Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 06:21 AM EST

PDB ID	:	1C1V
Title	:	RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF SERINE PROTEASES
Authors	:	Katz, B.A.; Luong, C.
Deposited on	:	1999-07-21
Resolution	:	1.98 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:

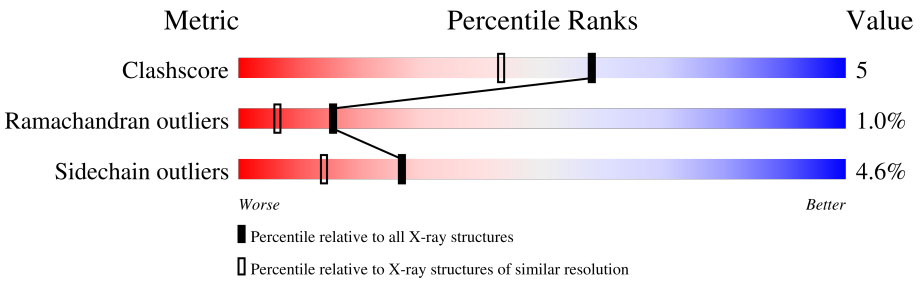
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.98 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	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)

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%

Mol	Chain	Length	Quality of chain
1	L	36	61% 31% 6% •
2	H	259	75% 19% • • •
3	I	11	64% 18% 18%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5639 atoms, of which 2918 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 Thrombin light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	L	36	565	177	278	48	61	1	0	0	0

- Molecule 2 is a protein called Thrombin heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	H	252	4052	1299	2013	360	366	14	0	0	0

- Molecule 3 is a protein called Hirudin-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	I	11	188	64	84	12	27	1	0	0	0

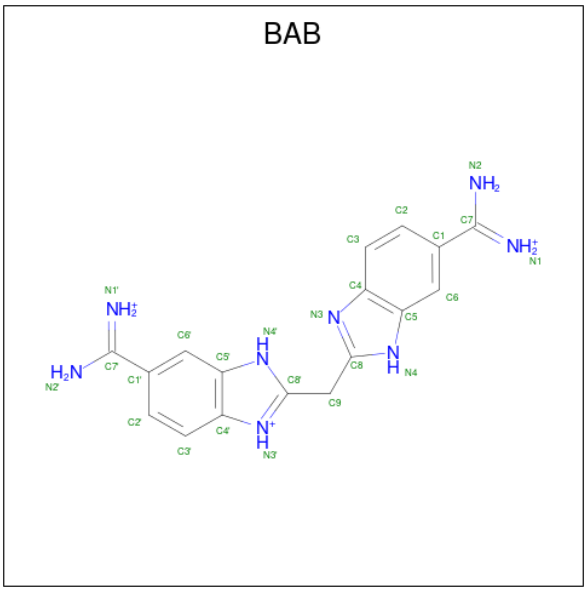
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	H	2	2	2	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
5	H	1	1	1	0	0

- Molecule 6 is BIS(5-AMIDINO-BENZIMIDAZOLYL)METHANE (three-letter code: BAB) (formula: $C_{17}H_{19}N_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
6	H	1	42	17	17	8	0	0

- Molecule 7 is water.

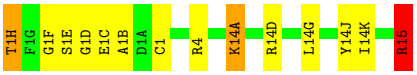
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	H	O		
7	L	35	105	70	35	0	1
			Total	H	O		
7	H	216	648	432	216	0	3
			Total	H	O		
7	I	12	36	24	12	0	1

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.

- Molecule 1: Thrombin light chain

Chain L:



- Molecule 2: Thrombin heavy chain

Chain H:

- Molecule 3: Hirudin-2

Chain I:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	72.47Å 72.09Å 73.11Å 90.00° 101.51° 90.00°	Depositor
Resolution (Å)	7.50 – 1.98 35.82 – 1.50	Depositor EDS
% Data completeness (in resolution range)	62.0 (7.50-1.98) 37.7 (35.82-1.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 1.50Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.204 , 0.248 0.217 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	0.5	Xtriage
Anisotropy	4.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.19 , 86.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.81	EDS
Total number of atoms	5639	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% 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: NA, ZN, TYS, BAB

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	L	1.50	0/290	1.39	0/384
2	H	1.41	6/2091 (0.3%)	1.71	50/2823 (1.8%)
3	I	1.54	0/88	1.30	0/115
All	All	1.43	6/2469 (0.2%)	1.66	50/3322 (1.5%)

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	L	0	2
2	H	0	10
All	All	0	12

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	223	GLU	CB-CG	5.84	1.63	1.52
2	H	213	TRP	CG-CD2	-5.55	1.34	1.43
2	H	29	TRP	CG-CD2	-5.42	1.34	1.43
2	H	96	TRP	CG-CD2	-5.20	1.34	1.43
2	H	60(D)	TRP	CG-CD2	-5.03	1.35	1.43
2	H	186	PHE	CA-CB	5.01	1.65	1.53

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	243	TRP	CD1-NE1-CE2	10.50	118.45	109.00
2	H	60(D)	TRP	CD1-NE1-CE2	9.94	117.94	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	141	TRP	CD1-NE1-CE2	9.85	117.86	109.00
2	H	221	TRP	CD1-NE1-CE2	9.51	117.56	109.00
2	H	60(D)	TRP	NE1-CE2-CZ2	9.02	140.32	130.40
2	H	96	TRP	CD1-NE1-CE2	8.85	116.97	109.00
2	H	213	TRP	NE1-CE2-CZ2	8.54	139.79	130.40
2	H	51	TRP	CD1-NE1-CE2	8.41	116.57	109.00
2	H	213	TRP	CD1-NE1-CE2	8.29	116.47	109.00
2	H	29	TRP	CD1-NE1-CE2	8.20	116.38	109.00
2	H	29	TRP	NE1-CE2-CZ2	8.07	139.27	130.40
2	H	60(D)	TRP	CG-CD1-NE1	-7.85	102.25	110.10
2	H	96	TRP	NE1-CE2-CZ2	7.65	138.81	130.40
2	H	51	TRP	NE1-CE2-CZ2	7.46	138.60	130.40
2	H	243	TRP	CG-CD1-NE1	-7.27	102.83	110.10
2	H	29	TRP	CG-CD1-NE1	-7.21	102.89	110.10
2	H	170	ARG	NE-CZ-NH2	-7.16	116.72	120.30
2	H	141	TRP	CG-CD1-NE1	-7.09	103.00	110.10
2	H	141	TRP	NE1-CE2-CZ2	6.95	138.04	130.40
2	H	243	TRP	NE1-CE2-CD2	-6.90	100.40	107.30
2	H	212	ARG	NE-CZ-NH2	-6.86	116.87	120.30
2	H	96	TRP	CG-CD1-NE1	-6.83	103.27	110.10
2	H	60(D)	TRP	NE1-CE2-CD2	-6.81	100.49	107.30
2	H	213	TRP	NE1-CE2-CD2	-6.72	100.58	107.30
2	H	221	TRP	NE1-CE2-CZ2	6.58	137.64	130.40
2	H	205	PHE	N-CA-C	-6.50	93.44	111.00
2	H	50	ARG	NE-CZ-NH2	-6.34	117.13	120.30
2	H	213	TRP	CG-CD1-NE1	-6.30	103.80	110.10
2	H	243	TRP	NE1-CE2-CZ2	6.23	137.25	130.40
2	H	221	TRP	CG-CD1-NE1	-6.22	103.88	110.10
2	H	141	TRP	NE1-CE2-CD2	-6.17	101.13	107.30
2	H	96	TRP	NE1-CE2-CD2	-5.95	101.35	107.30
2	H	119	HIS	CA-CB-CG	-5.84	103.67	113.60
2	H	67	ARG	NE-CZ-NH2	-5.83	117.39	120.30
2	H	51	TRP	NE1-CE2-CD2	-5.81	101.49	107.30
2	H	213	TRP	CG-CD2-CE3	-5.80	128.68	133.90
2	H	221	TRP	NE1-CE2-CD2	-5.78	101.52	107.30
2	H	29	TRP	CD1-CG-CD2	5.76	110.91	106.30
2	H	51	TRP	CG-CD1-NE1	-5.73	104.37	110.10
2	H	73	ARG	NE-CZ-NH2	-5.70	117.45	120.30
2	H	29	TRP	NE1-CE2-CD2	-5.70	101.60	107.30
2	H	29	TRP	CB-CG-CD2	-5.58	119.34	126.60
2	H	178	ARG	NE-CZ-NH2	-5.50	117.55	120.30
2	H	60(D)	TRP	CG-CD2-CE3	-5.49	128.96	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	137	ARG	NE-CZ-NH2	-5.38	117.61	120.30
2	H	76	TYR	CB-CG-CD2	-5.28	117.83	121.00
2	H	77(A)	ARG	NE-CZ-NH2	-5.25	117.67	120.30
2	H	159	VAL	N-CA-CB	-5.22	100.00	111.50
2	H	239	ARG	NE-CZ-NH2	-5.09	117.75	120.30
2	H	175	ASP	CB-CG-OD2	-5.07	113.74	118.30

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	178	ARG	Sidechain
2	H	180	ARG	Sidechain
2	H	193	ARG	Sidechain
2	H	212	ARG	Sidechain
2	H	227(A)	ARG	Sidechain
2	H	239	ARG	Sidechain
2	H	35	ARG	Sidechain
2	H	50	ARG	Sidechain
2	H	75	ARG	Sidechain
2	H	93	ARG	Sidechain
1	L	15	ARG	Sidechain
1	L	4	ARG	Sidechain

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	L	287	278	278	9	1
2	H	2039	2013	2010	15	2
3	I	104	84	81	2	0
4	H	2	0	0	0	0
5	H	1	0	0	0	0
6	H	25	17	19	0	0
7	H	216	432	0	0	3
7	I	12	24	0	0	0
7	L	35	70	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2721	2918	2388	23	3

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 5.

All (23) 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:L:1(D):GLY:HA3	1:L:1:CYS:SG	2.26	0.76
2:H:168:VAL:HB	2:H:187:CYS:SG	2.35	0.66
1:L:1(H):THR:HG23	2:H:48:SER:HB3	1.86	0.56
3:I:58:GLU:H	3:I:58:GLU:CD	2.10	0.55
2:H:31:VAL:CG1	2:H:66:VAL:HG13	2.38	0.53
1:L:1(F):GLY:HA2	2:H:241:LYS:HZ1	1.74	0.52
1:L:14(A):LYS:HB2	1:L:14(A):LYS:NZ	2.27	0.49
1:L:1(F):GLY:HA2	2:H:241:LYS:NZ	2.27	0.48
1:L:14(J):TYR:C	1:L:14(K):ILE:HG12	2.34	0.46
2:H:127:GLU:H	2:H:127:GLU:CD	2.18	0.46
2:H:17:VAL:O	2:H:194:GLY:HA2	2.15	0.46
2:H:181:ILE:HD12	2:H:233:PHE:CE2	2.51	0.45
2:H:206:VAL:HG12	2:H:215:GLN:HA	2.00	0.43
1:L:15:ARG:HD3	1:L:15:ARG:C	2.39	0.42
2:H:71:HIS:CD2	2:H:159:VAL:HG22	2.55	0.42
3:I:60:PRO:O	3:I:61:GLU:C	2.58	0.42
1:L:1(H):THR:N	1:L:1(D):GLY:O	2.44	0.42
1:L:14(G):LEU:HD22	1:L:14(G):LEU:N	2.35	0.42
2:H:36:LYS:O	2:H:38:GLN:HG2	2.20	0.42
2:H:85:LEU:HD22	2:H:106:MET:HB3	2.00	0.41
2:H:46:LEU:HD22	2:H:48:SER:O	2.20	0.41
2:H:206:VAL:HA	2:H:214:TYR:O	2.20	0.41
2:H:16:ILE:N	2:H:143:ASN:O	2.55	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:179:ILE:O	7:H:443:HOH:H2[4_546]	1.52	0.08
1:L:1(E):SER:OG	7:H:500:HOH:H2[4_556]	1.54	0.06
2:H:177:THR:O	7:H:550:HOH:H1[4_546]	1.58	0.02

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	L	34/36 (94%)	21 (62%)	12 (35%)	1 (3%)	4 0
2	H	248/259 (96%)	226 (91%)	22 (9%)	0	100 100
3	I	8/11 (73%)	4 (50%)	2 (25%)	2 (25%)	0 0
All	All	290/306 (95%)	251 (87%)	36 (12%)	3 (1%)	15 6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(B)	ALA
3	I	61	GLU
3	I	60	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	L	31/31 (100%)	26 (84%)	5 (16%)	2 0
2	H	220/225 (98%)	213 (97%)	7 (3%)	39 28
3	I	10/10 (100%)	10 (100%)	0	100 100
All	All	261/266 (98%)	249 (95%)	12 (5%)	27 14

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1(H)	THR
1	L	1(C)	GLU
1	L	14(A)	LYS
1	L	14(D)	ARG
1	L	15	ARG
2	H	46	LEU
2	H	50	ARG
2	H	94	TYR
2	H	119	HIS
2	H	159	VAL
2	H	210(B)	ASN
2	H	247	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	78	ASN
2	H	131	GLN
2	H	161	GLN
2	H	210(B)	ASN
3	I	65	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)

1 non-standard protein/DNA/RNA residue 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	$\#\|Z\| > 2$
3	TYS	I	63	3	15,16,17	1.37	2 (13%)	18,22,24	1.22	3 (16%)

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	TYS	I	63	3	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	63	TYS	OH-S	3.91	1.64	1.58
3	I	63	TYS	OH-CZ	-2.59	1.38	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	I	63	TYS	CG-CB-CA	-2.66	108.71	114.10
3	I	63	TYS	O3-S-OH	2.24	111.23	105.83
3	I	63	TYS	OH-S-O1	2.06	113.70	107.71

There are no chirality outliers.

There are no torsion outliers.

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)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
6	BAB	H	410	4	24,28,28	2.88	13 (54%)	22,41,41	1.86	6 (27%)

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
6	BAB	H	410	4	-	1/12/12/12	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	410	BAB	C9-C8	6.90	1.60	1.50
6	H	410	BAB	C1-C7	-5.38	1.37	1.47
6	H	410	BAB	C1'-C7'	-4.00	1.40	1.47
6	H	410	BAB	C6-C5	-3.98	1.35	1.41
6	H	410	BAB	C6'-C1'	3.62	1.43	1.37
6	H	410	BAB	C9-C8'	3.00	1.54	1.50
6	H	410	BAB	C3'-C4'	-2.93	1.36	1.41
6	H	410	BAB	C4'-N3'	-2.79	1.29	1.38
6	H	410	BAB	C3-C2	2.75	1.42	1.36
6	H	410	BAB	C5-N4	-2.43	1.31	1.38
6	H	410	BAB	C5-C4	-2.42	1.34	1.42
6	H	410	BAB	C2'-C1'	2.22	1.43	1.39
6	H	410	BAB	C4-N3	-2.15	1.31	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	410	BAB	C2'-C3'-C4'	-3.91	115.92	120.84
6	H	410	BAB	C2-C3-C4	-3.34	116.63	120.84
6	H	410	BAB	C9-C8'-N4'	3.33	131.86	122.54
6	H	410	BAB	N3-C8-N4	-2.26	108.99	115.89
6	H	410	BAB	C6-C1-C7	-2.23	116.53	120.29
6	H	410	BAB	C9-C8'-N3'	-2.17	116.47	122.54

There are no chirality outliers.

All (1) torsion outliers are listed below:

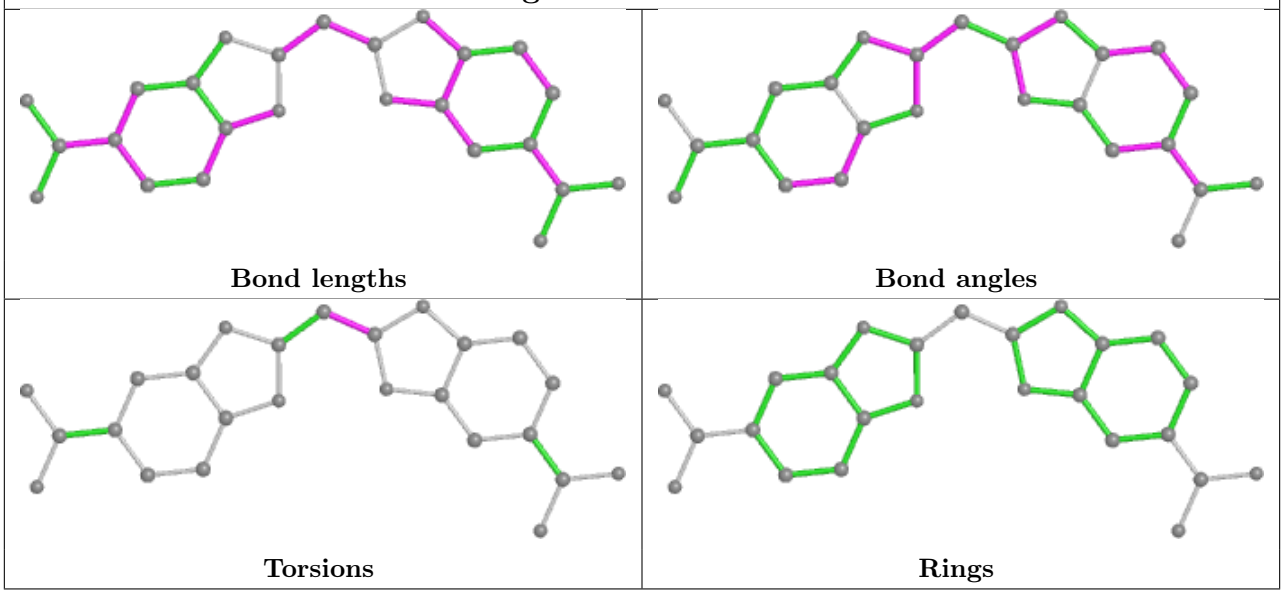
Mol	Chain	Res	Type	Atoms
6	H	410	BAB	N4-C8-C9-C8'

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 BAB H 410



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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

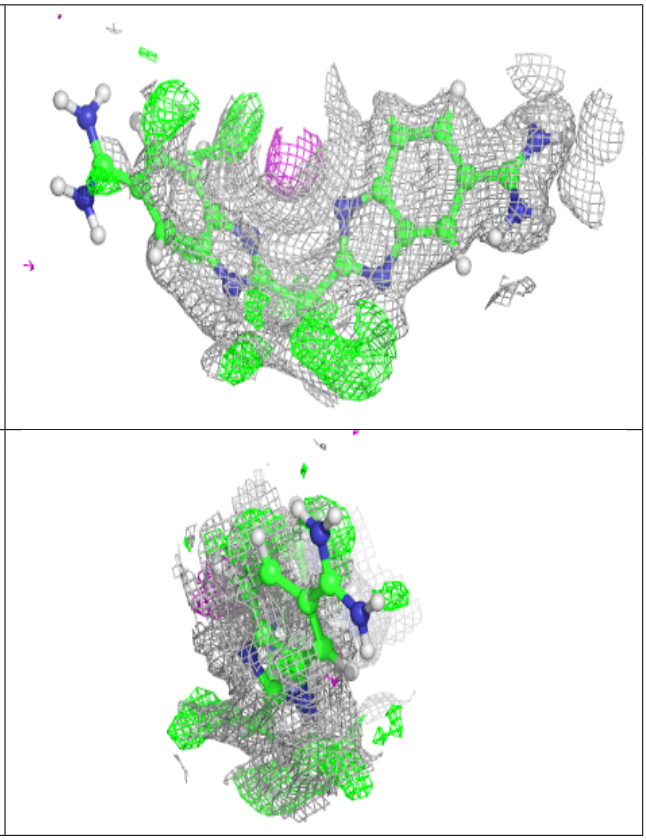
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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 BAB H 410:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.