



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 05:15 AM BST

PDB ID : 3GBM  
Title : Crystal Structure of Fab CR6261 in Complex with a H5N1 influenza virus hemagglutinin.  
Authors : Ekiert, D.C.; Elsliger, M.A.; Wilson, I.A.  
Deposited on : 2009-02-20  
Resolution : 2.70 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](mailto: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 ⓘ 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

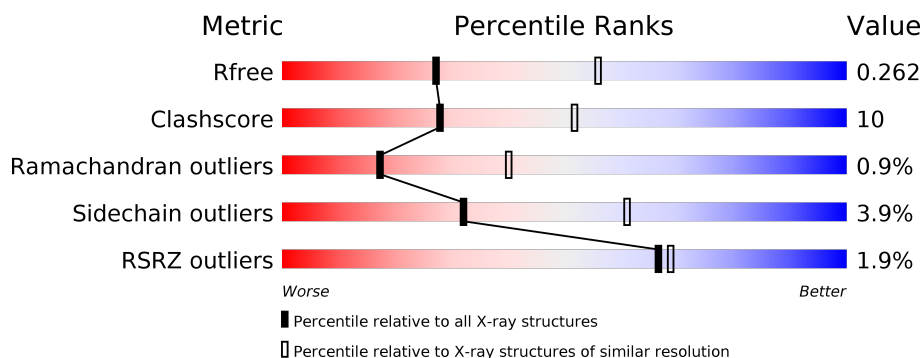
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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  $\leq 5\%$ . 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	A	334	<div> <div>75%</div> <div>19%</div> <div>• •</div> </div>
1	C	334	<div> <div>73%</div> <div>22%</div> <div>• •</div> </div>
2	B	177	<div> <div>87%</div> <div>12%</div> <div>•</div> </div>
2	D	177	<div> <div>85%</div> <div>12%</div> <div>•</div> </div>
3	H	226	<div> <div>%</div> <div>75%</div> <div>19%</div> <div>• 5%</div> </div>
3	I	226	<div> <div>4%</div> <div>74%</div> <div>18%</div> <div>• 6%</div> </div>

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Mol	Chain	Length	Quality of chain
4	L	221	
4	M	221	
5	E	2	
5	F	2	

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	BMA	A	4	-	-	-	X

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 14189 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	1	0
			2558	1616	438	489	15			
1	C	323	Total	C	N	O	S	0	1	0
			2485	1568	419	483	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	-	expression tag	UNP Q6DQ33
A	8	ASP	-	expression tag	UNP Q6DQ33
A	9	PRO	-	expression tag	UNP Q6DQ33
A	10	GLY	-	expression tag	UNP Q6DQ33
C	7	ALA	-	expression tag	UNP Q6DQ33
C	8	ASP	-	expression tag	UNP Q6DQ33
C	9	PRO	-	expression tag	UNP Q6DQ33
C	10	GLY	-	expression tag	UNP Q6DQ33

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	177	Total	C	N	O	S	0	0	0
			1407	874	246	279	8			
2	D	173	Total	C	N	O	S	0	0	0
			1373	852	239	274	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	175	SER	-	expression tag	UNP Q6DQ33
B	176	GLY	-	expression tag	UNP Q6DQ33
B	177	ARG	-	expression tag	UNP Q6DQ33
D	175	SER	-	expression tag	UNP Q6DQ33

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Chain	Residue	Modelled	Actual	Comment	Reference
D	176	GLY	-	expression tag	UNP Q6DQ33
D	177	ARG	-	expression tag	UNP Q6DQ33

- Molecule 3 is a protein called antibody (Fab).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	214	Total	C	N	O	S	0	0	0
			1572	1000	257	306	9			
3	I	213	Total	C	N	O	S	0	0	0
			1555	986	255	305	9			

- Molecule 4 is a protein called antibody (Fab).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	208	Total	C	N	O	S	0	0	0
			1498	943	244	307	4			
4	M	197	Total	C	N	O	S	0	0	0
			1415	892	230	289	4			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



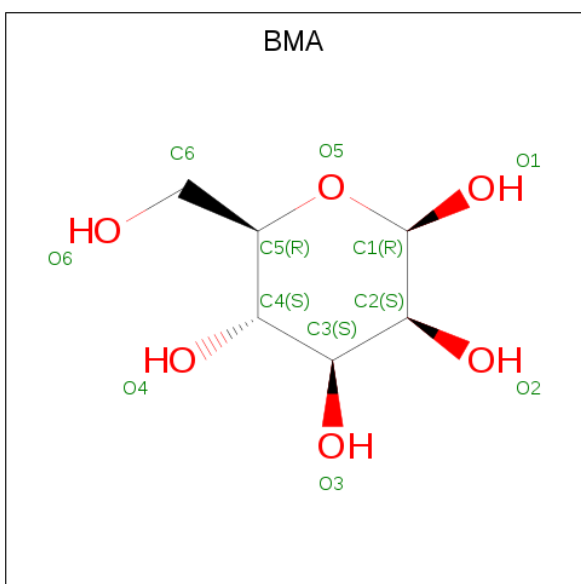
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 7 is beta-D-mannopyranose (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			11	6	5		
7	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 10 is water.

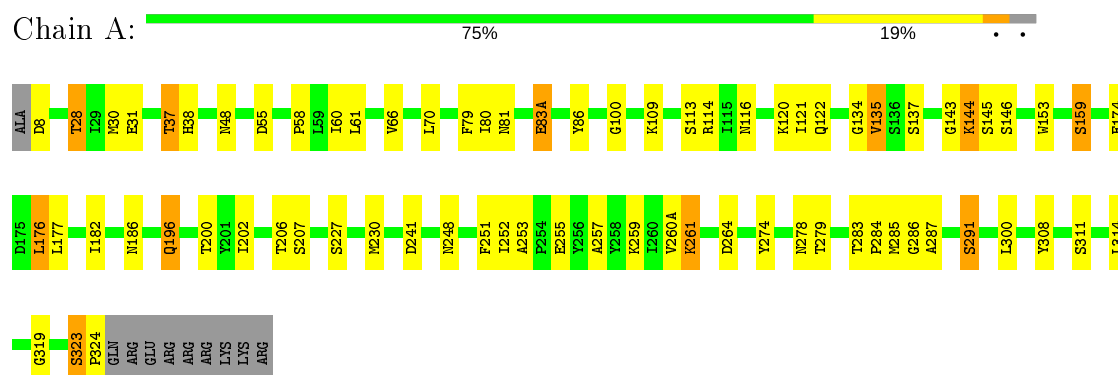
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	52	Total	O	0	0
			52	52		
10	B	38	Total	O	0	0
			38	38		
10	C	5	Total	O	0	0
			5	5		
10	D	24	Total	O	0	0
			24	24		
10	H	17	Total	O	0	0
			17	17		
10	L	6	Total	O	0	0
			6	6		
10	I	13	Total	O	0	0
			13	13		
10	M	9	Total	O	0	0
			9	9		



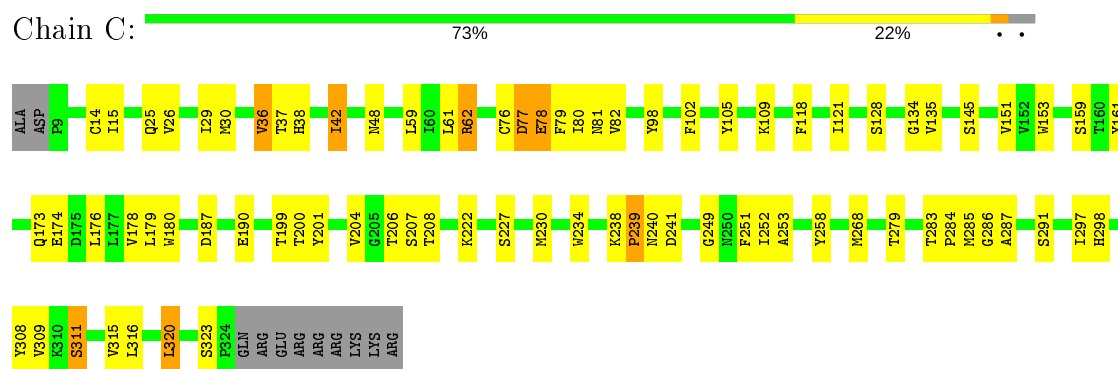
### 3 Residue-property plots

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 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.

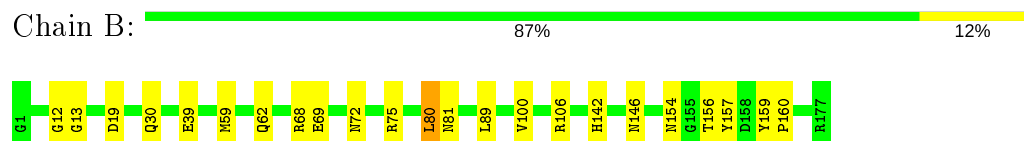
#### • Molecule 1: Hemagglutinin



#### • Molecule 1: Hemagglutinin



#### • Molecule 2: Hemagglutinin

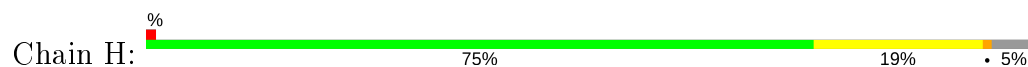


#### • Molecule 2: Hemagglutinin

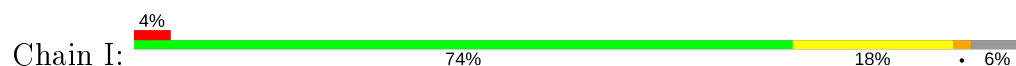




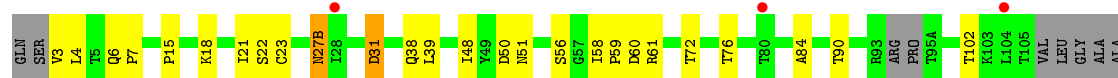
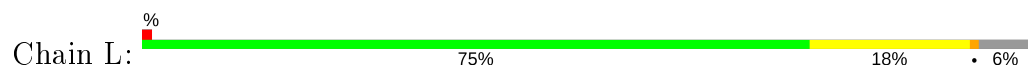
- Molecule 3: antibody (Fab)



- Molecule 3: antibody (Fab)



- Molecule 4: antibody (Fab)



- Molecule 4: antibody (Fab)



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

HA01  
HA02

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

HA01  
HA02

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	202.76 Å   202.76 Å   202.76 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	49.00 – 2.70 49.18 – 2.70	Depositor EDS
% Data completeness (in resolution range)	94.0 (49.00-2.70) 94.1 (49.18-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.69 Å)	Xtriage
Refinement program	REFMAC 5.5.0044	Depositor
R, $R_{free}$	0.203 , 0.261 0.205 , 0.262	Depositor DCC
$R_{free}$ test set	3645 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 57.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	14189	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.20% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BMA, NAG, EDO

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	0.64	0/2624	0.75	0/3569
1	C	0.53	0/2551	0.63	0/3481
2	B	0.74	0/1434	0.82	2/1930 (0.1%)
2	D	0.61	0/1400	0.66	0/1888
3	H	0.65	0/1612	0.67	0/2201
3	I	0.57	0/1594	0.65	0/2177
4	L	0.64	1/1535 (0.1%)	0.68	1/2109 (0.0%)
4	M	0.51	0/1447	0.60	0/1984
All	All	0.61	1/14197 (0.0%)	0.69	3/19339 (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
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	190	ARG	NE-CZ	13.00	1.50	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	190	ARG	CD-NE-CZ	-8.54	111.65	123.60
2	B	106	ARG	NE-CZ-NH2	-6.75	116.93	120.30
2	B	106	ARG	NE-CZ-NH1	5.66	123.13	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	323	SER	Peptide

## 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	A	2558	0	2468	63	0
1	C	2485	0	2322	75	0
2	B	1407	0	1295	17	0
2	D	1373	0	1233	18	0
3	H	1572	0	1520	38	0
3	I	1555	0	1490	31	0
4	L	1498	0	1376	30	0
4	M	1415	0	1298	23	0
5	E	28	0	25	0	0
5	F	28	0	25	0	0
6	A	28	0	26	0	0
6	B	14	0	13	0	0
6	C	14	0	13	1	0
6	D	14	0	13	0	0
7	A	11	0	10	0	0
7	C	11	0	10	0	0
8	A	4	0	6	0	0
8	C	4	0	6	0	0
9	B	6	0	8	1	0
10	A	52	0	0	3	0
10	B	38	0	0	0	0
10	C	5	0	0	0	0
10	D	24	0	0	0	0
10	H	17	0	0	0	0
10	I	13	0	0	0	0
10	L	6	0	0	0	0
10	M	9	0	0	1	0
All	All	14189	0	13157	268	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 10.

All (268) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:THR:HG22	1:C:38:HIS:CD2	1.70	1.24
1:C:42:ILE:CD1	1:C:316:LEU:HD12	1.82	1.09
1:A:37:THR:CG2	1:A:38:HIS:CD2	2.37	1.07
1:A:279:THR:HG21	1:A:287:ALA:HB1	1.36	1.05
1:C:37:THR:CG2	1:C:38:HIS:CD2	2.45	0.99
1:A:283:THR:HG22	1:A:285:MET:H	1.28	0.98
1:C:251:PHE:CE2	1:C:253:ALA:HB2	1.99	0.97
3:H:190:VAL:HG21	4:L:135:LEU:CD1	1.94	0.96
3:I:39:GLN:HE22	4:M:38:GLN:HE22	1.10	0.94
3:H:190:VAL:HG21	4:L:135:LEU:HD13	1.50	0.94
4:L:120:PRO:HD3	4:L:132:LEU:HD12	1.51	0.91
1:A:37:THR:HG22	1:A:38:HIS:CD2	2.04	0.90
3:H:39:GLN:HE22	4:L:38:GLN:HE22	1.19	0.89
1:A:37:THR:HG23	1:A:38:HIS:CD2	2.06	0.88
1:C:283:THR:HG22	1:C:285:MET:H	1.37	0.86
1:A:206:THR:HG22	1:A:207:SER:H	1.42	0.83
4:L:4:LEU:HD11	4:L:23:CYS:SG	2.18	0.83
1:A:113:SER:HB3	10:A:356:HOH:O	1.78	0.83
1:C:42:ILE:HD13	1:C:316:LEU:HD12	1.62	0.80
1:A:37:THR:CG2	1:A:38:HIS:HD2	1.95	0.80
1:A:206:THR:HG22	1:A:207:SER:N	1.98	0.79
3:H:121:VAL:HG21	3:H:210:VAL:HG21	1.65	0.78
1:A:206:THR:CG2	1:A:241:ASP:OD2	2.33	0.76
1:C:283:THR:HB	1:C:286:GLY:O	1.86	0.75
3:I:93:ALA:HB3	3:I:100(D):MET:CE	2.16	0.75
3:I:93:ALA:HB3	3:I:100(D):MET:HE2	1.68	0.75
4:M:19:VAL:HG23	4:M:75:ILE:HG23	1.68	0.74
4:L:39:LEU:HD23	4:L:84:ALA:HB2	1.70	0.73
1:A:159:SER:O	1:A:196:GLN:NE2	2.21	0.73
1:A:37:THR:HG22	1:A:38:HIS:HD2	1.53	0.73
1:A:279:THR:CG2	1:A:287:ALA:HB1	2.18	0.73
1:C:206:THR:HG22	1:C:207:SER:N	2.05	0.71
1:C:200:THR:CG2	1:C:201:TYR:N	2.54	0.71
1:A:283:THR:HB	1:A:286:GLY:O	1.90	0.71
1:C:206:THR:CG2	1:C:207:SER:N	2.55	0.70
3:I:154:VAL:HG22	3:I:210:VAL:HG22	1.72	0.70
1:C:37:THR:HG22	1:C:38:HIS:HD2	1.47	0.70
1:C:279:THR:HG21	1:C:287:ALA:HB1	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:VAL:CG2	2:D:104:ASN:ND2	2.56	0.69
3:H:190:VAL:CG2	4:L:135:LEU:HD13	2.22	0.68
3:I:20:VAL:HG11	3:I:107:THR:HG21	1.75	0.68
1:A:283:THR:HG22	1:A:285:MET:N	2.05	0.67
2:D:68:ARG:NH1	2:D:81:ASN:HD21	1.93	0.67
1:C:26:VAL:HG22	2:D:104:ASN:ND2	2.10	0.67
3:H:190:VAL:CG2	4:L:135:LEU:CD1	2.70	0.66
1:C:268:MET:HE3	1:C:284:PRO:HA	1.75	0.66
3:H:93:ALA:HB3	3:H:100(D):MET:CE	2.25	0.66
4:L:18:LYS:CB	4:L:76:THR:HG22	2.26	0.66
3:I:217:THR:HG22	3:I:219:VAL:HG23	1.78	0.65
4:L:120:PRO:HD3	4:L:132:LEU:CD1	2.26	0.65
4:L:159:VAL:HG22	4:L:179:LEU:HD13	1.79	0.64
1:C:320:LEU:CD1	1:C:320:LEU:N	2.59	0.64
4:L:144:VAL:HG12	4:L:198:HIS:HB2	1.79	0.64
1:C:98:TYR:CE2	1:C:230:MET:HE1	2.32	0.64
4:M:27(B):ASN:HD22	4:M:93:ARG:CD	2.11	0.63
2:D:42:GLN:HE22	3:I:98:TYR:H	1.46	0.63
1:C:320:LEU:HD12	1:C:320:LEU:N	2.14	0.63
1:C:206:THR:HG22	1:C:208:THR:H	1.64	0.62
2:B:68:ARG:NH1	2:B:81:ASN:HD21	1.96	0.62
2:D:48:VAL:O	2:D:52:VAL:HG23	2.00	0.62
2:D:68:ARG:HH11	2:D:81:ASN:HD21	1.48	0.62
1:C:135:VAL:CG1	1:C:145:SER:O	2.48	0.62
3:H:52:ILE:CG2	3:H:52(A):PRO:HD2	2.30	0.62
1:C:251:PHE:CZ	1:C:253:ALA:HB2	2.35	0.61
2:B:80:LEU:HD12	2:B:80:LEU:O	2.00	0.61
1:C:62:ARG:NH1	1:C:78:GLU:OE2	2.34	0.61
1:C:176:LEU:CD1	1:C:178:VAL:HG22	2.31	0.60
1:C:200:THR:HG21	1:C:249:GLY:O	2.01	0.60
1:A:60:ILE:HD13	1:A:274:TYR:HB2	1.83	0.60
1:C:42:ILE:HD12	1:C:316:LEU:HD12	1.80	0.60
1:C:187:ASP:OD2	1:C:190:GLU:N	2.35	0.60
3:H:90:TYR:CE2	3:H:109:VAL:HG13	2.37	0.60
1:A:135:VAL:HG22	1:A:146:SER:HA	1.84	0.59
2:D:42:GLN:HE22	3:I:98:TYR:N	2.01	0.59
1:A:176:LEU:HD21	1:A:257:ALA:HB1	1.85	0.59
1:C:98:TYR:CD2	1:C:230:MET:HE1	2.38	0.59
2:B:68:ARG:HH11	2:B:81:ASN:HD21	1.51	0.59
4:M:194:CYS:O	4:M:196:VAL:HG23	2.03	0.59
1:A:206:THR:HG23	1:A:241:ASP:OD2	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:121:VAL:CG2	3:H:210:VAL:HG21	2.34	0.58
1:C:151:VAL:HG22	1:C:252:ILE:HG22	1.86	0.58
3:I:40:ALA:HB3	3:I:43:GLN:HE21	1.68	0.58
1:C:79:PHE:O	1:C:81:ASN:N	2.37	0.58
3:H:52:ILE:HG23	3:H:52(A):PRO:HD2	1.86	0.58
1:A:55:ASP:O	1:A:278:ASN:ND2	2.36	0.57
1:C:297:ILE:N	1:C:297:ILE:HD13	2.20	0.57
1:C:200:THR:HG21	1:C:249:GLY:C	2.24	0.57
1:A:186:ASN:HD21	1:A:227:SER:C	2.08	0.57
1:C:42:ILE:HD11	1:C:316:LEU:HD12	1.84	0.57
4:L:3:VAL:O	4:L:3:VAL:HG13	2.04	0.57
1:C:200:THR:HG22	1:C:201:TYR:N	2.20	0.56
1:C:135:VAL:HG11	1:C:145:SER:O	2.03	0.56
2:D:49:THR:HG23	3:I:29:PHE:HB3	1.87	0.56
1:A:200:THR:HA	1:A:248:ASN:OD1	2.04	0.56
1:C:98:TYR:CD2	1:C:230:MET:CE	2.89	0.56
2:D:119:TYR:OH	2:D:132:GLU:HG2	2.05	0.55
3:H:93:ALA:HB3	3:H:100(D):MET:HE2	1.87	0.55
1:C:61:LEU:O	1:C:62:ARG:C	2.44	0.55
1:A:206:THR:CG2	1:A:207:SER:N	2.69	0.55
3:H:177:VAL:HG23	4:L:162:THR:HG22	1.88	0.55
4:M:27(B):ASN:OD1	4:M:28:ILE:N	2.35	0.55
1:C:230:MET:HG3	1:C:252:ILE:HD13	1.88	0.54
1:A:314:LEU:HD22	2:B:100:VAL:HG21	1.89	0.54
3:I:47:TRP:CZ2	3:I:49:GLY:HA2	2.42	0.54
4:M:159:VAL:HG22	10:M:216:HOH:O	2.07	0.54
4:M:136:ILE:HD13	4:M:196:VAL:HG11	1.88	0.54
1:C:308:TYR:HD2	2:D:89:LEU:HD22	1.73	0.54
1:C:26:VAL:HG23	1:C:315:VAL:O	2.08	0.54
4:L:50:ASP:O	4:L:51:ASN:HB2	2.05	0.54
3:I:187:LEU:HD12	3:I:187:LEU:C	2.28	0.54
3:I:137:THR:N	3:I:195:SER:HG	2.06	0.54
3:H:93:ALA:HB3	3:H:100(D):MET:HE1	1.90	0.54
1:A:176:LEU:HD23	1:A:177:LEU:N	2.23	0.54
3:H:121:VAL:HG11	3:H:210:VAL:HG21	1.89	0.53
4:M:19:VAL:HG21	4:M:104:LEU:HD11	1.89	0.53
4:M:84:ALA:HB3	4:M:86:TYR:CE1	2.44	0.53
1:C:134:GLY:HA3	1:C:153:TRP:HB3	1.89	0.53
1:C:200:THR:HG23	1:C:201:TYR:H	1.73	0.53
3:I:93:ALA:HB3	3:I:100(D):MET:HE1	1.91	0.53
1:A:230:MET:SD	1:A:252:ILE:HD11	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LEU:HD21	1:A:257:ALA:CB	2.39	0.52
4:L:22:SER:HA	4:L:72:THR:HG22	1.89	0.52
3:H:4:LEU:HD22	3:H:22:CYS:SG	2.49	0.52
1:C:151:VAL:CG2	1:C:252:ILE:HG22	2.40	0.52
2:B:72:ASN:HD22	2:B:75:ARG:NH2	2.07	0.52
3:I:217:THR:HG22	3:I:219:VAL:CG2	2.39	0.52
1:A:116:ASN:HB2	1:A:261:LYS:HG3	1.92	0.52
1:A:143:GLY:O	1:A:144:LYS:C	2.49	0.52
3:H:162:ASN:HD22	3:H:166:LEU:HD21	1.75	0.52
1:C:323:SER:OG	2:D:13:GLY:N	2.23	0.51
4:L:48:ILE:HD12	4:L:48:ILE:C	2.30	0.51
1:A:206:THR:HG22	1:A:241:ASP:OD2	2.08	0.51
1:C:206:THR:CG2	1:C:207:SER:H	2.22	0.51
3:H:39:GLN:HE22	4:L:38:GLN:NE2	1.97	0.51
4:M:37:GLN:HB2	4:M:47:LEU:HD11	1.93	0.51
1:A:291:SER:HB2	3:H:74:PHE:HB2	1.92	0.51
1:A:323:SER:HB3	1:A:324:PRO:CD	2.41	0.51
1:C:309:VAL:HG12	1:C:311:SER:H	1.76	0.51
3:I:152:VAL:HG12	3:I:187:LEU:HD21	1.91	0.51
10:A:383:HOH:O	2:B:13:GLY:HA2	2.10	0.50
4:M:36:TYR:HA	4:M:45:LYS:O	2.12	0.50
4:M:46:LEU:HD23	4:M:55:PRO:HG3	1.93	0.50
3:H:47:TRP:CZ2	3:H:49:GLY:HA2	2.46	0.50
3:H:140:LEU:HD21	3:H:191:VAL:HG13	1.93	0.50
4:L:27(B):ASN:HB2	4:L:90:THR:HG21	1.94	0.50
1:A:206:THR:CG2	1:A:207:SER:H	2.17	0.50
2:D:22:TYR:OH	2:D:111:HIS:ND1	2.38	0.50
1:A:100:GLY:HA3	1:A:230:MET:O	2.12	0.49
1:C:283:THR:HG23	1:C:298:HIS:HB3	1.94	0.49
2:D:42:GLN:NE2	3:I:98:TYR:H	2.09	0.49
3:I:30:ARG:NH1	3:I:32:TYR:O	2.46	0.49
1:C:206:THR:HG23	1:C:241:ASP:OD2	2.13	0.49
3:H:140:LEU:HD23	3:H:140:LEU:H	1.78	0.49
1:C:29:ILE:CG2	1:C:30:MET:N	2.76	0.48
1:A:323:SER:HB3	1:A:324:PRO:HD3	1.95	0.48
2:D:119:TYR:OH	2:D:132:GLU:CG	2.61	0.48
1:A:37:THR:HG23	1:A:38:HIS:NE2	2.29	0.48
3:H:157:TRP:CZ3	3:H:208:CYS:HB3	2.49	0.48
3:I:59:TYR:CD1	3:I:67:VAL:HG13	2.48	0.48
4:M:167:GLN:HE21	4:M:174:ALA:HB2	1.78	0.48
1:C:200:THR:HG23	1:C:201:TYR:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:52(A):PRO:O	3:H:54:PHE:N	2.47	0.48
3:H:140:LEU:CD2	3:H:191:VAL:HG13	2.44	0.48
4:L:21:ILE:HD13	4:L:102:THR:OG1	2.14	0.47
1:C:36:VAL:HG22	1:C:320:LEU:O	2.13	0.47
4:L:191:SER:HB2	4:L:208:THR:CG2	2.44	0.47
1:C:14:CYS:O	2:D:24:TYR:HA	2.14	0.47
1:A:308:TYR:HD2	2:B:89:LEU:HD22	1.78	0.47
3:H:36:TRP:CE2	3:H:80:MET:HB2	2.50	0.47
3:I:124:LEU:HB3	4:M:118:PHE:CE1	2.50	0.47
1:A:109:LYS:NZ	2:B:69:GLU:OE1	2.35	0.47
3:I:124:LEU:HD12	3:I:141:GLY:C	2.35	0.46
4:M:90:THR:HG22	4:M:97:VAL:HG13	1.96	0.46
4:L:21:ILE:CG2	4:L:102:THR:HG21	2.44	0.46
1:C:180:TRP:CZ2	1:C:204:VAL:HG11	2.51	0.46
3:H:17:SER:OG	3:H:82(A):SER:HB3	2.15	0.46
4:M:92:ASP:OD1	4:M:93:ARG:N	2.48	0.46
1:A:28:THR:HB	1:A:31:GLU:O	2.16	0.46
2:B:80:LEU:HD12	2:B:80:LEU:C	2.36	0.46
1:C:179:LEU:HD23	1:C:234:TRP:HB3	1.97	0.46
3:H:178:LEU:HD13	3:H:185:TYR:CE2	2.51	0.46
3:H:207:ILE:HG22	3:H:220:ASP:HB3	1.98	0.45
3:I:153:THR:O	3:I:153:THR:HG22	2.17	0.45
3:H:140:LEU:N	3:H:140:LEU:HD23	2.32	0.45
1:A:28:THR:HG22	1:A:31:GLU:H	1.81	0.45
1:C:38:HIS:CD2	2:D:21:TRP:HE1	2.34	0.45
1:C:174:GLU:OE2	1:C:174:GLU:N	2.50	0.45
4:M:9:SER:O	4:M:11:VAL:HG23	2.16	0.45
3:H:187:LEU:HD12	3:H:187:LEU:C	2.37	0.45
4:M:210:ALA:HB1	4:M:211:PRO:HD2	1.97	0.45
1:A:186:ASN:ND2	1:A:227:SER:CB	2.80	0.45
4:L:7:PRO:O	4:L:102:THR:HG22	2.17	0.45
2:B:30:GLN:HE22	2:B:146:ASN:H	1.64	0.45
1:C:230:MET:SD	1:C:252:ILE:HD11	2.57	0.45
3:H:190:VAL:HG21	4:L:135:LEU:HD12	1.91	0.45
1:A:122:GLN:NE2	1:A:255:GLU:OE2	2.50	0.44
2:B:156:THR:CG2	2:B:156:THR:O	2.66	0.44
1:C:15:ILE:N	1:C:15:ILE:HD13	2.32	0.44
1:C:268:MET:CE	1:C:284:PRO:HA	2.45	0.44
1:A:186:ASN:HD21	1:A:227:SER:CB	2.30	0.44
1:C:309:VAL:CG1	1:C:311:SER:OG	2.66	0.44
1:A:182:ILE:HD12	1:A:202:ILE:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:159:TYR:HB3	2:B:160:PRO:HD3	1.98	0.44
3:I:174:PHE:CE1	4:M:135:LEU:HD13	2.53	0.44
2:B:39:GLU:HG3	9:B:183:GOL:O3	2.18	0.43
4:M:48:ILE:HA	4:M:53:LYS:O	2.18	0.43
1:A:37:THR:HG22	1:A:319:GLY:HA3	1.98	0.43
3:H:144:VAL:HB	3:H:187:LEU:HD12	2.01	0.43
4:L:148:TRP:HB2	4:L:155:VAL:HG23	2.00	0.43
3:H:52:ILE:HG22	3:H:52(A):PRO:HD2	2.01	0.43
2:B:142:HIS:HE1	2:B:157:TYR:OH	2.00	0.43
3:I:193:VAL:HG11	3:I:206:TYR:CE1	2.53	0.43
3:H:121:VAL:HG21	3:H:210:VAL:CG2	2.43	0.43
1:C:76:CYS:O	1:C:78:GLU:N	2.52	0.43
1:C:291:SER:HB2	3:I:74:PHE:HB2	2.00	0.43
1:A:176:LEU:CD2	1:A:257:ALA:HB1	2.48	0.43
1:A:60:ILE:CD1	1:A:274:TYR:HB2	2.49	0.43
3:I:47:TRP:CH2	3:I:49:GLY:HA2	2.53	0.43
1:A:121:ILE:HD13	1:A:259:LYS:HD3	2.01	0.42
4:M:19:VAL:CG2	4:M:75:ILE:HG23	2.45	0.42
4:M:78:LEU:HD23	4:M:79:GLN:N	2.33	0.42
1:A:134:GLY:HA3	1:A:153:TRP:HB3	2.01	0.42
1:C:222:LYS:HG2	1:C:227:SER:HB2	2.01	0.42
2:D:4:GLY:O	2:D:9:PHE:HD2	2.03	0.42
3:H:124:LEU:HB3	4:L:118:PHE:CD1	2.54	0.42
2:B:19:ASP:N	2:B:19:ASP:OD1	2.41	0.42
1:C:238:LYS:O	1:C:239:PRO:C	2.57	0.42
3:I:87:THR:HG23	3:I:110:THR:HA	2.00	0.42
1:A:114:ARG:NH2	1:A:264:ASP:OD2	2.53	0.42
1:C:176:LEU:CD1	1:C:178:VAL:CG2	2.98	0.42
1:C:76:CYS:O	1:C:77:ASP:C	2.58	0.42
1:C:230:MET:CG	1:C:252:ILE:HD13	2.49	0.42
3:I:126:PRO:O	3:I:128:SER:N	2.53	0.42
4:L:58:ILE:HA	4:L:59:PRO:HD3	1.93	0.42
1:C:176:LEU:HD12	1:C:178:VAL:CG2	2.50	0.42
1:C:48:ASN:ND2	1:C:287:ALA:HB3	2.34	0.42
1:C:118:PHE:CD1	1:C:258:TYR:HB3	2.55	0.42
2:D:30:GLN:OE1	2:D:145:ASP:HB2	2.20	0.41
1:C:98:TYR:CZ	1:C:230:MET:HE1	2.54	0.41
1:C:105:TYR:CE2	1:C:109:LYS:HD2	2.55	0.41
3:I:52:ILE:HD12	3:I:56:THR:OG1	2.20	0.41
1:A:135:VAL:HG22	1:A:146:SER:CA	2.49	0.41
1:A:230:MET:SD	1:A:252:ILE:CD1	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:LYS:NZ	10:A:382:HOH:O	2.52	0.41
1:A:80:ILE:HG22	1:A:81:ASN:ND2	2.35	0.41
1:A:48:ASN:OD1	1:A:48:ASN:C	2.59	0.41
1:A:58:PRO:HB3	1:A:86:TYR:CE2	2.56	0.41
4:L:6:GLN:NE2	4:L:102:THR:HG23	2.36	0.41
1:A:28:THR:HG22	1:A:30:MET:H	1.86	0.41
1:C:161:TYR:CE2	1:C:249:GLY:HA2	2.56	0.41
3:H:52:ILE:HG23	3:H:98:TYR:O	2.21	0.41
1:A:251:PHE:CE2	1:A:253:ALA:HB2	2.56	0.41
1:C:268:MET:HE1	1:C:283:THR:C	2.41	0.41
1:C:98:TYR:CD2	1:C:230:MET:HE2	2.56	0.41
4:M:122:SER:HA	4:M:125:LEU:HD12	2.03	0.41
1:A:66:VAL:HG12	1:A:70:LEU:HD12	2.03	0.41
2:B:59:MET:HE2	2:B:62:GLN:OE1	2.21	0.41
4:L:120:PRO:CD	4:L:132:LEU:HD12	2.35	0.41
1:A:137:SER:HA	1:A:145:SER:HB2	2.02	0.40
1:A:284:PRO:HD3	1:A:300:LEU:O	2.21	0.40
3:I:59:TYR:CE1	3:I:67:VAL:HG13	2.56	0.40
1:A:83(A):GLU:HG3	1:A:261:LYS:HE2	2.04	0.40
1:A:61:LEU:HA	1:A:79:PHE:CZ	2.56	0.40
1:C:25:GLN:NE2	6:C:334:NAG:O7	2.55	0.40
3:I:37:VAL:HG21	3:I:100(D):MET:HE1	2.04	0.40
4:L:31:ASP:OD1	4:L:31:ASP:N	2.55	0.40
2:B:154:ASN:OD1	2:B:156:THR:HB	2.21	0.40
3:H:52:ILE:CD1	3:H:100:VAL:HG13	2.51	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	323/334 (97%)	306 (95%)	15 (5%)	2 (1%)	25 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	322/334 (96%)	293 (91%)	22 (7%)	7 (2%)	6	17
2	B	175/177 (99%)	170 (97%)	4 (2%)	1 (1%)	25	50
2	D	171/177 (97%)	167 (98%)	3 (2%)	1 (1%)	25	50
3	H	210/226 (93%)	201 (96%)	8 (4%)	1 (0%)	29	54
3	I	209/226 (92%)	195 (93%)	12 (6%)	2 (1%)	15	37
4	L	202/221 (91%)	187 (93%)	13 (6%)	2 (1%)	15	37
4	M	187/221 (85%)	165 (88%)	21 (11%)	1 (0%)	29	54
All	All	1799/1916 (94%)	1684 (94%)	98 (5%)	17 (1%)	17	40

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	80	ILE
3	I	127	SER
1	C	62	ARG
1	C	77	ASP
1	C	78	GLU
1	C	159	SER
1	C	199	THR
4	L	212	THR
4	M	204	THR
2	D	172	GLU
1	A	144	LYS
1	A	196	GLN
4	L	15	PRO
1	C	239	PRO
3	I	126	PRO
2	B	12	GLY
3	H	53	ILE

### 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	286/300 (95%)	274 (96%)	12 (4%)	30	58
1	C	271/300 (90%)	260 (96%)	11 (4%)	30	59
2	B	145/151 (96%)	144 (99%)	1 (1%)	84	94
2	D	138/151 (91%)	136 (99%)	2 (1%)	67	86
3	H	170/189 (90%)	160 (94%)	10 (6%)	19	43
3	I	168/189 (89%)	158 (94%)	10 (6%)	19	42
4	L	156/182 (86%)	149 (96%)	7 (4%)	27	55
4	M	146/182 (80%)	142 (97%)	4 (3%)	44	74
All	All	1480/1644 (90%)	1423 (96%)	57 (4%)	32	61

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASP
1	A	28	THR
1	A	37	THR
1	A	83(A)	GLU
1	A	135	VAL
1	A	159	SER
1	A	174	GLU
1	A	176	LEU
1	A	260(A)	VAL
1	A	261	LYS
1	A	291	SER
1	A	311	SER
2	B	80	LEU
1	C	36	VAL
1	C	42	ILE
1	C	59	LEU
1	C	82	VAL
1	C	102	PHE
1	C	121	ILE
1	C	128	SER
1	C	173	GLN
1	C	240	ASN
1	C	311	SER
1	C	320	LEU
2	D	19	ASP
2	D	27	SER
3	H	6	GLU

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Mol	Chain	Res	Type
3	H	43	GLN
3	H	56	THR
3	H	94	LYS
3	H	109	VAL
3	H	115	SER
3	H	116	THR
3	H	195	SER
3	H	205	THR
3	H	208	CYS
4	L	27(B)	ASN
4	L	31	ASP
4	L	56	SER
4	L	60	ASP
4	L	61	ARG
4	L	155	VAL
4	L	176	SER
3	I	6	GLU
3	I	80	MET
3	I	83	ARG
3	I	94	LYS
3	I	108	THR
3	I	137	THR
3	I	152	VAL
3	I	168	SER
3	I	195	SER
3	I	208	CYS
4	M	24	SER
4	M	75	ILE
4	M	145	THR
4	M	197	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	81	ASN
1	A	95	ASN
1	A	122	GLN
1	A	142	GLN
1	A	186	ASN
1	A	196	GLN
1	A	197	ASN

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Mol	Chain	Res	Type
1	A	278	ASN
2	B	30	GLN
2	B	50	ASN
2	B	72	ASN
2	B	81	ASN
2	B	117	ASN
2	B	142	HIS
2	B	146	ASN
1	C	38	HIS
1	C	95	ASN
1	C	150	ASN
1	C	197	ASN
1	C	278	ASN
2	D	42	GLN
2	D	50	ASN
2	D	72	ASN
2	D	81	ASN
2	D	117	ASN
2	D	125	GLN
2	D	142	HIS
2	D	161	GLN
3	H	64	GLN
3	H	172	HIS
3	H	179	GLN
4	L	37	GLN
4	L	38	GLN
3	I	43	GLN
3	I	172	HIS
4	M	38	GLN
4	M	79	GLN
4	M	167	GLN
4	M	185	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 ⓘ

4 monosaccharides 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	E	1	1,5	14,14,15	0.49	0	17,19,21	1.78	2 (11%)
5	NAG	E	2	5	14,14,15	0.74	0	17,19,21	1.47	4 (23%)
5	NAG	F	1	1,5	14,14,15	0.44	0	17,19,21	1.43	3 (17%)
5	NAG	F	2	5	14,14,15	0.58	0	17,19,21	2.59	4 (23%)

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	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	1/6/23/26	0/1/1/1
5	NAG	F	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	F	2	5	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	2	NAG	C1-O5-C5	7.73	122.67	112.19
5	E	1	NAG	C1-O5-C5	5.20	119.24	112.19
5	F	2	NAG	C4-C3-C2	-5.11	103.52	111.02
5	E	2	NAG	O5-C1-C2	3.33	116.54	111.29
5	F	1	NAG	C3-C4-C5	-2.97	104.93	110.24
5	E	2	NAG	C1-O5-C5	2.75	115.92	112.19
5	F	2	NAG	O4-C4-C5	2.73	116.09	109.30
5	E	2	NAG	C4-C3-C2	2.72	115.00	111.02
5	E	1	NAG	C6-C5-C4	-2.42	107.33	113.00
5	E	2	NAG	O5-C5-C4	-2.18	105.52	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	2	NAG	C1-C2-N2	2.14	114.14	110.49
5	F	1	NAG	C1-O5-C5	2.09	115.02	112.19
5	F	1	NAG	O5-C5-C6	2.05	110.42	107.20

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	1	NAG	O5-C5-C6-O6
5	F	2	NAG	O5-C5-C6-O6
5	F	1	NAG	C4-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 5.6 Ligand geometry ⓘ

10 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
6	NAG	C	334	1	14,14,15	0.93	1 (7%)	17,19,21	1.68	4 (23%)
6	NAG	D	182	2	14,14,15	1.19	1 (7%)	17,19,21	1.85	6 (35%)
6	NAG	B	182	2	14,14,15	0.58	0	17,19,21	2.26	2 (11%)
8	EDO	C	335	-	3,3,3	0.43	0	2,2,2	0.33	0
8	EDO	A	336	-	3,3,3	0.42	0	2,2,2	0.72	0
6	NAG	A	335	1	14,14,15	0.55	0	17,19,21	2.32	2 (11%)
7	BMA	A	4	-	11,11,12	0.40	0	15,15,17	0.98	0
9	GOL	B	183	-	5,5,5	0.36	0	5,5,5	0.47	0
7	BMA	C	4	-	11,11,12	0.42	0	15,15,17	1.45	4 (26%)
6	NAG	A	1	1	14,14,15	0.69	0	17,19,21	1.31	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
6	NAG	C	334	1	-	0/6/23/26	0/1/1/1
6	NAG	D	182	2	-	2/6/23/26	0/1/1/1
6	NAG	B	182	2	-	2/6/23/26	0/1/1/1
8	EDO	C	335	-	-	0/1/1/1	-
8	EDO	A	336	-	-	1/1/1/1	-
6	NAG	A	335	1	-	1/6/23/26	0/1/1/1
7	BMA	A	4	-	-	2/2/19/22	0/1/1/1
9	GOL	B	183	-	-	4/4/4/4	-
7	BMA	C	4	-	-	0/2/19/22	0/1/1/1
6	NAG	A	1	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	182	NAG	C1-C2	3.54	1.57	1.52
6	C	334	NAG	O5-C1	-2.14	1.40	1.43

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	335	NAG	C1-O5-C5	7.83	122.80	112.19
6	B	182	NAG	C1-O5-C5	7.78	122.74	112.19
6	D	182	NAG	C1-O5-C5	4.16	117.83	112.19
6	A	335	NAG	C4-C3-C2	-3.65	105.67	111.02
6	C	334	NAG	C4-C3-C2	3.42	116.04	111.02
6	A	1	NAG	C1-O5-C5	3.36	116.75	112.19
6	B	182	NAG	C6-C5-C4	-3.14	105.65	113.00
6	D	182	NAG	C2-N2-C7	3.12	127.35	122.90
7	C	4	BMA	O5-C1-C2	-3.02	106.11	110.77
7	C	4	BMA	O5-C5-C6	2.94	111.81	107.20
6	C	334	NAG	C1-C2-N2	-2.81	105.70	110.49
6	D	182	NAG	C1-C2-N2	2.64	115.00	110.49
6	C	334	NAG	C2-N2-C7	2.51	126.48	122.90
6	D	182	NAG	O5-C1-C2	2.30	114.91	111.29
6	D	182	NAG	O4-C4-C5	2.22	114.81	109.30
6	D	182	NAG	O7-C7-N2	2.13	125.87	121.95
7	C	4	BMA	C6-C5-C4	-2.11	108.07	113.00
7	C	4	BMA	O2-C2-C3	-2.03	106.07	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	334	NAG	O5-C5-C4	-2.00	105.95	110.83

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	183	GOL	C1-C2-C3-O3
6	B	182	NAG	C4-C5-C6-O6
6	D	182	NAG	O5-C5-C6-O6
6	D	182	NAG	C4-C5-C6-O6
6	B	182	NAG	O5-C5-C6-O6
7	A	4	BMA	O5-C5-C6-O6
9	B	183	GOL	O1-C1-C2-C3
9	B	183	GOL	O2-C2-C3-O3
7	A	4	BMA	C4-C5-C6-O6
9	B	183	GOL	O1-C1-C2-O2
6	A	335	NAG	C4-C5-C6-O6
8	A	336	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	334	NAG	1	0
9	B	183	GOL	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

### 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	324/334 (97%)	-0.18	0  	22, 45, 53, 60	0
1	C	323/334 (96%)	-0.06	0  	31, 57, 66, 70	0
2	B	177/177 (100%)	0.11	0  	18, 34, 46, 53	0
2	D	173/177 (97%)	0.09	0  	30, 45, 56, 62	0
3	H	214/226 (94%)	-0.13	3 (1%)  	28, 44, 65, 67	0
3	I	213/226 (94%)	0.01	9 (4%)  	37, 49, 72, 74	0
4	L	208/221 (94%)	0.11	3 (1%)  	47, 59, 78, 87	0
4	M	197/221 (89%)	0.44	19 (9%)  	49, 61, 75, 79	0
All	All	1829/1916 (95%)	0.02	34 (1%)  	18, 50, 70, 87	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	M	27(A)	SER	5.1
3	I	198	LEU	5.0
4	M	104	LEU	4.6
4	M	144	VAL	4.5
4	M	142	GLY	4.4
3	I	138	ALA	4.4
4	M	173	TYR	3.6
4	M	205	VAL	3.6
4	M	203	SER	3.6
4	M	140	TYR	3.6
3	I	205	THR	3.5
4	M	143	ALA	3.4
3	I	193	VAL	3.4
3	H	198	LEU	3.3
3	I	125	ALA	3.3
3	H	223	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
3	I	206	TYR	2.8
3	I	197	SER	2.7
4	L	28	ILE	2.7
3	H	206	TYR	2.6
4	M	157	ALA	2.6
3	I	127	SER	2.6
4	M	194	CYS	2.5
4	M	148	TRP	2.5
4	M	170	ASN	2.5
4	M	139	PHE	2.4
4	M	115	VAL	2.3
4	M	204	THR	2.3
4	L	104	LEU	2.2
4	M	190	ARG	2.2
4	M	106	VAL	2.1
4	M	196	VAL	2.1
3	I	194	PRO	2.1
4	L	80	THR	2.0

## 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
5	NAG	E	2	14/15	0.84	0.27	92,96,97,98	0
5	NAG	F	2	14/15	0.85	0.26	100,102,103,103	0
5	NAG	E	1	14/15	0.94	0.14	69,74,79,85	0
5	NAG	F	1	14/15	0.95	0.15	85,88,92,96	0

## 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
7	BMA	A	4	11/12	0.73	0.42	42,47,48,48	11
6	NAG	D	182	14/15	0.78	0.23	71,74,80,81	0
6	NAG	C	334	14/15	0.89	0.26	74,80,83,84	0
7	BMA	C	4	11/12	0.90	0.32	30,32,33,33	11
6	NAG	B	182	14/15	0.91	0.20	62,68,71,72	0
6	NAG	A	335	14/15	0.91	0.11	69,73,74,74	0
6	NAG	A	1	14/15	0.92	0.13	60,68,70,71	0
9	GOL	B	183	6/6	0.94	0.14	63,65,65,66	0
8	EDO	C	335	4/4	0.96	0.21	56,58,59,60	0
8	EDO	A	336	4/4	0.98	0.21	41,43,43,45	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.