



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:01 AM GMT

PDB ID : 2Z64
Title : Crystal structure of mouse TLR4 and mouse MD-2 complex
Authors : Lee, J.-O.; Kim, H.M.; Park, B.S.
Deposited on : 2007-07-22
Resolution : 2.84 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

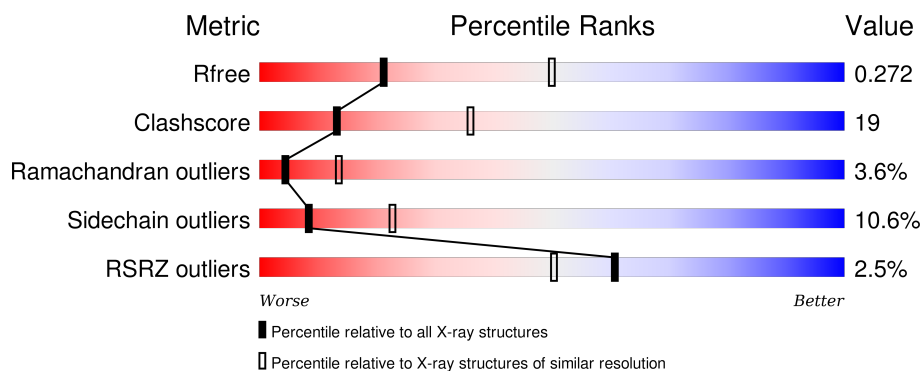
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.84 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3170 (2.88-2.80)
Clashscore	102246	3658 (2.88-2.80)
Ramachandran outliers	100387	3591 (2.88-2.80)
Sidechain outliers	100360	3594 (2.88-2.80)
RSRZ outliers	91569	3184 (2.88-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	599	<div> <div>7%</div> <div>54%</div> <div>40%</div> <div>6%</div> </div>
2	C	135	<div> <div>7%</div> <div>65%</div> <div>32%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6302 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 Toll-like receptor 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	599	Total	C	N	O	S	0	0	0
			4774	3055	785	906	28			

- Molecule 2 is a protein called Lymphocyte antigen 96.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	135	Total	C	N	O	S	0	0	0
			1093	706	182	198	7			

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

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

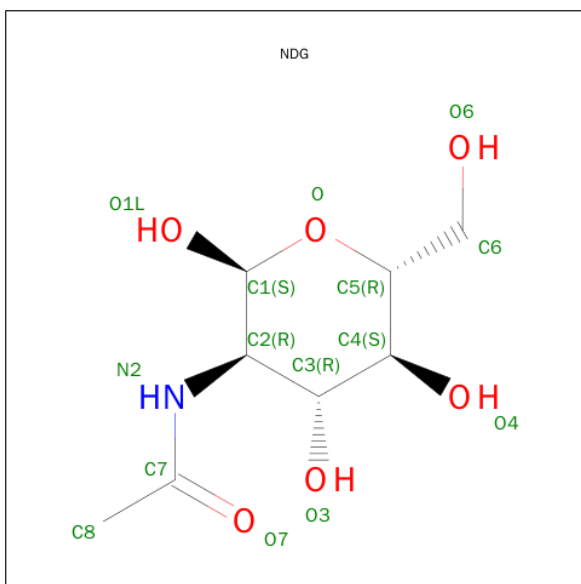
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			39	22	2	15		
4	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is SUGAR (2-(ACETYLAMINO)-2-DEOXY-A-D-GLUCOPYRANOSE) (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



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	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	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	4	Total	C	N	O	0	0
			49	28	2	19		

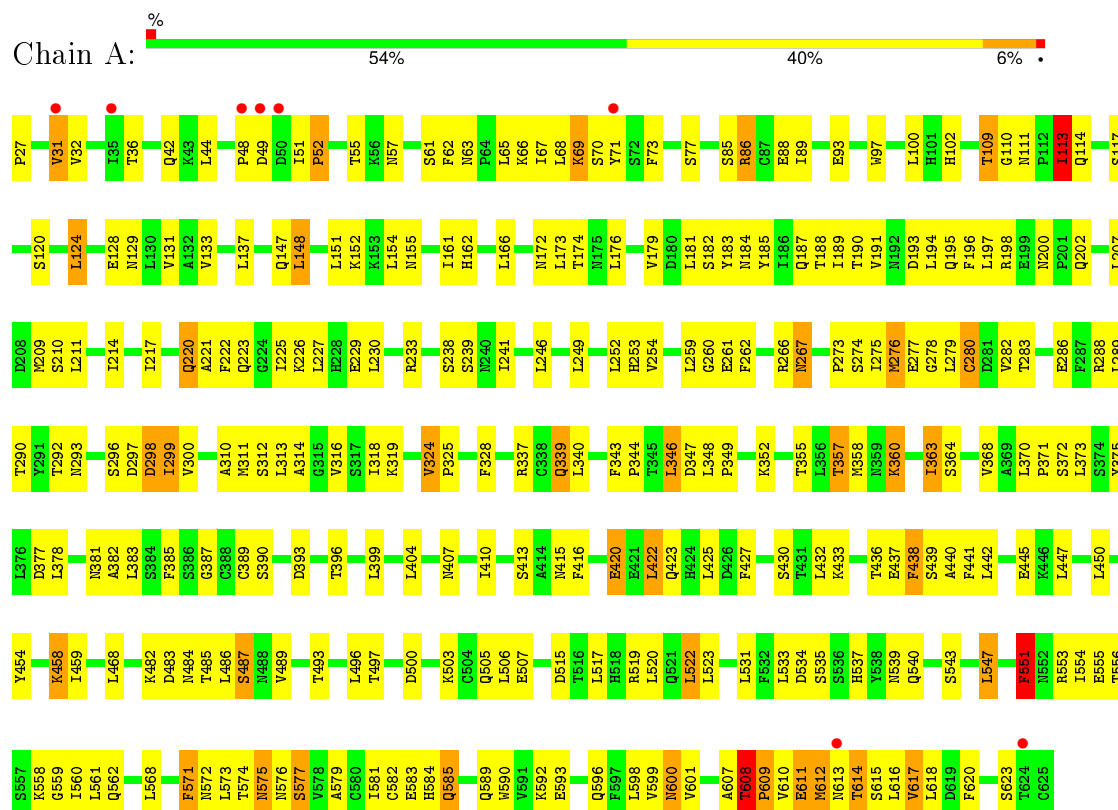
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	124	Total	O	0	0
			124	124		
8	C	30	Total	O	0	0
			30	30		

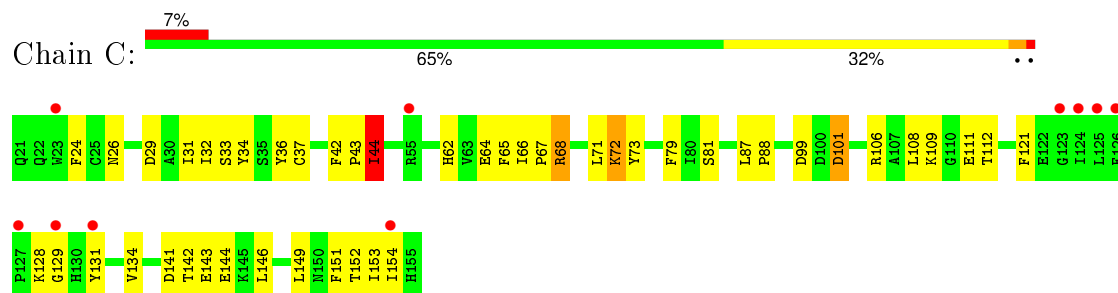
3 Residue-property plots

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: Toll-like receptor 4



• Molecule 2: Lymphocyte antigen 96



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.16Å 101.88Å 126.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.84 39.66 – 2.84	Depositor EDS
% Data completeness (in resolution range)	90.1 (20.00-2.84) 89.7 (39.66-2.84)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.46 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.242 , 0.290 0.227 , 0.272	Depositor DCC
R_{free} test set	1183 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	64.0	Xtriage
Anisotropy	0.408	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 23437 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6302	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.50	0/4874	0.66	1/6604 (0.0%)
2	C	0.56	0/1124	0.65	0/1519
All	All	0.51	0/5998	0.66	1/8123 (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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	154	LEU	CA-CB-CG	5.84	128.74	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	608	THR	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4774	0	4729	199	0
2	C	1093	0	1048	31	0
3	A	28	0	25	1	0
4	A	78	0	68	3	0
5	A	28	0	26	0	0
5	C	14	0	13	1	0
6	A	56	0	52	0	0
6	C	28	0	26	0	0
7	A	49	0	43	2	0
8	A	124	0	0	7	0
8	C	30	0	0	2	0
All	All	6302	0	6030	230	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 19.

All (230) 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:A:383:LEU:HB3	1:A:407:ASN:HD22	1.00	1.16
1:A:608:THR:HB	1:A:609:PRO:HD3	1.21	1.12
1:A:109:THR:HG23	1:A:133:VAL:HB	1.25	1.10
1:A:383:LEU:HB3	1:A:407:ASN:ND2	1.68	1.06
1:A:608:THR:HB	1:A:609:PRO:CD	2.01	0.91
1:A:404:LEU:HD12	1:A:427:PHE:HE2	1.44	0.82
1:A:381:ASN:C	1:A:383:LEU:H	1.85	0.81
1:A:166:LEU:HD22	1:A:197:LEU:HD21	1.61	0.80
1:A:97:TRP:HB3	1:A:124:LEU:HD13	1.65	0.79
1:A:582:CYS:O	1:A:585:GLN:HG3	1.82	0.79
1:A:233:ARG:HG3	8:A:1604:HOH:O	1.84	0.77
1:A:259:LEU:HD12	1:A:260:GLY:H	1.51	0.76
1:A:337:ARG:HA	1:A:358:MET:O	1.87	0.75
1:A:593:GLU:HB2	7:A:1533:NAG:H81	1.70	0.73
1:A:36:THR:HG23	1:A:57:ASN:HB2	1.71	0.72
1:A:598:LEU:HB2	1:A:601:VAL:HG22	1.72	0.70
1:A:222:PHE:HD2	1:A:225:ILE:HD11	1.57	0.69
1:A:296:SER:O	1:A:299:ILE:HG22	1.94	0.67
2:C:32:ILE:HG12	2:C:153:ILE:HG13	1.75	0.67
1:A:189:ILE:HG22	1:A:194:LEU:HD11	1.75	0.67
1:A:381:ASN:O	1:A:383:LEU:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:GLN:HA	1:A:447:LEU:HA	1.76	0.66
2:C:44:ILE:HD12	2:C:149:LEU:HD11	1.78	0.66
2:C:87:LEU:HB3	2:C:88:PRO:HD2	1.78	0.66
1:A:387:GLY:HA2	1:A:413:SER:HB3	1.77	0.65
1:A:589:GLN:HG3	7:A:1531:NAG:H5	1.78	0.65
3:A:1411:NAG:H83	4:A:1421:NAG:H3	1.79	0.64
1:A:89:ILE:H	1:A:111:ASN:HD22	1.45	0.63
1:A:346:LEU:O	1:A:368:VAL:HG23	1.99	0.63
1:A:319:LYS:HA	1:A:339:GLN:O	1.98	0.63
1:A:249:LEU:HB3	1:A:282:VAL:HG11	1.81	0.63
1:A:404:LEU:HD12	1:A:427:PHE:CE2	2.30	0.62
1:A:531:LEU:HA	1:A:553:ARG:O	1.98	0.62
1:A:556:THR:HG21	1:A:584:HIS:CG	2.34	0.62
2:C:67:PRO:HD2	2:C:111:GLU:O	1.99	0.62
4:A:1461:NAG:H61	4:A:1463:NAG:HN2	1.65	0.61
1:A:533:LEU:HD11	1:A:554:ILE:HD13	1.82	0.61
1:A:288:ARG:HD3	2:C:99:ASP:OD1	1.99	0.61
1:A:575:ASN:N	1:A:575:ASN:HD22	1.99	0.61
1:A:86:ARG:HH11	1:A:86:ARG:HB2	1.66	0.61
1:A:493:THR:HB	1:A:496:LEU:HD13	1.83	0.60
2:C:106:ARG:HB2	8:C:1540:HOH:O	2.01	0.60
1:A:581:ILE:HG22	1:A:583:GLU:H	1.66	0.60
1:A:137:LEU:HD12	1:A:161:ILE:HD11	1.83	0.60
1:A:222:PHE:CD2	1:A:225:ILE:HD11	2.38	0.59
1:A:612:MET:C	1:A:614:THR:H	2.06	0.58
1:A:381:ASN:C	1:A:383:LEU:N	2.57	0.58
1:A:355:THR:HA	1:A:377:ASP:HB3	1.85	0.58
1:A:579:ALA:HA	1:A:608:THR:OG1	2.04	0.58
1:A:226:LYS:HD2	8:A:1592:HOH:O	2.03	0.58
1:A:445:GLU:HB2	8:A:1550:HOH:O	2.03	0.57
2:C:72:LYS:O	2:C:73:TYR:HB2	2.04	0.57
1:A:486:LEU:HD13	1:A:506:LEU:HD11	1.87	0.57
1:A:458:LYS:O	1:A:458:LYS:HD3	2.05	0.57
2:C:68:ARG:O	2:C:109:LYS:HD3	2.06	0.56
1:A:290:THR:HA	1:A:314:ALA:O	2.04	0.56
1:A:276:MET:O	1:A:279:LEU:HB2	2.06	0.56
1:A:387:GLY:HA2	1:A:413:SER:CB	2.35	0.56
1:A:373:LEU:HB3	1:A:396:THR:HG21	1.87	0.56
1:A:363:ILE:HG13	1:A:383:LEU:HD23	1.88	0.55
1:A:117:SER:O	1:A:120:SER:OG	2.22	0.55
1:A:166:LEU:HD22	1:A:197:LEU:CD2	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:PRO:HA	1:A:371:PRO:HG2	1.88	0.55
1:A:279:LEU:HA	1:A:282:VAL:HG22	1.89	0.54
1:A:589:GLN:HE22	1:A:592:LYS:HD2	1.72	0.54
1:A:422:LEU:HD11	1:A:425:LEU:HD13	1.89	0.54
1:A:97:TRP:CB	1:A:124:LEU:HD13	2.38	0.54
1:A:166:LEU:CD2	1:A:197:LEU:HD21	2.35	0.54
2:C:131:TYR:HB2	2:C:153:ILE:HB	1.90	0.54
1:A:615:SER:HB3	1:A:618:LEU:HD23	1.90	0.54
1:A:276:MET:HG3	1:A:279:LEU:HD22	1.90	0.53
1:A:459:ILE:HG21	1:A:489:VAL:HG11	1.91	0.53
1:A:42:GLN:HB2	1:A:44:LEU:HG	1.91	0.53
1:A:608:THR:CB	1:A:609:PRO:HD3	2.14	0.53
1:A:162:HIS:HA	1:A:185:TYR:O	2.08	0.53
1:A:577:SER:HA	1:A:607:ALA:HB2	1.90	0.53
1:A:195:GLN:HA	1:A:198:ARG:HG3	1.91	0.52
1:A:555:GLU:O	1:A:556:THR:HG23	2.10	0.52
1:A:574:THR:CG2	1:A:600:ASN:HD22	2.23	0.52
1:A:189:ILE:CG2	1:A:194:LEU:HD11	2.39	0.52
1:A:484:ASN:HB2	1:A:507:GLU:OE1	2.09	0.52
1:A:97:TRP:HB3	1:A:124:LEU:CD1	2.38	0.52
1:A:198:ARG:HH11	1:A:198:ARG:HG3	1.75	0.52
1:A:447:LEU:HD21	1:A:450:LEU:HB2	1.92	0.51
1:A:522:LEU:C	1:A:522:LEU:HD13	2.30	0.51
1:A:246:LEU:HD22	1:A:279:LEU:HD11	1.93	0.51
1:A:179:VAL:HG12	1:A:181:LEU:HD11	1.93	0.51
1:A:497:THR:HA	1:A:520:LEU:HA	1.93	0.51
1:A:66:LYS:HE3	1:A:88:GLU:OE2	2.10	0.50
1:A:610:VAL:O	1:A:610:VAL:HG22	2.12	0.50
1:A:191:VAL:HG12	1:A:221:ALA:HA	1.93	0.50
1:A:226:LYS:O	1:A:227:LEU:HD23	2.11	0.50
1:A:300:VAL:HG11	1:A:313:LEU:HD11	1.94	0.50
1:A:220:GLN:HE21	1:A:223:GLN:HG2	1.76	0.50
1:A:238:SER:HB3	1:A:241:ILE:HG13	1.92	0.50
1:A:572:ASN:HA	1:A:599:VAL:HG12	1.94	0.50
2:C:128:LYS:HD3	2:C:129:GLY:H	1.75	0.49
1:A:200:ASN:HA	1:A:202:GLN:OE1	2.13	0.49
1:A:551:PHE:N	1:A:551:PHE:CD1	2.80	0.49
4:A:1461:NAG:H61	4:A:1463:NAG:N2	2.28	0.49
1:A:572:ASN:ND2	1:A:599:VAL:HG11	2.28	0.49
1:A:69:LYS:HD3	1:A:93:GLU:OE1	2.12	0.49
1:A:517:LEU:HA	8:A:1505:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:87:LEU:HB3	2:C:88:PRO:CD	2.43	0.49
1:A:577:SER:CA	1:A:607:ALA:HB2	2.43	0.49
1:A:583:GLU:HA	1:A:583:GLU:OE1	2.13	0.49
1:A:535:SER:HB2	1:A:559:GLY:O	2.13	0.49
1:A:441:PHE:HB3	1:A:468:LEU:HD21	1.94	0.49
1:A:427:PHE:CG	1:A:432:LEU:HD21	2.48	0.48
1:A:571:PHE:HB3	1:A:598:LEU:HD23	1.95	0.48
1:A:296:SER:C	1:A:298:ASP:H	2.17	0.48
1:A:313:LEU:HB3	1:A:316:VAL:HG21	1.96	0.48
1:A:220:GLN:HG2	1:A:223:GLN:HB2	1.94	0.48
1:A:267:ASN:OD1	1:A:293:ASN:HB2	2.13	0.48
1:A:551:PHE:HD1	1:A:551:PHE:N	2.12	0.48
1:A:343:PHE:HB2	1:A:364:SER:O	2.14	0.48
1:A:68:LEU:HD22	1:A:89:ILE:HD13	1.96	0.48
1:A:547:LEU:HB2	1:A:568:LEU:HD11	1.95	0.48
2:C:62:HIS:NE2	2:C:64:GLU:OE1	2.47	0.48
1:A:340:LEU:HD23	1:A:344:PRO:HD3	1.96	0.48
1:A:207:LEU:O	1:A:230:LEU:HA	2.14	0.47
1:A:172:ASN:O	1:A:174:THR:N	2.46	0.47
1:A:211:LEU:HD21	1:A:262:PHE:CE1	2.48	0.47
1:A:278:GLY:C	1:A:280:CYS:H	2.16	0.47
2:C:72:LYS:HD3	2:C:73:TYR:CE1	2.49	0.47
1:A:65:LEU:O	1:A:67:ILE:N	2.47	0.47
1:A:249:LEU:O	1:A:282:VAL:HG12	2.15	0.47
1:A:575:ASN:H	1:A:575:ASN:HD22	1.62	0.47
1:A:574:THR:HG21	1:A:600:ASN:ND2	2.30	0.47
2:C:24:PHE:HB3	2:C:33:SER:CB	2.44	0.47
1:A:52:PRO:HB2	1:A:55:THR:HG23	1.97	0.47
1:A:482:LYS:HE3	1:A:487:SER:HB3	1.97	0.47
1:A:611:GLU:OE2	1:A:614:THR:HG21	2.15	0.47
1:A:226:LYS:HG2	1:A:253:HIS:HB2	1.96	0.47
2:C:34:TYR:HB3	2:C:151:PHE:CD2	2.50	0.47
1:A:73:PHE:HB3	1:A:100:LEU:HD21	1.96	0.47
2:C:24:PHE:HE2	8:C:1543:HOH:O	1.98	0.46
2:C:79:PHE:HB2	2:C:134:VAL:CG2	2.45	0.46
1:A:238:SER:H	1:A:241:ILE:HD12	1.80	0.46
1:A:89:ILE:HG22	1:A:113:ILE:CG2	2.46	0.46
1:A:445:GLU:O	1:A:445:GLU:HG2	2.16	0.46
1:A:561:LEU:HB3	1:A:590:TRP:CD1	2.51	0.46
1:A:581:ILE:HG22	1:A:582:CYS:N	2.30	0.46
1:A:69:LYS:HG3	1:A:70:SER:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:LYS:HA	1:A:372:SER:O	2.16	0.46
1:A:195:GLN:NE2	8:A:1562:HOH:O	2.48	0.45
1:A:522:LEU:HD13	1:A:523:LEU:N	2.31	0.45
1:A:534:ASP:HB3	1:A:537:HIS:CD2	2.51	0.45
1:A:533:LEU:CD1	1:A:554:ILE:HD13	2.46	0.45
2:C:31:ILE:HG13	2:C:154:ILE:HB	1.98	0.45
1:A:71:TYR:HA	8:A:1517:HOH:O	2.15	0.45
2:C:142:THR:O	2:C:144:GLU:N	2.49	0.45
2:C:79:PHE:HB2	2:C:134:VAL:HG23	1.99	0.45
1:A:454:TYR:OH	1:A:503:LYS:HD2	2.17	0.45
1:A:437:GLU:HB3	1:A:438:PHE:HD2	1.81	0.45
1:A:399:LEU:O	1:A:422:LEU:HA	2.17	0.45
1:A:128:GLU:HA	1:A:151:LEU:HA	1.98	0.45
1:A:608:THR:CB	1:A:609:PRO:CD	2.84	0.44
1:A:259:LEU:HD12	1:A:260:GLY:N	2.27	0.44
1:A:577:SER:C	1:A:607:ALA:HB2	2.37	0.44
1:A:198:ARG:NH1	1:A:198:ARG:HG3	2.33	0.44
1:A:278:GLY:C	1:A:280:CYS:N	2.71	0.44
1:A:496:LEU:HB3	1:A:520:LEU:HD13	1.99	0.44
2:C:101:ASP:OD1	2:C:101:ASP:N	2.51	0.44
1:A:194:LEU:C	1:A:196:PHE:H	2.21	0.44
1:A:220:GLN:NE2	1:A:223:GLN:HG2	2.32	0.44
1:A:220:GLN:HG2	1:A:223:GLN:CB	2.48	0.44
1:A:438:PHE:N	1:A:438:PHE:HD2	2.15	0.44
1:A:288:ARG:HG3	1:A:312:SER:HB2	1.99	0.44
1:A:161:ILE:HB	1:A:184:ASN:OD1	2.17	0.44
1:A:189:ILE:HB	1:A:217:ILE:HG23	1.99	0.44
1:A:241:ILE:H	1:A:241:ILE:HG13	1.68	0.44
1:A:415:ASN:O	1:A:416:PHE:HB2	2.18	0.44
1:A:77:SER:O	1:A:102:HIS:HD2	2.00	0.44
1:A:133:VAL:HG21	2:C:108:LEU:HD12	2.00	0.43
1:A:438:PHE:N	1:A:438:PHE:CD2	2.85	0.43
1:A:555:GLU:O	1:A:556:THR:CG2	2.66	0.43
1:A:68:LEU:HA	1:A:68:LEU:HD12	1.92	0.43
2:C:72:LYS:O	2:C:73:TYR:CB	2.66	0.43
2:C:24:PHE:HB3	2:C:33:SER:HA	2.00	0.43
1:A:599:VAL:HG22	1:A:600:ASN:ND2	2.34	0.43
1:A:194:LEU:HD12	1:A:194:LEU:H	1.83	0.43
1:A:410:ILE:HD12	1:A:430:SER:HB3	2.00	0.43
2:C:66:ILE:HG12	2:C:112:THR:HA	2.01	0.43
2:C:36:TYR:OH	2:C:43:PRO:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:SER:HB2	1:A:275:ILE:HD11	2.00	0.43
1:A:616:LEU:C	1:A:618:LEU:H	2.22	0.43
1:A:390:SER:O	1:A:393:ASP:HB2	2.18	0.43
1:A:89:ILE:O	1:A:113:ILE:HG23	2.19	0.42
1:A:293:ASN:ND2	8:A:1566:HOH:O	2.52	0.42
1:A:182:SER:HA	1:A:210:SER:O	2.19	0.42
1:A:48:PRO:HB2	1:A:51:ILE:HG13	2.01	0.42
1:A:539:ASN:O	1:A:540:GLN:HB2	2.18	0.42
1:A:152:LYS:O	1:A:176:LEU:HD12	2.20	0.42
1:A:31:VAL:HG23	1:A:32:VAL:HG23	2.00	0.42
1:A:252:LEU:HG	1:A:254:VAL:HG23	2.01	0.42
1:A:375:TYR:CE2	1:A:377:ASP:HB2	2.55	0.42
1:A:500:ASP:C	1:A:500:ASP:OD1	2.58	0.42
1:A:190:THR:O	1:A:193:ASP:N	2.51	0.42
1:A:316:VAL:HG12	1:A:318:ILE:H	1.85	0.42
1:A:61:SER:HB3	1:A:85:SER:HB2	2.01	0.42
1:A:420:GLU:CD	1:A:420:GLU:H	2.23	0.42
1:A:274:SER:O	1:A:277:GLU:HB2	2.19	0.42
1:A:148:LEU:HA	1:A:148:LEU:HD12	1.88	0.42
1:A:324:VAL:HG12	1:A:348:LEU:HD21	2.01	0.42
1:A:44:LEU:N	1:A:63:ASN:OD1	2.53	0.41
2:C:26:ASN:OD1	5:C:1501:NAG:N2	2.53	0.41
1:A:370:LEU:HA	1:A:371:PRO:HD2	1.75	0.41
2:C:24:PHE:HB3	2:C:33:SER:HB3	2.02	0.41
1:A:131:VAL:HG13	1:A:133:VAL:HG23	2.02	0.41
1:A:531:LEU:HD23	1:A:553:ARG:HB2	2.02	0.41
1:A:517:LEU:C	1:A:519:ARG:H	2.24	0.41
1:A:222:PHE:HB3	1:A:252:LEU:HB2	2.03	0.41
1:A:286:GLU:HG3	1:A:310:ALA:CB	2.50	0.41
2:C:42:PHE:N	2:C:42:PHE:CD2	2.89	0.41
1:A:325:PRO:HG2	1:A:328:PHE:CD2	2.56	0.41
1:A:196:PHE:HD2	1:A:197:LEU:HD22	1.86	0.41
1:A:249:LEU:HB3	1:A:282:VAL:CG1	2.50	0.41
1:A:355:THR:HG22	1:A:357:THR:HG22	2.01	0.41
1:A:62:PHE:HE1	2:C:68:ARG:HA	1.86	0.41
1:A:522:LEU:C	1:A:522:LEU:CD1	2.89	0.41
1:A:261:GLU:OE2	1:A:267:ASN:HA	2.20	0.41
1:A:86:ARG:HH12	1:A:110:GLY:HA3	1.86	0.41
1:A:311:MET:HB2	1:A:311:MET:HE2	1.93	0.41
1:A:187:GLN:HA	1:A:214:ILE:HA	2.03	0.41
1:A:113:ILE:H	1:A:113:ILE:HG12	1.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:612:MET:C	1:A:614:THR:N	2.70	0.40
2:C:31:ILE:O	2:C:31:ILE:HG13	2.21	0.40
1:A:573:LEU:O	1:A:576:ASN:ND2	2.54	0.40
1:A:179:VAL:HB	1:A:207:LEU:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	597/599 (100%)	495 (83%)	79 (13%)	23 (4%)	4	12
2	C	133/135 (98%)	115 (86%)	15 (11%)	3 (2%)	8	25
All	All	730/734 (100%)	610 (84%)	94 (13%)	26 (4%)	4	13

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	382	ALA
1	A	440	ALA
1	A	608	THR
2	C	143	GLU
1	A	347	ASP
1	A	609	PRO
2	C	37	CYS
1	A	266	ARG
1	A	442	LEU
1	A	505	GLN
2	C	44	ILE
1	A	360	LYS
1	A	577	SER
1	A	613	ASN

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Mol	Chain	Res	Type
1	A	623	SER
1	A	114	GLN
1	A	483	ASP
1	A	487	SER
1	A	551	PHE
1	A	560	ILE
1	A	612	MET
1	A	52	PRO
1	A	113	ILE
1	A	363	ILE
1	A	273	PRO
1	A	617	VAL

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	558/558 (100%)	498 (89%)	60 (11%)	8	22
2	C	122/122 (100%)	110 (90%)	12 (10%)	10	27
All	All	680/680 (100%)	608 (89%)	72 (11%)	8	23

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	PRO
1	A	31	VAL
1	A	49	ASP
1	A	69	LYS
1	A	86	ARG
1	A	109	THR
1	A	113	ILE
1	A	124	LEU
1	A	129	ASN
1	A	147	GLN
1	A	148	LEU

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Mol	Chain	Res	Type
1	A	155	ASN
1	A	173	LEU
1	A	183	TYR
1	A	188	THR
1	A	209	MET
1	A	220	GLN
1	A	229	GLU
1	A	267	ASN
1	A	276	MET
1	A	280	CYS
1	A	283	THR
1	A	289	LEU
1	A	292	THR
1	A	297	ASP
1	A	298	ASP
1	A	299	ILE
1	A	324	VAL
1	A	339	GLN
1	A	346	LEU
1	A	357	THR
1	A	360	LYS
1	A	378	LEU
1	A	385	PHE
1	A	389	CYS
1	A	420	GLU
1	A	422	LEU
1	A	433	LYS
1	A	436	THR
1	A	438	PHE
1	A	439	SER
1	A	458	LYS
1	A	485	THR
1	A	515	ASP
1	A	522	LEU
1	A	543	SER
1	A	547	LEU
1	A	551	PHE
1	A	558	LYS
1	A	562	GLN
1	A	571	PHE
1	A	575	ASN
1	A	585	GLN

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Mol	Chain	Res	Type
1	A	596	GLN
1	A	600	ASN
1	A	608	THR
1	A	611	GLU
1	A	614	THR
1	A	617	VAL
1	A	620	PHE
2	C	29	ASP
2	C	44	ILE
2	C	65	PHE
2	C	68	ARG
2	C	71	LEU
2	C	72	LYS
2	C	81	SER
2	C	101	ASP
2	C	121	PHE
2	C	141	ASP
2	C	146	LEU
2	C	152	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	HIS
1	A	111	ASN
1	A	147	GLN
1	A	155	ASN
1	A	175	ASN
1	A	195	GLN
1	A	220	GLN
1	A	228	HIS
1	A	235	ASN
1	A	247	GLN
1	A	255	HIS
1	A	293	ASN
1	A	339	GLN
1	A	401	HIS
1	A	407	ASN
1	A	428	GLN
1	A	484	ASN
1	A	521	GLN
1	A	537	HIS

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Mol	Chain	Res	Type
1	A	539	ASN
1	A	575	ASN
1	A	589	GLN
1	A	594	GLN
1	A	596	GLN
1	A	600	ASN
2	C	22	GLN
2	C	83	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

12 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	$\# Z > 2$
3	NAG	A	1411	1,3	14,14,15	0.56	0	15,19,21	1.65	4 (26%)
3	NAG	A	1412	3	14,14,15	0.54	0	15,19,21	2.52	1 (6%)
4	NAG	A	1421	1,4	14,14,15	0.52	0	15,19,21	0.97	1 (6%)
4	NAG	A	1422	4	14,14,15	0.44	0	15,19,21	0.87	0
4	BMA	A	1423	4	11,11,12	0.63	0	14,15,17	1.08	2 (14%)
4	NAG	A	1461	1,4	14,14,15	0.62	0	15,19,21	1.54	3 (20%)
4	NAG	A	1463	4	14,14,15	0.40	0	15,19,21	1.27	2 (13%)
4	BMA	A	1464	4	11,11,12	0.61	0	14,15,17	0.46	0
7	NAG	A	1531	7	14,14,15	0.54	0	15,19,21	1.01	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	FUL	A	1532	7	10,10,11	0.64	0	14,14,16	1.65	3 (21%)
7	NAG	A	1533	7	14,14,15	0.58	0	15,19,21	1.15	1 (6%)
7	BMA	A	1534	7	11,11,12	0.59	0	14,15,17	0.92	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
3	NAG	A	1411	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1412	3	-	0/6/23/26	0/1/1/1
4	NAG	A	1421	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1422	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1423	4	-	0/2/19/22	0/1/1/1
4	NAG	A	1461	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1463	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1464	4	-	0/2/19/22	0/1/1/1
7	NAG	A	1531	7	-	0/6/23/26	0/1/1/1
7	FUL	A	1532	7	-	0/0/17/20	0/1/1/1
7	NAG	A	1533	7	-	0/6/23/26	0/1/1/1
7	BMA	A	1534	7	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1463	NAG	C4-C3-C2	-2.71	107.02	111.23
4	A	1421	NAG	C2-N2-C7	-2.67	119.61	123.04
3	A	1411	NAG	C2-N2-C7	-2.62	119.68	123.04
4	A	1461	NAG	O4-C4-C3	-2.43	104.86	110.34
3	A	1411	NAG	O4-C4-C3	-2.34	105.06	110.34
7	A	1533	NAG	C4-C3-C2	-2.25	107.73	111.23
3	A	1411	NAG	C4-C3-C2	2.05	114.42	111.23
4	A	1423	BMA	C2-C3-C4	2.06	114.54	111.04
7	A	1532	FUL	C2-C3-C4	2.18	114.74	111.04
4	A	1461	NAG	C1-O5-C5	2.33	115.21	112.25
4	A	1423	BMA	C3-C4-C5	2.41	114.39	110.20
7	A	1532	FUL	O5-C5-C6	2.66	110.52	106.13
4	A	1463	NAG	C1-O5-C5	3.14	116.23	112.25
4	A	1461	NAG	C4-C3-C2	3.98	117.41	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1411	NAG	C1-O5-C5	4.36	117.78	112.25
7	A	1532	FUL	C1-C2-C3	4.46	114.82	109.54
3	A	1412	NAG	C1-O5-C5	9.05	123.73	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1411	NAG	1	0
4	A	1421	NAG	1	0
4	A	1461	NAG	2	0
4	A	1463	NAG	2	0
7	A	1531	NAG	1	0
7	A	1533	NAG	1	0

5.6 Ligand geometry

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	A	1431	1	14,14,15	0.58	0	15,19,21	1.05	1 (6%)
6	NDG	A	1441	1	14,14,15	0.50	0	15,19,21	1.19	1 (6%)
6	NDG	A	1451	1	14,14,15	0.47	0	15,19,21	1.11	1 (6%)
6	NDG	A	1471	1	14,14,15	0.50	0	15,19,21	0.80	0
6	NDG	A	1481	1	14,14,15	0.67	0	15,19,21	0.92	0
5	NAG	A	1491	1	14,14,15	0.60	0	15,19,21	1.24	2 (13%)
5	NAG	C	1501	2	14,14,15	0.75	1 (7%)	15,19,21	1.35	1 (6%)
6	NDG	C	1511	2	14,14,15	0.49	0	15,19,21	0.95	1 (6%)
6	NDG	C	1521	2	14,14,15	0.73	0	15,19,21	1.17	1 (6%)

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	A	1431	1	-	0/6/23/26	0/1/1/1
6	NDG	A	1441	1	-	0/6/23/26	0/1/1/1
6	NDG	A	1451	1	-	1/6/23/26	0/1/1/1
6	NDG	A	1471	1	-	0/6/23/26	0/1/1/1
6	NDG	A	1481	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1491	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1501	2	-	1/6/23/26	0/1/1/1
6	NDG	C	1511	2	-	0/6/23/26	0/1/1/1
6	NDG	C	1521	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1501	NAG	C1-C2	2.27	1.55	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1521	NDG	C4-C3-C2	2.40	114.96	111.23
5	A	1491	NAG	C1-O5-C5	2.51	115.44	112.25
6	C	1511	NDG	C1-O-C5	2.53	115.45	112.25
6	A	1441	NDG	C3-C4-C5	2.61	114.75	110.20
6	A	1451	NDG	C1-O-C5	3.05	116.12	112.25
5	A	1491	NAG	C2-N2-C7	3.17	127.11	123.04
5	A	1431	NAG	C1-O5-C5	3.23	116.35	112.25
5	C	1501	NAG	C1-O5-C5	3.98	117.30	112.25

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1501	NAG	O7-C7-N2-C2
6	A	1481	NDG	O7-C7-N2-C2
6	A	1451	NDG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1501	NAG	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	599/599 (100%)	0.01	8 (1%) 79 72	8, 28, 46, 66	0
2	C	135/135 (100%)	0.30	10 (7%) 17 10	4, 30, 44, 69	2 (1%)
All	All	734/734 (100%)	0.06	18 (2%) 61 50	4, 28, 45, 69	2 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	126	PHE	5.3
2	C	124	ILE	4.8
1	A	48	PRO	3.5
2	C	125	LEU	3.4
2	C	127	PRO	3.3
2	C	55	ARG	3.0
1	A	71	TYR	2.9
2	C	131	TYR	2.5
1	A	31	VAL	2.4
2	C	123	GLY	2.4
1	A	624	THR	2.3
1	A	49	ASP	2.2
1	A	50	ASP	2.2
2	C	154	ILE	2.2
2	C	129	GLY	2.1
1	A	35	ILE	2.1
1	A	613	ASN	2.1
2	C	23	TRP	2.0

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

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

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	A	1411	14/15	0.92	0.16	0.02	28,38,47,54	0
4	NAG	A	1421	14/15	0.97	0.10	-1.79	18,28,33,43	0
7	BMA	A	1534	11/12	0.80	0.19	-	87,92,94,95	0
4	NAG	A	1463	14/15	0.84	0.19	-	72,82,86,93	0
7	NAG	A	1533	14/15	0.76	0.17	-	74,78,80,87	0
3	NAG	A	1412	14/15	0.92	0.18	-	41,47,54,61	0
7	FUL	A	1532	10/11	0.78	0.32	-	87,92,94,96	0
4	NAG	A	1461	14/15	0.93	0.20	-	39,45,63,67	0
4	BMA	A	1464	11/12	0.70	0.25	-	94,97,101,102	0
4	BMA	A	1423	11/12	0.57	0.25	-	90,95,96,97	0
7	NAG	A	1531	14/15	0.82	0.15	-	67,72,77,82	0
4	NAG	A	1422	14/15	0.95	0.17	-	51,56,68,81	0

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	NDG	C	1521	14/15	0.83	0.26	0.87	22,49,73,76	0
5	NAG	A	1431	14/15	0.71	0.23	-	82,91,94,95	0
6	NDG	A	1451	14/15	0.75	0.32	-	79,85,88,89	0
5	NAG	A	1491	14/15	0.61	0.43	-	80,88,94,96	0
6	NDG	A	1481	14/15	0.77	0.29	-	57,65,69,70	0
6	NDG	A	1441	14/15	0.75	0.36	-	48,59,65,66	0
5	NAG	C	1501	14/15	0.84	0.17	-	65,71,85,86	0
6	NDG	A	1471	14/15	0.85	0.21	-	54,63,72,75	0
6	NDG	C	1511	14/15	0.92	0.31	-	38,42,44,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.