Full wwPDB X-ray Structure Validation Report (i)

Aug 9, 2020 – 03:37 PM BST

PDB ID	:	1D3T
Title	:	CRYSTAL STRUCTURE OF HUMAN ALPHA THROMBIN IN COMPLEX WITH BENZO[B]THIOPHENE INHIBITOR 1
Authors	:	Chirgadze, N.Y.
Deposited on	:	1999-09-30
Resolution	:	3.00 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:

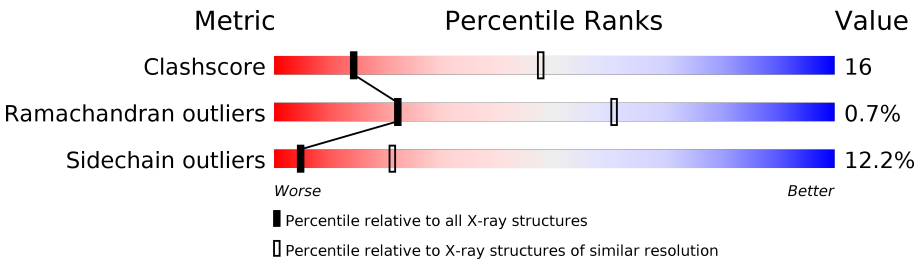
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 3.00 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	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	36	50% 25% • 22%
2	B	259	61% 31% • •
3	H	12	42% 33% 25%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2419 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 ALPHA-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	28	231	145	37	48	1	0	0	0

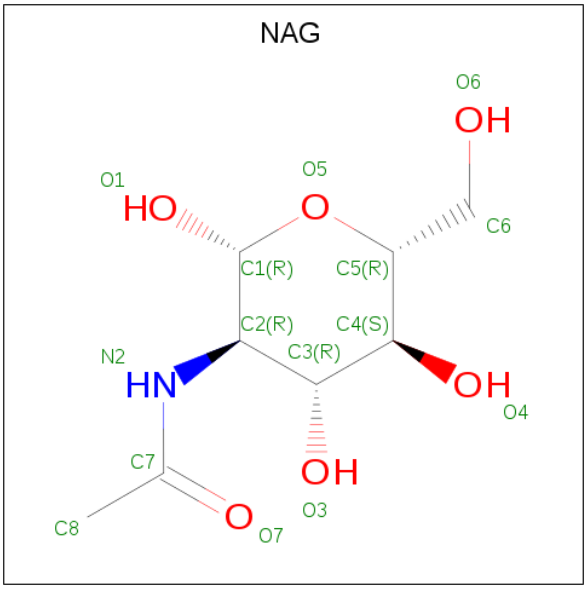
- Molecule 2 is a protein called ALPHA-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	250	2025	1292	358	361	14	3	0	0

- Molecule 3 is a protein called HIRUGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	12	108	66	13	28	1	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

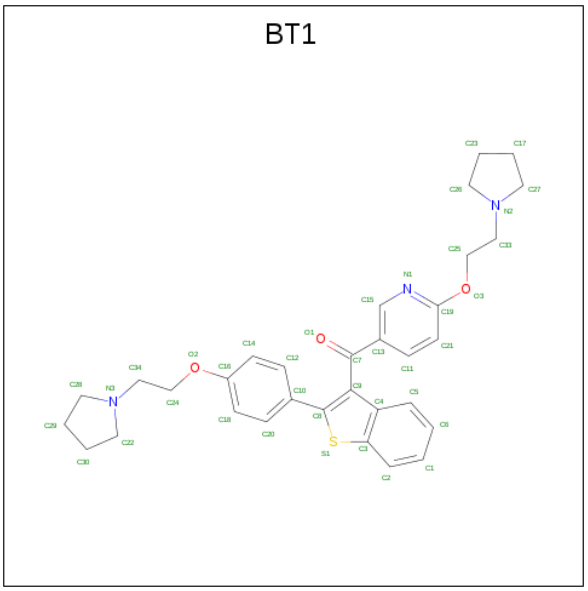


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	B	1	14	8	1	5	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
5	B	2	2	2	0	0

- Molecule 6 is {2-[4-(2-PYRROLIDIN-1-YL-ETHOXY)-PHENYL]-BENZO[B]THIOPHEN-3-YL}-[4-(2-PYRROLIDIN-1-YL-ETHOXY)-PHENYL]-METHANONE (three-letter code: BT1) (formula: $C_{32}H_{35}N_3O_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
6	B	1	39	32	3	3	1	0	0

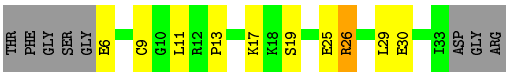
3 Residue-property plots (i)

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.

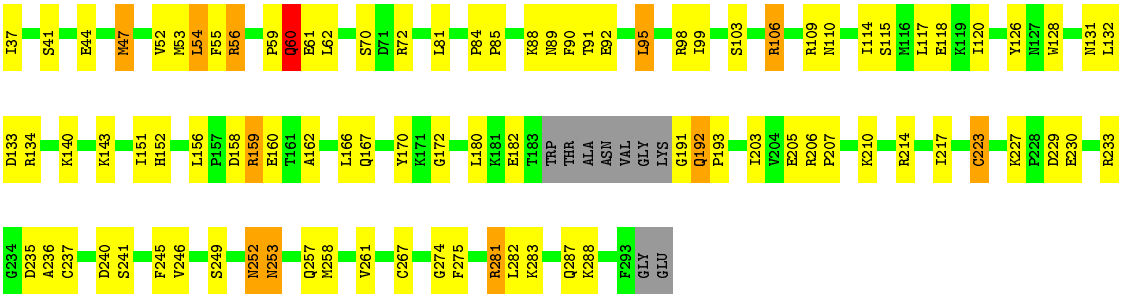
- Molecule 1: ALPHA-THROMBIN

Chain A:



- Molecule 2: ALPHA-THROMBIN

Chain B:



- Molecule 3: HIRUGEN

Chain H:

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	71.14Å 71.85Å 72.96Å 90.00° 100.50° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00	Depositor
% Data completeness (in resolution range)	78.6 (20.00-3.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 98.0	Depositor
R, R_{free}	0.172 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2419	wwPDB-VP
Average B, all atoms (Å^2)	19.0	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: NA, BT1, NAG, TYS

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	0.51	0/233	0.63	0/310
2	B	0.47	0/2077	0.70	0/2806
3	H	0.85	0/92	0.91	0/120
All	All	0.49	0/2402	0.70	0/3236

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	231	0	228	7	0
2	B	2025	0	2000	64	0
3	H	108	0	85	5	0
4	B	14	0	13	0	0
5	B	2	0	0	0	0
6	B	39	0	35	2	0
All	All	2419	0	2361	74	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 16.

All (74) 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)
2:B:281:ARG:HH11	2:B:281:ARG:HG3	1.42	0.83
2:B:95:LEU:HD22	2:B:95:LEU:H	1.45	0.79
3:H:311:GLN:HG2	3:H:311:GLN:OXT	1.85	0.76
2:B:180:LEU:HD21	2:B:193:PRO:HB3	1.68	0.75
2:B:95:LEU:HD22	2:B:95:LEU:N	2.05	0.72
2:B:281:ARG:HH11	2:B:281:ARG:CG	2.03	0.71
2:B:237:CYS:O	2:B:240:ASP:HB2	1.91	0.69
2:B:118:GLU:OE2	2:B:140:LYS:HD3	1.93	0.68
2:B:106:ARG:HG2	3:H:303:GLU:OE1	1.95	0.67
2:B:131:ASN:HA	6:B:400:BT1:H231	1.78	0.65
2:B:182:GLU:HB2	2:B:267:CYS:HB2	1.80	0.63
1:A:6:GLU:HB2	1:A:9:CYS:HB3	1.84	0.60
2:B:99:ILE:HG22	2:B:151:ILE:HG12	1.84	0.59
2:B:160:GLU:H	2:B:160:GLU:CD	2.05	0.59
2:B:98:ARG:HG2	2:B:114:ILE:HG12	1.86	0.58
1:A:25:GLU:O	1:A:29:LEU:HD23	2.04	0.57
2:B:109:ARG:O	2:B:110:ASN:HB2	2.04	0.57
2:B:166:LEU:HD23	2:B:203:ILE:HD13	1.87	0.56
2:B:88:LYS:HD2	2:B:90:PHE:CE2	2.40	0.56
2:B:160:GLU:N	2:B:160:GLU:CD	2.61	0.54
2:B:249:SER:HB3	2:B:252:ASN:HD21	1.73	0.54
2:B:223:CYS:HA	2:B:274:GLY:O	2.09	0.53
2:B:37:ILE:N	2:B:240:ASP:OD1	2.42	0.53
2:B:126:TYR:CZ	2:B:128:TRP:HB3	2.44	0.52
2:B:81:LEU:HD23	2:B:120:ILE:HG21	1.91	0.52
2:B:88:LYS:HD2	2:B:90:PHE:HE2	1.74	0.52
3:H:308:GLU:CD	3:H:308:GLU:H	2.12	0.52
1:A:13:PRO:HA	1:A:17:LYS:HG3	1.91	0.52
2:B:162:ALA:HA	2:B:258:MET:CE	2.41	0.51
2:B:281:ARG:NH1	2:B:281:ARG:CG	2.68	0.51
2:B:95:LEU:N	2:B:95:LEU:CD2	2.74	0.50
2:B:252:ASN:HD22	2:B:252:ASN:C	2.15	0.50
2:B:81:LEU:HD23	2:B:120:ILE:CG2	2.41	0.49
1:A:26:ARG:HH21	1:A:26:ARG:HG2	1.76	0.49
2:B:205:GLU:CD	2:B:205:GLU:H	2.16	0.48
2:B:249:SER:HB3	2:B:252:ASN:ND2	2.28	0.48
2:B:191:GLY:C	2:B:192:GLN:HE21	2.17	0.48
2:B:241:SER:HA	2:B:261:VAL:CG1	2.44	0.48
2:B:166:LEU:HD23	2:B:203:ILE:CD1	2.44	0.47
2:B:59:PRO:O	2:B:61:GLU:HG2	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ARG:O	1:A:30:GLU:HG3	2.15	0.47
2:B:283:LYS:HE2	2:B:287:GLN:HE22	1.80	0.46
2:B:84:PRO:HB2	2:B:85:PRO:HD3	1.97	0.46
2:B:55:PHE:HE1	3:H:302:PHE:CD2	2.33	0.46
2:B:56:ARG:O	2:B:60:GLN:HA	2.16	0.46
2:B:72:ARG:NH2	2:B:118:GLU:OE2	2.49	0.45
2:B:223:CYS:HB3	2:B:275:PHE:CE1	2.52	0.45
1:A:11:LEU:O	2:B:152:HIS:CD2	2.70	0.45
2:B:126:TYR:CE1	2:B:132:LEU:HD22	2.52	0.44
2:B:131:ASN:O	2:B:132:LEU:HB2	2.17	0.44
2:B:159:ARG:HB3	2:B:159:ARG:HH11	1.81	0.44
2:B:206:ARG:N	2:B:207:PRO:CD	2.81	0.44
2:B:54:LEU:HD22	2:B:54:LEU:HA	1.81	0.43
2:B:167:GLN:O	2:B:170:TYR:HB2	2.18	0.43
2:B:235:ASP:OD1	2:B:236:ALA:N	2.51	0.43
2:B:128:TRP:HA	2:B:132:LEU:HD23	1.99	0.43
2:B:227:LYS:HB2	2:B:230:GLU:HG3	2.00	0.42
2:B:134:ARG:HG2	2:B:282:LEU:HD21	2.00	0.42
1:A:29:LEU:N	1:A:29:LEU:HD22	2.34	0.42
2:B:252:ASN:HD22	2:B:253:ASN:N	2.18	0.42
2:B:95:LEU:CD2	2:B:117:LEU:HD12	2.50	0.42
2:B:172:GLY:HA3	2:B:245:PHE:CZ	2.54	0.42
2:B:52:VAL:HG12	2:B:53:MET:N	2.35	0.42
2:B:133:ASP:O	2:B:134:ARG:HB2	2.20	0.41
2:B:246:VAL:HG12	2:B:257:GLN:HA	2.03	0.41
2:B:241:SER:HA	2:B:261:VAL:HB	2.03	0.41
2:B:126:TYR:HE1	2:B:132:LEU:HD22	1.85	0.41
2:B:192:GLN:CA	2:B:192:GLN:HE21	2.33	0.41
6:B:400:BT1:H252	6:B:400:BT1:H271	1.50	0.41
2:B:53:MET:HG3	2:B:62:LEU:CD1	2.51	0.41
2:B:92:GLU:HG2	2:B:118:GLU:O	2.21	0.41
3:H:306:PRO:HG2	3:H:309:TYS:HE1	2.02	0.41
2:B:205:GLU:HB3	2:B:207:PRO:HD2	2.03	0.41
2:B:44:GLU:O	2:B:47:MET:HB2	2.21	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	26/36 (72%)	24 (92%)	2 (8%)	0	100	100
2	B	246/259 (95%)	221 (90%)	23 (9%)	2 (1%)	19	57
3	H	9/12 (75%)	8 (89%)	1 (11%)	0	100	100
All	All	281/307 (92%)	253 (90%)	26 (9%)	2 (1%)	22	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	89	ASN
2	B	60	GLN

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	26/31 (84%)	24 (92%)	2 (8%)	13	42
2	B	219/225 (97%)	193 (88%)	26 (12%)	5	22
3	H	10/10 (100%)	7 (70%)	3 (30%)	0	1
All	All	255/266 (96%)	224 (88%)	31 (12%)	5	21

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	26	ARG
2	B	41	SER
2	B	47	MET
2	B	54	LEU
2	B	56	ARG
2	B	60	GLN
2	B	70	SER
2	B	91	THR
2	B	95	LEU
2	B	103	SER
2	B	106	ARG
2	B	115	SER
2	B	143	LYS
2	B	156	LEU
2	B	158	ASP
2	B	159	ARG
2	B	192	GLN
2	B	210	LYS
2	B	214	ARG
2	B	217	ILE
2	B	223	CYS
2	B	229	ASP
2	B	233	ARG
2	B	252	ASN
2	B	253	ASN
2	B	281	ARG
2	B	288	LYS
3	H	304	GLU
3	H	308	GLU
3	H	311	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	167	GLN
2	B	192	GLN
2	B	252	ASN
2	B	287	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	H	309	3	15,16,17	4.60	13 (86%)	18,22,24	2.03	6 (33%)

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	H	309	3	-	0/10/11/13	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	309	TYS	CE1-CZ	7.47	1.53	1.38
3	H	309	TYS	CE2-CD2	7.39	1.52	1.38
3	H	309	TYS	CE1-CD1	6.91	1.51	1.38
3	H	309	TYS	CD2-CG	6.21	1.52	1.38
3	H	309	TYS	CE2-CZ	5.05	1.48	1.38
3	H	309	TYS	CD1-CG	4.50	1.48	1.38
3	H	309	TYS	OH-S	-4.04	1.52	1.58
3	H	309	TYS	O1-S	3.59	1.60	1.45
3	H	309	TYS	CB-CG	-3.44	1.43	1.51
3	H	309	TYS	OH-CZ	-3.21	1.37	1.42
3	H	309	TYS	O2-S	3.20	1.59	1.45
3	H	309	TYS	O3-S	2.49	1.65	1.50
3	H	309	TYS	CB-CA	2.16	1.58	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	309	TYS	O3-S-OH	4.25	116.06	105.83
3	H	309	TYS	CB-CG-CD1	-3.42	114.12	120.91
3	H	309	TYS	CE1-CD1-CG	-3.28	116.52	121.03
3	H	309	TYS	CD2-CG-CD1	2.79	122.56	118.17
3	H	309	TYS	CB-CA-C	-2.46	106.86	111.47
3	H	309	TYS	CD1-CE1-CZ	2.41	122.69	119.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	309	TYS	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
4	NAG	B	500	2	14,14,15	1.40	2 (14%)	17,19,21	1.59	1 (5%)
6	BT1	B	400	-	39,44,44	5.07	24 (61%)	49,60,60	3.01	16 (32%)

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
4	NAG	B	500	2	-	1/6/23/26	0/1/1/1
6	BT1	B	400	-	-	6/21/38/38	0/6/6/6

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	400	BT1	C15-C13	9.99	1.55	1.39
6	B	400	BT1	C6-C5	9.68	1.58	1.36
6	B	400	BT1	C11-C13	9.26	1.55	1.39
6	B	400	BT1	C19-N1	9.08	1.47	1.32
6	B	400	BT1	C21-C11	8.85	1.54	1.38
6	B	400	BT1	C20-C18	8.77	1.54	1.38
6	B	400	BT1	C1-C2	8.56	1.56	1.36
6	B	400	BT1	C18-C16	7.76	1.54	1.38
6	B	400	BT1	C14-C12	7.42	1.52	1.38
6	B	400	BT1	C14-C16	7.33	1.53	1.38
6	B	400	BT1	C9-C7	-6.64	1.42	1.50
6	B	400	BT1	C21-C19	6.48	1.54	1.39
6	B	400	BT1	C6-C1	5.67	1.53	1.38
6	B	400	BT1	C20-C10	4.49	1.48	1.39
6	B	400	BT1	C10-C8	4.39	1.52	1.48
6	B	400	BT1	C12-C10	3.97	1.47	1.39
6	B	400	BT1	O3-C19	3.24	1.43	1.36
6	B	400	BT1	C27-N2	2.76	1.52	1.47
6	B	400	BT1	C15-N1	2.73	1.40	1.34
6	B	400	BT1	C2-C3	2.67	1.48	1.40
6	B	400	BT1	C26-N2	2.44	1.52	1.47
6	B	400	BT1	C28-N3	2.42	1.52	1.47
6	B	400	BT1	C13-C7	2.37	1.53	1.49
4	B	500	NAG	O4-C4	2.36	1.48	1.43
4	B	500	NAG	O3-C3	2.32	1.48	1.43
6	B	400	BT1	C22-N3	2.04	1.51	1.47

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	400	BT1	C28-N3-C22	10.22	113.99	104.04
6	B	400	BT1	C15-N1-C19	9.48	124.97	116.63
6	B	400	BT1	C9-C7-C13	6.49	128.59	119.53
6	B	400	BT1	C27-N2-C26	5.95	109.83	104.04
6	B	400	BT1	C21-C19-N1	-5.40	116.81	124.87

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	500	NAG	C1-O5-C5	5.28	119.35	112.19
6	B	400	BT1	O1-C7-C9	-4.90	113.80	119.49
6	B	400	BT1	C33-N2-C26	-3.99	102.20	113.29
6	B	400	BT1	O3-C19-N1	3.57	125.12	119.27
6	B	400	BT1	C34-N3-C22	2.99	121.59	113.29
6	B	400	BT1	O3-C25-C33	2.96	114.97	107.68
6	B	400	BT1	C34-N3-C28	2.52	120.30	113.29
6	B	400	BT1	O2-C24-C34	2.43	113.67	107.68
6	B	400	BT1	C6-C1-C2	-2.40	117.07	120.44
6	B	400	BT1	C25-O3-C19	-2.29	113.99	117.59
6	B	400	BT1	C5-C4-C9	-2.20	131.12	135.49
6	B	400	BT1	C11-C21-C19	2.03	120.34	117.72

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	400	BT1	C25-C33-N2-C27
6	B	400	BT1	O3-C25-C33-N2
6	B	400	BT1	N1-C19-O3-C25
6	B	400	BT1	C24-C34-N3-C22
6	B	400	BT1	O2-C24-C34-N3
6	B	400	BT1	C21-C19-O3-C25
4	B	500	NAG	C3-C2-N2-C7

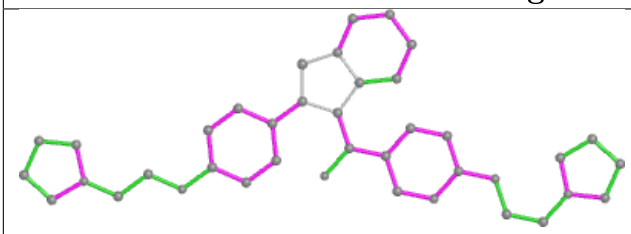
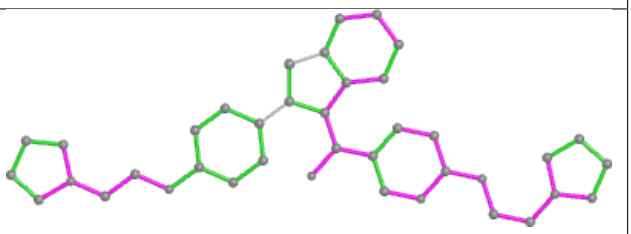
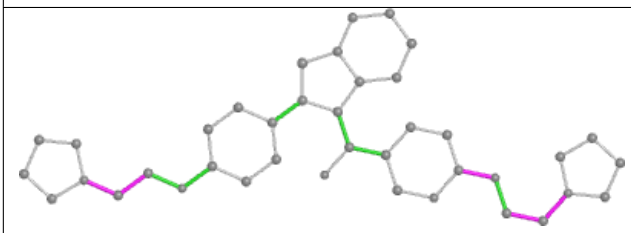
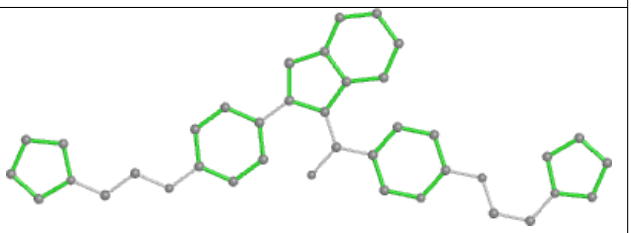
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	400	BT1	2	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 BT1 B 400	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.