (0%)	47	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	597	GLU

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	233/280 (83%)	233 (100%)	0	100	100
1	B	222/280 (79%)	222 (100%)	0	100	100
All	All	455/560 (81%)	455 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	608	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](#)

Of 9 ligands modelled in this entry, 7 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
3	4MH	B	905	-	35,35,35	2.26	5 (14%)	46,48,48	2.32	13 (28%)
3	4MH	A	904	-	35,35,35	2.25	5 (14%)	46,48,48	2.34	11 (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
3	4MH	B	905	-	-	8/24/34/34	0/3/3/3
3	4MH	A	904	-	-	10/24/34/34	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	904	4MH	C06-N05	8.25	1.47	1.34
3	B	905	4MH	C06-N05	8.19	1.46	1.34
3	B	905	4MH	C24-N25	7.22	1.46	1.35
3	A	904	4MH	C24-N25	6.99	1.46	1.35
3	A	904	4MH	C10-N12	5.75	1.46	1.33
3	B	905	4MH	C10-N12	5.68	1.46	1.33
3	B	905	4MH	S20-N23	2.75	1.65	1.60
3	A	904	4MH	S20-N23	2.73	1.65	1.60
3	B	905	4MH	C09-C10	2.29	1.54	1.50
3	A	904	4MH	C09-C10	2.21	1.54	1.50

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	905	4MH	O22-S20-O21	-10.64	101.28	118.76
3	A	904	4MH	O22-S20-O21	-10.62	101.30	118.76
3	A	904	4MH	N07-C06-N33	-5.77	121.08	126.55
3	B	905	4MH	N07-C06-N33	-5.74	121.11	126.55
3	B	905	4MH	C08-C09-C24	3.88	118.34	114.55
3	A	904	4MH	C08-C09-C24	3.68	118.16	114.55
3	A	904	4MH	O22-S20-C17	3.56	111.32	107.35
3	A	904	4MH	O21-S20-C17	3.44	111.19	107.35
3	B	905	4MH	O22-S20-C17	3.43	111.18	107.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	905	4MH	O21-S20-C17	3.09	110.80	107.35
3	A	904	4MH	C24-C09-C10	3.02	121.70	120.69
3	B	905	4MH	O22-S20-N23	2.91	111.68	107.36
3	A	904	4MH	O22-S20-N23	2.76	111.46	107.36
3	A	904	4MH	C08-N07-C06	2.66	119.89	115.88
3	A	904	4MH	O21-S20-N23	2.61	111.24	107.36
3	B	905	4MH	O21-S20-N23	2.54	111.14	107.36
3	B	905	4MH	C08-N07-C06	2.47	119.61	115.88
3	A	904	4MH	C09-C08-N07	-2.46	120.57	124.28
3	B	905	4MH	C09-C08-N07	-2.44	120.59	124.28
3	B	905	4MH	C06-N33-C24	2.32	121.71	116.39
3	B	905	4MH	C27-C26-N25	-2.16	107.23	110.60
3	A	904	4MH	C06-N33-C24	2.08	121.16	116.39
3	B	905	4MH	N05-C06-N07	2.03	120.26	117.22
3	B	905	4MH	C24-C09-C10	2.01	121.36	120.69

There are no chirality outliers.

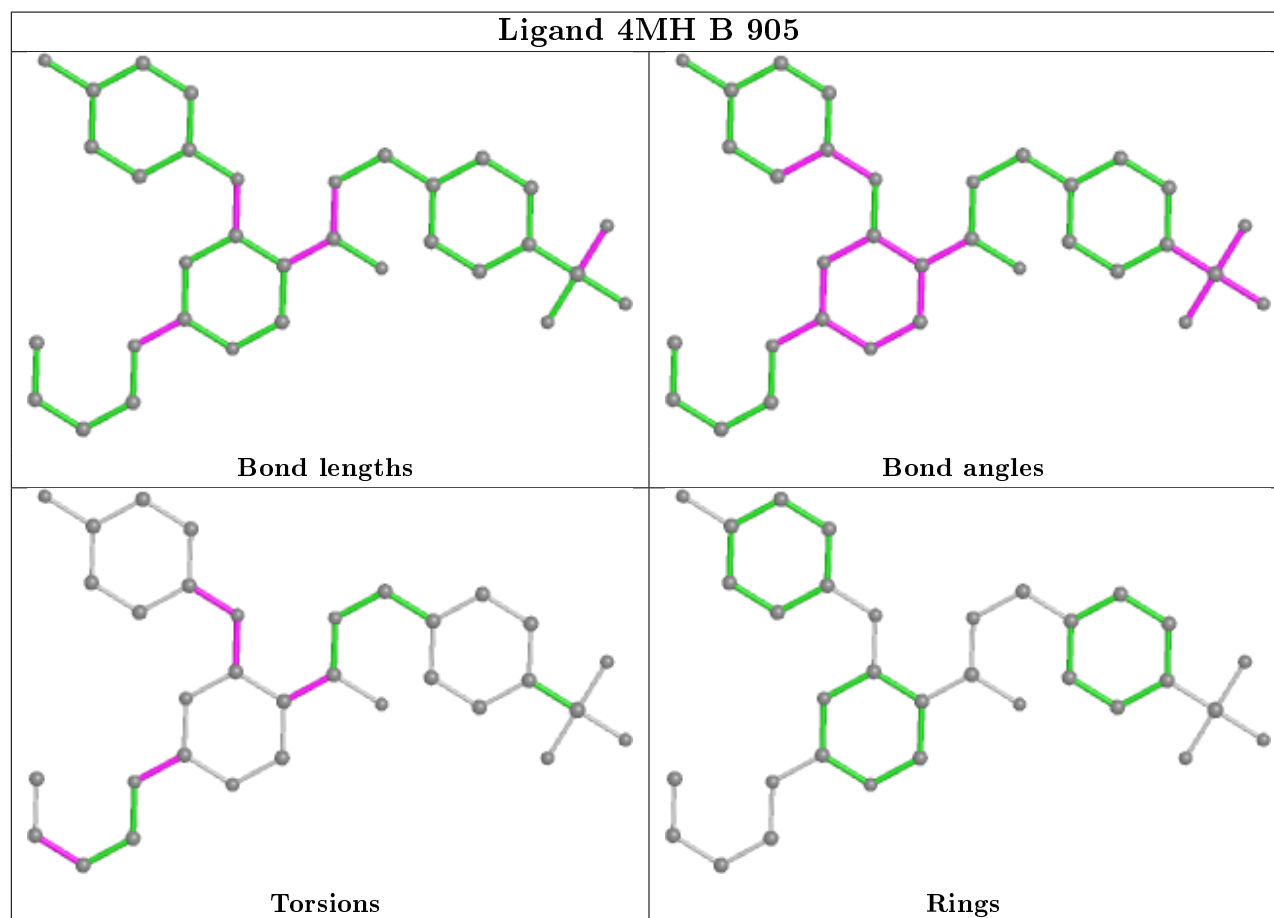
All (18) torsion outliers are listed below:

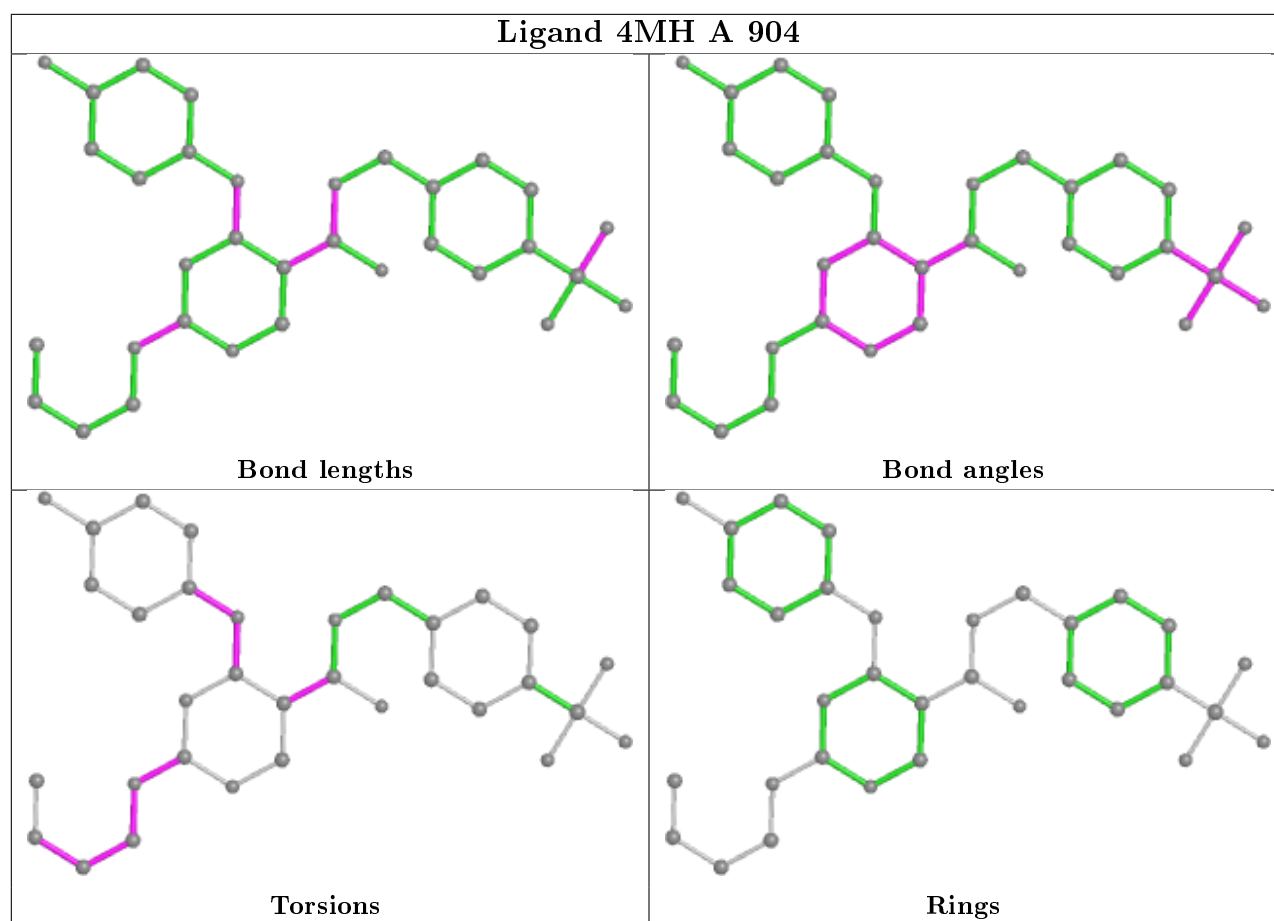
Mol	Chain	Res	Type	Atoms
3	B	905	4MH	N07-C06-N05-C04
3	B	905	4MH	N33-C06-N05-C04
3	B	905	4MH	C09-C24-N25-C26
3	B	905	4MH	N33-C24-N25-C26
3	B	905	4MH	C32-C26-N25-C24
3	A	904	4MH	C03-C04-N05-C06
3	A	904	4MH	N07-C06-N05-C04
3	A	904	4MH	N33-C06-N05-C04
3	A	904	4MH	C09-C24-N25-C26
3	A	904	4MH	N33-C24-N25-C26
3	A	904	4MH	C32-C26-N25-C24
3	A	904	4MH	C08-C09-C10-O11
3	A	904	4MH	C08-C09-C10-N12
3	A	904	4MH	C01-C02-C03-C04
3	B	905	4MH	C08-C09-C10-O11
3	B	905	4MH	C08-C09-C10-N12
3	B	905	4MH	C01-C02-C03-C04
3	A	904	4MH	C02-C03-C04-N05

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 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	256/313 (81%)	0.71	23 (8%) 9 6	20, 38, 69, 92	0
1	B	246/313 (78%)	0.93	41 (16%) 1 1	18, 38, 74, 99	0
All	All	502/626 (80%)	0.82	64 (12%) 3 2	18, 38, 71, 99	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	664	ILE	5.6
1	B	597	GLU	5.5
1	A	777	TYR	4.9
1	B	775	ARG	4.9
1	B	666	LYS	4.7
1	A	690	THR	4.5
1	B	772	LEU	4.5
1	B	581	VAL	4.1
1	B	773	ALA	4.1
1	B	763	PRO	3.8
1	B	586	LEU	3.7
1	B	774	ASP	3.7
1	A	621	MET	3.7
1	A	810	TYR	3.6
1	A	625	ASN	3.6
1	B	776	VAL	3.5
1	B	643	ASP	3.4
1	A	665	PRO	3.4
1	A	658	GLU	3.2
1	A	629	ARG	3.2
1	B	777	TYR	3.2
1	B	826	LEU	3.1
1	B	810	TYR	3.1
1	A	632	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	596	GLY	2.9
1	B	620	THR	2.9
1	A	743	GLY	2.8
1	B	825	CYS	2.8
1	B	824	ASP	2.8
1	A	862	PRO	2.7
1	B	698	GLN	2.7
1	B	856	LYS	2.7
1	A	775	ARG	2.7
1	A	636	SER	2.6
1	B	767	ILE	2.6
1	B	814	LEU	2.6
1	B	578	GLU	2.6
1	B	598	PHE	2.6
1	A	623	LEU	2.6
1	A	776	VAL	2.6
1	B	690	THR	2.6
1	B	663	GLY	2.5
1	A	657	ILE	2.5
1	B	667	PRO	2.4
1	B	722	ARG	2.4
1	B	657	ILE	2.4
1	A	720	LEU	2.3
1	B	659	MET	2.3
1	B	842	LEU	2.3
1	B	661	SER	2.3
1	A	774	ASP	2.3
1	B	580	VAL	2.2
1	B	602	MET	2.2
1	A	630	GLU	2.2
1	B	862	PRO	2.2
1	B	619	LYS	2.2
1	A	722	ARG	2.1
1	A	580	VAL	2.1
1	B	658	GLU	2.1
1	A	626	SER	2.0
1	B	607	LYS	2.0
1	A	691	GLY	2.0
1	B	660	SER	2.0
1	B	641	MET	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](#)

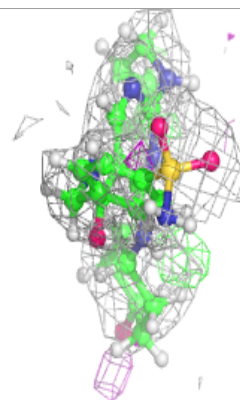
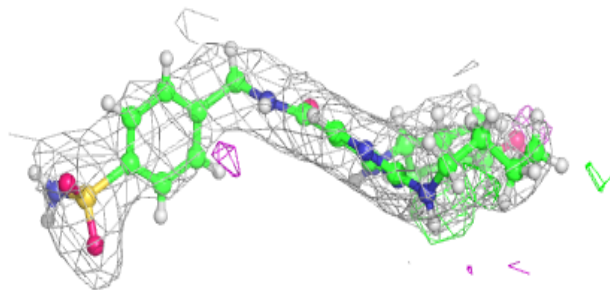
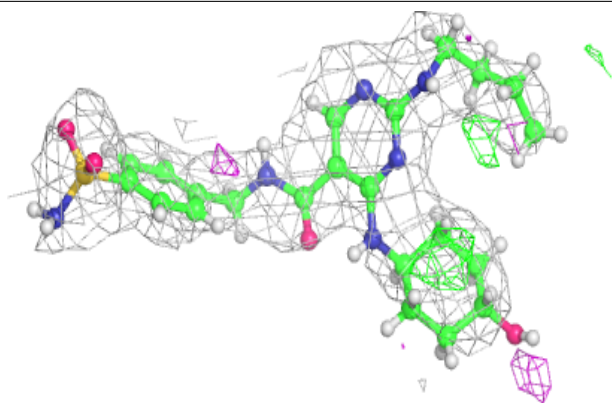
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CL	A	903	1/1	0.87	0.23	63,63,63,63	0
3	4MH	B	905	33/33	0.88	0.24	23,47,81,98	0
3	4MH	A	904	33/33	0.90	0.22	26,49,66,81	0
2	CL	A	902	1/1	0.92	0.14	24,24,24,24	0
4	MG	B	904	1/1	0.93	0.16	34,34,34,34	0
2	CL	A	901	1/1	0.96	0.23	40,40,40,40	0
2	CL	B	902	1/1	0.97	0.20	51,51,51,51	0
2	CL	B	901	1/1	0.98	0.13	27,27,27,27	0
2	CL	B	903	1/1	0.99	0.05	36,36,36,36	0

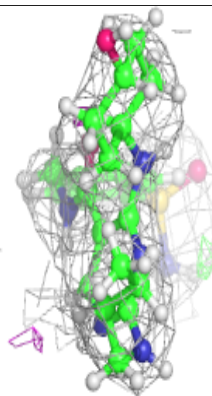
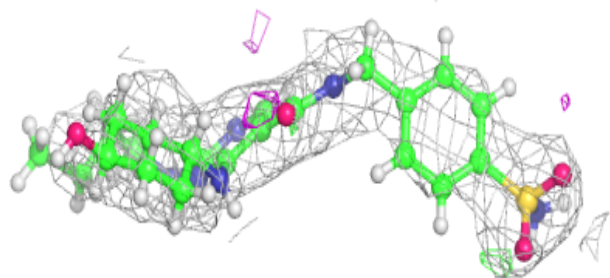
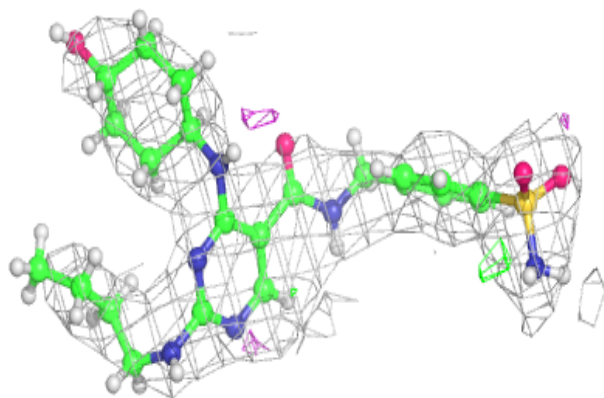
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4MH B 905:

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

**Electron density around 4MH A 904:**

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



6.5 Other polymers

There are no such residues in this entry.