Full wwPDB X-ray Structure Validation Report (i)

Oct 11, 2021 – 07:33 AM EDT

PDB ID	:	2Q15
Title	:	Structure of BACE complexed to compound 3a
Authors	:	Sharff, A.J.
Deposited on	:	2007-05-23
Resolution	:	2.40 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 (1)) were used in the production of this report:

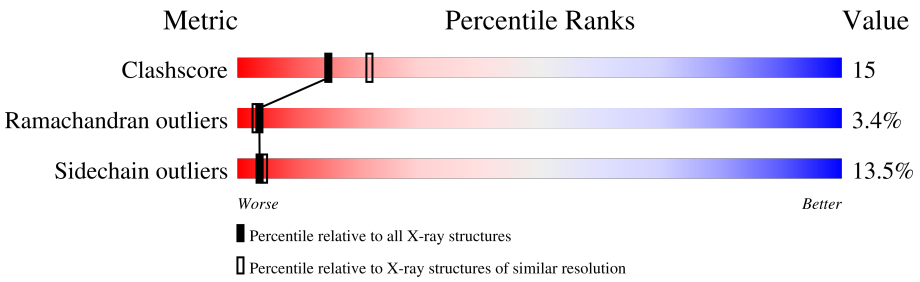
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	385	66% 24% 9% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3217 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.

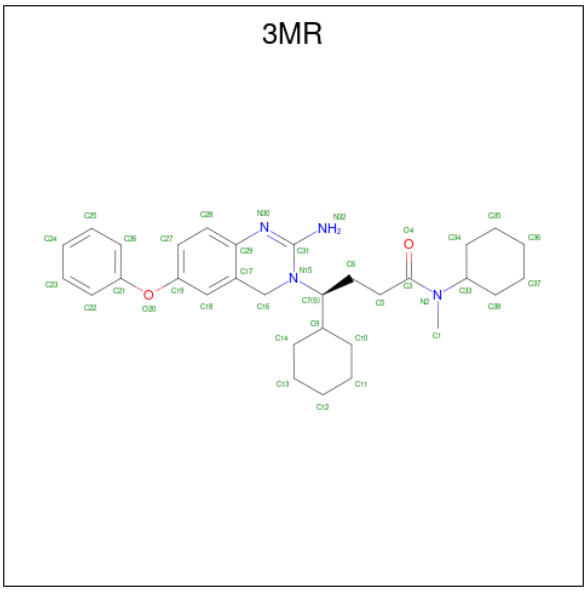
- Molecule 1 is a protein called Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	385	3023	1935	502	572	14	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	GLN	ASN	engineered mutation	UNP P56817
A	111	GLN	ASN	engineered mutation	UNP P56817
A	162	GLN	ASN	engineered mutation	UNP P56817
A	293	GLN	ASN	engineered mutation	UNP P56817

- Molecule 2 is (4S)-4-(2-AMINO-6-PHENOXYQUINAZOLIN-3(4H)-YL)-N,4-DICYCLOHEXYL-N-METHYLBUTANAMIDE (three-letter code: 3MR) (formula: $C_{31}H_{42}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	37	31	4	2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	157	157	157	0	0

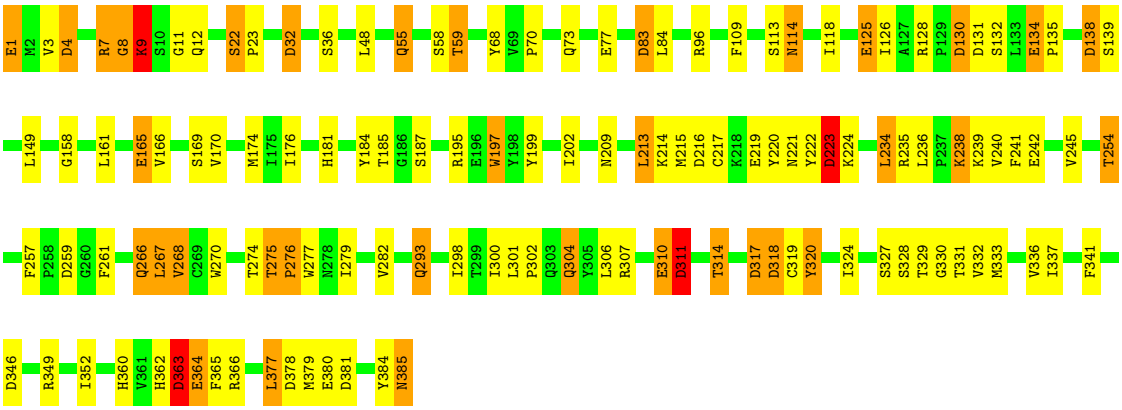
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: Beta-secretase 1

Chain A: 66% 24% 9%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	102.35Å 102.35Å 169.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.54 – 2.40	Depositor
% Data completeness (in resolution range)	99.8 (29.54-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	REFMAC 5.1.29	Depositor
R, R_{free}	0.252 , 0.344	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3217	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

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: 3MR

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	1.09	0/3100	1.13	19/4216 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	83	ASP	CB-CG-OD2	7.95	125.45	118.30
1	A	363	ASP	CB-CG-OD2	7.80	125.32	118.30
1	A	318	ASP	CB-CG-OD2	7.56	125.11	118.30
1	A	311	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	346	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	131	ASP	CB-CG-OD2	6.25	123.93	118.30
1	A	223	ASP	CB-CG-OD1	-6.22	112.70	118.30
1	A	223	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	138	ASP	CB-CG-OD2	6.02	123.72	118.30
1	A	32	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	378	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	4	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	138	ASP	CB-CG-OD1	-5.54	113.31	118.30
1	A	114	ASN	N-CA-C	5.51	125.89	111.00
1	A	55	GLN	CB-CA-C	-5.36	99.67	110.40
1	A	130	ASP	CB-CG-OD2	5.27	123.04	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	8	GLY	N-CA-C	5.23	126.18	113.10
1	A	185	THR	OG1-CB-CG2	-5.16	98.14	110.00
1	A	84	LEU	CA-CB-CG	5.11	127.06	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	197	TRP	Peptide
1	A	7	ARG	Peptide

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	3023	0	2933	87	0
2	A	37	0	42	6	0
3	A	157	0	0	3	0
All	All	3217	0	2975	91	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 15.

All (91) 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:1:GLU:OE1	1:A:1:GLU:N	2.05	0.87
1:A:293:GLN:HE21	1:A:377:LEU:HD23	1.43	0.83
1:A:293:GLN:NE2	1:A:377:LEU:HA	1.95	0.82
2:A:386:3MR:H381	2:A:386:3MR:H51	1.63	0.79
1:A:9:LYS:HB3	1:A:12:GLN:H	1.50	0.75
1:A:234:LEU:HB2	1:A:336:VAL:HG21	1.69	0.74
1:A:267:LEU:HD11	1:A:319:CYS:HB3	1.69	0.73
2:A:386:3MR:C16	2:A:386:3MR:H102	2.21	0.71
1:A:349:ARG:HB3	1:A:349:ARG:CZ	2.20	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:386:3MR:H102	2:A:386:3MR:H162	1.74	0.70
1:A:363:ASP:OD1	1:A:364:GLU:N	2.26	0.69
1:A:8:GLY:O	1:A:166:VAL:HG22	1.94	0.69
2:A:386:3MR:H381	2:A:386:3MR:C5	2.24	0.68
1:A:293:GLN:HE22	1:A:377:LEU:HA	1.58	0.67
1:A:270:TRP:O	1:A:317:ASP:O	2.14	0.65
1:A:384:TYR:C	1:A:385:ASN:OD1	2.39	0.61
1:A:222:TYR:O	1:A:223:ASP:CB	2.48	0.61
1:A:222:TYR:O	1:A:223:ASP:HB3	2.01	0.61
1:A:224:LYS:NZ	1:A:329:THR:O	2.17	0.61
1:A:301:LEU:HB3	1:A:302:PRO:HD2	1.84	0.59
1:A:234:LEU:HB2	1:A:336:VAL:CG2	2.33	0.59
1:A:215:MET:O	1:A:216:ASP:C	2.41	0.59
1:A:238:LYS:HZ2	1:A:242:GLU:HG2	1.69	0.58
1:A:241:PHE:CE2	1:A:245:VAL:HG21	2.39	0.57
1:A:241:PHE:CZ	1:A:245:VAL:HG21	2.38	0.57
1:A:241:PHE:CZ	1:A:245:VAL:CG2	2.87	0.57
1:A:118:ILE:HD12	2:A:386:3MR:H362	1.87	0.57
1:A:209:ASN:HA	1:A:282:VAL:HG22	1.87	0.56
1:A:234:LEU:O	1:A:324:ILE:HA	2.05	0.56
1:A:293:GLN:NE2	1:A:377:LEU:HD23	2.17	0.56
1:A:224:LYS:O	1:A:330:GLY:HA3	2.05	0.55
1:A:304:GLN:O	1:A:336:VAL:HG12	2.06	0.55
1:A:4:ASP:O	1:A:170:VAL:HG11	2.06	0.55
1:A:128:ARG:NH1	3:A:482:HOH:O	2.41	0.54
1:A:1:GLU:H3	1:A:1:GLU:CD	2.03	0.53
1:A:267:LEU:HD12	1:A:268:VAL:N	2.24	0.53
1:A:384:TYR:C	1:A:384:TYR:CD2	2.82	0.53
1:A:261:PHE:HB2	1:A:266:GLN:HE21	1.73	0.53
1:A:300:ILE:C	1:A:301:LEU:HD23	2.28	0.53
1:A:238:LYS:NZ	1:A:242:GLU:HG2	2.24	0.53
1:A:132:SER:HB3	3:A:432:HOH:O	2.10	0.51
1:A:181:HIS:CD2	1:A:184:TYR:CZ	2.99	0.51
1:A:320:TYR:CD1	1:A:320:TYR:N	2.78	0.51
1:A:384:TYR:O	1:A:385:ASN:OD1	2.29	0.50
1:A:174:MET:CE	1:A:176:ILE:HD11	2.41	0.50
1:A:7:ARG:HG3	1:A:170:VAL:HG13	1.92	0.50
1:A:282:VAL:HG13	1:A:366:ARG:HH11	1.76	0.50
1:A:310:GLU:O	1:A:311:ASP:O	2.29	0.49
1:A:293:GLN:NE2	1:A:377:LEU:CA	2.72	0.49
1:A:202:ILE:HD11	1:A:380:GLU:OE2	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:ARG:HD2	3:A:494:HOH:O	2.11	0.49
1:A:217:CYS:HA	1:A:220:TYR:CD1	2.47	0.49
1:A:7:ARG:CG	1:A:170:VAL:HG22	2.44	0.47
1:A:7:ARG:HG2	1:A:170:VAL:HG22	1.96	0.47
1:A:8:GLY:HA2	1:A:166:VAL:HG13	1.97	0.46
1:A:36:SER:OG	1:A:126:ILE:HG13	2.16	0.46
1:A:174:MET:HE3	1:A:176:ILE:HD11	1.96	0.46
1:A:241:PHE:O	1:A:245:VAL:HG23	2.15	0.46
1:A:161:LEU:HD22	1:A:165:GLU:O	2.15	0.46
1:A:134:GLU:HA	1:A:135:PRO:HD3	1.83	0.46
1:A:236:LEU:HD23	1:A:331:THR:HG23	1.99	0.45
1:A:32:ASP:OD2	2:A:386:3MR:N30	2.50	0.45
1:A:8:GLY:O	1:A:9:LYS:HB2	2.16	0.44
1:A:125:GLU:OE1	1:A:195:ARG:NH1	2.50	0.44
1:A:241:PHE:CE1	1:A:245:VAL:CG2	3.01	0.44
1:A:363:ASP:OD1	1:A:365:PHE:N	2.50	0.44
1:A:9:LYS:NZ	1:A:11:GLY:HA3	2.32	0.43
1:A:83:ASP:O	1:A:96:ARG:HA	2.18	0.43
1:A:199:TYR:HB3	1:A:352:ILE:HD11	2.00	0.43
1:A:213:LEU:O	1:A:215:MET:N	2.50	0.43
1:A:293:GLN:HE21	1:A:377:LEU:CD2	2.21	0.43
1:A:333:MET:HG2	1:A:337:ILE:HG13	2.00	0.43
1:A:298:ILE:HB	1:A:341:PHE:CZ	2.54	0.43
1:A:59:THR:O	1:A:96:ARG:NH2	2.52	0.43
1:A:275:THR:HA	1:A:276:PRO:HD3	1.73	0.43
1:A:301:LEU:HB3	1:A:302:PRO:CD	2.47	0.43
1:A:219:GLU:O	1:A:240:VAL:CG2	2.67	0.42
1:A:3:VAL:O	1:A:4:ASP:CB	2.66	0.42
1:A:238:LYS:NZ	1:A:242:GLU:OE2	2.47	0.42
1:A:268:VAL:HG13	1:A:270:TRP:CZ3	2.54	0.42
1:A:360:HIS:CD2	1:A:360:HIS:C	2.93	0.42
1:A:113:SER:O	1:A:114:ASN:CB	2.66	0.42
1:A:8:GLY:O	1:A:9:LYS:CB	2.68	0.41
1:A:48:LEU:HD21	1:A:109:PHE:CG	2.55	0.41
1:A:125:GLU:O	1:A:125:GLU:HG3	2.19	0.41
1:A:134:GLU:CG	1:A:139:SER:OG	2.69	0.41
1:A:235:ARG:HB2	1:A:332:VAL:HB	2.01	0.41
1:A:68:TYR:CD2	1:A:70:PRO:HD3	2.56	0.40
1:A:22:SER:HA	1:A:23:PRO:C	2.41	0.40
1:A:267:LEU:HD12	1:A:267:LEU:C	2.41	0.40
1:A:277:TRP:CE3	1:A:302:PRO:HG2	2.56	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	383/385 (100%)	335 (88%)	35 (9%)	13 (3%)	3 3

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	THR
1	A	310	GLU
1	A	311	ASP
1	A	318	ASP
1	A	364	GLU
1	A	9	LYS
1	A	158	GLY
1	A	214	LYS
1	A	223	ASP
1	A	314	THR
1	A	363	ASP
1	A	362	HIS
1	A	276	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	327/328 (100%)	283 (86%)	44 (14%)	4 4

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	9	LYS
1	A	22	SER
1	A	55	GLN
1	A	58	SER
1	A	59	THR
1	A	73	GLN
1	A	77	GLU
1	A	125	GLU
1	A	130	ASP
1	A	134	GLU
1	A	138	ASP
1	A	149	LEU
1	A	165	GLU
1	A	169	SER
1	A	187	SER
1	A	197	TRP
1	A	213	LEU
1	A	221	ASN
1	A	234	LEU
1	A	238	LYS
1	A	239	LYS
1	A	254	THR
1	A	257	PHE
1	A	259	ASP
1	A	266	GLN
1	A	267	LEU
1	A	268	VAL
1	A	274	THR
1	A	275	THR
1	A	279	ILE
1	A	293	GLN
1	A	304	GLN
1	A	306	LEU
1	A	307	ARG
1	A	314	THR
1	A	317	ASP
1	A	320	TYR
1	A	327	SER
1	A	328	SER
1	A	377	LEU
1	A	379	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	381	ASP
1	A	385	ASN

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	28	ASN
1	A	181	HIS
1	A	266	GLN
1	A	293	GLN
1	A	304	GLN
1	A	360	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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	3MR	A	386	-	41,41,41	0.94	2 (4%)	48,56,56	1.91	15 (31%)

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	3MR	A	386	-	-	5/25/53/53	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	386	3MR	C31-N15	3.95	1.42	1.35
2	A	386	3MR	C31-N32	2.34	1.38	1.34

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	386	3MR	C36-C35-C34	-4.18	102.89	111.42
2	A	386	3MR	C18-C17-C29	4.12	122.53	118.91
2	A	386	3MR	C28-C29-C17	-3.66	116.03	119.97
2	A	386	3MR	C10-C9-C7	-3.53	105.05	112.22
2	A	386	3MR	C36-C37-C38	-3.47	104.34	111.42
2	A	386	3MR	C6-C7-C9	-3.23	108.12	113.36
2	A	386	3MR	C35-C34-C33	-3.14	104.57	110.82
2	A	386	3MR	C13-C14-C9	-2.95	106.89	111.93
2	A	386	3MR	C17-C16-N15	-2.83	107.30	111.88
2	A	386	3MR	C28-C29-N30	2.81	122.33	118.59
2	A	386	3MR	C16-C17-C29	-2.46	117.72	120.31
2	A	386	3MR	C28-C27-C19	2.39	122.65	119.73
2	A	386	3MR	N15-C31-N30	-2.33	121.25	125.11
2	A	386	3MR	C27-C19-C18	-2.30	117.38	120.53
2	A	386	3MR	C29-N30-C31	-2.04	115.97	117.92

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	386	3MR	C34-C33-N2-C1
2	A	386	3MR	C38-C33-N2-C1
2	A	386	3MR	C34-C33-N2-C3
2	A	386	3MR	C38-C33-N2-C3
2	A	386	3MR	C3-C5-C6-C7

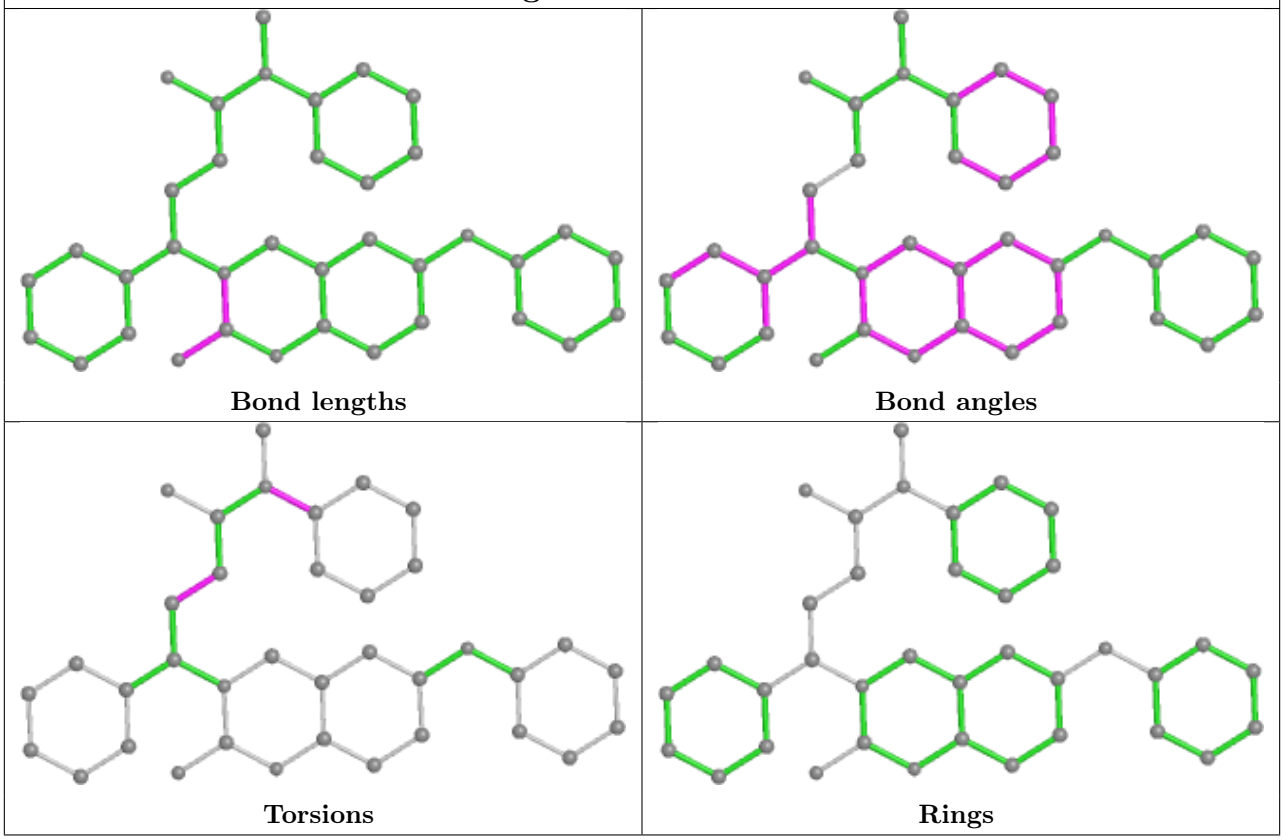
There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	386	3MR	6	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 3MR A 386



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.