



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 03:52 PM GMT

PDB ID : 3PMH  
Title : Mechanism of Sulfotyrosine-Mediated Glycoprotein Ib Interaction with Two Distinct alpha-Thrombin Sites  
Authors : Varughese, K.I.; Celikel, R.  
Deposited on : 2010-11-16  
Resolution : 3.20 Å (reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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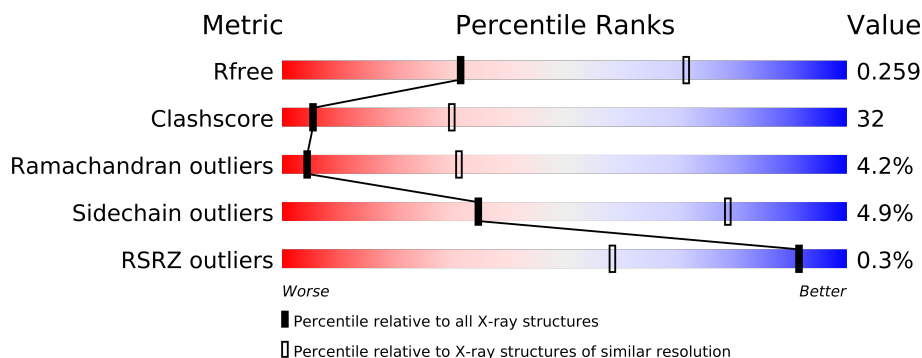
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.20 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))
$R_{free}$	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	36	
2	B	259	
3	G	290	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4723 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ALPHA-CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	36	Total	C	N	O	S	0	0	0
			287	177	48	61	1			

- Molecule 2 is a protein called THROMBIN BETA-CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	259	Total	C	N	O	S	0	0	0
			2093	1334	370	375	14			

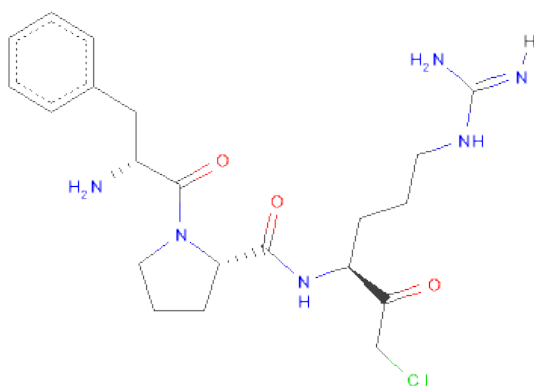
- Molecule 3 is a protein called Platelet glycoprotein Ib alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	284	Total	C	N	O	S	0	0	0
			2237	1427	363	436	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	65	ALA	CYS	ENGINEERED MUTATION	UNP P07359

- Molecule 4 is D-PHENYLALANYL-N-[(3S)-6-CARBAMIMIDAMIDO-1-CHLORO-2-OXO HEXAN-3-YL]-L-PROLINAMIDE (three-letter code: 0G7) (formula: C<sub>21</sub>H<sub>31</sub>ClN<sub>6</sub>O<sub>3</sub>).

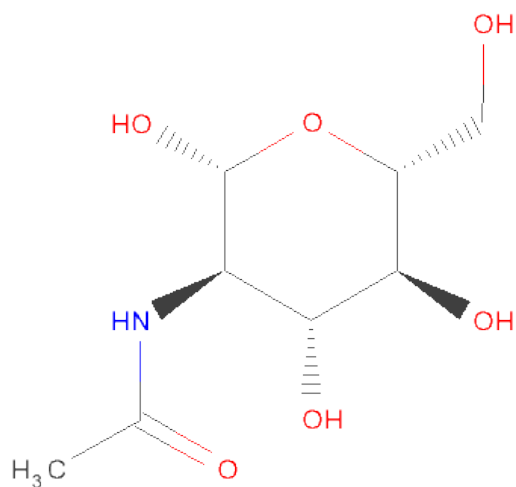


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	Cl	N	O	
			31	21	1	6	3	

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

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

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



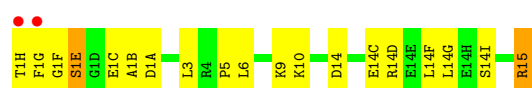
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	G	1	Total	C	N	O	0	0
			14	8	1	5		

### 3 Residue-property plots

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.

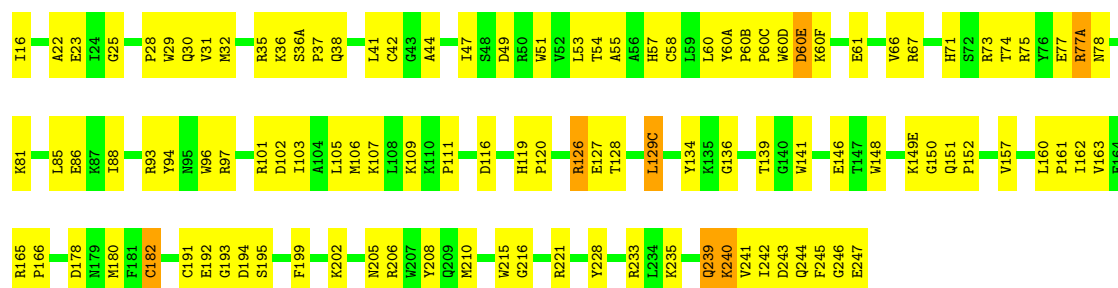
#### • Molecule 1: THROMBIN ALPHA-CHAIN

Chain A: 



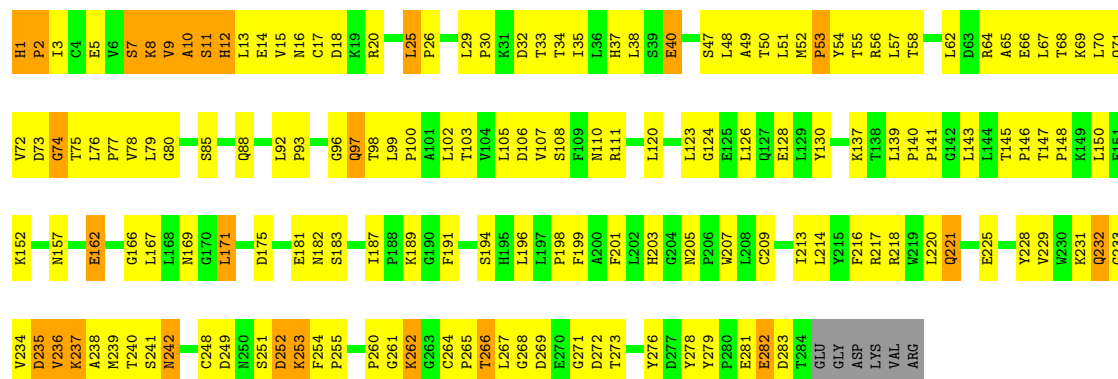
#### • Molecule 2: THROMBIN BETA-CHAIN

Chain B: 



#### • Molecule 3: Platelet glycoprotein Ib alpha chain

Chain G: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.66Å 67.66Å 329.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.20 47.34 – 3.19	Depositor EDS
% Data completeness (in resolution range)	94.2 (50.00-3.20) 88.9 (47.34-3.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.49 (at 3.19Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.220 , 0.263 0.223 , 0.259	Depositor DCC
$R_{free}$ test set	615 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	56.8	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 16.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 12905 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4723	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 0G7, MAN, 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	0.42	0/290	0.69	0/384
2	B	0.44	0/2148	0.70	0/2903
3	G	0.37	0/2235	0.65	0/3050
All	All	0.41	0/4673	0.68	0/6337

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	287	0	278	32	0
2	B	2093	0	2063	110	0
3	G	2237	0	2225	179	0
4	B	31	0	28	20	0
5	B	61	0	52	1	0
6	G	14	0	13	3	0
All	All	4723	0	4659	303	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including



hydrogens) of the entry. The overall clashscore for this entry is 32.

All (303) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:126:ARG:CD	2:B:126:ARG:H	1.56	1.13
2:B:126:ARG:HD2	2:B:126:ARG:N	1.66	1.11
3:G:25:LEU:HD23	3:G:25:LEU:H	1.18	1.09
2:B:195:SER:HB3	4:B:301:OG7:O2	1.55	1.03
3:G:124:GLY:HA2	3:G:146:PRO:O	1.63	0.98
3:G:48:LEU:HD12	3:G:72:VAL:HA	1.43	0.97
3:G:25:LEU:HD21	3:G:50:THR:HG21	1.47	0.97
2:B:126:ARG:HD2	2:B:126:ARG:H	0.81	0.95
2:B:37:PRO:HG2	3:G:278:TYS:O2	1.69	0.93
2:B:193:GLY:N	4:B:301:OG7:CL1	2.39	0.92
2:B:73:ARG:HH22	3:G:282:GLU:HG2	1.32	0.91
2:B:202:LYS:HE2	2:B:205:ASN:ND2	1.84	0.91
4:B:301:OG7:HD1	4:B:301:OG7:N	1.88	0.89
4:B:301:OG7:HB	4:B:301:OG7:H29	1.53	0.89
2:B:42:CYS:SG	2:B:195:SER:OG	2.30	0.88
3:G:68:THR:HG22	3:G:88:GLN:HB2	1.56	0.88
3:G:49:ALA:HB2	3:G:73:ASP:HB2	1.53	0.87
2:B:195:SER:CB	4:B:301:OG7:O2	2.22	0.86
3:G:201:PHE:CE2	3:G:237:LYS:HG2	2.10	0.86
3:G:13:LEU:HB2	3:G:33:THR:HA	1.56	0.86
3:G:58:THR:HG22	3:G:78:VAL:HG12	1.56	0.85
1:A:15:ARG:HH11	1:A:15:ARG:HG2	1.42	0.84
3:G:17:CYS:HA	3:G:20:ARG:HE	1.45	0.81
1:A:1(C):GLU:HG2	1:A:1(B):ALA:N	1.94	0.81
3:G:14:GLU:HG3	3:G:35:ILE:HB	1.63	0.78
2:B:73:ARG:NH2	3:G:282:GLU:HG2	1.97	0.78
3:G:267:LEU:HD23	3:G:267:LEU:H	1.47	0.77
3:G:75:THR:HG22	3:G:77:PRO:HD3	1.67	0.76
2:B:85:LEU:HD11	2:B:106:MET:HE1	1.68	0.76
3:G:201:PHE:HE2	3:G:237:LYS:HG2	1.51	0.75
3:G:137:LYS:HE2	6:G:601:NAG:H81	1.66	0.75
2:B:149(E):LYS:HG3	3:G:283:ASP:HB3	1.68	0.75
3:G:17:CYS:HB2	3:G:38:LEU:HD23	1.69	0.75
4:B:301:OG7:H29	4:B:301:OG7:CB	2.17	0.74
3:G:248:CYS:HB2	3:G:254:PHE:HB3	1.70	0.74
3:G:25:LEU:CD2	3:G:25:LEU:H	1.99	0.74
3:G:52:MET:HB3	3:G:53:PRO:HD3	1.68	0.74
2:B:195:SER:HB3	4:B:301:OG7:C2	2.18	0.73
3:G:8:LYS:N	3:G:8:LYS:HD3	2.04	0.72
3:G:145:THR:HB	3:G:146:PRO:HD3	1.70	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:73:ARG:HH12	3:G:282:GLU:HB3	1.56	0.71
3:G:25:LEU:HD21	3:G:50:THR:CG2	2.20	0.70
3:G:150:LEU:HB3	3:G:171:LEU:HD12	1.73	0.70
3:G:242:ASN:HD22	3:G:242:ASN:C	1.94	0.69
3:G:74:GLY:O	3:G:98:THR:HG23	1.93	0.69
1:A:1(C):GLU:HG2	1:A:1(B):ALA:H	1.55	0.69
3:G:40:GLU:HA	3:G:64:ARG:O	1.93	0.69
3:G:79:LEU:HD23	3:G:99:LEU:HD13	1.74	0.68
2:B:146:GLU:OE2	2:B:221:ARG:HD2	1.94	0.67
2:B:148:TRP:HA	3:G:279:TYS:O2	1.92	0.67
2:B:193:GLY:H	4:B:301:OG7:C3	2.06	0.67
4:B:301:OG7:N	4:B:301:OG7:CD1	2.57	0.67
3:G:276:TYS:HD2	3:G:278:TYS:O1	1.94	0.66
3:G:75:THR:HG22	3:G:77:PRO:CD	2.26	0.66
1:A:1(G):PHE:CE2	1:A:1(E):SER:HB2	2.30	0.66
2:B:57:HIS:NE2	4:B:301:OG7:O2	2.24	0.66
3:G:49:ALA:HB2	3:G:73:ASP:CB	2.25	0.64
3:G:25:LEU:HD23	3:G:25:LEU:N	2.02	0.64
1:A:1(C):GLU:C	1:A:1(A):ASP:H	1.99	0.64
3:G:34:THR:HA	3:G:56:ARG:O	1.98	0.64
3:G:214:LEU:O	3:G:217:ARG:HB3	1.98	0.63
3:G:218:ARG:NH2	3:G:273:THR:HB	2.13	0.63
4:B:301:OG7:CD2	4:B:301:OG7:H29	2.29	0.63
3:G:218:ARG:HH21	3:G:273:THR:HB	1.62	0.63
3:G:124:GLY:CA	3:G:146:PRO:O	2.45	0.62
1:A:6:LEU:HD21	2:B:116:ASP:HB3	1.80	0.62
3:G:67:LEU:HD23	3:G:68:THR:N	2.15	0.62
3:G:232:GLN:N	3:G:232:GLN:HE21	1.97	0.62
3:G:97:GLN:NE2	3:G:97:GLN:H	1.98	0.62
4:B:301:OG7:CD	4:B:301:OG7:HB	2.27	0.62
2:B:136:GLY:HA3	2:B:199:PHE:CZ	2.36	0.61
2:B:202:LYS:CE	2:B:205:ASN:ND2	2.61	0.61
3:G:137:LYS:HE2	6:G:601:NAG:C8	2.31	0.61
3:G:228:TYR:CD2	3:G:241:SER:HA	2.35	0.60
1:A:1(H):THR:HA	2:B:243:ASP:HA	1.82	0.60
3:G:120:LEU:HD12	3:G:143:LEU:O	2.00	0.60
1:A:1(G):PHE:HE2	1:A:1(E):SER:HB2	1.66	0.60
3:G:17:CYS:HA	3:G:20:ARG:NE	2.16	0.60
1:A:1(H):THR:HA	2:B:243:ASP:CA	2.32	0.59
2:B:235:LYS:O	2:B:239:GLN:HG2	2.02	0.59
2:B:77(A):ARG:HG3	2:B:78:ASN:OD1	2.01	0.59
2:B:246:GLY:O	2:B:247:GLU:HB3	2.03	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:165:ARG:HB2	2:B:166:PRO:HD3	1.83	0.59
3:G:128:GLU:HG2	3:G:152:LYS:HB2	1.84	0.59
2:B:96:TRP:CZ3	2:B:97:ARG:HG3	2.37	0.59
3:G:25:LEU:HD11	3:G:50:THR:HG22	1.84	0.58
3:G:75:THR:O	3:G:76:LEU:HD23	2.03	0.58
3:G:209:CYS:HA	3:G:213:ILE:HG21	1.85	0.58
3:G:80:GLY:O	3:G:102:LEU:HD12	2.04	0.58
3:G:13:LEU:HD12	3:G:32:ASP:C	2.24	0.57
3:G:9:VAL:O	3:G:10:ALA:HB3	2.05	0.57
3:G:228:TYR:CE2	3:G:241:SER:HA	2.39	0.57
2:B:150:GLY:N	3:G:281:GLU:HG3	2.20	0.57
3:G:29:LEU:HB2	3:G:54:TYR:HE2	1.69	0.57
3:G:267:LEU:CD2	3:G:267:LEU:H	2.16	0.57
1:A:1(F):GLY:O	1:A:1(E):SER:HB3	2.05	0.57
3:G:15:VAL:HG11	3:G:29:LEU:HD13	1.86	0.57
2:B:150:GLY:H	3:G:281:GLU:HG3	1.69	0.57
2:B:35:ARG:HB2	2:B:41:LEU:HD21	1.85	0.57
1:A:6:LEU:HD12	2:B:25:GLY:HA3	1.86	0.56
2:B:163:VAL:HB	2:B:182:CYS:SG	2.45	0.56
1:A:15:ARG:NH1	1:A:15:ARG:HG2	2.13	0.56
2:B:93:ARG:HB3	2:B:101:ARG:NH1	2.21	0.56
2:B:31:VAL:CG1	2:B:66:VAL:HG13	2.35	0.56
3:G:1:HIS:N	3:G:2:PRO:CD	2.69	0.55
2:B:191:CYS:O	2:B:194:ASP:HB2	2.05	0.55
1:A:5:PRO:HA	1:A:9:LYS:HD2	1.89	0.55
3:G:67:LEU:HD11	3:G:70:LEU:HD13	1.88	0.55
2:B:178:ASP:O	2:B:233:ARG:HD3	2.07	0.55
3:G:12:HIS:C	3:G:12:HIS:CD2	2.80	0.55
3:G:7:SER:C	3:G:8:LYS:HD3	2.26	0.55
1:A:1(H):THR:HA	2:B:243:ASP:O	2.07	0.55
2:B:105:LEU:HD12	2:B:241:VAL:HG21	1.88	0.55
3:G:157:ASN:HD21	3:G:181:GLU:HG3	1.71	0.55
2:B:57:HIS:O	2:B:60(F):LYS:HE3	2.07	0.55
1:A:14(C):GLU:O	1:A:14(G):LEU:HD23	2.07	0.55
3:G:97:GLN:H	3:G:97:GLN:CD	2.10	0.55
3:G:218:ARG:HD2	3:G:271:GLY:H	1.72	0.54
2:B:126:ARG:CD	2:B:126:ARG:N	2.40	0.54
2:B:85:LEU:HD11	2:B:106:MET:CE	2.37	0.53
2:B:202:LYS:NZ	2:B:205:ASN:HD21	2.05	0.53
1:A:1(C):GLU:CG	1:A:1(B):ALA:N	2.69	0.53
2:B:202:LYS:HE2	2:B:205:ASN:HD22	1.72	0.53
3:G:217:ARG:HH12	3:G:221:GLN:HE22	1.57	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:G:126:LEU:HD23	3:G:147:THR:HG21	1.91	0.53
3:G:68:THR:HG22	3:G:88:GLN:CB	2.35	0.53
3:G:9:VAL:HG12	3:G:12:HIS:NE2	2.24	0.53
3:G:236:VAL:O	3:G:238:ALA:N	2.32	0.52
2:B:127:GLU:HA	2:B:127:GLU:OE1	2.09	0.52
2:B:150:GLY:HA3	3:G:281:GLU:HG3	1.90	0.52
1:A:14(C):GLU:OE2	2:B:202:LYS:NZ	2.36	0.52
3:G:67:LEU:HD23	3:G:69:LYS:N	2.25	0.52
2:B:22:ALA:HB2	2:B:157:VAL:CG2	2.40	0.52
3:G:47:SER:HB3	3:G:50:THR:OG1	2.10	0.51
2:B:60(A):TYR:CE2	2:B:60(C):PRO:HB2	2.45	0.51
3:G:146:PRO:C	3:G:148:PRO:HD3	2.31	0.51
3:G:253:LYS:C	3:G:255:PRO:HD3	2.30	0.51
2:B:86:GLU:HB2	2:B:109:LYS:HA	1.92	0.51
4:B:301:OG7:CG	4:B:301:OG7:H29	2.40	0.51
3:G:34:THR:O	3:G:57:LEU:HD12	2.10	0.51
3:G:225:GLU:HG2	3:G:225:GLU:O	2.10	0.51
3:G:18:ASP:O	3:G:20:ARG:HG3	2.11	0.51
2:B:73:ARG:NH1	3:G:282:GLU:HB3	2.24	0.50
3:G:53:PRO:HB2	3:G:54:TYR:CD1	2.46	0.50
2:B:60:LEU:HG	2:B:60(B):PRO:HD3	1.93	0.50
2:B:73:ARG:HG3	2:B:141:TRP:HB3	1.93	0.50
2:B:51:TRP:CZ2	2:B:107:LYS:HD3	2.46	0.50
3:G:33:THR:HG22	3:G:54:TYR:HD2	1.75	0.50
1:A:1(C):GLU:CG	1:A:1(B):ALA:H	2.23	0.50
3:G:167:LEU:HB3	3:G:191:PHE:HE1	1.76	0.50
3:G:9:VAL:O	3:G:9:VAL:HG13	2.11	0.50
1:A:15:ARG:CG	1:A:15:ARG:NH1	2.75	0.50
1:A:1(C):GLU:C	1:A:1(A):ASP:N	2.66	0.49
3:G:106:ASP:HA	3:G:130:TYR:HB2	1.94	0.49
3:G:76:LEU:HD12	3:G:79:LEU:HD22	1.94	0.49
3:G:12:HIS:O	3:G:12:HIS:HD2	1.94	0.49
2:B:60(D):TRP:O	2:B:60(E):ASP:C	2.51	0.49
3:G:175:ASP:HA	3:G:198:PRO:HD2	1.95	0.49
3:G:231:LYS:O	3:G:232:GLN:HB3	2.12	0.49
1:A:1(H):THR:CA	2:B:243:ASP:HA	2.42	0.49
1:A:5:PRO:O	1:A:10:LYS:HG3	2.11	0.49
3:G:187:ILE:HG13	3:G:216:PHE:CD1	2.48	0.49
3:G:232:GLN:HG2	3:G:233:GLY:N	2.26	0.49
3:G:162:GLU:HG3	3:G:162:GLU:O	2.12	0.49
2:B:22:ALA:HB2	2:B:157:VAL:HG23	1.95	0.49
2:B:67:ARG:HH12	3:G:196:LEU:CD2	2.26	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:75:ARG:O	2:B:77:GLU:HG3	2.14	0.48
2:B:73:ARG:NH1	2:B:152:PRO:O	2.40	0.48
3:G:218:ARG:NH1	3:G:272:ASP:OD1	2.46	0.48
2:B:58:CYS:SG	2:B:195:SER:OG	2.63	0.48
1:A:1(H):THR:N	2:B:245:PHE:O	2.47	0.48
3:G:157:ASN:ND2	3:G:181:GLU:HB2	2.28	0.48
3:G:171:LEU:HD22	3:G:171:LEU:N	2.29	0.48
3:G:12:HIS:O	3:G:12:HIS:CD2	2.66	0.48
3:G:65:ALA:C	3:G:66:GLU:HG2	2.34	0.47
2:B:30:GLN:NE2	2:B:139:THR:OG1	2.40	0.47
2:B:22:ALA:O	2:B:71:HIS:HE1	1.96	0.47
3:G:187:ILE:HB	3:G:216:PHE:HB2	1.96	0.47
2:B:150:GLY:CA	3:G:281:GLU:HG3	2.45	0.47
3:G:198:PRO:HB2	3:G:199:PHE:CD1	2.50	0.47
2:B:202:LYS:HZ3	2:B:205:ASN:HD21	1.63	0.47
3:G:248:CYS:O	3:G:251:SER:HB3	2.13	0.47
2:B:67:ARG:NH1	3:G:196:LEU:CD2	2.77	0.47
3:G:137:LYS:NZ	6:G:601:NAG:O7	2.37	0.47
2:B:239:GLN:HA	2:B:239:GLN:HE21	1.79	0.47
2:B:134:TYR:O	2:B:162:ILE:HG13	2.15	0.47
3:G:78:VAL:HG12	3:G:78:VAL:O	2.14	0.47
3:G:254:PHE:N	3:G:255:PRO:HD3	2.30	0.47
2:B:36:LYS:NZ	3:G:194:SER:HB2	2.30	0.47
3:G:171:LEU:HD22	3:G:171:LEU:H	1.79	0.47
3:G:5:GLU:HA	3:G:5:GLU:OE1	2.15	0.47
3:G:38:LEU:HB2	3:G:62:LEU:HD23	1.97	0.47
3:G:64:ARG:HG3	3:G:64:ARG:HH11	1.80	0.47
4:B:301:OG7:H29	4:B:301:OG7:HD2	1.97	0.46
3:G:203:HIS:CD2	3:G:229:VAL:HA	2.50	0.46
3:G:102:LEU:HD21	3:G:105:LEU:HD13	1.96	0.46
2:B:16:ILE:N	2:B:194:ASP:OD2	2.48	0.46
1:A:1(F):GLY:O	2:B:49:ASP:OD1	2.34	0.46
1:A:3:LEU:HD21	2:B:206:ARG:HG2	1.97	0.45
1:A:1(C):GLU:O	1:A:1(B):ALA:HB3	2.15	0.45
3:G:267:LEU:HD23	3:G:267:LEU:N	2.25	0.45
3:G:58:THR:HA	3:G:79:LEU:HA	1.98	0.45
3:G:249:ASP:C	3:G:251:SER:H	2.20	0.45
1:A:14:ASP:HB2	2:B:23:GLU:OE1	2.17	0.45
3:G:261:GLY:O	3:G:264:CYS:SG	2.75	0.45
2:B:57:HIS:ND1	2:B:102:ASP:OD2	2.50	0.45
2:B:105:LEU:HD12	2:B:241:VAL:CG2	2.47	0.44
3:G:107:VAL:O	3:G:107:VAL:HG12	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:G:92:LEU:HA	3:G:93:PRO:HD3	1.86	0.44
1:A:1(B):ALA:C	2:B:206:ARG:HH12	2.21	0.44
3:G:139:LEU:HA	3:G:140:PRO:HD3	1.79	0.44
2:B:28:PRO:HG2	2:B:29:TRP:CE3	2.52	0.44
3:G:282:GLU:H	3:G:282:GLU:CD	2.21	0.44
3:G:16:ASN:HD22	3:G:37:HIS:HB2	1.83	0.44
3:G:20:ARG:HH11	3:G:20:ARG:HG2	1.83	0.44
2:B:35:ARG:O	2:B:38:GLN:HA	2.18	0.44
4:B:301:OG7:CD	4:B:301:OG7:CB	2.86	0.44
3:G:53:PRO:O	3:G:54:TYR:C	2.56	0.44
3:G:11:SER:O	3:G:56:ARG:NH2	2.50	0.44
3:G:106:ASP:OD2	3:G:108:SER:HB2	2.17	0.44
2:B:61:GLU:HG3	2:B:88:ILE:HG13	1.99	0.44
2:B:208:TYR:HB2	2:B:210:MET:HE1	2.00	0.44
3:G:205:ASN:HB2	3:G:207:TRP:NE1	2.33	0.44
3:G:3:ILE:HG22	3:G:20:ARG:HD3	2.00	0.43
3:G:252:ASP:O	3:G:254:PHE:N	2.50	0.43
2:B:216:GLY:O	4:B:301:OG7:N	2.51	0.43
2:B:37:PRO:CG	3:G:278:TYS:O2	2.54	0.43
2:B:85:LEU:CD1	2:B:106:MET:CE	2.95	0.43
3:G:79:LEU:HD23	3:G:99:LEU:HD22	1.99	0.43
3:G:166:GLY:CA	3:G:169:ASN:ND2	2.82	0.43
3:G:47:SER:HB3	3:G:50:THR:HG1	1.83	0.43
3:G:9:VAL:O	3:G:10:ALA:CB	2.66	0.43
3:G:218:ARG:HD2	3:G:271:GLY:N	2.34	0.43
3:G:1:HIS:H3	3:G:2:PRO:HD3	1.84	0.43
3:G:157:ASN:ND2	3:G:181:GLU:CB	2.81	0.43
2:B:160:LEU:HA	2:B:161:PRO:HD3	1.94	0.43
2:B:53:LEU:HD11	2:B:103:ILE:HD11	2.00	0.43
2:B:215:TRP:HB2	4:B:301:OG7:O	2.19	0.43
1:A:14(F):LEU:O	1:A:14(I):SER:HB2	2.19	0.43
3:G:265:PRO:O	3:G:266:THR:O	2.37	0.43
2:B:85:LEU:HD13	2:B:106:MET:HE2	2.01	0.43
3:G:242:ASN:O	3:G:242:ASN:ND2	2.50	0.43
2:B:228:TYR:CD1	2:B:228:TYR:N	2.86	0.43
3:G:76:LEU:N	3:G:77:PRO:HD3	2.34	0.43
3:G:79:LEU:HD23	3:G:99:LEU:CD1	2.46	0.43
2:B:246:GLY:O	2:B:247:GLU:CB	2.67	0.43
3:G:196:LEU:O	3:G:198:PRO:HD3	2.19	0.42
3:G:218:ARG:HD2	3:G:271:GLY:HA2	2.01	0.42
2:B:31:VAL:HG13	2:B:66:VAL:HG13	2.00	0.42
2:B:215:TRP:HA	4:B:301:OG7:HG2	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1(E):SER:HB3	2:B:49:ASP:OD1	2.20	0.42
3:G:85:SER:HA	3:G:108:SER:O	2.19	0.42
3:G:49:ALA:CB	3:G:73:ASP:HB2	2.37	0.42
1:A:1(F):GLY:O	1:A:1(E):SER:CB	2.66	0.42
3:G:25:LEU:HD11	3:G:50:THR:CG2	2.49	0.42
2:B:32:MET:HB3	2:B:67:ARG:HB2	2.02	0.42
3:G:140:PRO:HA	3:G:141:PRO:HD3	1.96	0.42
3:G:106:ASP:OD2	3:G:108:SER:CB	2.67	0.42
2:B:31:VAL:HB	2:B:44:ALA:HB3	2.02	0.42
3:G:98:THR:C	3:G:100:PRO:HD3	2.40	0.42
3:G:182:ASN:HB3	3:G:183:SER:H	1.68	0.42
2:B:36(A):SER:HA	2:B:37:PRO:C	2.39	0.42
3:G:15:VAL:HG23	3:G:33:THR:OG1	2.19	0.42
2:B:139:THR:HG22	2:B:157:VAL:HG13	2.02	0.42
2:B:109:LYS:HE3	2:B:109:LYS:HB2	1.89	0.42
3:G:33:THR:CG2	3:G:54:TYR:HD2	2.33	0.42
3:G:14:GLU:HG3	3:G:35:ILE:CB	2.43	0.41
3:G:8:LYS:O	3:G:9:VAL:HB	2.19	0.41
3:G:25:LEU:N	3:G:25:LEU:CD2	2.74	0.41
3:G:8:LYS:HB2	3:G:9:VAL:H	1.66	0.41
2:B:81:LYS:HD3	2:B:81:LYS:HA	1.88	0.41
2:B:195:SER:OG	4:B:301:OG7:O2	2.38	0.41
3:G:48:LEU:HD12	3:G:72:VAL:HG13	2.02	0.41
2:B:193:GLY:N	4:B:301:OG7:C3	2.77	0.41
3:G:29:LEU:O	3:G:30:PRO:C	2.58	0.41
3:G:128:GLU:HB3	3:G:130:TYR:CE1	2.55	0.41
3:G:29:LEU:HB2	3:G:54:TYR:CE2	2.50	0.41
2:B:241:VAL:HG23	2:B:242:ILE:N	2.35	0.41
3:G:201:PHE:CZ	3:G:237:LYS:HG2	2.52	0.41
3:G:51:LEU:O	3:G:52:MET:C	2.59	0.41
3:G:110:ASN:HB3	3:G:111:ARG:H	1.76	0.41
1:A:1(C):GLU:O	1:A:1(A):ASP:N	2.54	0.41
2:B:49:ASP:O	2:B:111:PRO:HA	2.19	0.41
3:G:47:SER:HA	3:G:71:GLN:HB2	2.03	0.41
3:G:233:GLY:C	3:G:235:ASP:H	2.23	0.41
3:G:102:LEU:HD23	3:G:123:LEU:HD13	2.02	0.41
2:B:47:ILE:HG12	2:B:51:TRP:O	2.21	0.41
3:G:97:GLN:NE2	3:G:97:GLN:N	2.68	0.41
3:G:225:GLU:CG	3:G:225:GLU:O	2.68	0.41
3:G:216:PHE:O	3:G:220:LEU:HG	2.21	0.41
5:B:303:NAG:O3	5:B:304:MAN:C1	2.69	0.41
2:B:240:LYS:O	2:B:244:GLN:HB2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:G:260:PRO:C	3:G:262:LYS:H	2.25	0.41
3:G:201:PHE:N	3:G:201:PHE:CD1	2.89	0.40
2:B:94:TYR:CZ	2:B:96:TRP:HB3	2.56	0.40
2:B:54:THR:OG1	2:B:55:ALA:N	2.54	0.40
3:G:218:ARG:HD2	3:G:271:GLY:CA	2.52	0.40
3:G:102:LEU:HD23	3:G:123:LEU:CD1	2.52	0.40
2:B:119:HIS:HA	2:B:120:PRO:HD3	1.81	0.40
2:B:128:THR:HG23	2:B:129(C):LEU:HD22	2.04	0.40
3:G:103:THR:C	3:G:126:LEU:HD12	2.41	0.40
3:G:88:GLN:OE1	3:G:111:ARG:HD2	2.21	0.40
3:G:12:HIS:C	3:G:12:HIS:HD2	2.24	0.40

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	A	34/36 (94%)	28 (82%)	5 (15%)	1 (3%)	7	43
2	B	257/259 (99%)	240 (93%)	15 (6%)	2 (1%)	27	77
3	G	279/290 (96%)	209 (75%)	49 (18%)	21 (8%)	2	12
All	All	570/585 (97%)	477 (84%)	69 (12%)	24 (4%)	4	31

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	77(A)	ARG
3	G	2	PRO
3	G	9	VAL
3	G	189	LYS
3	G	234	VAL
3	G	240	THR
3	G	252	ASP
3	G	253	LYS

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Mol	Chain	Res	Type
3	G	266	THR
3	G	10	ALA
3	G	55	THR
3	G	74	GLY
3	G	237	LYS
1	A	1(E)	SER
2	B	60(E)	ASP
3	G	53	PRO
3	G	171	LEU
3	G	262	LYS
3	G	40	GLU
3	G	269	ASP
3	G	236	VAL
3	G	26	PRO
3	G	96	GLY
3	G	268	GLY

### 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	A	31/31 (100%)	29 (94%)	2 (6%)	24	68
2	B	225/225 (100%)	216 (96%)	9 (4%)	42	83
3	G	251/256 (98%)	237 (94%)	14 (6%)	30	75
All	All	507/512 (99%)	482 (95%)	25 (5%)	35	79

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14(D)	ARG
1	A	15	ARG
2	B	74	THR
2	B	126	ARG
2	B	129(C)	LEU
2	B	151	GLN
2	B	180	MET

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Mol	Chain	Res	Type
2	B	182	CYS
2	B	192	GLU
2	B	239	GLN
2	B	240	LYS
3	G	1	HIS
3	G	7	SER
3	G	8	LYS
3	G	11	SER
3	G	12	HIS
3	G	25	LEU
3	G	97	GLN
3	G	162	GLU
3	G	221	GLN
3	G	232	GLN
3	G	235	ASP
3	G	239	MET
3	G	242	ASN
3	G	282	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	30	GLN
2	B	38	GLN
2	B	71	HIS
2	B	151	GLN
2	B	205	ASN
2	B	209	GLN
2	B	239	GLN
3	G	12	HIS
3	G	16	ASN
3	G	37	HIS
3	G	61	ASN
3	G	71	GLN
3	G	86	HIS
3	G	97	GLN
3	G	127	GLN
3	G	169	ASN
3	G	195	HIS
3	G	223	ASN
3	G	226	ASN
3	G	232	GLN

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Mol	Chain	Res	Type
3	G	242	ASN
3	G	247	GLN
3	G	250	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

3 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	G	276	3	16,16,17	4.78	3 (18%)	20,22,24	1.09	2 (10%)
3	TYS	G	278	3	16,16,17	4.56	4 (25%)	20,22,24	1.18	2 (10%)
3	TYS	G	279	3	16,16,17	4.99	4 (25%)	20,22,24	1.16	2 (10%)

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	G	276	3	-	0/9/11/13	0/1/1/1
3	TYS	G	278	3	-	0/9/11/13	0/1/1/1
3	TYS	G	279	3	-	0/9/11/13	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	279	TYS	O-C	18.65	1.24	1.11
3	G	276	TYS	O-C	17.55	1.23	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	278	TYS	O-C	17.07	1.23	1.11
3	G	276	TYS	OH-S	-6.06	1.52	1.63
3	G	279	TYS	OH-S	-5.33	1.54	1.63
3	G	278	TYS	OH-S	-5.05	1.54	1.63
3	G	276	TYS	OH-CZ	-3.61	1.38	1.42
3	G	279	TYS	OH-CZ	-3.21	1.38	1.42
3	G	279	TYS	CA-C	3.00	1.53	1.48
3	G	278	TYS	CA-C	2.66	1.53	1.48
3	G	278	TYS	OH-CZ	-2.39	1.39	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	278	TYS	C-CA-N	-3.36	110.47	113.83
3	G	276	TYS	OH-CZ-CE1	3.32	124.22	118.70
3	G	279	TYS	OH-CZ-CE1	3.18	123.98	118.70
3	G	278	TYS	OH-CZ-CE1	2.67	123.14	118.70
3	G	279	TYS	OH-CZ-CE2	-2.37	114.77	118.70
3	G	276	TYS	OH-CZ-CE2	-2.25	114.97	118.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

5 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
5	NAG	B	302	2,5	12,14,15	1.21	1 (8%)	15,19,21	1.91	4 (26%)
5	NAG	B	303	5	12,14,15	0.62	0	15,19,21	0.88	0
5	MAN	B	304	5	10,11,12	0.56	0	11,15,17	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	MAN	B	305	5	10,11,12	0.57	0	11,15,17	0.25	0
5	MAN	B	306	5	10,11,12	0.50	0	11,15,17	0.35	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	NAG	B	302	2,5	-	0/6/23/26	0/1/1/1
5	NAG	B	303	5	-	0/6/23/26	0/1/1/1
5	MAN	B	304	5	-	0/2/19/22	0/1/1/1
5	MAN	B	305	5	-	0/2/19/22	0/1/1/1
5	MAN	B	306	5	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	302	NAG	C8-C7	2.53	1.55	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	302	NAG	O5-C5-C6	-4.50	102.25	106.98
5	B	302	NAG	C8-C7-N2	3.67	123.27	116.11
5	B	302	NAG	C2-N2-C7	-2.44	118.99	123.09
5	B	302	NAG	O7-C7-C8	-2.28	117.60	122.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

2 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	$\# Z  > 2$
4	0G7	B	301	-	32,32,32	3.03	3 (9%)	42,42,42	1.89	5 (11%)
6	NAG	G	601	3	12,14,15	1.09	2 (16%)	15,19,21	1.00	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	0G7	B	301	-	-	1/33/43/43	0/2/2/2
6	NAG	G	601	3	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	301	0G7	C3-C2	-16.62	1.25	1.51
4	B	301	0G7	O2-C2	2.80	1.26	1.21
6	G	601	NAG	C3-C2	2.32	1.57	1.52
4	B	301	0G7	C3-CL1	2.07	1.83	1.76
6	G	601	NAG	C4-C3	2.02	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	301	0G7	C2-C3-CL1	10.19	127.04	112.74
4	B	301	0G7	CB-CA-C	3.02	115.61	108.77
4	B	301	0G7	O2-C2-C3	-2.48	118.59	122.76
4	B	301	0G7	C3-C2-CA2	2.33	120.77	116.39
4	B	301	0G7	C2-CA2-N2	2.04	114.59	110.20

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	301	0G7	CA2-C2-C3-CL1

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	A	36/36 (100%)	-0.02	2 (5%) 24 5	40, 63, 136, 153	0
2	B	259/259 (100%)	-0.33	0 100 100	26, 49, 76, 101	0
3	G	284/290 (97%)	-0.02	0 100 100	38, 81, 127, 139	1 (0%)
All	All	579/585 (98%)	-0.16	2 (0%) 91 58	26, 62, 122, 153	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1(H)	THR	5.0
1	A	1(G)	PHE	2.1

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

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	TYS	G	278	16/17	0.24	-	84,94,100,101	4
3	TYS	G	279	16/17	0.21	-	67,75,87,89	0
3	TYS	G	276	16/17	0.34	-	97,103,120,122	4

### 6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	NAG	B	302	14/15	0.19	-	93,101,107,118	0
5	MAN	B	306	11/12	0.36	-	128,134,137,139	0
5	NAG	B	303	14/15	0.17	-	99,104,108,112	0
5	MAN	B	304	11/12	0.18	-	104,112,116,118	0
5	MAN	B	305	11/12	0.28	-	78,90,98,99	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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
6	NAG	G	601	14/15	0.20	-	86,102,107,112	0
4	OG7	B	301	31/31	0.25	-	20,36,44,56	0

## 6.5 Other polymers

There are no such residues in this entry.