



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:01 AM GMT

PDB ID : 3GXT
Title : Crystal structure of alpha-galactosidase A at pH 4.5 complexed with 1-deoxy galactonijirimycin
Authors : Lieberman, R.L.
Deposited on : 2009-04-02
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
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

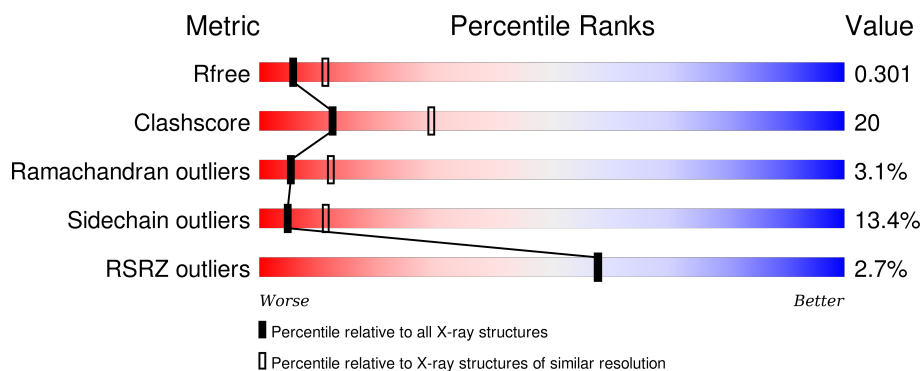
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

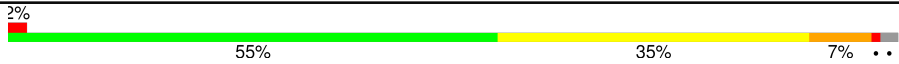

The reported resolution of this entry is 2.70 Å.

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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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 ≥ 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	398	 2% 55% 35% 7% ..
1	B	398	 4% 58% 33% 6% ..

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
2	NAG	A	639	-	-	-	X
3	MAN	A	696	X	-	-	-
4	SO4	A	2	-	-	X	-
4	SO4	B	4	-	-	-	X
6	NAG	B	639	-	-	-	X
7	NAG	B	692	X	-	-	-
7	MAN	B	694	X	-	-	-
8	MAN	B	717	X	-	-	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6573 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 Alpha-galactosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3122	1988	534	574	26			
1	B	391	Total	C	N	O	S	0	0	0
			3131	1993	536	576	26			

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

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

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

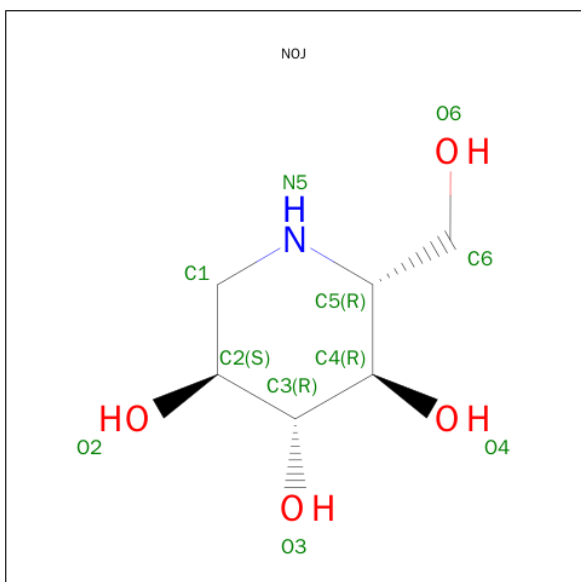
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	2	Total	C	O	0	0
			22	12	10		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



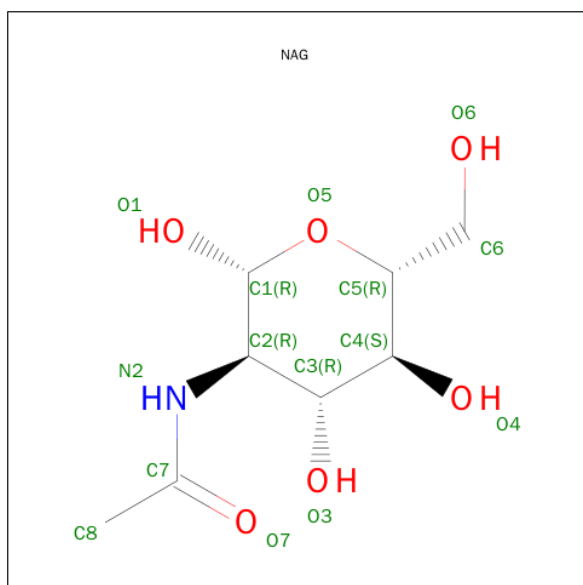
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 1-DEOXYNOJIRIMYCIN (three-letter code: NOJ) (formula: C₆H₁₃NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			11	6	1	4		
5	B	1	Total	C	N	O	0	0
			11	6	1	4		

- 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	B	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	B	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 8 is a polymer of unknown type called SUGAR (3-MER).

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

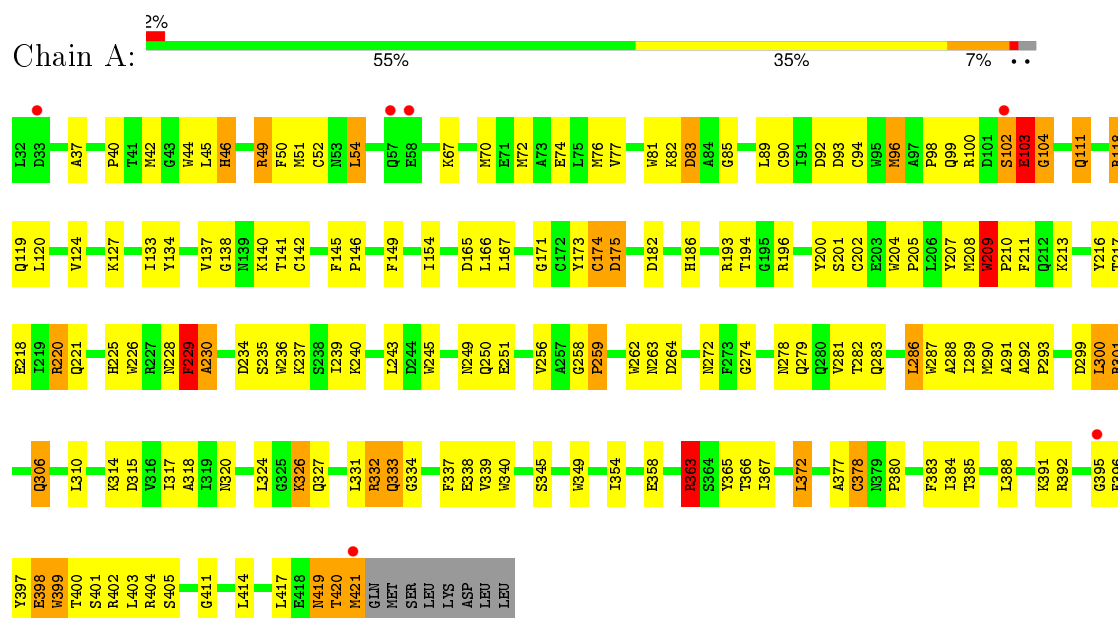
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	36	Total 36	O 36	0	0
9	B	28	Total 28	O 28	0	0

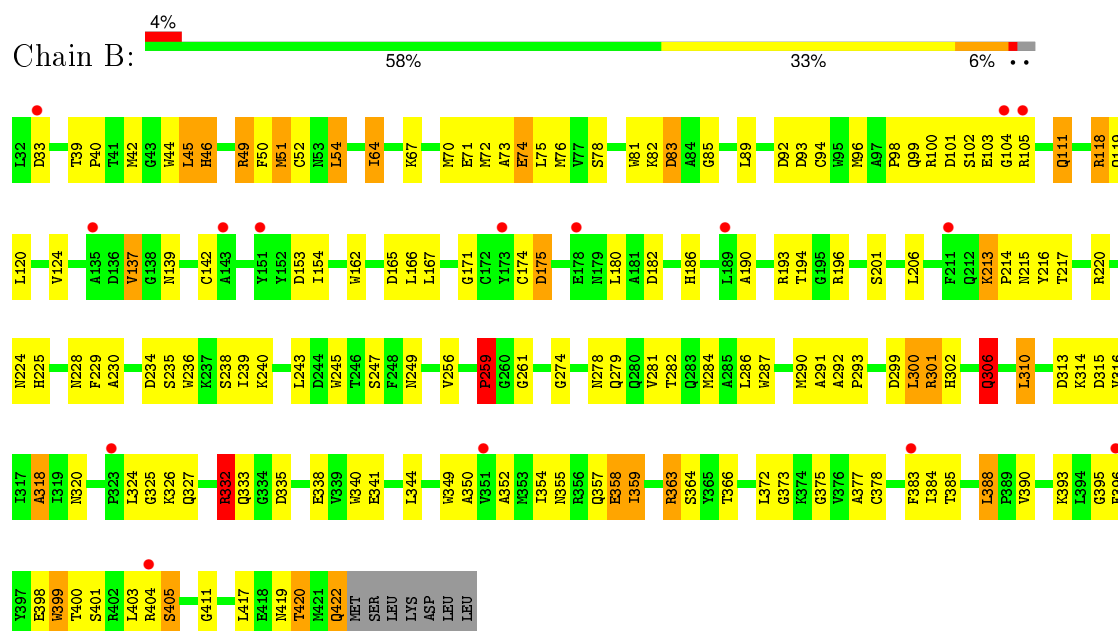
3 Residue-property plots

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: Alpha-galactosidase A



• Molecule 1: Alpha-galactosidase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.61Å 89.61Å 216.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.90 – 2.70 19.90 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.3 (19.90-2.70) 97.3 (19.90-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.242 , 0.306 0.238 , 0.301	Depositor DCC
R_{free} test set	1400 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	45.8	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 65.2	EDS
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 27633 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6573	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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: SO4, NAG, NOJ, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.84	2/3209 (0.1%)	0.91	5/4358 (0.1%)
1	B	0.79	0/3218	0.88	2/4370 (0.0%)
All	All	0.81	2/6427 (0.0%)	0.90	7/8728 (0.1%)

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	4
1	B	0	2
3	A	1	0
7	B	2	0
8	B	1	0
All	All	4	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	90	CYS	CB-SG	-5.34	1.73	1.81
1	A	229	PHE	CE1-CZ	5.13	1.47	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	332	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	392	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	A	286	LEU	CA-CB-CG	-5.30	103.11	115.30
1	A	220	ARG	NE-CZ-NH2	-5.25	117.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	388	LEU	CA-CB-CG	5.14	127.12	115.30
1	A	102	SER	C-N-CA	5.08	134.40	121.70
1	A	363	ARG	NE-CZ-NH2	-5.05	117.77	120.30

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	696	MAN	C1
7	B	692	NAG	C1
7	B	694	MAN	C1
8	B	717	MAN	C1

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	SER	Peptide
1	A	103	GLU	Peptide
1	A	104	GLY	Peptide
1	A	209	TRP	Peptide
1	B	102	SER	Peptide
1	B	420	THR	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	3122	0	2981	124	0
1	B	3131	0	2991	112	0
2	A	84	0	75	10	0
3	A	22	0	19	1	0
4	A	15	0	0	3	0
4	B	10	0	0	2	0
5	A	11	0	13	2	0
5	B	11	0	13	3	0
6	B	14	0	13	2	0
7	B	50	0	43	3	0
8	B	39	0	34	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	36	0	0	3	0
9	B	28	0	0	9	0
All	All	6573	0	6182	248	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 20.

All (248) 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:103:GLU:HB3	1:A:104:GLY:HA3	1.15	1.15
1:A:332:ARG:HG3	1:A:332:ARG:HH11	1.08	1.12
1:B:332:ARG:HH11	1:B:332:ARG:HG3	1.28	0.95
1:A:363:ARG:HG2	1:A:363:ARG:HH11	1.34	0.93
1:A:103:GLU:HB3	1:A:104:GLY:CA	2.04	0.88
8:B:716:NAG:H83	9:B:441:HOH:O	1.75	0.86
1:A:175:ASP:OD2	2:A:639:NAG:O7	1.94	0.83
1:A:332:ARG:CG	1:A:332:ARG:HH11	1.90	0.83
1:A:332:ARG:HG3	1:A:332:ARG:NH1	1.86	0.82
1:B:224:ASN:O	1:B:261:GLY:HA2	1.80	0.82
1:B:228:ASN:HB3	1:B:245:TRP:CH2	2.15	0.81
1:A:290:MET:O	1:A:327:GLN:HG3	1.83	0.79
1:A:228:ASN:HB3	1:A:245:TRP:CH2	2.18	0.78
1:B:363:ARG:HG2	1:B:363:ARG:HH11	1.47	0.78
1:A:175:ASP:OD2	1:A:175:ASP:N	2.09	0.76
8:B:715:NAG:H5	9:B:21:HOH:O	1.85	0.75
1:B:215:ASN:HD21	8:B:715:NAG:C1	2.00	0.74
2:A:692:NAG:H61	2:A:693:NAG:H82	1.71	0.73
1:B:215:ASN:ND2	8:B:715:NAG:O5	2.19	0.72
1:A:142:CYS:HB2	5:A:430:NOJ:O6	1.89	0.72
1:A:377:ALA:O	1:A:378:CYS:HB2	1.89	0.71
1:B:335:ASP:OD1	9:B:440:HOH:O	2.07	0.71
1:A:332:ARG:NH1	9:A:25:HOH:O	2.20	0.71
1:A:120:LEU:O	1:A:124:VAL:HG23	1.93	0.69
1:A:100:ARG:HD3	1:A:104:GLY:O	1.93	0.68
4:A:2:SO4:O4	9:A:12:HOH:O	2.11	0.68
1:B:83:ASP:OD2	1:B:83:ASP:N	2.26	0.67
1:A:103:GLU:CB	1:A:104:GLY:HA3	2.08	0.67
1:B:332:ARG:HH11	1:B:332:ARG:CG	2.05	0.67
1:B:290:MET:O	1:B:327:GLN:HG3	1.95	0.67
1:B:228:ASN:HB3	1:B:245:TRP:HH2	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:MET:O	1:A:327:GLN:CG	2.43	0.66
1:A:380:PRO:HD3	1:A:421:MET:HG3	1.79	0.65
1:B:299:ASP:OD1	1:B:301:ARG:HB2	1.97	0.64
1:B:73:ALA:HB2	1:B:89:LEU:HD22	1.79	0.64
1:B:142:CYS:HB2	5:B:1:NOJ:H62	1.79	0.63
1:A:54:LEU:HD12	1:A:54:LEU:H	1.64	0.62
1:A:299:ASP:OD1	1:A:301:ARG:HB2	1.99	0.62
2:A:692:NAG:C6	2:A:693:NAG:H82	2.29	0.62
1:B:340:TRP:HB2	1:B:352:ALA:HB3	1.82	0.62
1:A:118:ARG:HA	1:A:118:ARG:HE	1.65	0.61
1:A:384:ILE:HG12	1:A:417:LEU:HG	1.83	0.61
1:A:46:HIS:CD2	1:A:92:ASP:H	2.18	0.60
1:B:142:CYS:HB2	5:B:1:NOJ:C6	2.32	0.60
1:A:384:ILE:HD12	1:A:397:TYR:CD1	2.37	0.59
1:A:210:PRO:HD2	1:A:211:PHE:HD2	1.67	0.59
1:A:377:ALA:O	1:A:378:CYS:CB	2.49	0.59
1:A:77:VAL:HG21	1:A:127:LYS:HD2	1.85	0.58
1:B:338:GLU:HB2	1:B:354:ILE:HB	1.86	0.58
1:A:243:LEU:HD22	1:A:286:LEU:HD22	1.86	0.58
1:B:72:MET:O	1:B:76:MET:HG3	2.04	0.57
1:A:349:TRP:CD1	1:A:377:ALA:HB2	2.39	0.57
1:B:118:ARG:NH2	1:B:162:TRP:O	2.37	0.57
1:B:175:ASP:N	1:B:175:ASP:OD2	2.36	0.57
1:B:39:THR:HB	1:B:40:PRO:HD2	1.86	0.57
1:B:234:ASP:OD1	1:B:274:GLY:N	2.38	0.56
1:B:215:ASN:ND2	8:B:715:NAG:C1	2.67	0.56
1:A:237:LYS:HD3	9:A:439:HOH:O	2.04	0.56
1:B:315:ASP:O	1:B:318:ALA:HB3	2.06	0.56
7:B:692:NAG:H5	7:B:693:NAG:H82	1.86	0.56
1:B:120:LEU:O	1:B:124:VAL:HG23	2.06	0.56
1:B:332:ARG:HG3	1:B:332:ARG:NH1	2.06	0.55
1:A:380:PRO:CD	1:A:421:MET:HG3	2.36	0.55
1:B:67:LYS:HA	1:B:70:MET:HB2	1.87	0.55
1:A:83:ASP:OD2	1:A:83:ASP:N	2.39	0.55
1:B:422:GLN:NE2	1:B:422:GLN:C	2.60	0.55
1:A:286:LEU:HD21	1:A:354:ILE:HD11	1.89	0.55
1:B:118:ARG:HE	1:B:118:ARG:HA	1.72	0.55
1:B:72:MET:SD	1:B:300:LEU:HB2	2.47	0.55
1:B:234:ASP:OD1	1:B:274:GLY:HA3	2.06	0.55
1:B:196:ARG:NH1	4:B:4:SO4:O4	2.38	0.55
7:B:694:MAN:H62	9:B:442:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:GLN:C	1:B:422:GLN:HE21	2.10	0.55
1:A:72:MET:O	1:A:76:MET:HG3	2.06	0.54
1:B:111:GLN:H	1:B:111:GLN:HE21	1.54	0.54
1:B:76:MET:SD	1:B:89:LEU:HD13	2.48	0.54
1:A:363:ARG:CG	1:A:363:ARG:HH11	2.15	0.54
1:B:175:ASP:OD2	6:B:639:NAG:O7	2.25	0.54
1:A:166:LEU:HD23	1:A:167:LEU:N	2.23	0.54
1:A:76:MET:SD	1:A:89:LEU:HD13	2.48	0.54
1:A:111:GLN:HE21	1:A:111:GLN:H	1.56	0.53
1:B:341:GLU:HA	1:B:350:ALA:O	2.08	0.53
1:A:292:ALA:O	1:A:320:ASN:ND2	2.35	0.53
1:A:216:TYR:HB3	1:A:256:VAL:HG21	1.90	0.53
1:A:154:ILE:HD12	1:A:154:ILE:N	2.24	0.53
1:A:286:LEU:CD2	1:A:354:ILE:HD11	2.39	0.52
1:B:358:GLU:O	1:B:359:ILE:HB	2.10	0.52
1:A:118:ARG:CA	1:A:118:ARG:HE	2.22	0.52
1:B:302:HIS:HA	9:B:7:HOH:O	2.09	0.52
1:A:337:PHE:CE2	1:A:365:TYR:HB2	2.45	0.52
1:A:72:MET:SD	1:A:300:LEU:HB2	2.49	0.52
1:A:67:LYS:HA	1:A:70:MET:HB2	1.92	0.52
1:A:243:LEU:HD22	1:A:286:LEU:CD2	2.40	0.51
1:B:278:ASN:HB3	1:B:411:GLY:CA	2.41	0.51
1:B:236:TRP:CD1	1:B:240:LYS:HE2	2.45	0.51
1:B:306:GLN:N	9:B:444:HOH:O	2.08	0.51
1:A:250:GLN:O	1:A:251:GLU:C	2.48	0.51
1:B:349:TRP:CD1	1:B:377:ALA:HB2	2.46	0.51
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.92	0.51
2:A:692:NAG:H61	2:A:693:NAG:C8	2.37	0.51
1:B:100:ARG:HD3	1:B:104:GLY:O	2.10	0.51
1:B:290:MET:O	1:B:327:GLN:CG	2.58	0.51
1:B:217:THR:HG21	8:B:715:NAG:H82	1.92	0.50
1:A:154:ILE:H	1:A:154:ILE:HD12	1.77	0.50
1:B:383:PHE:HD1	1:B:396:PHE:CE1	2.29	0.50
1:A:40:PRO:HB2	1:A:293:PRO:HA	1.93	0.50
1:A:363:ARG:HG2	1:A:363:ARG:NH1	2.12	0.50
1:A:175:ASP:OD2	2:A:639:NAG:C7	2.59	0.50
2:A:693:NAG:O4	3:A:694:MAN:H4	2.12	0.50
1:A:93:ASP:OD1	1:A:94:CYS:N	2.45	0.50
1:A:236:TRP:CD1	1:A:240:LYS:HE2	2.47	0.50
1:B:234:ASP:O	1:B:274:GLY:HA3	2.12	0.49
1:A:337:PHE:CZ	1:A:365:TYR:HB2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:THR:HG22	1:A:404:ARG:HA	1.94	0.49
1:B:363:ARG:CG	1:B:363:ARG:HH11	2.22	0.49
1:A:420:THR:CA	1:A:421:MET:HB2	2.43	0.49
1:A:200:TYR:CE2	1:A:202:CYS:SG	3.06	0.49
1:B:139:ASN:HD21	6:B:639:NAG:C7	2.25	0.49
1:B:236:TRP:CE3	1:B:279:GLN:HG2	2.47	0.49
1:A:37:ALA:HB1	1:A:262:TRP:HE1	1.78	0.49
1:A:228:ASN:HB3	1:A:245:TRP:HH2	1.73	0.48
1:B:82:LYS:O	1:B:85:GLY:N	2.47	0.48
1:B:384:ILE:HG12	1:B:417:LEU:HG	1.94	0.48
1:B:93:ASP:OD1	1:B:94:CYS:N	2.47	0.48
1:A:264:ASP:OD1	1:A:264:ASP:C	2.52	0.48
1:A:141:THR:HG23	1:A:145:PHE:O	2.13	0.48
1:A:208:MET:O	1:A:209:TRP:C	2.51	0.48
1:B:234:ASP:OD1	1:B:274:GLY:CA	2.62	0.48
1:A:137:VAL:HG12	1:A:171:GLY:HA2	1.95	0.48
1:A:338:GLU:HB2	1:A:354:ILE:HB	1.96	0.48
1:A:140:LYS:HB2	1:A:173:TYR:CD2	2.50	0.47
1:A:226:TRP:NE1	1:A:263:ASN:OD1	2.42	0.47
1:B:355:ASN:HD21	1:B:363:ARG:HD3	1.79	0.47
1:A:76:MET:HA	1:A:81:TRP:CD1	2.50	0.47
1:A:377:ALA:HA	1:A:419:ASN:HB2	1.96	0.47
1:A:340:TRP:N	1:A:340:TRP:CD1	2.81	0.47
1:B:46:HIS:CD2	1:B:92:ASP:H	2.33	0.47
1:B:75:LEU:O	1:B:78:SER:N	2.48	0.47
1:B:40:PRO:HB2	1:B:293:PRO:HA	1.97	0.47
1:A:367:ILE:HD11	1:A:372:LEU:HD11	1.97	0.47
2:A:639:NAG:H62	2:A:640:NAG:C1	2.45	0.47
1:B:340:TRP:CD1	1:B:340:TRP:N	2.81	0.47
1:A:201:SER:HB2	1:A:225:HIS:CE1	2.50	0.47
1:B:201:SER:HB2	1:B:225:HIS:CE1	2.51	0.46
1:A:193:ARG:O	1:A:194:THR:C	2.53	0.46
1:B:52:CYS:O	1:B:54:LEU:HD12	2.16	0.46
1:A:388:LEU:HB2	1:A:414:LEU:HB3	1.97	0.46
1:B:137:VAL:HG12	1:B:171:GLY:HA2	1.97	0.46
1:B:332:ARG:NH2	4:B:3:SO4:O1	2.49	0.46
1:A:288:ALA:HA	1:A:320:ASN:HB2	1.97	0.46
1:A:236:TRP:CE3	1:A:279:GLN:HG2	2.51	0.46
1:B:378:CYS:O	1:B:399:TRP:HD1	1.99	0.46
1:A:52:CYS:SG	1:A:52:CYS:O	2.73	0.46
1:A:138:GLY:O	1:A:149:PHE:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:ALA:HB3	1:A:327:GLN:HG3	1.98	0.46
1:B:206:LEU:O	1:B:206:LEU:HD12	2.16	0.46
1:B:284:MET:HG2	1:B:310:LEU:HD22	1.98	0.46
1:A:324:LEU:CD1	1:A:326:LYS:HG3	2.46	0.46
1:A:378:CYS:H	1:A:419:ASN:HB2	1.81	0.45
1:A:182:ASP:O	1:A:186:HIS:HB2	2.16	0.45
1:A:331:LEU:N	1:A:339:VAL:O	2.50	0.45
1:A:317:ILE:O	1:A:318:ALA:C	2.54	0.45
1:A:333:GLN:HG2	1:A:334:GLY:N	2.32	0.45
1:B:153:ASP:HB2	1:B:154:ILE:HD12	1.99	0.45
1:B:383:PHE:HD1	1:B:396:PHE:CD1	2.35	0.45
1:B:390:VAL:HG22	9:B:443:HOH:O	2.17	0.45
1:B:355:ASN:ND2	1:B:363:ARG:HD3	2.32	0.45
1:B:71:GLU:OE1	1:B:301:ARG:HD2	2.17	0.45
1:A:225:HIS:HB3	1:A:262:TRP:HB2	1.99	0.45
1:B:281:VAL:O	1:B:282:THR:C	2.53	0.45
1:A:378:CYS:SG	1:A:417:LEU:HD23	2.57	0.44
1:B:49:ARG:CG	1:B:50:PHE:CE2	3.00	0.44
1:B:193:ARG:O	1:B:194:THR:C	2.55	0.44
1:A:278:ASN:HB3	1:A:411:GLY:CA	2.46	0.44
1:A:363:ARG:NH1	1:A:363:ARG:CG	2.78	0.44
1:B:291:ALA:HB3	1:B:327:GLN:HG3	1.98	0.44
1:B:259:PRO:HD3	1:B:325:GLY:HA3	2.00	0.44
1:B:76:MET:HA	1:B:81:TRP:CD1	2.53	0.44
1:B:51:MET:O	1:B:64:ILE:HD11	2.17	0.44
1:A:82:LYS:O	1:A:85:GLY:N	2.47	0.44
1:A:402:ARG:NH2	4:A:2:SO4:O1	2.48	0.44
1:B:393:LYS:NZ	9:B:435:HOH:O	2.50	0.44
1:B:166:LEU:HD23	1:B:167:LEU:N	2.32	0.44
1:A:96:MET:HB2	1:A:96:MET:HE3	1.82	0.44
7:B:695:MAN:O3	9:B:438:HOH:O	2.16	0.44
1:B:216:TYR:HB3	1:B:256:VAL:HG21	2.00	0.44
1:B:71:GLU:CD	1:B:301:ARG:HD2	2.37	0.44
1:B:373:GLY:C	1:B:375:GLY:H	2.20	0.44
1:A:49:ARG:HG3	1:A:50:PHE:CD2	2.53	0.44
1:B:213:LYS:HA	1:B:214:PRO:HD3	1.79	0.44
1:B:49:ARG:HG3	1:B:50:PHE:CD2	2.53	0.43
1:B:137:VAL:HG11	1:B:180:LEU:HD12	2.00	0.43
1:B:49:ARG:NH1	1:B:299:ASP:HB2	2.33	0.43
1:B:239:ILE:O	1:B:240:LYS:C	2.56	0.43
1:A:333:GLN:C	1:A:333:GLN:HE21	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:692:NAG:H61	2:A:693:NAG:C7	2.49	0.43
1:A:209:TRP:C	1:A:211:PHE:H	2.18	0.43
1:B:313:ASP:CG	1:B:316:VAL:HG23	2.39	0.43
1:B:292:ALA:O	1:B:320:ASN:ND2	2.43	0.43
1:B:417:LEU:N	1:B:417:LEU:HD12	2.33	0.43
1:A:324:LEU:HB2	1:A:345:SER:HB3	2.01	0.43
1:B:220:ARG:NH1	1:B:256:VAL:O	2.50	0.43
1:A:383:PHE:HD1	1:A:396:PHE:CE1	2.37	0.42
1:A:207:TYR:O	1:A:210:PRO:CD	2.67	0.42
1:A:218:GLU:O	1:A:221:GLN:HB2	2.19	0.42
1:B:182:ASP:O	1:B:186:HIS:HB2	2.18	0.42
1:A:378:CYS:O	1:A:399:TRP:HD1	2.01	0.42
1:A:324:LEU:HD11	1:A:326:LYS:HG3	2.01	0.42
1:A:42:MET:HB2	1:A:85:GLY:O	2.18	0.42
1:A:234:ASP:O	1:A:274:GLY:HA3	2.18	0.42
1:B:142:CYS:CB	5:B:1:NOJ:H62	2.47	0.42
1:A:258:GLY:O	1:A:259:PRO:C	2.58	0.42
1:B:366:THR:HG22	1:B:404:ARG:HA	2.00	0.42
1:B:50:PHE:CD2	1:B:50:PHE:N	2.87	0.42
1:A:220:ARG:NH1	1:A:256:VAL:O	2.53	0.42
1:B:363:ARG:NH1	1:B:363:ARG:HG2	2.26	0.42
1:B:42:MET:HB2	1:B:85:GLY:O	2.20	0.42
1:A:54:LEU:HD12	1:A:54:LEU:N	2.32	0.42
1:A:229:PHE:CD1	1:A:230:ALA:N	2.86	0.42
1:A:76:MET:HA	1:A:81:TRP:HB2	2.01	0.42
1:B:103:GLU:HB3	1:B:104:GLY:H	1.20	0.42
1:A:315:ASP:O	1:A:318:ALA:HB3	2.19	0.42
1:A:383:PHE:HD1	1:A:396:PHE:CD1	2.38	0.42
1:A:281:VAL:O	1:A:282:THR:C	2.57	0.42
1:B:190:ALA:O	1:B:194:THR:HG23	2.20	0.42
1:A:333:GLN:HG2	1:A:334:GLY:H	1.85	0.41
1:A:239:ILE:HD12	1:A:283:GLN:HG3	2.02	0.41
1:A:50:PHE:CD2	1:A:50:PHE:N	2.88	0.41
1:B:364:SER:HA	1:B:405:SER:O	2.21	0.41
1:A:174:CYS:HA	2:A:639:NAG:O7	2.19	0.41
1:B:154:ILE:HD12	1:B:154:ILE:N	2.35	0.41
1:A:142:CYS:CB	5:A:430:NOJ:O6	2.66	0.41
1:A:237:LYS:N	4:A:1:SO4:O3	2.52	0.41
1:B:236:TRP:CD2	1:B:279:GLN:HG2	2.55	0.41
1:A:217:THR:CG2	2:A:715:NAG:H5	2.51	0.41
1:A:209:TRP:C	1:A:211:PHE:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ILE:CG1	1:A:134:TYR:H	2.34	0.41
1:B:286:LEU:HD21	1:B:354:ILE:HD11	2.03	0.41
1:A:216:TYR:CB	1:A:256:VAL:HG21	2.51	0.41
1:B:243:LEU:HD22	1:B:286:LEU:HD22	2.02	0.41
1:B:45:LEU:HD22	1:B:92:ASP:HB2	2.03	0.40
1:B:76:MET:HA	1:B:81:TRP:HD1	1.86	0.40
1:B:166:LEU:HD23	1:B:167:LEU:C	2.42	0.40
1:A:289:ILE:HD13	1:A:289:ILE:HA	1.80	0.40
1:B:101:ASP:OD2	1:B:105:ARG:HB2	2.22	0.40
1:B:49:ARG:HG3	1:B:50:PHE:CE2	2.57	0.40
1:A:236:TRP:CD2	1:A:279:GLN:HG2	2.57	0.40
1:B:229:PHE:CG	1:B:230:ALA:N	2.88	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	388/398 (98%)	332 (86%)	43 (11%)	13 (3%)	5	10
1	B	389/398 (98%)	333 (86%)	45 (12%)	11 (3%)	6	15
All	All	777/796 (98%)	665 (86%)	88 (11%)	24 (3%)	5	12

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	GLU
1	A	230	ALA
1	B	51	MET
1	B	359	ILE
1	B	420	THR
1	A	395	GLY

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Mol	Chain	Res	Type
1	B	306	GLN
1	B	395	GLY
1	A	98	PRO
1	A	259	PRO
1	A	398	GLU
1	B	98	PRO
1	B	259	PRO
1	A	146	PRO
1	A	272	ASN
1	A	306	GLN
1	B	318	ALA
1	A	51	MET
1	A	378	CYS
1	A	420	THR
1	B	33	ASP
1	B	74	GLU
1	A	209	TRP
1	B	64	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	331/339 (98%)	289 (87%)	42 (13%)	5	13
1	B	332/339 (98%)	285 (86%)	47 (14%)	4	10
All	All	663/678 (98%)	574 (87%)	89 (13%)	5	11

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	TRP
1	A	45	LEU
1	A	46	HIS
1	A	49	ARG
1	A	54	LEU

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Mol	Chain	Res	Type
1	A	74	GLU
1	A	83	ASP
1	A	96	MET
1	A	99	GLN
1	A	111	GLN
1	A	118	ARG
1	A	119	GLN
1	A	165	ASP
1	A	174	CYS
1	A	175	ASP
1	A	196	ARG
1	A	213	LYS
1	A	229	PHE
1	A	235	SER
1	A	249	ASN
1	A	287	TRP
1	A	300	LEU
1	A	301	ARG
1	A	306	GLN
1	A	310	LEU
1	A	314	LYS
1	A	326	LYS
1	A	332	ARG
1	A	333	GLN
1	A	358	GLU
1	A	363	ARG
1	A	372	LEU
1	A	385	THR
1	A	391	LYS
1	A	398	GLU
1	A	399	TRP
1	A	400	THR
1	A	401	SER
1	A	403	LEU
1	A	405	SER
1	A	419	ASN
1	A	421	MET
1	B	44	TRP
1	B	45	LEU
1	B	46	HIS
1	B	49	ARG
1	B	54	LEU

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Mol	Chain	Res	Type
1	B	74	GLU
1	B	83	ASP
1	B	96	MET
1	B	99	GLN
1	B	111	GLN
1	B	118	ARG
1	B	119	GLN
1	B	137	VAL
1	B	165	ASP
1	B	174	CYS
1	B	175	ASP
1	B	213	LYS
1	B	235	SER
1	B	238	SER
1	B	247	SER
1	B	249	ASN
1	B	259	PRO
1	B	287	TRP
1	B	300	LEU
1	B	301	ARG
1	B	306	GLN
1	B	310	LEU
1	B	314	LYS
1	B	324	LEU
1	B	326	LYS
1	B	332	ARG
1	B	333	GLN
1	B	344	LEU
1	B	357	GLN
1	B	358	GLU
1	B	363	ARG
1	B	372	LEU
1	B	385	THR
1	B	388	LEU
1	B	398	GLU
1	B	399	TRP
1	B	400	THR
1	B	401	SER
1	B	403	LEU
1	B	405	SER
1	B	419	ASN
1	B	422	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	A	111	GLN
1	A	115	HIS
1	A	122	ASN
1	A	212	GLN
1	A	221	GLN
1	A	333	GLN
1	A	357	GLN
1	B	99	GLN
1	B	111	GLN
1	B	115	HIS
1	B	122	ASN
1	B	139	ASN
1	B	212	GLN
1	B	333	GLN
1	B	357	GLN
1	B	419	ASN
1	B	422	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 ⓘ

15 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
2	NAG	A	639	1,2	14,14,15	0.62	0	15,19,21	2.26	2 (13%)
2	NAG	A	640	2	14,14,15	0.55	0	15,19,21	2.16	3 (20%)
2	NAG	A	692	1,2	14,14,15	0.76	0	15,19,21	2.74	6 (40%)
2	NAG	A	693	2	14,14,15	0.93	0	15,19,21	2.76	4 (26%)
3	MAN	A	694	3	11,11,12	0.77	0	14,15,17	2.40	5 (35%)
3	MAN	A	696	3	11,11,12	0.96	1 (9%)	14,15,17	1.94	6 (42%)
2	NAG	A	715	1,2	14,14,15	0.78	0	15,19,21	1.57	3 (20%)
2	NAG	A	716	2	14,14,15	0.62	0	15,19,21	1.27	1 (6%)
7	NAG	B	692	1,7	14,14,15	0.65	0	15,19,21	1.79	2 (13%)
7	NAG	B	693	7	14,14,15	0.68	0	15,19,21	1.42	2 (13%)
7	MAN	B	694	7	11,11,12	0.76	0	14,15,17	1.67	3 (21%)
7	MAN	B	695	7	11,11,12	1.15	1 (9%)	14,15,17	2.13	5 (35%)
8	NAG	B	715	8	14,14,15	0.57	0	15,19,21	2.32	5 (33%)
8	NAG	B	716	8	14,14,15	0.70	0	15,19,21	1.78	3 (20%)
8	MAN	B	717	8	11,11,12	0.81	0	14,15,17	2.58	3 (21%)

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
2	NAG	A	639	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	640	2	-	0/6/23/26	0/1/1/1
2	NAG	A	692	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	693	2	-	0/6/23/26	0/1/1/1
3	MAN	A	694	3	-	0/2/19/22	0/1/1/1
3	MAN	A	696	3	1/1/4/5	0/2/19/22	1/1/1/1
2	NAG	A	715	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	716	2	-	0/6/23/26	0/1/1/1
7	NAG	B	692	1,7	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	B	693	7	-	0/6/23/26	0/1/1/1
7	MAN	B	694	7	1/1/4/5	0/2/19/22	0/1/1/1
7	MAN	B	695	7	-	0/2/19/22	0/1/1/1
8	NAG	B	715	8	-	0/6/23/26	0/1/1/1
8	NAG	B	716	8	-	0/6/23/26	0/1/1/1
8	MAN	B	717	8	1/1/4/5	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	696	MAN	C2-C3	2.34	1.55	1.52
7	B	695	MAN	C2-C3	2.92	1.56	1.52

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	692	NAG	C3-C4-C5	-4.00	103.22	110.20
2	A	715	NAG	C3-C4-C5	-3.65	103.83	110.20
3	A	694	MAN	C3-C4-C5	-3.45	104.19	110.20
8	B	716	NAG	O4-C4-C3	-3.39	102.71	110.34
3	A	694	MAN	C2-C3-C4	-3.08	105.82	111.04
2	A	693	NAG	O7-C7-C8	-2.96	116.63	122.06
2	A	640	NAG	C3-C2-N2	-2.79	103.87	110.56
7	B	692	NAG	O4-C4-C5	-2.67	102.16	109.24
2	A	693	NAG	O3-C3-C4	-2.66	104.34	110.34
7	B	694	MAN	C1-C2-C3	-2.66	106.39	109.54
8	B	717	MAN	C1-C2-C3	-2.49	106.59	109.54
7	B	695	MAN	C1-O5-C5	-2.46	109.12	112.25
2	A	692	NAG	C6-C5-C4	-2.43	107.03	113.02
3	A	696	MAN	O5-C1-C2	-2.42	106.94	110.86
2	A	692	NAG	C3-C2-N2	-2.28	105.09	110.56
3	A	696	MAN	C3-C4-C5	-2.26	106.25	110.20
8	B	715	NAG	O7-C7-C8	-2.26	117.92	122.06
7	B	694	MAN	O5-C1-C2	-2.00	107.61	110.86
2	A	692	NAG	C2-N2-C7	2.08	125.71	123.04
8	B	717	MAN	O2-C2-C1	2.08	113.39	109.21
3	A	696	MAN	O2-C2-C3	2.15	114.45	110.12
2	A	693	NAG	C3-C2-N2	2.21	115.86	110.56
3	A	696	MAN	O3-C3-C2	2.25	114.06	110.00
2	A	692	NAG	O5-C5-C6	2.50	112.77	107.35
8	B	715	NAG	O5-C5-C6	2.62	113.02	107.35
2	A	715	NAG	C4-C3-C2	2.69	115.41	111.23
7	B	693	NAG	C3-C4-C5	2.83	115.13	110.20
2	A	715	NAG	C2-N2-C7	2.84	126.69	123.04
3	A	694	MAN	O4-C4-C3	2.90	116.88	110.34
7	B	695	MAN	O2-C2-C3	2.97	116.10	110.12
2	A	639	NAG	O3-C3-C4	3.09	117.31	110.34
8	B	716	NAG	O4-C4-C5	3.18	117.67	109.24
7	B	695	MAN	C2-C3-C4	3.21	116.49	111.04
3	A	696	MAN	C1-C2-C3	3.30	113.44	109.54
8	B	715	NAG	C3-C4-C5	3.40	116.13	110.20
7	B	693	NAG	C1-O5-C5	3.55	116.76	112.25
3	A	696	MAN	C1-O5-C5	3.57	116.77	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	715	NAG	C4-C3-C2	3.75	117.05	111.23
2	A	716	NAG	C1-O5-C5	3.78	117.04	112.25
7	B	695	MAN	C1-C2-C3	3.83	114.08	109.54
2	A	640	NAG	C2-N2-C7	3.93	128.09	123.04
7	B	695	MAN	O5-C5-C6	4.00	116.01	107.35
3	A	694	MAN	C1-C2-C3	4.07	114.35	109.54
8	B	716	NAG	C1-O5-C5	4.09	117.44	112.25
3	A	694	MAN	O3-C3-C4	4.10	119.57	110.34
7	B	692	NAG	C1-O5-C5	4.52	117.99	112.25
7	B	694	MAN	C3-C4-C5	4.60	118.21	110.20
2	A	640	NAG	C1-O5-C5	5.63	119.39	112.25
8	B	715	NAG	C1-O5-C5	5.78	119.58	112.25
2	A	639	NAG	C1-O5-C5	6.94	121.05	112.25
2	A	692	NAG	C1-O5-C5	8.01	122.41	112.25
8	B	717	MAN	C1-O5-C5	8.12	122.55	112.25
2	A	693	NAG	C1-O5-C5	8.88	123.52	112.25

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	B	692	NAG	C1
3	A	696	MAN	C1
7	B	694	MAN	C1
8	B	717	MAN	C1

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	696	MAN	C1-C2-C3-C4-C5-O5

12 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	639	NAG	4	0
2	A	640	NAG	1	0
2	A	692	NAG	4	0
2	A	693	NAG	5	0
3	A	694	MAN	1	0
2	A	715	NAG	1	0
7	B	692	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	693	NAG	1	0
7	B	694	MAN	1	0
7	B	695	MAN	1	0
8	B	715	NAG	5	0
8	B	716	NAG	1	0

5.6 Ligand geometry [i](#)

8 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	SO4	A	1	-	4,4,4	0.39	0	6,6,6	1.65	1 (16%)
4	SO4	A	2	-	4,4,4	0.24	0	6,6,6	0.66	0
5	NOJ	A	430	-	11,11,11	0.93	1 (9%)	11,15,15	3.04	6 (54%)
4	SO4	A	5	-	4,4,4	0.38	0	6,6,6	0.29	0
5	NOJ	B	1	-	11,11,11	1.57	2 (18%)	11,15,15	3.21	5 (45%)
4	SO4	B	3	-	4,4,4	0.17	0	6,6,6	0.27	0
4	SO4	B	4	-	4,4,4	0.20	0	6,6,6	0.30	0
6	NAG	B	639	-	14,14,15	0.68	0	15,19,21	2.41	5 (33%)

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	SO4	A	1	-	-	0/0/0/0	0/0/0/0
4	SO4	A	2	-	-	0/0/0/0	0/0/0/0
5	NOJ	A	430	-	-	0/2/19/19	0/1/1/1
4	SO4	A	5	-	-	0/0/0/0	0/0/0/0
5	NOJ	B	1	-	-	0/2/19/19	0/1/1/1
4	SO4	B	3	-	-	0/0/0/0	0/0/0/0
4	SO4	B	4	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	639	-	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1	NOJ	C2-C3	2.03	1.55	1.52
5	A	430	NOJ	C1-C2	2.14	1.54	1.52
5	B	1	NOJ	C1-C2	3.94	1.56	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1	NOJ	C3-C4-C5	-8.56	97.92	111.23
5	A	430	NOJ	C2-C3-C4	-6.44	100.10	111.04
5	A	430	NOJ	C3-C4-C5	-4.68	103.96	111.23
6	B	639	NAG	O7-C7-C8	-2.77	116.97	122.06
5	A	430	NOJ	C1-C2-C3	-2.66	107.25	110.29
6	B	639	NAG	O3-C3-C4	-2.50	104.72	110.34
5	A	430	NOJ	O6-C6-C5	-2.14	105.41	111.12
5	B	1	NOJ	C2-C3-C4	-2.02	107.61	111.04
5	A	430	NOJ	O2-C2-C3	2.23	114.60	110.12
5	B	1	NOJ	O4-C4-C5	2.28	113.63	109.11
5	B	1	NOJ	C6-C5-N5	2.81	117.06	110.05
6	B	639	NAG	C2-N2-C7	3.15	127.08	123.04
4	A	1	SO4	O2-S-O1	3.25	119.80	109.50
5	A	430	NOJ	O3-C3-C2	3.42	116.17	110.00
6	B	639	NAG	C3-C4-C5	3.53	116.35	110.20
5	B	1	NOJ	O3-C3-C2	3.92	117.08	110.00
6	B	639	NAG	C1-O5-C5	5.78	119.59	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	SO4	1	0
4	A	2	SO4	2	0
5	A	430	NOJ	2	0
5	B	1	NOJ	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	3	SO4	1	0
4	B	4	SO4	1	0
6	B	639	NAG	2	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	390/398 (97%)	0.04	6 (1%) 76 76	54, 57, 59, 72	0
1	B	391/398 (98%)	0.15	15 (3%) 44 44	54, 57, 59, 71	0
All	All	781/796 (98%)	0.09	21 (2%) 58 58	54, 57, 59, 72	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	421	MET	4.4
1	A	102	SER	3.8
1	A	57	GLN	3.3
1	A	58	GLU	3.2
1	B	396	PHE	2.9
1	B	404	ARG	2.8
1	B	105	ARG	2.8
1	B	135	ALA	2.7
1	B	189	LEU	2.6
1	B	143	ALA	2.6
1	B	33	ASP	2.3
1	B	104	GLY	2.3
1	B	383	PHE	2.3
1	A	33	ASP	2.3
1	A	395	GLY	2.2
1	B	211	PHE	2.1
1	B	351	VAL	2.1
1	B	323	PRO	2.1
1	B	151	TYR	2.0
1	B	173	TYR	2.0
1	B	178	GLU	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. 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
2	NAG	A	639	14/15	0.90	0.26	2.16	66,71,72,73	0
7	NAG	B	692	14/15	0.92	0.24	0.75	62,64,68,68	0
2	NAG	A	693	14/15	0.92	0.25	0.00	59,64,66,66	0
2	NAG	A	692	14/15	0.93	0.15	-0.46	42,49,51,54	0
3	MAN	A	696	11/12	0.70	0.48	-	102,103,106,106	0
3	MAN	A	694	11/12	0.84	0.38	-	103,103,104,104	0
8	NAG	B	716	14/15	0.74	0.44	-	106,108,109,111	0
8	NAG	B	715	14/15	0.77	0.33	-	101,104,105,105	0
2	NAG	A	640	14/15	0.80	0.35	-	65,72,75,77	0
2	NAG	A	716	14/15	0.83	0.44	-	79,84,87,88	0
7	MAN	B	694	11/12	0.81	0.35	-	74,78,81,81	0
2	NAG	A	715	14/15	0.85	0.37	-	71,75,77,81	0
8	MAN	B	717	11/12	0.67	0.42	-	112,113,113,114	0
7	MAN	B	695	11/12	0.94	0.21	-	66,69,71,72	0
7	NAG	B	693	14/15	0.88	0.28	-	71,73,75,76	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. 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	NAG	B	639	14/15	0.69	0.36	3.19	107,109,110,110	0
4	SO4	B	4	5/5	0.95	0.33	2.78	81,82,83,83	0
4	SO4	B	3	5/5	0.97	0.23	1.02	85,85,86,87	0
4	SO4	A	1	5/5	0.92	0.21	0.84	58,58,59,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	NOJ	B	1	11/11	0.89	0.22	0.46	46,52,56,56	0
4	SO4	A	2	5/5	0.95	0.17	-0.44	68,68,70,70	0
5	NOJ	A	430	11/11	0.96	0.15	-0.59	55,57,59,62	0
4	SO4	A	5	5/5	0.81	0.46	-	115,116,116,116	0

6.5 Other polymers [i](#)

There are no such residues in this entry.