



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:33 PM UTC

PDB ID : 1NQI / pdb_00001nqi
Title : crystal structure of lactose synthase, a 1:1 complex between beta1,4-galactosyltransferase and alpha-lactalbumin in the presence of GlcNAc
Authors : Ramakrishnan, B.; Qasba, P.K.
Deposited on : 2003-01-21
Resolution : 2.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

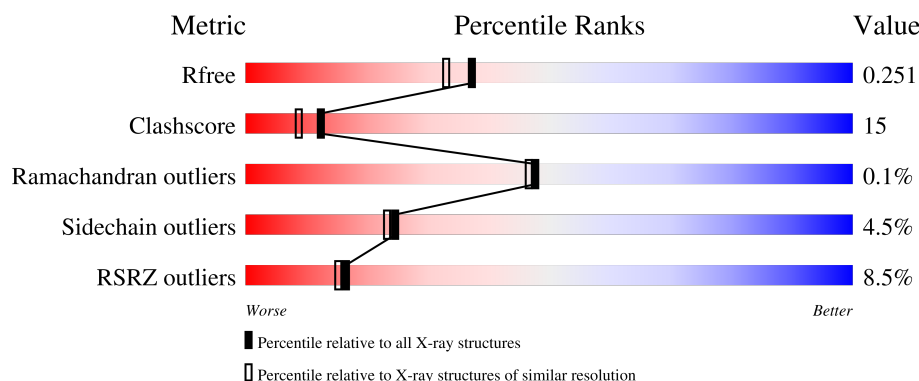
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	123	2% 81% 15% . .
1	C	123	7% 80% 15% .
2	B	286	2% 72% 20% . 5%
2	D	286	17% 51% 37% 7% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7198 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-LACTALBUMIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	123	Total	C	N	O	S	0	0	0
			980	620	156	195	9			
1	C	123	Total	C	N	O	S	0	0	0
			980	620	156	195	9			

- Molecule 2 is a protein called BETA-1,4-GALACTOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	272	Total	C	N	O	S	0	0	0
			2218	1424	382	398	14			
2	D	272	Total	C	N	O	S	0	0	0
			2218	1424	382	398	14			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	117	ALA	-	SEE REMARK 999	UNP P08037
B	118	SER	-	SEE REMARK 999	UNP P08037
B	119	MET	-	SEE REMARK 999	UNP P08037
B	120	THR	-	SEE REMARK 999	UNP P08037
B	121	GLY	-	SEE REMARK 999	UNP P08037
B	122	GLY	-	SEE REMARK 999	UNP P08037
B	123	GLN	-	SEE REMARK 999	UNP P08037
B	124	GLN	-	SEE REMARK 999	UNP P08037
B	125	MET	-	SEE REMARK 999	UNP P08037
B	126	GLY	-	SEE REMARK 999	UNP P08037
B	127	ARG	-	SEE REMARK 999	UNP P08037
B	128	GLY	-	SEE REMARK 999	UNP P08037
B	129	SER	-	SEE REMARK 999	UNP P08037
D	117	ALA	-	SEE REMARK 999	UNP P08037
D	118	SER	-	SEE REMARK 999	UNP P08037
D	119	MET	-	SEE REMARK 999	UNP P08037

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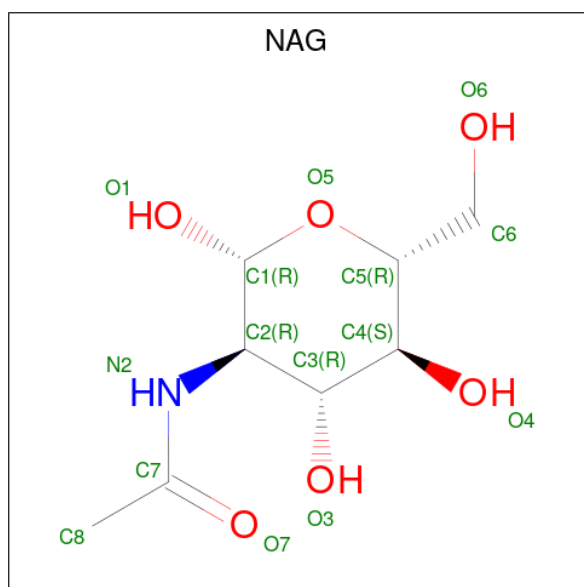
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Chain	Residue	Modelled	Actual	Comment	Reference
D	120	THR	-	SEE REMARK 999	UNP P08037
D	121	GLY	-	SEE REMARK 999	UNP P08037
D	122	GLY	-	SEE REMARK 999	UNP P08037
D	123	GLN	-	SEE REMARK 999	UNP P08037
D	124	GLN	-	SEE REMARK 999	UNP P08037
D	125	MET	-	SEE REMARK 999	UNP P08037
D	126	GLY	-	SEE REMARK 999	UNP P08037
D	127	ARG	-	SEE REMARK 999	UNP P08037
D	128	GLY	-	SEE REMARK 999	UNP P08037
D	129	SER	-	SEE REMARK 999	UNP P08037

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O 15 8 1 6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			15	8	1	6		

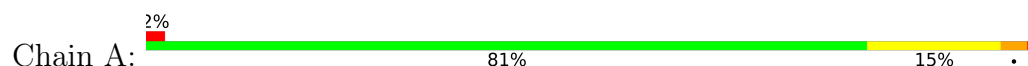
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	155	Total	O	0	0
			155	155		
5	B	244	Total	O	0	0
			244	244		
5	C	157	Total	O	0	0
			157	157		
5	D	214	Total	O	0	0
			214	214		

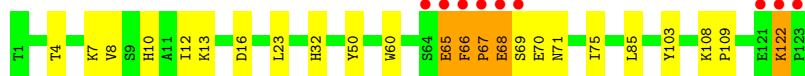
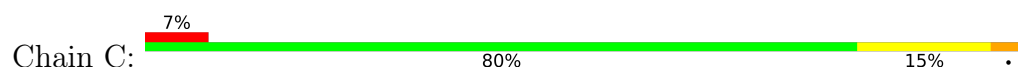
3 Residue-property plots

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.

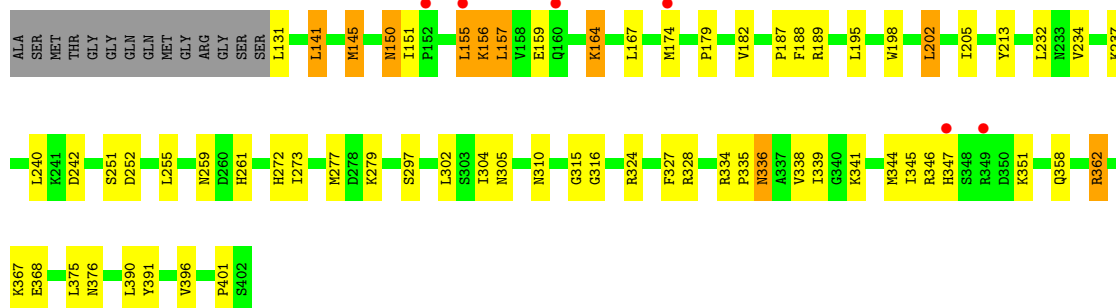
• Molecule 1: ALPHA-LACTALBUMIN



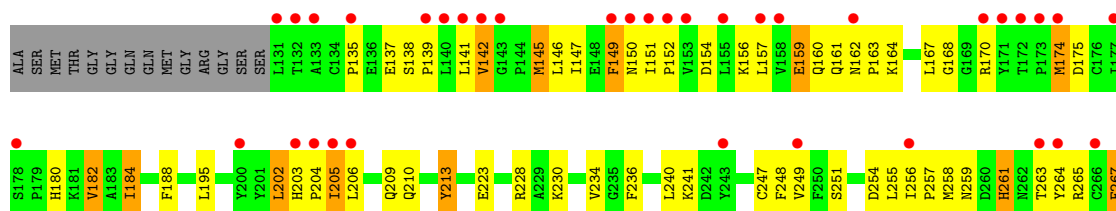
• Molecule 1: ALPHA-LACTALBUMIN

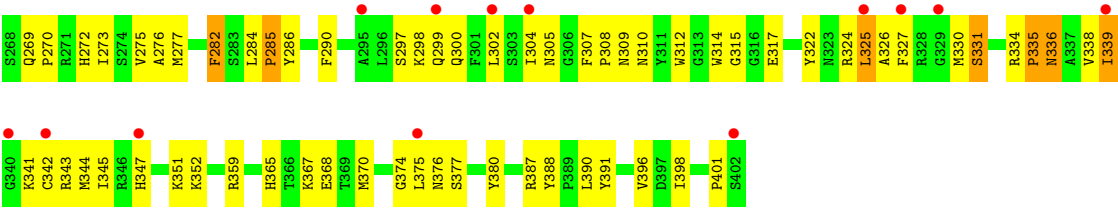


• Molecule 2: BETA-1,4-GALACTOSYLTRANSFERASE



• Molecule 2: BETA-1,4-GALACTOSYLTRANSFERASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.16Å 96.38Å 99.48Å 90.00° 100.98° 90.00°	Depositor
Resolution (Å)	24.50 – 2.00 24.50 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.1 (24.50-2.00) 95.1 (24.50-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.99Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.210 , 0.258 0.204 , 0.251	Depositor DCC
R_{free} test set	6887 reflections (10.04%)	wwPDB-VP
Wilson B-factor (Å ²)	23.0	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7198	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.67	0/1001	1.12	9/1350 (0.7%)
1	C	0.68	0/1001	1.33	11/1350 (0.8%)
2	B	0.68	1/2278 (0.0%)	1.06	15/3085 (0.5%)
2	D	0.66	0/2278	1.16	21/3085 (0.7%)
All	All	0.67	1/6558 (0.0%)	1.15	56/8870 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	145	MET	SD-CE	-8.53	1.58	1.79

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	67	PRO	N-CA-C	14.63	131.75	114.20
1	C	68	GLU	N-CA-C	12.39	128.87	112.88
2	D	182	VAL	N-CA-C	9.88	122.13	107.80
2	D	315	GLY	N-CA-C	9.59	124.08	112.48
1	C	122	LYS	N-CA-C	9.50	121.71	109.93
1	A	60	TRP	N-CA-C	8.95	124.89	112.45
1	C	66	PHE	CA-C-N	8.49	129.55	120.12
1	C	66	PHE	C-N-CA	8.49	129.55	120.12
2	B	182	VAL	N-CA-C	8.35	119.90	107.80
1	A	103	TYR	N-CA-C	-8.20	102.34	111.28
2	D	149	PHE	N-CA-C	8.05	120.10	110.44
2	B	315	GLY	N-CA-C	7.92	122.06	112.48
1	C	50	TYR	N-CA-C	7.82	122.14	109.40
2	D	285	PRO	N-CA-C	-7.74	103.44	113.57
1	A	69	SER	N-CA-C	-7.62	99.54	110.59
2	D	213	TYR	N-CA-C	7.15	120.27	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	261	HIS	N-CA-C	-7.12	104.59	113.28
2	D	273	ILE	N-CA-C	7.09	119.10	111.58
2	B	335	PRO	N-CA-C	-7.04	100.64	111.13
2	D	282	PHE	N-CA-C	6.93	121.03	112.58
2	D	359	ARG	N-CA-C	6.90	119.68	111.33
1	A	50	TYR	N-CA-C	6.78	120.46	109.40
2	D	251	SER	N-CA-C	6.72	120.59	108.69
2	B	202	LEU	N-CA-C	6.70	118.66	111.36
1	C	70	GLU	N-CA-C	-6.69	104.06	111.82
1	A	66	PHE	CA-C-N	6.60	128.09	119.84
1	A	66	PHE	C-N-CA	6.60	128.09	119.84
1	C	60	TRP	N-CA-C	6.59	121.54	112.04
2	D	159	GLU	N-CA-C	6.58	120.41	112.38
2	D	335	PRO	N-CA-C	-6.57	101.34	111.13
2	D	314	TRP	N-CA-C	6.54	119.96	110.28
2	B	316	GLY	N-CA-C	6.51	123.68	115.42
1	A	15	ILE	N-CA-C	-6.31	106.55	113.43
2	B	213	TYR	N-CA-C	6.31	119.47	109.81
2	B	310	ASN	N-CA-C	6.31	120.00	112.93
2	D	241	LYS	N-CA-C	-6.30	105.90	113.97
2	D	322	TYR	N-CA-C	-6.12	104.53	111.14
2	D	188	PHE	N-CA-C	6.08	118.53	108.99
2	B	273	ILE	N-CA-C	6.05	117.02	111.81
2	B	188	PHE	N-CA-C	5.95	118.15	108.76
2	B	252	ASP	N-CA-C	-5.93	102.29	110.35
2	D	202	LEU	N-CA-C	5.79	118.54	111.82
1	A	12	ILE	N-CA-C	5.64	117.59	112.29
2	D	205	ILE	N-CA-C	5.62	115.82	110.53
2	D	309	ASN	N-CA-C	-5.56	106.85	113.97
2	D	310	ASN	N-CA-C	5.53	119.66	113.02
2	D	396	VAL	N-CA-C	5.50	117.82	108.86
1	A	85	LEU	N-CA-C	5.44	119.76	113.18
2	B	242	ASP	N-CA-C	5.36	118.28	111.69
2	B	251	SER	N-CA-C	5.36	117.82	108.76
1	C	16	ASP	N-CA-C	5.31	117.87	109.96
2	B	179	PRO	N-CA-C	-5.20	107.85	114.35
1	C	109	PRO	N-CA-C	5.20	120.39	113.57
1	C	103	TYR	N-CA-C	-5.14	105.68	111.28
2	B	297	SER	N-CA-C	-5.08	103.83	110.53
2	B	362	ARG	N-CA-C	5.00	116.73	111.28

There are no chirality outliers.

There are no planarity outliers.

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	980	0	936	14	0
1	C	980	0	936	15	0
2	B	2218	0	2185	45	0
2	D	2218	0	2185	123	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	B	15	0	15	0	0
4	D	15	0	15	1	0
5	A	155	0	0	2	0
5	B	244	0	0	4	0
5	C	157	0	0	3	0
5	D	214	0	0	12	0
All	All	7198	0	6272	196	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 15.

All (196) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:270:PRO:HD3	2:D:330:MET:HE2	1.23	1.08
2:D:325:LEU:HD13	2:D:326:ALA:N	1.73	1.02
2:D:270:PRO:HD3	2:D:330:MET:CE	1.89	1.01
2:B:150:ASN:HD22	2:B:151:ILE:H	1.09	0.97
2:D:270:PRO:CD	2:D:330:MET:HE2	1.94	0.97
2:B:155:LEU:HD12	2:B:155:LEU:H	1.27	0.96
2:D:305:ASN:HD21	2:D:376:ASN:H	1.22	0.84
2:B:150:ASN:ND2	2:B:151:ILE:H	1.76	0.82
2:B:155:LEU:O	2:B:159:GLU:HG3	1.82	0.79
1:C:71:ASN:HD21	1:C:75:ILE:H	1.31	0.79
2:B:150:ASN:HD22	2:B:151:ILE:N	1.80	0.78
2:B:305:ASN:HD21	2:B:376:ASN:H	1.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:277:MET:HE3	2:B:344:MET:HE3	1.67	0.77
2:D:182:VAL:HG22	2:D:247:CYS:HB3	1.66	0.77
2:D:325:LEU:CD2	2:D:330:MET:HB2	2.14	0.76
2:D:142:VAL:HG13	5:D:993:HOH:O	1.85	0.76
2:B:150:ASN:ND2	2:B:150:ASN:H	1.85	0.74
2:B:279:LYS:HG3	2:B:346:ARG:NH2	2.03	0.74
2:D:150:ASN:HB3	5:D:1578:HOH:O	1.87	0.74
2:D:336:ASN:HD22	2:D:338:VAL:H	1.36	0.72
2:D:160:GLN:O	2:D:163:PRO:HD3	1.89	0.72
2:D:157:LEU:O	2:D:161:GLN:HG3	1.89	0.71
2:D:305:ASN:ND2	2:D:376:ASN:H	1.90	0.70
2:D:167:LEU:HD11	2:D:387:ARG:HB3	1.73	0.70
2:D:336:ASN:ND2	2:D:338:VAL:H	1.88	0.70
2:D:230:LYS:HD3	2:D:398:ILE:HB	1.76	0.68
2:D:275:VAL:HG13	2:D:284:LEU:HD21	1.76	0.68
2:B:336:ASN:HD22	2:B:336:ASN:C	2.02	0.67
2:D:325:LEU:HD22	2:D:330:MET:HB2	1.75	0.67
2:D:145:MET:HA	5:D:1606:HOH:O	1.95	0.67
2:D:160:GLN:NE2	2:D:161:GLN:HG3	2.09	0.67
1:C:10:HIS:O	1:C:13:LYS:HG2	1.94	0.67
1:C:10:HIS:HA	1:C:13:LYS:HE2	1.77	0.66
2:B:164:LYS:HD2	2:B:174:MET:HE3	1.78	0.66
2:D:135:PRO:HG2	2:D:210:GLN:HE22	1.61	0.65
1:A:64:SER:O	1:A:67:PRO:HD3	1.97	0.65
2:D:347:HIS:HB2	5:D:1233:HOH:O	1.96	0.65
2:D:297:SER:OG	2:D:300:GLN:HG3	1.95	0.65
2:D:223:GLU:O	2:D:352:LYS:HE2	1.97	0.65
1:A:71:ASN:HD21	1:A:75:ILE:H	1.44	0.64
2:D:336:ASN:ND2	2:D:339:ILE:H	1.96	0.64
2:D:335:PRO:HB2	2:D:339:ILE:HG12	1.80	0.64
2:B:150:ASN:HD22	2:B:150:ASN:H	1.45	0.64
2:D:336:ASN:HD22	2:D:336:ASN:C	2.06	0.63
1:C:4:THR:H	1:C:7:LYS:HD2	1.63	0.63
2:D:257:PRO:HD3	2:D:264:TYR:OH	1.97	0.63
2:D:162:ASN:C	5:D:1669:HOH:O	2.42	0.62
2:D:184:ILE:HD12	2:D:184:ILE:N	2.14	0.62
2:D:149:PHE:HE2	2:D:256:ILE:HG13	1.63	0.62
2:D:150:ASN:O	2:D:151:ILE:HD13	2.00	0.62
2:D:156:LYS:O	2:D:159:GLU:HB2	2.00	0.62
2:B:336:ASN:ND2	2:B:339:ILE:H	1.98	0.62
2:B:327:PHE:CZ	2:B:367:LYS:HB2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:326:ALA:HA	5:D:1461:HOH:O	1.99	0.61
2:D:167:LEU:CD1	2:D:387:ARG:HB3	2.31	0.61
2:D:180:HIS:CE1	2:D:265:ARG:HD2	2.35	0.61
2:D:174:MET:SD	2:D:174:MET:N	2.75	0.60
2:D:259:ASN:OD1	2:D:261:HIS:HB2	2.01	0.60
2:D:336:ASN:HD21	2:D:339:ILE:H	1.50	0.60
2:B:164:LYS:HD2	2:B:174:MET:CE	2.33	0.59
2:B:358:GLN:O	2:B:362:ARG:HG3	2.02	0.59
1:C:65:GLU:HB3	1:C:66:PHE:CD2	2.37	0.59
2:D:327:PHE:CZ	2:D:367:LYS:HB2	2.38	0.58
2:D:325:LEU:CD1	2:D:326:ALA:N	2.59	0.58
1:C:8:VAL:O	1:C:12:ILE:HG12	2.04	0.58
2:D:255:LEU:HD21	2:D:277:MET:HE3	1.83	0.58
1:A:13:LYS:HE3	5:A:1226:HOH:O	2.03	0.57
1:A:121:GLU:HG2	5:A:1290:HOH:O	2.04	0.57
1:C:69:SER:HA	5:C:1173:HOH:O	2.04	0.57
2:D:154:ASP:OD1	2:D:156:LYS:HB2	2.05	0.57
2:D:325:LEU:HD13	2:D:326:ALA:H	1.64	0.57
2:D:202:LEU:HD21	2:D:257:PRO:HD2	1.86	0.57
2:D:138:SER:HB2	2:D:210:GLN:HE21	1.70	0.57
2:D:298:LYS:O	2:D:302:LEU:HD13	2.05	0.56
2:D:276:ALA:HB1	2:D:282:PHE:C	2.30	0.56
2:D:138:SER:HB3	2:D:141:LEU:HD13	1.89	0.55
2:D:365:HIS:O	2:D:368:GLU:HG2	2.07	0.55
2:D:236:PHE:HE1	2:D:248:PHE:CE2	2.25	0.55
2:D:167:LEU:HD11	2:D:387:ARG:CB	2.36	0.55
1:A:75:ILE:HD11	1:A:79:LYS:HB2	1.87	0.55
2:D:135:PRO:CG	2:D:210:GLN:HE22	2.19	0.54
2:B:150:ASN:ND2	2:B:151:ILE:N	2.48	0.54
2:D:325:LEU:HD21	2:D:330:MET:C	2.31	0.54
2:D:305:ASN:O	2:D:374:GLY:HA3	2.08	0.54
2:D:167:LEU:C	2:D:167:LEU:HD13	2.33	0.53
2:D:236:PHE:CE1	2:D:248:PHE:CE2	2.96	0.53
2:D:282:PHE:CD2	2:D:341:LYS:HE3	2.43	0.53
1:A:12:ILE:O	1:A:15:ILE:HG22	2.08	0.53
2:B:141:LEU:HD23	2:B:261:HIS:CD2	2.43	0.53
2:D:263:THR:HG21	2:D:265:ARG:HD3	1.91	0.53
1:C:13:LYS:HD3	1:C:23:LEU:HD11	1.91	0.53
2:B:259:ASN:OD1	2:B:261:HIS:HB2	2.09	0.53
2:D:275:VAL:HG21	2:D:335:PRO:HD2	1.90	0.53
2:D:272:HIS:CD2	2:D:290:PHE:HA	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:259:ASN:C	2:D:261:HIS:H	2.17	0.52
2:D:275:VAL:CG2	2:D:335:PRO:HD2	2.39	0.52
2:D:145:MET:HE2	2:D:146:LEU:O	2.10	0.51
2:B:345:ILE:O	2:B:347:HIS:CD2	2.64	0.51
2:D:325:LEU:HD13	2:D:326:ALA:CA	2.41	0.51
1:C:32:HIS:HD2	4:D:527:NAG:O1	1.94	0.51
1:A:70:GLU:O	1:A:71:ASN:C	2.54	0.51
2:D:258:MET:HG3	2:D:342:CYS:HA	1.93	0.51
2:D:269:GLN:HB3	2:D:331:SER:O	2.11	0.51
2:D:149:PHE:CE2	2:D:256:ILE:HG13	2.45	0.50
2:D:170:ARG:NH1	2:D:213:TYR:O	2.41	0.50
2:D:175:ASP:HB2	5:D:1172:HOH:O	2.11	0.50
2:B:150:ASN:ND2	2:B:150:ASN:N	2.52	0.49
2:B:336:ASN:HD22	2:B:338:VAL:H	1.59	0.49
2:D:147:ILE:HB	2:D:343:ARG:HD2	1.94	0.49
2:D:267:PHE:N	2:D:267:PHE:CD1	2.81	0.49
2:D:157:LEU:O	2:D:160:GLN:NE2	2.46	0.48
2:B:336:ASN:ND2	2:B:338:VAL:H	2.12	0.48
2:B:336:ASN:HD21	2:B:339:ILE:H	1.58	0.48
2:B:150:ASN:HD22	2:B:150:ASN:N	2.04	0.48
1:C:32:HIS:HE1	5:C:952:HOH:O	1.97	0.48
2:D:307:PHE:HB3	2:D:308:PRO:HD2	1.96	0.48
2:D:343:ARG:HH11	2:D:343:ARG:HG2	1.79	0.48
1:C:66:PHE:HB2	1:C:67:PRO:HD2	1.96	0.47
2:D:270:PRO:CD	2:D:330:MET:CE	2.70	0.47
2:D:255:LEU:CD2	2:D:344:MET:HB2	2.44	0.47
2:B:344:MET:HE2	5:B:1100:HOH:O	2.14	0.47
1:A:55:ILE:HB	1:A:80:LEU:HD13	1.97	0.46
2:D:269:GLN:O	2:D:270:PRO:C	2.58	0.46
2:B:156:LYS:HD3	2:B:156:LYS:HA	1.76	0.46
2:D:230:LYS:O	2:D:234:VAL:HG23	2.16	0.46
2:D:336:ASN:ND2	2:D:339:ILE:HG23	2.30	0.46
2:D:255:LEU:CD2	2:D:277:MET:HE3	2.45	0.46
2:D:305:ASN:HD21	2:D:376:ASN:N	2.02	0.46
2:D:285:PRO:HG2	2:D:286:TYR:CD2	2.49	0.46
2:D:182:VAL:HG11	2:D:249:VAL:HG23	1.99	0.45
2:D:184:ILE:N	2:D:184:ILE:CD1	2.80	0.45
2:D:205:ILE:O	2:D:209:GLN:HG3	2.16	0.45
1:A:75:ILE:HD11	1:A:79:LYS:CB	2.46	0.45
1:C:108:LYS:HD2	5:C:1625:HOH:O	2.15	0.45
2:D:159:GLU:C	5:D:1669:HOH:O	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:336:ASN:HD22	2:D:338:VAL:N	2.11	0.45
2:B:131:LEU:HB2	5:B:1422:HOH:O	2.15	0.45
2:D:375:LEU:C	2:D:377:SER:H	2.25	0.45
2:D:324:ARG:O	2:D:370:MET:HE1	2.16	0.45
2:D:228:ARG:HD3	2:D:317:GLU:OE1	2.17	0.45
2:B:237:LYS:HE2	5:B:1277:HOH:O	2.17	0.45
2:B:304:ILE:HB	2:B:324:ARG:HB3	1.99	0.45
2:D:351:LYS:HE2	2:D:351:LYS:HB2	1.78	0.45
2:B:272:HIS:HB3	2:B:334:ARG:HG2	1.99	0.44
2:D:325:LEU:CD2	2:D:330:MET:C	2.90	0.44
1:C:122:LYS:HA	1:C:122:LYS:HD3	1.67	0.44
2:D:272:HIS:HB3	2:D:334:ARG:HG2	1.99	0.44
1:A:2:GLU:OE1	2:B:346:ARG:NH2	2.51	0.44
2:D:135:PRO:HB2	2:D:137:GLU:O	2.17	0.43
2:D:336:ASN:ND2	2:D:336:ASN:C	2.75	0.43
2:B:198:TRP:CZ2	2:B:202:LEU:HG	2.53	0.43
2:B:390:LEU:O	2:B:391:TYR:HB3	2.17	0.43
2:D:142:VAL:HB	5:D:1040:HOH:O	2.18	0.43
2:D:304:ILE:O	2:D:305:ASN:HB3	2.18	0.43
2:B:279:LYS:HE3	2:B:346:ARG:NH2	2.34	0.42
2:D:307:PHE:O	2:D:374:GLY:HA2	2.17	0.42
1:A:65:GLU:H	1:A:65:GLU:HG2	1.24	0.42
2:D:325:LEU:CD1	2:D:326:ALA:H	2.29	0.42
2:B:255:LEU:HD23	2:B:255:LEU:HA	1.75	0.42
2:D:299:GLN:HE21	2:D:299:GLN:HA	1.84	0.42
2:B:336:ASN:C	2:B:336:ASN:ND2	2.71	0.42
2:D:259:ASN:C	2:D:261:HIS:N	2.77	0.42
2:D:168:GLY:N	2:D:388:TYR:O	2.45	0.42
2:B:279:LYS:HG3	2:B:346:ARG:CZ	2.50	0.42
2:D:154:ASP:OD1	2:D:156:LYS:CB	2.67	0.42
2:D:312:TRP:CD2	2:D:401:PRO:HG3	2.55	0.42
2:D:390:LEU:O	2:D:391:TYR:HB3	2.20	0.42
2:D:159:GLU:HB3	5:D:1295:HOH:O	2.19	0.42
2:B:157:LEU:HD13	2:B:157:LEU:HA	1.90	0.42
1:C:71:ASN:HD21	1:C:75:ILE:N	2.09	0.42
2:B:187:PRO:HD3	2:B:232:LEU:HD21	2.01	0.41
2:D:300:GLN:HG2	2:D:330:MET:HE1	2.01	0.41
2:D:352:LYS:HE3	2:D:352:LYS:HA	2.03	0.41
2:D:380:TYR:HA	5:D:1499:HOH:O	2.20	0.41
2:B:234:VAL:HG11	2:B:396:VAL:HG11	2.02	0.41
2:D:203:HIS:HB2	2:D:204:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:261:HIS:HB3	2:D:339:ILE:HD12	2.03	0.41
2:D:300:GLN:CG	2:D:330:MET:HE1	2.51	0.41
2:D:325:LEU:HD13	2:D:325:LEU:C	2.40	0.41
2:D:343:ARG:HG2	2:D:343:ARG:NH1	2.35	0.41
1:A:60:TRP:O	1:A:73:CYS:HB2	2.21	0.41
2:D:327:PHE:CE1	2:D:367:LYS:HB2	2.56	0.41
2:D:202:LEU:O	2:D:206:LEU:HG	2.21	0.41
2:D:269:GLN:OE1	2:D:330:MET:HB3	2.21	0.41
2:D:299:GLN:HA	2:D:299:GLN:NE2	2.36	0.41
1:A:8:VAL:O	1:A:12:ILE:HG12	2.21	0.41
1:A:85:LEU:O	1:A:89:ILE:HG13	2.20	0.40
2:B:145:MET:HE1	2:B:205:ILE:CD1	2.51	0.40
2:B:328:ARG:HD3	2:B:328:ARG:HA	1.79	0.40
2:B:338:VAL:O	2:B:341:LYS:HG3	2.21	0.40
2:B:401:PRO:HG2	5:B:1590:HOH:O	2.21	0.40
2:D:138:SER:CB	2:D:210:GLN:HE21	2.34	0.40
2:D:254:ASP:O	2:D:345:ILE:HG13	2.21	0.40
1:C:108:LYS:HE2	1:C:108:LYS:HB3	1.98	0.40
2:D:139:PRO:C	5:D:1310:HOH:O	2.65	0.40
2:D:150:ASN:O	2:D:150:ASN:CG	2.64	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	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
1	C	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
2	B	270/286 (94%)	260 (96%)	10 (4%)	0	100	100
2	D	270/286 (94%)	255 (94%)	14 (5%)	1 (0%)	30	27
All	All	782/818 (96%)	749 (96%)	32 (4%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	152	PRO

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	109/109 (100%)	107 (98%)	2 (2%)	51	58
1	C	109/109 (100%)	106 (97%)	3 (3%)	38	41
2	B	245/254 (96%)	230 (94%)	15 (6%)	17	14
2	D	245/254 (96%)	233 (95%)	12 (5%)	22	20
All	All	708/726 (98%)	676 (96%)	32 (4%)	24	23

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	GLU
1	A	85	LEU
2	B	141	LEU
2	B	150	ASN
2	B	155	LEU
2	B	156	LYS
2	B	157	LEU
2	B	164	LYS
2	B	167	LEU
2	B	189	ARG
2	B	195	LEU
2	B	240	LEU
2	B	302	LEU
2	B	336	ASN
2	B	351	LYS
2	B	368	GLU
2	B	375	LEU
1	C	65	GLU
1	C	68	GLU

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Mol	Chain	Res	Type
1	C	85	LEU
2	D	142	VAL
2	D	145	MET
2	D	164	LYS
2	D	174	MET
2	D	184	ILE
2	D	195	LEU
2	D	240	LEU
2	D	267	PHE
2	D	325	LEU
2	D	331	SER
2	D	336	ASN
2	D	339	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	45	ASN
1	A	71	ASN
2	B	150	ASN
2	B	160	GLN
2	B	161	GLN
2	B	194	HIS
2	B	219	ASN
2	B	261	HIS
2	B	305	ASN
2	B	310	ASN
2	B	336	ASN
2	B	347	HIS
2	B	386	GLN
1	C	32	HIS
1	C	43	ASN
1	C	45	ASN
1	C	71	ASN
2	D	150	ASN
2	D	161	GLN
2	D	162	ASN
2	D	180	HIS
2	D	190	ASN
2	D	210	GLN
2	D	219	ASN

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Mol	Chain	Res	Type
2	D	299	GLN
2	D	305	ASN
2	D	310	ASN
2	D	336	ASN
2	D	347	HIS

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	D	527	-	15,15,15	0.94	0	21,21,21	0.87	2 (9%)
4	NAG	B	403	-	15,15,15	1.16	1 (6%)	21,21,21	0.83	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	527	-	-	0/6/26/26	0/1/1/1
4	NAG	B	403	-	-	0/6/26/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	403	NAG	C2-N2	3.81	1.51	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	527	NAG	C8-C7-N2	-2.26	112.36	116.12
4	D	527	NAG	O7-C7-N2	2.02	125.56	121.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	527	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	123/123 (100%)	-0.13	3 (2%) 59 59	13, 21, 45, 64	0
1	C	123/123 (100%)	-0.04	9 (7%) 21 19	11, 21, 46, 72	0
2	B	272/286 (95%)	-0.11	6 (2%) 62 61	11, 24, 46, 60	0
2	D	272/286 (95%)	1.01	49 (18%) 3 3	16, 33, 57, 66	0
All	All	790/818 (96%)	0.28	67 (8%) 16 15	11, 26, 52, 72	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	67	PRO	4.7
2	D	339	ILE	4.4
2	D	243	TYR	4.3
2	D	132	THR	4.2
1	C	69	SER	4.1
1	C	68	GLU	4.0
1	C	66	PHE	3.9
2	D	135	PRO	3.7
1	C	123	PRO	3.7
1	A	66	PHE	3.7
2	D	151	ILE	3.6
2	D	133	ALA	3.6
2	D	142	VAL	3.4
2	D	200	TYR	3.4
2	D	157	LEU	3.3
2	D	325	LEU	3.3
2	B	347	HIS	3.2
2	D	295	ALA	3.1
1	C	121	GLU	3.1
2	D	402	SER	3.1
1	C	122	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
2	D	173	PRO	2.9
2	B	155	LEU	2.8
2	D	342	CYS	2.8
2	B	349	ARG	2.8
2	D	178	SER	2.8
2	D	150	ASN	2.8
2	D	162	ASN	2.7
2	D	205	ILE	2.7
2	D	263	THR	2.7
2	D	139	PRO	2.7
2	B	174	MET	2.7
1	C	65	GLU	2.6
2	B	152	PRO	2.6
2	D	249	VAL	2.6
2	D	329	GLY	2.6
2	D	149	PHE	2.6
2	D	266	CYS	2.6
2	D	158	VAL	2.6
2	D	204	PRO	2.6
2	D	174	MET	2.5
2	D	327	PHE	2.5
2	D	143	GLY	2.5
2	D	171	TYR	2.5
2	D	152	PRO	2.4
2	D	141	LEU	2.4
2	D	347	HIS	2.4
2	D	340	GLY	2.3
2	D	131	LEU	2.3
2	D	140	LEU	2.3
2	D	155	LEU	2.3
2	D	206	LEU	2.3
2	D	302	LEU	2.3
1	C	64	SER	2.3
2	D	256	ILE	2.3
2	D	375	LEU	2.2
2	D	177	ILE	2.2
2	D	304	ILE	2.2
2	D	172	THR	2.2
2	D	153	VAL	2.2
1	A	65	GLU	2.2
1	A	67	PRO	2.1
2	D	170	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	299	GLN	2.1
2	D	203	HIS	2.1
2	D	264	TYR	2.1
2	B	160	GLN	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](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	D	527	15/15	0.97	0.05	14,15,18,20	0
4	NAG	B	403	15/15	0.98	0.04	12,15,17,19	0
3	CA	A	124	1/1	0.99	0.02	18,18,18,18	0
3	CA	C	526	1/1	0.99	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.