



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 06:32 pm GMT

PDB ID : 4E7R  
Title : Thrombin in complex with 3-amidinophenylalanine inhibitor  
Authors : Ruehmann, E.; Heine, A.; Klebe, G.  
Deposited on : 2012-03-19  
Resolution : 2.25 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

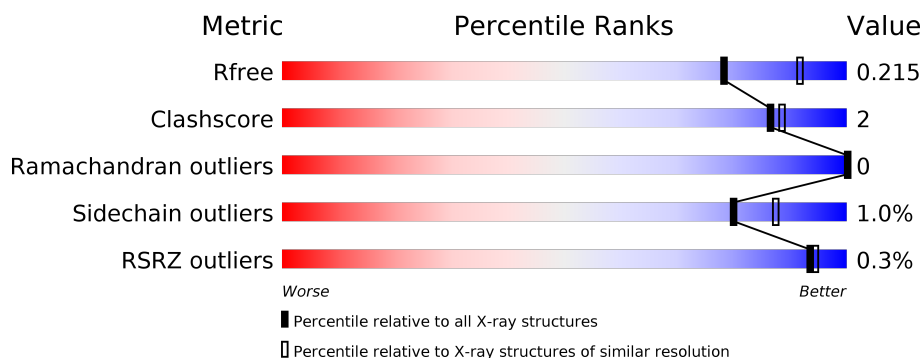
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	100719	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (2.26-2.26)

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  $\geq 3$ , 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	36	<div> <div style="width: 78%;"></div> <div style="width: 22%;"></div> </div>
1	M	36	<div> <div style="width: 75%;"></div> <div style="width: 22%;"></div> </div>
2	G	259	<div> <div style="width: 91%;"></div> <div style="width: 5%;"></div> <div style="width: 4%;"></div> </div>
2	H	259	<div> <div style="width: 92%;"></div> <div style="width: 5%;"></div> <div style="width: 3%;"></div> </div>
3	I	11	<div> <div style="width: 9%;"></div> <div style="width: 64%;"></div> <div style="width: 36%;"></div> </div>
3	J	11	<div> <div style="width: 100%;"></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
7	PO4	G	1305	-	-	-	X
8	GOL	G	1306	-	-	-	X
8	GOL	H	306	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 5034 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 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	28	Total	C	N	O	S	0	0	0
			217	137	33	46	1			
1	M	28	Total	C	N	O	S	0	0	0
			217	137	33	46	1			

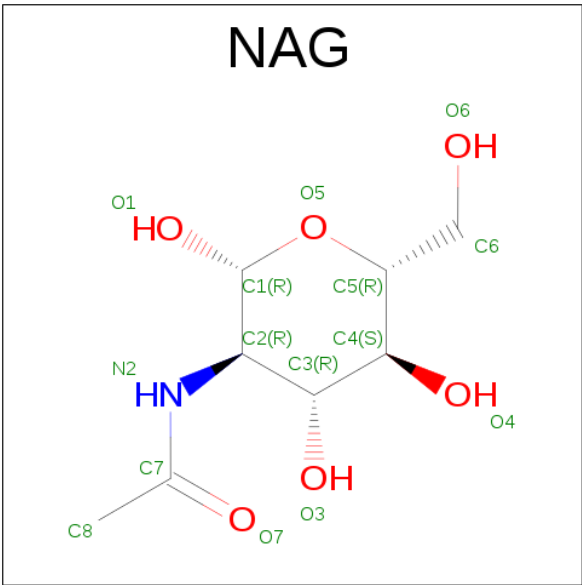
- Molecule 2 is a protein called Thrombin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	250	Total	C	N	O	S	0	1	0
			2007	1281	356	356	14			
2	G	250	Total	C	N	O	S	0	3	0
			2009	1281	355	359	14			

- Molecule 3 is a protein called Hirudin variant-2.

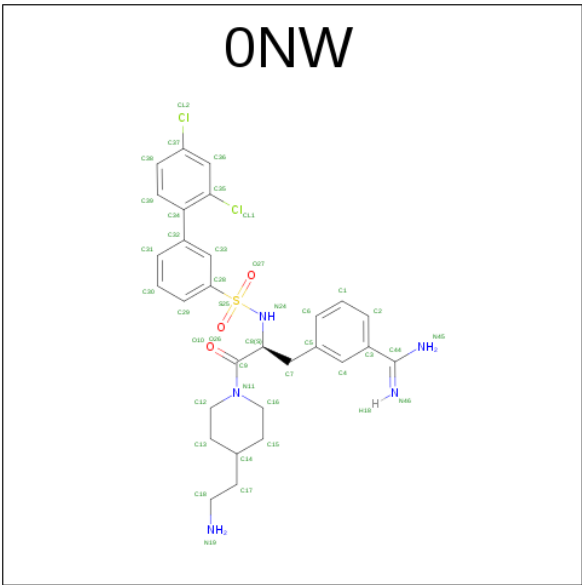
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	11	Total	C	N	O	S	0	0	0
			91	58	11	21	1			
3	J	11	Total	C	N	O	S	0	0	0
			88	57	11	19	1			

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 5 is 3-[(2S)-3-[4-(2-AMINOETHYL)PIPERIDIN-1-YL]-2-[(2',4'-DICHLOROBIPHENYL-3-YL)SULFONYL]AMINO}-3-OXOPROPYL]BENZENECARBOXIMIDAMIDE (three-letter code: ONW) (formula: C<sub>29</sub>H<sub>33</sub>Cl<sub>2</sub>N<sub>5</sub>O<sub>3</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	H	1	Total	C	Cl	N	O	S	0	0
			40	29	2	5	3	1		

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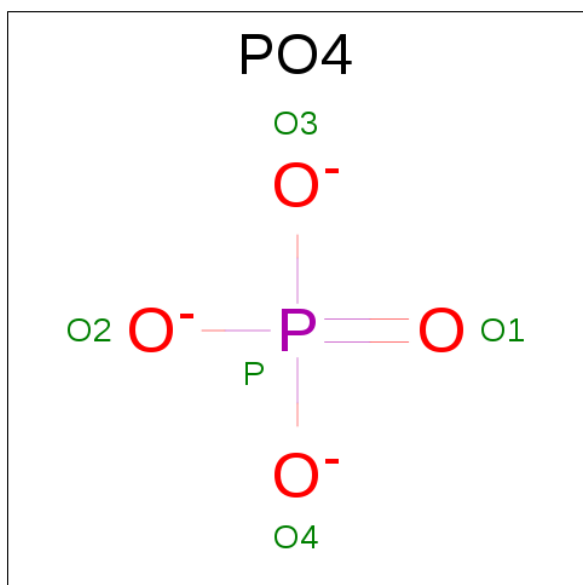
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	Cl	N	O	S	
			40	29	2	5	3	1	
									0
									0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	2	Total	Na		
			2	2	0	0
6	G	2	Total	Na		
			2	2	0	0

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	H	1	Total	O	P		
			5	4	1	0	0
7	G	1	Total	O	P		
			5	4	1	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	H	1	Total	C	O	0	0
			6	3	3		
8	H	1	Total	C	O	0	0
			6	3	3		
8	G	1	Total	C	O	0	0
			6	3	3		


- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	L	16	Total	O	0	0
			16	16		
9	M	16	Total	O	0	0
			16	16		
9	H	109	Total	O	0	0
			109	109		
9	G	120	Total	O	0	0
			120	120		
9	I	1	Total	O	0	0
			1	1		
9	J	3	Total	O	0	0
			3	3		

### 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.

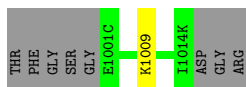
- Molecule 1: Thrombin light chain

Chain L: 



- Molecule 1: Thrombin light chain

Chain M: 



- Molecule 2: Thrombin heavy chain

Chain H: 



- Molecule 2: Thrombin heavy chain

Chain G: 



- Molecule 3: Hirudin variant-2

Chain I: 



- Molecule 3: Hirudin variant-2

Chain J: 



There are no outlier residues recorded for this chain.

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.24Å 50.28Å 71.84Å 97.61° 96.61° 90.57°	Depositor
Resolution (Å)	29.26 – 2.25 29.26 – 2.25	Depositor EDS
% Data completeness (in resolution range)	95.1 (29.26-2.25) 91.1 (29.26-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.71 (at 2.24Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.2_869)	Depositor
R, $R_{free}$	0.171 , 0.223 0.160 , 0.215	Depositor DCC
$R_{free}$ test set	1586 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.7	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 26.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.267 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5034	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, NA, PO4, ONW, 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	L	0.43	0/219	0.67	0/294
1	M	0.40	0/219	0.58	0/294
2	G	0.39	1/2069 (0.0%)	0.63	3/2801 (0.1%)
2	H	0.38	0/2062	0.62	2/2789 (0.1%)
3	I	0.31	0/75	0.44	0/100
3	J	0.33	0/72	0.39	0/96
All	All	0.39	1/4716 (0.0%)	0.62	5/6374 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1060(G)	ASN	CG-ND2	5.27	1.46	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1233	ARG	NE-CZ-NH2	-12.02	114.29	120.30
2	G	1233	ARG	NE-CZ-NH1	11.66	126.13	120.30
2	H	233	ARG	NE-CZ-NH2	10.52	125.56	120.30
2	H	233	ARG	NE-CZ-NH1	-10.43	115.08	120.30
2	G	1233	ARG	CD-NE-CZ	5.60	131.43	123.60

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	L	217	0	205	0	0
1	M	217	0	202	0	0
2	G	2009	0	1958	9	0
2	H	2007	0	1962	7	0
3	I	91	0	68	2	0
3	J	88	0	64	0	0
4	G	14	0	13	1	0
4	H	14	0	13	0	0
5	G	40	0	32	1	0
5	H	40	0	32	3	0
6	G	2	0	0	0	0
6	H	2	0	0	0	0
7	G	5	0	0	0	0
7	H	5	0	0	0	0
8	G	6	0	8	2	0
8	H	12	0	16	3	0
9	G	120	0	0	0	0
9	H	109	0	0	2	0
9	I	1	0	0	0	0
9	J	3	0	0	0	0
9	L	16	0	0	0	0
9	M	16	0	0	0	0
All	All	5034	0	4573	23	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 2.

The worst 5 of 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)
2:G:1165[B]:ARG:HG3	8:G:1306:GOL:H31	1.64	0.80
2:H:50:ARG:NH2	2:H:108:LEU:O	2.27	0.68
2:H:57:HIS:HD2	5:H:302:ONW:H30	1.63	0.64
2:H:144:LEU:HD21	2:H:152:PRO:HB3	1.81	0.62
2:G:1144:LEU:HD21	2:G:1152:PRO:HB3	1.84	0.60

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	26/36 (72%)	25 (96%)	1 (4%)	0	100	100
1	M	26/36 (72%)	25 (96%)	1 (4%)	0	100	100
2	G	249/259 (96%)	242 (97%)	7 (3%)	0	100	100
2	H	247/259 (95%)	239 (97%)	8 (3%)	0	100	100
3	I	8/11 (73%)	8 (100%)	0	0	100	100
3	J	8/11 (73%)	8 (100%)	0	0	100	100
All	All	564/612 (92%)	547 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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	23/31 (74%)	23 (100%)	0	100	100
1	M	23/31 (74%)	22 (96%)	1 (4%)	33	39
2	G	213/225 (95%)	212 (100%)	1 (0%)	91	94
2	H	213/225 (95%)	211 (99%)	2 (1%)	82	89
3	I	7/10 (70%)	6 (86%)	1 (14%)	4	2
3	J	6/10 (60%)	6 (100%)	0	100	100
All	All	485/532 (91%)	480 (99%)	5 (1%)	80	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	1009	LYS
2	H	33	LEU
2	H	85	LEU
2	G	1033	LEU
3	I	564	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
3	TYS	I	563	3	16,16,17	2.47	3 (18%)	19,22,24	0.85	0
3	TYS	J	1563	3	16,16,17	2.54	4 (25%)	19,22,24	0.83	1 (5%)

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	563	3	-	0/9/11/13	0/1/1/1
3	TYS	J	1563	3	-	0/9/11/13	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	1563	TYS	OH-S	-8.64	1.48	1.63
3	I	563	TYS	OH-S	-8.58	1.48	1.63
3	J	1563	TYS	O2-S	2.17	1.53	1.45
3	I	563	TYS	CD2-CG	2.19	1.43	1.38
3	J	1563	TYS	CD2-CG	2.33	1.43	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	1563	TYS	O-C-CA	-2.25	118.81	125.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	563	TYS	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 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	G	1301	2	14,14,15	1.92	4 (28%)	15,19,21	1.15	1 (6%)
5	0NW	G	1302	-	43,43,43	1.82	4 (9%)	58,61,61	1.54	7 (12%)
7	PO4	G	1305	-	4,4,4	0.66	0	6,6,6	0.45	0
8	GOL	G	1306	-	5,5,5	1.00	0	5,5,5	1.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	H	301	2	14,14,15	0.61	0	15,19,21	4.27	7 (46%)
5	0NW	H	302	-	43,43,43	1.86	4 (9%)	58,61,61	1.49	4 (6%)
7	PO4	H	305	-	4,4,4	0.68	0	6,6,6	0.45	0
8	GOL	H	306	-	5,5,5	1.07	0	5,5,5	1.30	0
8	GOL	H	307	-	5,5,5	0.99	0	5,5,5	1.26	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	NAG	G	1301	2	-	0/6/23/26	0/1/1/1
5	0NW	G	1302	-	-	0/34/44/44	0/4/4/4
7	PO4	G	1305	-	-	0/0/0/0	0/0/0/0
8	GOL	G	1306	-	-	0/4/4/4	0/0/0/0
4	NAG	H	301	2	-	0/6/23/26	0/1/1/1
5	0NW	H	302	-	-	0/34/44/44	0/4/4/4
7	PO4	H	305	-	-	0/0/0/0	0/0/0/0
8	GOL	H	306	-	-	0/4/4/4	0/0/0/0
8	GOL	H	307	-	-	0/4/4/4	0/0/0/0

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	302	0NW	C28-S25	-10.73	1.61	1.76
5	G	1302	0NW	C28-S25	-10.45	1.61	1.76
5	H	302	0NW	C44-N45	-3.38	1.26	1.33
4	G	1301	NAG	C4-C3	-3.25	1.44	1.52
5	G	1302	0NW	C44-N45	-2.90	1.27	1.33

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	301	NAG	C4-C3-C2	-10.01	96.34	111.02
5	H	302	0NW	O26-S25-O27	-7.39	110.10	119.55
5	G	1302	0NW	O26-S25-O27	-6.48	111.26	119.55
4	H	301	NAG	O7-C7-N2	-2.13	117.83	121.92
4	H	301	NAG	C6-C5-C4	-2.11	108.06	113.00

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1301	NAG	1	0
5	G	1302	0NW	1	0
8	G	1306	GOL	2	0
5	H	302	0NW	3	0
8	H	306	GOL	2	0
8	H	307	GOL	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	L	28/36 (77%)	-0.94	0	100   100	18, 28, 57, 72	0
1	M	28/36 (77%)	-0.90	0	100   100	18, 28, 54, 60	0
2	G	250/259 (96%)	-0.88	1 (0%)	92   93	16, 27, 48, 66	0
2	H	250/259 (96%)	-0.88	0	100   100	15, 27, 49, 71	0
3	I	10/11 (90%)	-0.02	1 (10%)	8   8	44, 60, 73, 78	0
3	J	10/11 (90%)	-0.25	0	100   100	35, 50, 64, 68	0
All	All	576/612 (94%)	-0.86	2 (0%)	93   94	15, 28, 55, 78	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	1186(C)	GLY	2.4
3	I	564	LEU	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	TYS	J	1563	16/17	0.96	0.10	-	32,44,67,76	0
3	TYS	I	563	16/17	0.97	0.09	-	27,43,64,70	0

### 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. 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
8	GOL	H	306	6/6	0.94	0.17	4.81	28,41,53,56	0
8	GOL	G	1306	6/6	0.92	0.16	3.31	29,42,52,52	0
7	PO4	G	1305	5/5	0.92	0.13	2.85	38,85,90,93	5
6	NA	H	303	1/1	0.95	0.12	0.91	37,37,37,37	0
6	NA	G	1304	1/1	0.96	0.12	0.24	41,41,41,41	0
7	PO4	H	305	5/5	0.96	0.09	-0.14	34,68,79,85	0
6	NA	G	1303	1/1	0.91	0.09	-0.18	37,37,37,37	0
5	0NW	G	1302	40/40	0.98	0.08	-0.27	12,27,42,64	0
5	0NW	H	302	40/40	0.98	0.08	-0.29	15,28,48,51	0
6	NA	H	304	1/1	0.87	0.06	-1.81	29,29,29,29	0
8	GOL	H	307	6/6	0.92	0.12	-	42,56,66,68	0
4	NAG	G	1301	14/15	0.86	0.12	-	52,62,73,85	0
4	NAG	H	301	14/15	0.86	0.16	-	44,73,85,93	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.