



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:22 PM GMT

PDB ID : 1TB6
Title : 2.5A Crystal Structure of the Antithrombin-Thrombin-Heparin Ternary Complex
Authors : Li, W.; Johnson, D.J.; Esmon, C.T.; Huntington, J.A.
Deposited on : 2004-05-19
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

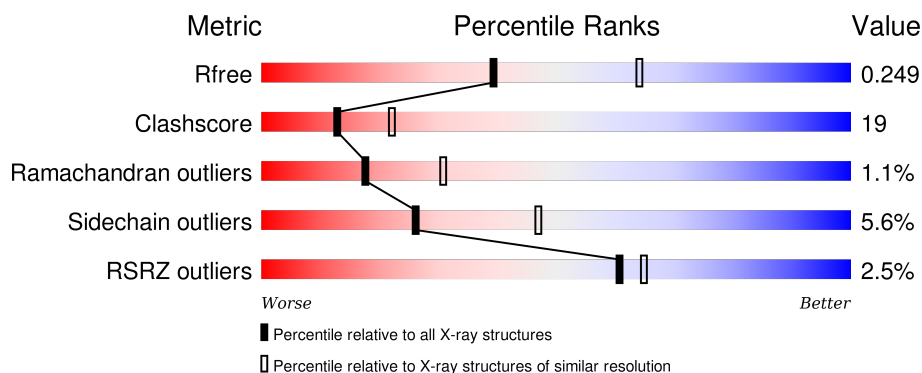
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	L	49	<div> <div>6%</div> <div> <div></div> <div>55%</div> <div>29%</div> <div>•</div> <div>12%</div> </div> </div>
2	H	259	<div> <div>2%</div> <div> <div></div> <div>68%</div> <div>30%</div> <div>•</div> </div> </div>
3	I	432	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>•</div> <div>5%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MPD	H	781	-	-	-	X
5	MPD	H	782	-	-	X	X
5	MPD	H	783	-	-	-	X
5	MPD	H	784	-	-	-	X
5	MPD	I	864	-	-	-	X
5	MPD	I	865	-	-	-	X
5	MPD	I	867	-	-	-	X
6	GU6	I	434	X	-	-	-
6	GU1	I	445	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6324 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 thrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	43	Total	C	N	O	S	0	0	0
			343	219	52	71	1			

- Molecule 2 is a protein called thrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	259	Total	C	N	O	S	0	0	0
			2070	1324	362	370	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	195	ALA	SER	ENGINEERED	UNP P00734

- Molecule 3 is a protein called Antithrombin-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	412	Total	C	N	O	S	0	0	0
			3271	2091	553	607	20			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	137	ALA	SER	ENGINEERED	UNP P01008
I	317	CYS	VAL	ENGINEERED	UNP P01008
I	401	CYS	THR	ENGINEERED	UNP P01008

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	H	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).

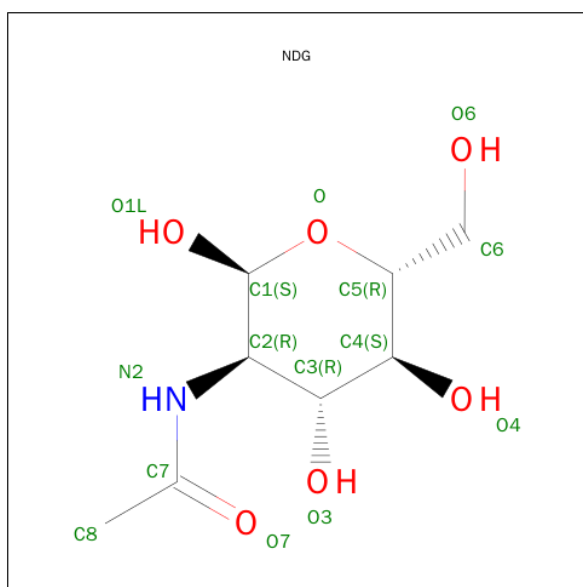


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			8	6	2		
5	H	1	Total	C	O	0	0
			8	6	2		
5	H	1	Total	C	O	0	0
			8	6	2		
5	H	1	Total	C	O	0	0
			8	6	2		
5	I	1	Total	C	O	0	0
			8	6	2		
5	I	1	Total	C	O	0	0
			8	6	2		
5	I	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is a polymer of unknown type called SUGAR (16-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	I	16	Total	C	O	S	0	0
			278	127	134	17		

- Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	I	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	I	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 9 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	I	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	L	3	Total	O	0	0
			3	3		
10	H	47	Total	O	0	0
			47	47		
10	I	96	Total	O	0	0
			96	96		

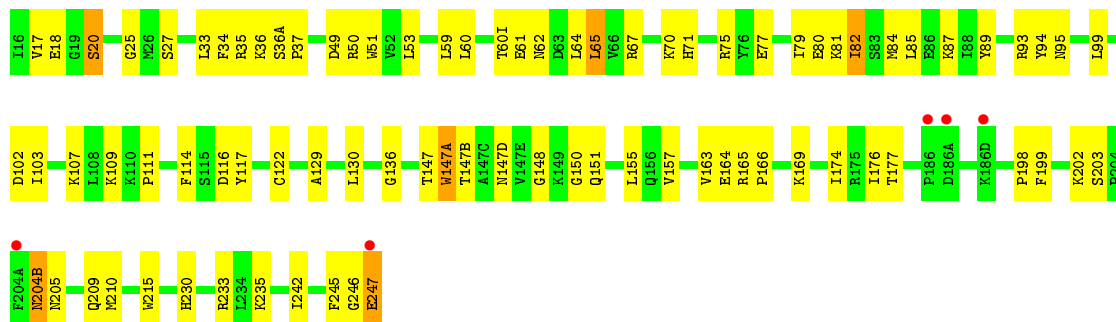
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

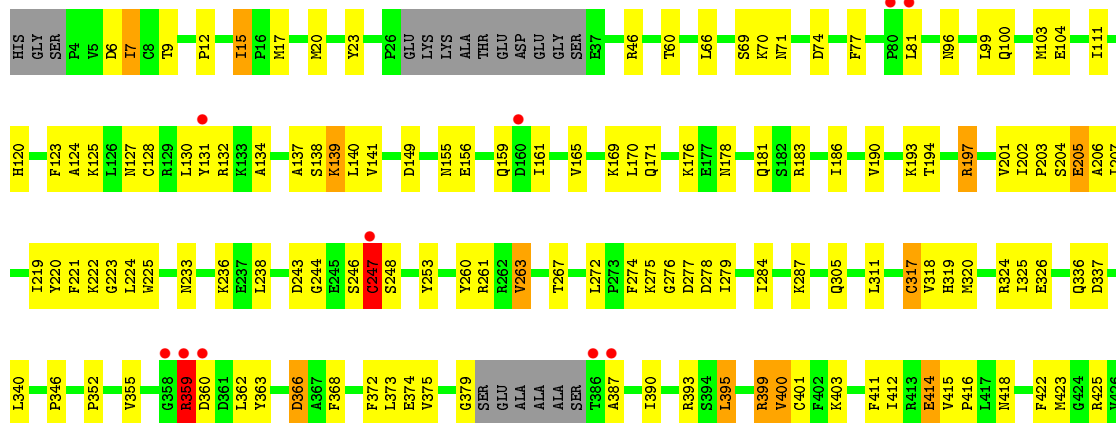
• Molecule 1: thrombin



• Molecule 2: thrombin



• Molecule 3: Antithrombin-III



K427
I428
P429
C430
V431
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.41Å 88.40Å 117.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.46 – 2.50 37.46 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.4 (37.46-2.50) 99.4 (37.46-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.51Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.208 , 0.245 0.215 , 0.249	Depositor DCC
R_{free} test set	1301 reflections (4.03%)	DCC
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.4	EDS
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 32246 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6324	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 3.43% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MPD, BMA, NAG, NDG, GU3, GU2, GU1, GU0, GU6, GU5, GU4, GU9, GU8, FUC, MAN

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	0.34	0/350	0.60	0/470
2	H	0.36	0/2125	0.67	1/2876 (0.0%)
3	I	0.40	0/3337	0.67	1/4508 (0.0%)
All	All	0.38	0/5812	0.67	2/7854 (0.0%)

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
6	I	4	0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	317	CYS	CA-CB-SG	6.18	125.12	114.00
2	H	247	GLU	N-CA-C	5.56	126.00	111.00

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	I	434	GU6	C4,C3,C5,C2

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	L	343	0	315	26	0
2	H	2070	0	2022	77	0
3	I	3271	0	3248	116	1
4	H	38	0	34	4	0
5	H	32	0	56	9	0
5	I	32	0	56	5	0
6	I	278	0	191	32	0
7	I	14	0	13	1	0
8	I	61	0	52	2	0
9	I	39	0	34	0	0
10	H	47	0	0	3	0
10	I	96	0	0	5	0
10	L	3	0	0	0	0
All	All	6324	0	6021	234	1

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 19.

The worst 5 of 234 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)
3:I:324:ARG:HH12	3:I:374:GLU:HG3	1.21	1.02
3:I:7:ILE:HD13	3:I:7:ILE:H	1.25	0.98
1:L:1(I):ARG:HG2	1:L:1(I):ARG:HH11	1.39	0.85
2:H:71:HIS:HB2	5:H:782:MPD:H11	1.59	0.84
3:I:355:VAL:HG21	3:I:360:ASP:HB3	1.59	0.83

All (1) 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)
3:I:207:ILE:O	3:I:399:ARG:NH2[4_455]	2.19	0.01

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	41/49 (84%)	35 (85%)	6 (15%)	0	100	100
2	H	257/259 (99%)	237 (92%)	20 (8%)	0	100	100
3	I	406/432 (94%)	378 (93%)	20 (5%)	8 (2%)	9	15
All	All	704/740 (95%)	650 (92%)	46 (6%)	8 (1%)	17	31

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	247	CYS
3	I	359	ARG
3	I	387	ALA
3	I	205	GLU
3	I	111	ILE

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	36/43 (84%)	32 (89%)	4 (11%)	8	14
2	H	218/224 (97%)	209 (96%)	9 (4%)	37	63
3	I	358/382 (94%)	337 (94%)	21 (6%)	24	44
All	All	612/649 (94%)	578 (94%)	34 (6%)	26	47

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	69	SER
3	I	171	GLN
3	I	414	GLU
3	I	139	LYS
2	H	60(I)	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	65	HIS
3	I	120	HIS
3	I	319	HIS
3	I	55	ASN
3	I	305	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

27 carbohydrates 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	$\# Z > 2$
4	NDG	H	778	2,4	14,14,15	0.64	0	15,19,21	1.30	3 (20%)
4	NAG	H	779	4	14,14,15	0.60	0	15,19,21	0.63	0
4	FUC	H	780	4	10,10,11	0.63	0	14,14,16	0.84	1 (7%)
6	GU4	I	433	6	27,28,28	1.89	4 (14%)	37,45,45	1.13	4 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GU6	I	434	6	22,23,24	3.36	9 (40%)	25,36,38	2.84	8 (32%)
6	GU0	I	435	6	22,23,24	1.88	4 (18%)	25,36,38	0.83	1 (4%)
6	GU5	I	436	6	16,17,18	1.31	1 (6%)	19,24,26	0.98	1 (5%)
6	GU8	I	437	6	13,14,15	0.52	0	16,18,20	0.90	1 (6%)
6	GU9	I	438	6	13,14,15	0.62	0	16,18,20	1.09	1 (6%)
6	GU8	I	439	6	13,14,15	0.53	0	16,18,20	0.90	1 (6%)
6	GU9	I	440	6	13,14,15	0.56	0	16,18,20	0.77	0
6	GU8	I	441	6	13,14,15	0.54	0	16,18,20	0.71	0
6	GU9	I	442	6	13,14,15	0.56	0	16,18,20	0.80	0
6	GU8	I	443	6	13,14,15	0.52	0	16,18,20	0.92	0
6	GU5	I	444	6	16,17,18	1.32	1 (6%)	19,24,26	0.72	0
6	GU1	I	445	6	10,14,15	0.54	0	12,19,21	0.89	0
6	GU6	I	446	6	22,23,24	1.89	4 (18%)	25,36,38	0.99	2 (8%)
6	GU2	I	447	6	10,14,15	0.57	0	12,19,21	0.61	0
6	GU3	I	448	6	21,21,22	1.61	3 (14%)	26,31,33	1.07	1 (3%)
8	NAG	I	841	8,3	14,14,15	0.63	0	15,19,21	0.71	1 (6%)
8	NAG	I	842	8	14,14,15	0.60	0	15,19,21	0.89	1 (6%)
8	BMA	I	843	8	11,11,12	0.66	0	14,15,17	1.15	2 (14%)
8	MAN	I	844	8	11,11,12	0.61	0	14,15,17	0.68	1 (7%)
8	MAN	I	845	8	11,11,12	0.61	0	14,15,17	0.58	0
9	NAG	I	861	9,3	14,14,15	0.54	0	15,19,21	0.78	1 (6%)
9	NAG	I	862	9	14,14,15	0.66	0	15,19,21	0.72	1 (6%)
9	BMA	I	863	9	11,11,12	0.60	0	14,15,17	0.52	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
4	NDG	H	778	2,4	-	0/6/23/26	0/1/1/1
4	NAG	H	779	4	-	0/6/23/26	0/1/1/1
4	FUC	H	780	4	-	0/0/17/20	0/1/1/1
6	GU4	I	433	6	-	0/21/41/41	0/1/1/1
6	GU6	I	434	6	4/4/7/8	0/16/32/36	0/1/1/1
6	GU0	I	435	6	-	0/16/32/36	0/1/1/1
6	GU5	I	436	6	-	0/10/26/30	0/1/1/1
6	GU8	I	437	6	-	0/7/23/27	0/1/1/1
6	GU9	I	438	6	-	0/7/23/27	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GU8	I	439	6	-	0/7/23/27	0/1/1/1
6	GU9	I	440	6	-	0/7/23/27	0/1/1/1
6	GU8	I	441	6	-	0/7/23/27	0/1/1/1
6	GU9	I	442	6	-	0/7/23/27	0/1/1/1
6	GU8	I	443	6	-	0/7/23/27	0/1/1/1
6	GU5	I	444	6	-	0/10/26/30	0/1/1/1
6	GU1	I	445	6	-	0/4/24/28	0/1/1/1
6	GU6	I	446	6	-	0/16/32/36	0/1/1/1
6	GU2	I	447	6	-	0/4/24/28	1/1/1/1
6	GU3	I	448	6	-	0/15/31/35	0/1/1/1
8	NAG	I	841	8,3	-	0/6/23/26	0/1/1/1
8	NAG	I	842	8	-	0/6/23/26	0/1/1/1
8	BMA	I	843	8	-	0/2/19/22	0/1/1/1
8	MAN	I	844	8	-	0/2/19/22	1/1/1/1
8	MAN	I	845	8	-	0/2/19/22	1/1/1/1
9	NAG	I	861	9,3	-	0/6/23/26	0/1/1/1
9	NAG	I	862	9	-	0/6/23/26	0/1/1/1
9	BMA	I	863	9	-	0/2/19/22	0/1/1/1

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	I	434	GU6	O3-C3	-7.19	1.36	1.47
6	I	434	GU6	C4-C3	-6.61	1.39	1.52
6	I	434	GU6	C2-C3	-4.87	1.39	1.52
6	I	434	GU6	O2-C2	-4.72	1.36	1.46
6	I	434	GU6	C4-C5	-4.68	1.39	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	448	GU3	C2-O2-S2	-3.98	111.20	118.77
6	I	433	GU4	C2-O2-S2	-3.41	112.27	118.77
6	I	438	GU9	C4-C5-C6	-3.31	106.01	112.59
6	I	434	GU6	C2-O2-S2	-3.20	112.67	118.77
4	H	778	NDG	C4-C3-C2	-2.98	106.59	111.23

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	I	434	GU6	C4
6	I	434	GU6	C3

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Mol	Chain	Res	Type	Atom
6	I	434	GU6	C5
6	I	434	GU6	C2

There are no torsion outliers.

All (3) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	I	844	MAN	C1-C2-C3-C4-C5-O5
6	I	447	GU2	C1-C2-C3-C4-C5-O5
8	I	845	MAN	C1-C2-C3-C4-C5-O5

17 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	778	NDG	4	0
4	H	780	FUC	2	0
6	I	434	GU6	1	0
6	I	436	GU5	2	0
6	I	437	GU8	4	0
6	I	438	GU9	4	0
6	I	439	GU8	5	0
6	I	440	GU9	4	0
6	I	441	GU8	5	0
6	I	442	GU9	3	0
6	I	443	GU8	2	0
6	I	444	GU5	6	0
6	I	445	GU1	7	0
6	I	446	GU6	2	0
6	I	447	GU2	2	0
6	I	448	GU3	1	0
8	I	841	NAG	2	0

5.6 Ligand geometry

9 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
5	MPD	H	781	-	6,7,7	0.62	0	7,10,10	0.43	0
5	MPD	H	782	-	6,7,7	0.65	0	7,10,10	0.63	0
5	MPD	H	783	-	6,7,7	0.44	0	7,10,10	0.40	0
5	MPD	H	784	-	6,7,7	0.49	0	7,10,10	0.41	0
7	NDG	I	801	3	14,14,15	0.69	0	15,19,21	0.79	0
5	MPD	I	864	-	6,7,7	0.49	0	7,10,10	0.47	0
5	MPD	I	865	-	6,7,7	0.56	0	7,10,10	0.48	0
5	MPD	I	866	-	6,7,7	0.47	0	7,10,10	0.41	0
5	MPD	I	867	-	6,7,7	0.43	0	7,10,10	0.52	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
5	MPD	H	781	-	-	0/5/5/5	0/0/0/0
5	MPD	H	782	-	-	0/5/5/5	0/0/0/0
5	MPD	H	783	-	-	0/5/5/5	0/0/0/0
5	MPD	H	784	-	-	0/5/5/5	0/0/0/0
7	NDG	I	801	3	-	0/6/23/26	0/1/1/1
5	MPD	I	864	-	-	0/5/5/5	0/0/0/0
5	MPD	I	865	-	-	0/5/5/5	0/0/0/0
5	MPD	I	866	-	-	0/5/5/5	0/0/0/0
5	MPD	I	867	-	-	0/5/5/5	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	781	MPD	2	0
5	H	782	MPD	6	0
5	H	783	MPD	1	0
7	I	801	NDG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	864	MPD	2	0
5	I	865	MPD	2	0
5	I	867	MPD	1	0

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	L	43/49 (87%)	0.27	3 (6%) 19 22	47, 64, 77, 90	0
2	H	259/259 (100%)	0.01	5 (1%) 70 73	22, 42, 60, 83	0
3	I	412/432 (95%)	0.11	10 (2%) 62 66	22, 40, 70, 82	0
All	All	714/740 (96%)	0.09	18 (2%) 61 65	22, 42, 70, 90	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	1(R)	SER	7.8
3	I	358	GLY	4.0
3	I	359	ARG	3.9
3	I	387	ALA	3.6
2	H	247	GLU	3.2

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	GU6	I	434	23/24	0.89	0.19	0.97	41,52,64,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
8	NAG	I	842	14/15	0.92	0.17	0.34	46,58,66,78	0
8	NAG	I	841	14/15	0.96	0.18	0.04	42,48,50,51	0
6	GU6	I	446	23/24	0.92	0.17	-0.40	53,65,70,71	0
6	GU1	I	445	14/15	0.92	0.17	-0.77	58,59,62,63	0
6	GU4	I	433	28/28	0.95	0.13	-1.18	43,54,60,61	0
6	GU0	I	435	23/24	0.96	0.13	-1.50	28,43,47,51	0
6	GU5	I	444	17/18	0.96	0.11	-1.54	47,54,57,57	0
6	GU2	I	447	14/15	0.93	0.22	-	65,66,70,70	0
8	MAN	I	845	11/12	0.54	0.56	-	118,123,125,125	0
9	BMA	I	863	11/12	0.58	0.42	-	106,108,108,109	0
4	FUC	H	780	10/11	0.64	0.39	-	86,89,91,92	0
6	GU9	I	440	14/15	0.92	0.35	-	73,75,77,77	0
8	MAN	I	844	11/12	0.48	0.60	-	119,122,123,124	0
4	NDG	H	778	14/15	0.82	0.29	-	67,74,84,86	0
6	GU8	I	441	14/15	0.88	0.29	-	74,75,76,77	0
8	BMA	I	843	11/12	0.78	0.26	-	91,103,110,115	0
6	GU3	I	448	21/22	0.94	0.14	-	58,63,74,75	0
6	GU9	I	442	14/15	0.91	0.18	-	71,74,76,76	0
6	GU9	I	438	14/15	0.80	0.25	-	70,75,76,76	0
4	NAG	H	779	14/15	0.78	0.48	-	89,92,94,94	0
6	GU5	I	436	17/18	0.95	0.11	-	43,46,51,53	0
9	NAG	I	862	14/15	0.54	0.56	-	102,104,106,107	0
9	NAG	I	861	14/15	0.56	0.36	-	87,92,94,98	0
6	GU8	I	443	14/15	0.88	0.22	-	63,69,71,72	0
6	GU8	I	439	14/15	0.91	0.26	-	76,77,79,79	0
6	GU8	I	437	14/15	0.92	0.16	-	49,55,59,62	0

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
5	MPD	H	782	8/8	0.64	0.52	12.42	97,99,100,100	0
5	MPD	I	867	8/8	0.79	0.29	5.67	98,98,99,99	0
5	MPD	H	781	8/8	0.88	0.31	4.36	76,76,77,78	0
5	MPD	H	784	8/8	0.85	0.31	3.44	77,77,78,78	0
5	MPD	H	783	8/8	0.87	0.23	2.64	68,69,73,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	MPD	I	864	8/8	0.87	0.34	2.27	83,84,86,87	0
5	MPD	I	865	8/8	0.90	0.25	2.10	72,73,74,75	0
5	MPD	I	866	8/8	0.92	0.22	1.03	89,90,91,91	0
7	NDG	I	801	14/15	0.72	0.41	-	78,82,84,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.