



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:38 PM GMT

PDB ID : 4J0M
Title : Crystal structure of BRL1 (LRR) in complex with brassinolide
Authors : Chai, J.; She, J.; Han, Z.; Zhou, B.
Deposited on : 2013-01-31
Resolution : 2.50 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

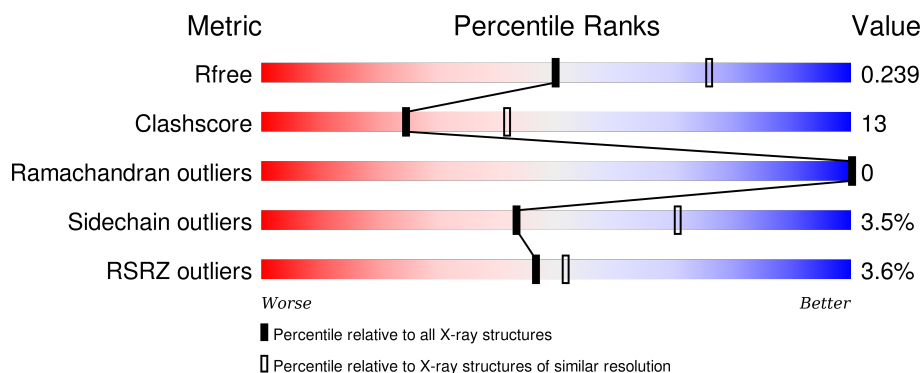
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	740	<div> <div>4%</div> <div>79%</div> <div>18%</div> <div>..</div> </div>
1	B	740	<div> <div>3%</div> <div>78%</div> <div>19%</div> <div>..</div> </div>

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	801	-	-	-	X
2	NAG	B	803	-	-	-	X
3	NAG	B	802	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11785 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 Serine/threonine-protein kinase BRI1-like 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	724	Total	C	N	O	S	0	0	0
			5455	3446	913	1067	29			
1	B	724	Total	C	N	O	S	0	0	0
			5455	3446	913	1067	29			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	759	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
A	760	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
A	761	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
A	762	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
A	763	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
A	764	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	759	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	760	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	761	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	762	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	763	HIS	-	EXPRESSION TAG	UNP Q9ZWC8
B	764	HIS	-	EXPRESSION TAG	UNP Q9ZWC8

- 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		
2	B	2	Total	C	N	O	0	0
			28	16	2	10		

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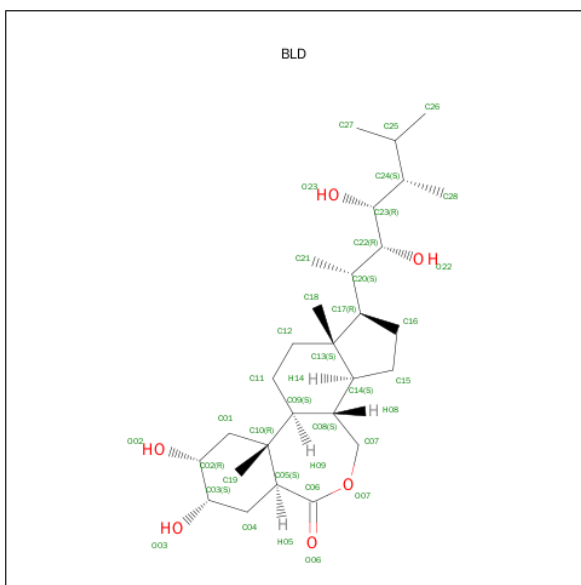
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	2	Total	C	N	O	0	0
			28	16	2	10		
2	B	2	Total	C	N	O	0	0
			28	16	2	10		
2	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is BRASSINOLIDE (three-letter code: BLD) (formula: $C_{28}H_{48}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 34 28 6	0	0
4	B	1	Total C O 34 28 6	0	0

- Molecule 5 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	6	Total 72	C 40	N 2	O 30	0	0
5	B	6	Total 72	C 40	N 2	O 30	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	210	Total O 210 210	0	0
6	B	201	Total O 201 201	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.86 Å 83.40 Å 264.06 Å 90.00° 97.24° 90.00°	Depositor
Resolution (Å)	29.83 – 2.50 29.83 – 2.49	Depositor EDS
% Data completeness (in resolution range)	94.5 (29.83-2.50) 93.9 (29.83-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 2.51 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.187 , 0.239 0.193 , 0.239	Depositor DCC
R_{free} test set	3773 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	3 of 75143 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11785	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BLD, BMA, NAG, 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	0.43	0/5561	0.67	0/7559
1	B	0.42	0/5561	0.66	1/7559 (0.0%)
All	All	0.42	0/11122	0.66	1/15118 (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	B	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	B	156	VAL	CB-CA-C	-5.11	101.69	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	120	SER	Peptide

5.2 Too-close contacts

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5455	0	5391	144	0
1	B	5455	0	5390	133	1
2	A	84	0	74	3	0
2	B	112	0	100	1	0
3	A	28	0	26	2	0
3	B	28	0	26	0	0
4	A	34	0	48	5	0
4	B	34	0	48	5	0
5	A	72	0	55	7	0
5	B	72	0	54	1	0
6	A	210	0	0	8	0
6	B	201	0	0	11	0
All	All	11785	0	11212	291	1

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 13.

All (291) 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:B:120:SER:HB3	1:B:145:TYR:HB2	1.26	1.17
1:B:118:GLY:H	1:B:142:MET:HE3	1.06	1.15
1:A:95:LEU:HD22	1:A:142:MET:HE2	1.30	1.12
1:B:590:GLU:HG2	1:B:624:THR:HG21	1.25	1.12
1:A:510:ARG:HH11	1:A:510:ARG:HG2	1.06	1.11
1:A:95:LEU:H	1:A:118:GLY:HA2	1.07	1.11
1:A:399:GLN:HG3	1:A:402:PRO:HD3	1.28	1.11
1:B:398:LEU:HD23	1:B:399:GLN:H	1.01	1.09
1:A:590:GLU:HG2	1:A:624:THR:HG21	1.12	1.08
1:A:95:LEU:HB2	1:A:142:MET:HE3	1.34	1.07
1:B:399:GLN:HG2	1:B:400:SER:H	1.20	1.02
1:A:153:LEU:HD21	1:A:156:VAL:HG22	1.41	1.02
1:A:399:GLN:HG2	1:A:401:SER:HA	1.41	1.01
1:A:95:LEU:H	1:A:118:GLY:CA	1.75	0.98
1:B:448:MET:CE	1:B:473:LYS:HD2	1.98	0.94
1:A:590:GLU:HG2	1:A:624:THR:CG2	1.97	0.93
1:B:398:LEU:HD23	1:B:399:GLN:N	1.83	0.93
1:A:95:LEU:N	1:A:118:GLY:HA2	1.82	0.93
1:A:480:LEU:N	1:A:501:MET:HE1	1.83	0.93
1:B:477:LEU:HB2	1:B:501:MET:HE1	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:ARG:NH1	1:A:510:ARG:HG2	1.85	0.90
1:B:590:GLU:CG	1:B:624:THR:HG21	2.01	0.89
1:A:400:SER:N	1:A:401:SER:HA	1.88	0.89
1:A:590:GLU:CG	1:A:624:THR:HG21	2.02	0.89
1:B:498:CYS:O	1:B:522:LEU:HD22	1.73	0.88
1:B:400:SER:N	1:B:401:SER:HA	1.89	0.88
3:A:815:NAG:O3	3:A:815:NAG:H82	1.75	0.87
1:A:281:GLN:HB3	5:A:805:NAG:H81	1.55	0.87
1:B:118:GLY:N	1:B:142:MET:HE3	1.90	0.86
1:B:305:VAL:HG23	1:B:306:ILE:HG13	1.56	0.86
1:A:399:GLN:CG	1:A:402:PRO:HD3	2.04	0.85
1:B:398:LEU:CD2	1:B:399:GLN:H	1.90	0.85
1:B:117:GLY:HA2	1:B:142:MET:HE1	1.55	0.84
1:A:399:GLN:OE1	6:A:1080:HOH:O	1.94	0.84
1:A:153:LEU:HD21	1:A:156:VAL:CG2	2.06	0.84
1:B:120:SER:HB3	1:B:145:TYR:CB	2.08	0.83
1:B:590:GLU:HG2	1:B:624:THR:CG2	2.08	0.83
1:B:477:LEU:O	1:B:501:MET:HE2	1.78	0.83
1:B:457:MET:HE2	1:B:462:LEU:HD11	1.60	0.82
1:A:399:GLN:HG2	1:A:400:SER:H	1.44	0.82
1:A:119:ASP:CG	1:A:120:SER:H	1.83	0.81
1:B:153:LEU:HD21	1:B:156:VAL:HG22	1.62	0.81
1:A:399:GLN:HG2	1:A:400:SER:N	1.95	0.80
1:A:281:GLN:HB3	5:A:805:NAG:C8	2.12	0.79
1:A:258:ILE:HD12	1:A:263:LEU:CD1	2.12	0.78
1:A:497:ARG:HD2	6:A:1104:HOH:O	1.83	0.77
1:B:477:LEU:CB	1:B:501:MET:HE1	2.13	0.77
1:B:418:VAL:HG21	1:B:457:MET:CE	2.16	0.76
1:A:399:GLN:CG	1:A:400:SER:H	1.96	0.76
1:A:119:ASP:HA	1:A:141:SER:OG	1.85	0.75
1:B:118:GLY:H	1:B:142:MET:CE	1.94	0.75
1:B:418:VAL:HG21	1:B:457:MET:HE3	1.68	0.75
1:B:468:GLU:OE1	6:B:1007:HOH:O	2.03	0.75
1:B:603:GLU:OE2	1:B:605:GLU:HB2	1.87	0.74
1:B:399:GLN:HG2	1:B:400:SER:N	2.00	0.74
1:B:258:ILE:HD11	1:B:284:LEU:HD22	1.69	0.74
1:B:501:MET:SD	6:B:1000:HOH:O	2.46	0.72
1:B:117:GLY:CA	1:B:142:MET:HE1	2.19	0.72
1:A:558:ASN:OD1	2:A:801:NAG:H2	1.88	0.72
1:B:467:PRO:O	1:B:470:VAL:HG23	1.89	0.72
1:B:448:MET:HE1	1:B:473:LYS:HD2	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:SER:N	1:B:401:SER:CA	2.53	0.71
1:A:603:GLU:OE2	1:A:605:GLU:HB2	1.91	0.71
1:A:480:LEU:H	1:A:501:MET:HE1	1.57	0.70
1:B:258:ILE:HD12	1:B:263:LEU:CD1	2.22	0.70
1:B:443:PRO:HD2	1:B:446:ILE:HD12	1.73	0.69
1:A:95:LEU:HB2	1:A:142:MET:CE	2.17	0.69
1:B:165:GLY:HA3	6:B:1018:HOH:O	1.92	0.69
1:A:258:ILE:HD12	1:A:263:LEU:HD11	1.72	0.69
1:A:443:PRO:HD2	1:A:446:ILE:HD12	1.73	0.69
1:B:151:SER:HA	1:B:174:LEU:HD22	1.75	0.69
1:A:310:SER:OG	1:A:332:ASN:OD1	2.11	0.69
1:A:418:VAL:HG21	1:A:457:MET:CE	2.23	0.68
4:A:804:BLD:H221	4:A:804:BLD:H112	1.73	0.68
1:A:479:THR:C	1:A:501:MET:HE1	2.14	0.68
1:A:105:GLN:HB3	1:A:128:GLN:HG3	1.75	0.66
1:A:41:PHE:CD1	1:A:98:LEU:HD21	2.30	0.66
1:A:95:LEU:HD22	1:A:142:MET:CE	2.18	0.66
1:A:558:ASN:OD1	2:A:801:NAG:C2	2.40	0.66
1:B:374:CYS:HB3	6:B:1054:HOH:O	1.94	0.65
1:A:479:THR:HA	1:A:501:MET:CE	2.26	0.65
1:B:501:MET:CE	6:B:1000:HOH:O	2.44	0.65
1:A:281:GLN:CB	5:A:805:NAG:H81	2.28	0.64
1:A:399:GLN:HG2	1:A:401:SER:CA	2.24	0.64
1:A:418:VAL:HG12	1:A:446:ILE:HD11	1.79	0.64
1:B:277:GLN:O	1:B:303:THR:HG21	1.98	0.64
1:A:174:LEU:O	1:A:200:PRO:HG3	1.99	0.63
1:A:95:LEU:HB3	1:A:118:GLY:HA3	1.81	0.63
1:A:418:VAL:HG21	1:A:457:MET:HE3	1.81	0.62
1:B:418:VAL:CG2	1:B:457:MET:HE3	2.29	0.62
4:A:804:BLD:C12	4:A:804:BLD:H221	2.29	0.62
1:A:372:THR:HG22	1:A:395:PHE:CD1	2.35	0.62
1:B:392:PRO:HB2	1:B:395:PHE:CD2	2.34	0.62
1:A:132:LEU:HD13	1:A:142:MET:HE1	1.82	0.61
1:B:399:GLN:C	1:B:401:SER:HA	2.20	0.61
1:A:631:THR:HG22	4:A:804:BLD:H228	1.81	0.61
1:A:153:LEU:CD2	1:A:156:VAL:CG2	2.78	0.61
1:A:258:ILE:HD11	1:A:284:LEU:HD22	1.80	0.61
1:B:123:SER:OG	1:B:124:ASP:N	2.33	0.60
5:A:806:NAG:H83	5:A:806:NAG:H3	1.82	0.60
1:A:642:ILE:HD13	1:A:642:ILE:N	2.16	0.60
1:B:95:LEU:HB2	1:B:142:MET:HE2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLN:CG	1:A:400:SER:N	2.60	0.60
1:A:119:ASP:CG	1:A:120:SER:N	2.54	0.60
1:B:448:MET:HE2	1:B:473:LYS:HD2	1.79	0.60
1:B:392:PRO:HG2	1:B:395:PHE:HE2	1.66	0.60
4:B:801:BLD:H112	4:B:801:BLD:H221	1.82	0.60
1:B:41:PHE:CD1	1:B:98:LEU:HD21	2.36	0.60
1:A:119:ASP:OD2	1:A:120:SER:N	2.33	0.59
1:A:684:GLY:HA3	1:A:706:SER:OG	2.02	0.59
1:A:510:ARG:HH11	1:A:510:ARG:CG	1.95	0.59
3:A:815:NAG:HO3	3:A:815:NAG:H82	1.68	0.59
1:A:358:VAL:CG2	1:A:382:LEU:HD23	2.33	0.58
1:A:255:THR:HB	1:A:281:GLN:HB2	1.85	0.58
1:A:59:TYR:CE1	1:A:60:GLU:HG3	2.39	0.58
1:A:479:THR:CA	1:A:501:MET:HE1	2.33	0.58
1:A:596:ARG:HD3	1:A:648:TYR:CE2	2.38	0.58
1:B:501:MET:HE3	6:B:1000:HOH:O	2.02	0.58
1:A:753:ARG:NH1	1:A:754:PRO:HD2	2.18	0.57
1:B:631:THR:HG22	4:B:801:BLD:H228	1.85	0.57
1:B:118:GLY:HA3	1:B:120:SER:OG	2.04	0.57
1:A:399:GLN:C	1:A:401:SER:HA	2.24	0.57
1:B:59:TYR:CE1	1:B:60:GLU:HG3	2.39	0.57
1:B:279:LEU:HD23	1:B:300:LEU:HD22	1.87	0.57
1:A:510:ARG:NH1	1:A:510:ARG:CG	2.61	0.56
1:B:477:LEU:HB2	1:B:501:MET:CE	2.31	0.56
1:B:418:VAL:HG12	1:B:446:ILE:HD11	1.87	0.56
1:B:41:PHE:CE1	1:B:98:LEU:HD11	2.40	0.56
1:B:676:THR:HG22	1:B:698:ASN:HB2	1.86	0.56
1:A:716:LEU:HD22	1:A:733:LEU:CD1	2.36	0.56
1:A:400:SER:N	1:A:401:SER:CA	2.67	0.56
1:A:501:MET:CE	1:A:503:TRP:O	2.53	0.56
1:A:479:THR:HA	1:A:501:MET:HE1	1.88	0.56
1:A:479:THR:HA	1:A:501:MET:HE3	1.87	0.56
1:B:718:VAL:HG13	1:B:723:LEU:HD12	1.88	0.55
1:A:32:PHE:HE2	1:A:59:TYR:HH	1.52	0.55
1:A:480:LEU:H	1:A:501:MET:CE	2.19	0.55
1:B:166:LYS:N	6:B:1018:HOH:O	2.38	0.55
1:A:317:GLU:HG2	1:A:339:SER:O	2.07	0.55
1:B:358:VAL:CG2	1:B:382:LEU:HD23	2.36	0.55
1:B:433:LEU:HB2	1:B:457:MET:HG2	1.87	0.55
1:A:37:LEU:HD21	1:A:97:ASN:O	2.06	0.55
1:B:418:VAL:HG12	1:B:446:ILE:CD1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:ASP:OD1	1:B:310:SER:HB2	2.07	0.55
1:B:358:VAL:HG23	1:B:382:LEU:HD23	1.89	0.54
1:B:281:GLN:HB3	5:B:808:NAG:H81	1.90	0.54
1:B:59:TYR:CZ	1:B:60:GLU:HG3	2.43	0.54
1:B:590:GLU:CB	1:B:624:THR:HG21	2.38	0.54
5:A:806:NAG:C3	5:A:806:NAG:H83	2.37	0.54
1:B:32:PHE:HZ	1:B:59:TYR:HH	1.50	0.54
1:B:614:ARG:HB2	1:B:614:ARG:NH1	2.23	0.53
1:A:418:VAL:HG21	1:A:457:MET:HE1	1.90	0.53
1:B:54:LEU:HD22	1:B:57:TRP:CE2	2.44	0.53
1:B:468:GLU:OE2	1:B:494:SER:HB2	2.07	0.53
1:A:80:VAL:HG23	1:A:105:GLN:HG3	1.90	0.53
1:B:421:GLU:O	1:B:424:LYS:HB2	2.09	0.53
1:B:418:VAL:HG11	1:B:446:ILE:HD13	1.91	0.52
1:A:716:LEU:CD2	1:A:733:LEU:CD1	2.88	0.52
1:A:706:SER:HB2	6:A:916:HOH:O	2.10	0.52
1:B:150:CYS:O	1:B:174:LEU:HD22	2.10	0.52
1:A:501:MET:HE3	1:A:503:TRP:O	2.10	0.51
4:B:801:BLD:H221	4:B:801:BLD:C12	2.40	0.51
1:A:322:PHE:O	1:A:325:CYS:HB2	2.10	0.51
1:B:409:ILE:HG21	1:B:414:LEU:HD11	1.91	0.51
1:A:716:LEU:HD22	1:A:733:LEU:HD11	1.93	0.51
1:A:418:VAL:CG2	1:A:457:MET:HE3	2.40	0.51
1:B:418:VAL:HG21	1:B:457:MET:HE1	1.91	0.51
1:B:738:VAL:CG1	6:B:1044:HOH:O	2.59	0.51
1:A:395:PHE:HB2	6:A:1015:HOH:O	2.10	0.50
1:A:409:ILE:HG21	1:A:414:LEU:HD11	1.93	0.50
1:A:247:LEU:N	1:A:248:PRO:CD	2.74	0.50
1:B:217:PHE:O	1:B:244:PRO:HG3	2.12	0.50
1:A:132:LEU:CD1	1:A:142:MET:HE1	2.42	0.50
1:A:502:ILE:HD11	1:A:578:SER:HB3	1.94	0.49
1:B:267:ILE:HD11	1:B:314:PHE:CZ	2.48	0.49
1:A:392:PRO:HG2	1:A:395:PHE:HE2	1.77	0.49
1:B:344:ASN:HB2	1:B:368:PRO:HB3	1.95	0.49
1:B:454:ASP:HA	1:B:479:THR:HG22	1.94	0.49
5:A:806:NAG:C8	5:A:806:NAG:H3	2.43	0.48
1:B:398:LEU:HD22	1:B:399:GLN:O	2.13	0.48
1:A:79:ILE:HD12	1:A:101:LEU:HD22	1.95	0.48
1:B:95:LEU:HB2	1:B:142:MET:CE	2.43	0.48
1:A:308:ASP:OD1	1:A:310:SER:HB2	2.13	0.48
1:A:241:ASP:C	1:A:242:LYS:HG3	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:247:LEU:N	1:B:248:PRO:CD	2.76	0.48
1:A:467:PRO:O	1:A:470:VAL:HG23	2.14	0.48
1:A:691:VAL:HG22	1:A:715:ASP:HB3	1.96	0.48
1:A:418:VAL:CG1	1:A:446:ILE:CD1	2.92	0.47
1:A:76:ASP:N	1:A:76:ASP:OD2	2.47	0.47
1:A:267:ILE:HD11	1:A:314:PHE:CZ	2.50	0.47
1:A:461:ASN:HB2	6:A:1053:HOH:O	2.15	0.47
1:B:418:VAL:CG1	1:B:446:ILE:CD1	2.93	0.47
1:B:738:VAL:HG12	6:B:1044:HOH:O	2.14	0.47
1:B:429:LYS:HB3	1:B:429:LYS:HE3	1.66	0.47
1:B:447:TRP:O	1:B:474:GLY:HA3	2.14	0.47
1:A:153:LEU:CD2	1:A:156:VAL:HG22	2.27	0.47
1:A:635:PHE:HE2	1:A:642:ILE:HD11	1.78	0.47
1:A:93:LEU:HD21	1:A:142:MET:HE1	1.96	0.47
5:A:806:NAG:C3	5:A:806:NAG:C8	2.92	0.46
1:B:579:VAL:HG12	1:B:633:TYR:OH	2.15	0.46
1:B:581:GLY:HA2	1:B:630:MET:HG3	1.97	0.46
1:A:41:PHE:CE1	1:A:98:LEU:HD11	2.50	0.46
1:B:380:LEU:CD2	1:B:395:PHE:CZ	2.98	0.46
1:B:37:LEU:HD21	1:B:97:ASN:O	2.15	0.46
1:B:686:LEU:O	1:B:710:LEU:HD22	2.16	0.46
1:B:610:GLU:OE1	2:B:807:NAG:H82	2.16	0.46
1:A:358:VAL:HG23	1:A:382:LEU:HD23	1.98	0.46
1:A:434:SER:OG	1:A:456:VAL:HG12	2.16	0.46
1:B:153:LEU:CD2	1:B:156:VAL:HG22	2.38	0.45
1:A:418:VAL:HG12	1:A:446:ILE:CD1	2.44	0.45
1:B:545:ASN:O	1:B:547:LYS:HD2	2.16	0.45
1:A:45:SER:O	1:A:91:GLY:HA3	2.16	0.45
1:A:734:THR:HB	1:A:750:VAL:HG12	1.97	0.45
1:B:392:PRO:HB2	1:B:395:PHE:CE2	2.52	0.45
1:A:398:LEU:HG	1:A:398:LEU:O	2.16	0.45
1:B:398:LEU:CD2	1:B:399:GLN:N	2.64	0.45
1:B:691:VAL:HG23	4:B:801:BLD:H02	1.98	0.44
4:A:804:BLD:H20	4:A:804:BLD:H24	1.79	0.44
2:A:811:NAG:H62	2:A:812:NAG:C1	2.47	0.44
1:A:564:PRO:HG2	1:A:567:LEU:HG	2.00	0.44
1:A:470:VAL:HG12	1:A:471:CYS:SG	2.58	0.44
1:A:405:GLU:OE2	6:A:999:HOH:O	2.21	0.44
1:B:418:VAL:CG1	1:B:446:ILE:HD13	2.47	0.44
1:A:241:ASP:HB3	1:A:242:LYS:HG3	2.00	0.44
1:B:37:LEU:C	1:B:37:LEU:HD23	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:576:PRO:HA	1:A:633:TYR:CE1	2.53	0.44
1:B:153:LEU:HD21	1:B:156:VAL:CG2	2.41	0.44
1:B:258:ILE:HD12	1:B:263:LEU:HD11	1.98	0.44
1:B:218:SER:HB3	1:B:242:LYS:O	2.17	0.44
1:B:635:PHE:HB3	1:B:664:TYR:CE1	2.53	0.43
1:A:83:ASP:OD1	1:A:85:ARG:NH2	2.47	0.43
1:B:457:MET:CE	1:B:462:LEU:HD11	2.39	0.43
1:B:174:LEU:O	1:B:200:PRO:HG3	2.18	0.43
1:A:32:PHE:HE2	1:A:59:TYR:OH	2.01	0.43
1:B:434:SER:OG	1:B:456:VAL:HG12	2.18	0.43
1:A:392:PRO:HB2	1:A:395:PHE:CE2	2.52	0.43
1:A:392:PRO:HB2	1:A:395:PHE:CD2	2.54	0.43
1:B:718:VAL:HG13	1:B:718:VAL:O	2.18	0.43
1:A:473:LYS:HA	1:A:473:LYS:HD2	1.81	0.43
1:B:413:TYR:CD2	1:B:413:TYR:N	2.87	0.43
1:B:654:PHE:C	1:B:654:PHE:CD2	2.92	0.43
1:A:143:VAL:HG22	1:A:158:ILE:HD12	1.99	0.43
1:A:40:ALA:O	1:A:44:ASN:HB2	2.19	0.43
1:B:158:ILE:O	1:B:158:ILE:HG22	2.18	0.42
1:B:259:SER:HB3	1:B:283:SER:OG	2.19	0.42
1:B:32:PHE:CE2	1:B:59:TYR:CE1	3.07	0.42
1:A:689:ILE:O	1:A:689:ILE:HG23	2.18	0.42
1:B:143:VAL:HG22	1:B:158:ILE:HD12	2.00	0.42
1:A:679:ILE:HD12	1:A:703:LEU:HD23	2.01	0.42
1:A:417:THR:HB	6:A:971:HOH:O	2.19	0.42
1:B:596:ARG:HD3	1:B:648:TYR:CD2	2.54	0.42
1:A:95:LEU:CB	1:A:118:GLY:HA3	2.49	0.42
4:B:801:BLD:O06	4:B:801:BLD:C19	2.67	0.42
1:B:587:VAL:HB	1:B:599:GLY:CA	2.49	0.42
1:A:418:VAL:HG11	1:A:446:ILE:HD13	2.01	0.42
1:B:380:LEU:HD22	1:B:395:PHE:CZ	2.55	0.42
1:A:59:TYR:HD1	1:A:60:GLU:N	2.18	0.42
1:B:245:ILE:O	1:B:248:PRO:HD2	2.20	0.42
1:B:53:VAL:HG21	1:B:87:SER:HB3	2.02	0.41
1:B:590:GLU:HG2	1:B:624:THR:CB	2.50	0.41
1:A:80:VAL:HG22	1:A:80:VAL:O	2.21	0.41
1:A:372:THR:HG22	1:A:395:PHE:CE1	2.55	0.41
1:A:31:ASP:C	1:A:32:PHE:CD2	2.93	0.41
1:B:546:CYS:HB3	6:B:901:HOH:O	2.19	0.41
1:A:281:GLN:N	1:A:281:GLN:OE1	2.54	0.41
4:A:804:BLD:H119	4:A:804:BLD:H08	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ARG:CD	1:A:648:TYR:CD2	3.04	0.41
1:B:477:LEU:C	1:B:501:MET:HE2	2.39	0.41
1:A:247:LEU:HB3	1:A:248:PRO:HD3	2.03	0.41
1:A:686:LEU:HD23	1:A:686:LEU:HA	1.86	0.41
1:B:80:VAL:HG22	1:B:80:VAL:O	2.21	0.41
1:B:423:GLY:HA3	1:B:445:GLU:HB3	2.02	0.41
1:A:260:ARG:HG2	1:A:286:HIS:HB2	2.02	0.41
1:B:117:GLY:CA	1:B:142:MET:CE	2.95	0.41
1:A:457:MET:HB2	1:A:482:LEU:CD2	2.51	0.41
1:A:93:LEU:O	1:A:117:GLY:CA	2.69	0.41
1:A:470:VAL:C	1:A:472:VAL:H	2.23	0.41
1:B:550:ILE:HB	1:B:642:ILE:HG12	2.03	0.41
1:B:550:ILE:HA	1:B:641:MET:HA	2.02	0.41
1:A:271:GLU:OE1	1:A:271:GLU:HA	2.19	0.41
1:B:305:VAL:HG21	6:B:983:HOH:O	2.21	0.41
1:A:32:PHE:N	1:A:32:PHE:CD2	2.89	0.41
1:B:293:ILE:HA	1:B:294:PRO:HD3	1.94	0.41
1:A:591:GLY:HA3	1:A:595:CYS:SG	2.60	0.40
1:A:733:LEU:HD13	1:A:733:LEU:HA	1.89	0.40
1:B:182:LEU:HB2	1:B:208:LEU:HD23	2.02	0.40
1:A:132:LEU:CD1	1:A:142:MET:CE	2.99	0.40
1:B:520:GLY:O	1:B:545:ASN:ND2	2.49	0.40
1:A:588:ARG:NH1	1:A:627:TYR:OH	2.54	0.40
1:B:477:LEU:O	1:B:501:MET:CE	2.60	0.40
1:A:546:CYS:HB3	6:A:901:HOH:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:ASP:OD1	1:B:541:ARG:NH1[1_545]	1.99	0.21

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	720/740 (97%)	685 (95%)	35 (5%)	0	100	100
1	B	720/740 (97%)	693 (96%)	27 (4%)	0	100	100
All	All	1440/1480 (97%)	1378 (96%)	62 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	627/641 (98%)	604 (96%)	23 (4%)	41	68
1	B	627/641 (98%)	606 (97%)	21 (3%)	45	73
All	All	1254/1282 (98%)	1210 (96%)	44 (4%)	43	70

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	TYR
1	A	76	ASP
1	A	158	ILE
1	A	186	ILE
1	A	212	ASN
1	A	220	LEU
1	A	225	CYS
1	A	241	ASP
1	A	255	THR
1	A	325	CYS
1	A	349	LYS
1	A	371	LEU
1	A	435	PHE
1	A	453	SER
1	A	510	ARG

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Mol	Chain	Res	Type
1	A	579	VAL
1	A	593	THR
1	A	613	GLU
1	A	618	VAL
1	A	630	MET
1	A	687	LYS
1	A	718	VAL
1	A	722	ASN
1	B	76	ASP
1	B	119	ASP
1	B	121	SER
1	B	123	SER
1	B	149	LYS
1	B	186	ILE
1	B	225	CYS
1	B	310	SER
1	B	349	LYS
1	B	353	ILE
1	B	369	ILE
1	B	397	SER
1	B	409	ILE
1	B	435	PHE
1	B	479	THR
1	B	604	PHE
1	B	614	ARG
1	B	628	SER
1	B	630	MET
1	B	718	VAL
1	B	733	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

26 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	801	1,2	14,14,15	0.48	0	15,19,21	1.84	2 (13%)
2	NAG	A	802	2	14,14,15	0.44	0	15,19,21	1.43	1 (6%)
5	NAG	A	805	1,5	14,14,15	0.56	0	15,19,21	1.92	4 (26%)
5	NAG	A	806	5	14,14,15	1.82	4 (28%)	15,19,21	1.85	5 (33%)
5	BMA	A	807	5	11,11,12	1.06	1 (9%)	14,15,17	1.65	3 (21%)
5	MAN	A	808	5	11,11,12	1.40	3 (27%)	14,15,17	1.98	3 (21%)
5	MAN	A	809	5	11,11,12	3.85	1 (9%)	14,15,17	1.45	2 (14%)
5	MAN	A	810	5	11,11,12	1.98	4 (36%)	14,15,17	1.67	2 (14%)
2	NAG	A	811	1,2	14,14,15	1.89	3 (21%)	15,19,21	2.22	4 (26%)
2	NAG	A	812	2	14,14,15	1.61	2 (14%)	15,19,21	2.54	4 (26%)
2	NAG	A	813	1,2	14,14,15	0.57	0	15,19,21	0.68	0
2	NAG	A	814	2	14,14,15	0.45	0	15,19,21	0.98	2 (13%)
2	NAG	B	803	1,2	14,14,15	0.44	0	15,19,21	2.22	4 (26%)
2	NAG	B	804	2	14,14,15	0.46	0	15,19,21	1.15	2 (13%)
2	NAG	B	806	1,2	14,14,15	0.49	0	15,19,21	1.90	1 (6%)
2	NAG	B	807	2	14,14,15	0.45	0	15,19,21	1.62	1 (6%)
5	NAG	B	808	1,5	14,14,15	2.03	6 (42%)	15,19,21	1.81	2 (13%)
5	NAG	B	809	5	14,14,15	2.24	5 (35%)	15,19,21	1.81	1 (6%)
5	BMA	B	810	5	11,11,12	1.02	1 (9%)	14,15,17	1.60	3 (21%)
5	MAN	B	811	5	11,11,12	1.65	3 (27%)	14,15,17	1.90	5 (35%)
5	MAN	B	812	5	11,11,12	2.15	4 (36%)	14,15,17	3.07	5 (35%)
5	MAN	B	813	5	11,11,12	2.29	5 (45%)	14,15,17	1.49	3 (21%)
2	NAG	B	814	1,2	14,14,15	0.64	0	15,19,21	1.08	2 (13%)
2	NAG	B	815	2	14,14,15	0.54	0	15,19,21	1.34	1 (6%)
2	NAG	B	816	1,2	14,14,15	0.61	0	15,19,21	0.92	1 (6%)
2	NAG	B	817	2	14,14,15	0.49	0	15,19,21	0.82	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
2	NAG	A	801	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	802	2	-	0/6/23/26	0/1/1/1
5	NAG	A	805	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	806	5	-	0/6/23/26	0/1/1/1
5	BMA	A	807	5	-	0/2/19/22	0/1/1/1
5	MAN	A	808	5	-	0/2/19/22	0/1/1/1
5	MAN	A	809	5	-	0/2/19/22	0/1/1/1
5	MAN	A	810	5	-	0/2/19/22	0/1/1/1
2	NAG	A	811	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	812	2	-	0/6/23/26	0/1/1/1
2	NAG	A	813	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	814	2	-	0/6/23/26	0/1/1/1
2	NAG	B	803	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	804	2	-	0/6/23/26	0/1/1/1
2	NAG	B	806	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	807	2	-	0/6/23/26	0/1/1/1
5	NAG	B	808	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	809	5	-	0/6/23/26	0/1/1/1
5	BMA	B	810	5	-	0/2/19/22	0/1/1/1
5	MAN	B	811	5	-	0/2/19/22	0/1/1/1
5	MAN	B	812	5	-	0/2/19/22	0/1/1/1
5	MAN	B	813	5	-	0/2/19/22	0/1/1/1
2	NAG	B	814	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	815	2	-	0/6/23/26	0/1/1/1
2	NAG	B	816	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	817	2	-	0/6/23/26	0/1/1/1

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	809	MAN	O6-C6	-12.55	0.88	1.42
5	B	809	NAG	O5-C1	-4.93	1.35	1.43
5	B	813	MAN	O5-C1	-4.47	1.36	1.43
5	B	808	NAG	O5-C1	-4.42	1.36	1.43
5	B	812	MAN	O5-C1	-4.09	1.36	1.43
5	B	811	MAN	O5-C1	-3.77	1.37	1.43
5	A	806	NAG	O5-C1	-3.63	1.37	1.43
2	A	811	NAG	O5-C1	-3.38	1.38	1.43
5	A	810	MAN	O5-C1	-3.35	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	809	NAG	O5-C5	-3.28	1.36	1.43
5	B	813	MAN	O5-C5	-3.28	1.36	1.43
2	A	811	NAG	C2-N2	-3.22	1.40	1.46
5	A	810	MAN	O5-C5	-3.17	1.36	1.43
2	A	812	NAG	O5-C1	-3.06	1.38	1.43
5	A	810	MAN	O4-C4	-3.04	1.35	1.43
5	B	812	MAN	O3-C3	-2.98	1.35	1.43
5	A	806	NAG	O5-C5	-2.94	1.37	1.43
5	B	808	NAG	C2-N2	-2.93	1.41	1.46
5	B	813	MAN	O2-C2	-2.90	1.36	1.43
5	B	812	MAN	O4-C4	-2.87	1.36	1.43
5	B	813	MAN	O4-C4	-2.86	1.36	1.43
5	A	806	NAG	O3-C3	-2.86	1.36	1.43
2	A	811	NAG	O3-C3	-2.86	1.36	1.43
5	B	809	NAG	C2-N2	-2.69	1.41	1.46
5	B	812	MAN	O5-C5	-2.69	1.37	1.43
5	B	811	MAN	O4-C4	-2.66	1.36	1.43
5	B	808	NAG	O3-C3	-2.63	1.36	1.43
5	B	809	NAG	O3-C3	-2.62	1.36	1.43
5	B	809	NAG	O7-C7	-2.50	1.17	1.23
5	B	813	MAN	O3-C3	-2.48	1.37	1.43
2	A	812	NAG	C2-N2	-2.43	1.42	1.46
5	A	808	MAN	O4-C4	-2.42	1.37	1.43
5	A	808	MAN	O2-C2	-2.41	1.37	1.43
5	A	807	BMA	O5-C1	-2.41	1.39	1.43
5	B	808	NAG	O4-C4	-2.38	1.37	1.43
5	A	808	MAN	O5-C1	-2.31	1.39	1.43
5	B	808	NAG	C1-C2	-2.31	1.49	1.52
5	A	810	MAN	O3-C3	-2.29	1.37	1.43
5	B	811	MAN	O2-C2	-2.21	1.38	1.43
5	A	806	NAG	C7-N2	-2.20	1.25	1.34
5	B	810	BMA	O5-C1	-2.19	1.40	1.43
5	B	808	NAG	O5-C5	-2.04	1.38	1.43

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	812	NAG	C3-C4-C5	-6.62	98.65	110.20
5	B	812	MAN	O5-C5-C6	-6.48	93.33	107.35
5	B	809	NAG	C3-C4-C5	-5.65	100.34	110.20
2	A	811	NAG	C6-C5-C4	-5.27	100.02	113.02
5	A	805	NAG	C2-N2-C7	-4.88	116.77	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	808	MAN	C2-C3-C4	-4.60	103.23	111.04
2	A	812	NAG	C2-N2-C7	-4.56	117.18	123.04
2	B	815	NAG	C2-N2-C7	-4.49	117.27	123.04
5	B	811	MAN	C2-C3-C4	-4.45	103.48	111.04
2	A	811	NAG	O3-C3-C4	-3.72	101.97	110.34
2	A	812	NAG	C4-C3-C2	-3.60	105.64	111.23
5	B	812	MAN	C1-C2-C3	-3.52	105.38	109.54
5	B	810	BMA	O5-C1-C2	-3.43	105.30	110.86
5	A	806	NAG	C4-C3-C2	-2.95	106.65	111.23
5	B	813	MAN	C6-C5-C4	-2.87	105.93	113.02
5	A	807	BMA	O5-C1-C2	-2.71	106.45	110.86
2	A	812	NAG	C3-C2-N2	-2.59	104.36	110.56
5	B	812	MAN	O2-C2-C3	-2.51	105.06	110.12
5	B	813	MAN	O4-C4-C3	-2.49	104.74	110.34
2	B	804	NAG	C2-N2-C7	-2.46	119.88	123.04
5	A	810	MAN	C6-C5-C4	-2.46	106.94	113.02
5	B	808	NAG	C6-C5-C4	-2.38	107.15	113.02
2	A	814	NAG	C2-N2-C7	-2.28	120.11	123.04
2	B	814	NAG	C2-N2-C7	-2.18	120.24	123.04
5	A	809	MAN	O3-C3-C2	-2.14	106.13	110.00
2	B	803	NAG	C6-C5-C4	-2.13	107.76	113.02
5	B	812	MAN	O5-C1-C2	-2.12	107.42	110.86
5	A	806	NAG	C3-C4-C5	-2.09	106.56	110.20
2	A	811	NAG	C3-C4-C5	-2.07	106.59	110.20
5	A	805	NAG	C6-C5-C4	-2.06	107.94	113.02
2	A	801	NAG	C3-C2-N2	-2.02	105.72	110.56
5	B	811	MAN	C1-C2-C3	2.05	111.97	109.54
2	B	803	NAG	C2-N2-C7	2.11	125.75	123.04
2	B	803	NAG	C3-C4-C5	2.14	113.94	110.20
5	A	807	BMA	C1-O5-C5	2.15	114.98	112.25
2	B	816	NAG	C4-C3-C2	2.19	114.63	111.23
5	B	811	MAN	O3-C3-C2	2.26	114.07	110.00
5	B	810	BMA	O3-C3-C2	2.27	114.10	110.00
5	B	813	MAN	C1-C2-C3	2.35	112.32	109.54
5	B	810	BMA	C1-O5-C5	2.42	115.32	112.25
5	B	811	MAN	O6-C6-C5	2.47	119.48	111.33
5	A	806	NAG	O3-C3-C2	2.52	114.10	109.11
5	A	805	NAG	C3-C4-C5	2.62	114.76	110.20
5	A	808	MAN	O6-C6-C5	2.64	120.06	111.33
2	A	814	NAG	C1-O5-C5	2.67	115.64	112.25
2	B	804	NAG	C1-O5-C5	2.71	115.69	112.25
2	B	814	NAG	C1-O5-C5	2.80	115.80	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	811	MAN	C1-O5-C5	2.99	116.04	112.25
5	A	807	BMA	O3-C3-C2	3.10	115.60	110.00
5	A	806	NAG	C2-N2-C7	3.26	127.23	123.04
5	A	805	NAG	C1-O5-C5	3.47	116.66	112.25
5	A	809	MAN	C1-O5-C5	3.58	116.79	112.25
5	A	810	MAN	C1-O5-C5	3.59	116.81	112.25
5	A	808	MAN	C1-O5-C5	4.19	117.56	112.25
5	A	806	NAG	C3-C2-N2	4.28	120.82	110.56
2	A	811	NAG	C1-O5-C5	4.57	118.05	112.25
2	A	802	NAG	C1-O5-C5	4.67	118.17	112.25
5	B	808	NAG	C1-O5-C5	5.37	119.07	112.25
2	B	807	NAG	C1-O5-C5	5.47	119.19	112.25
2	A	801	NAG	C1-O5-C5	6.63	120.66	112.25
2	B	806	NAG	C1-O5-C5	6.91	121.02	112.25
2	B	803	NAG	C1-O5-C5	7.27	121.48	112.25
5	B	812	MAN	C1-O5-C5	7.89	122.26	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
2	A	801	NAG	2	0
5	A	805	NAG	3	0
5	A	806	NAG	4	0
2	A	811	NAG	1	0
2	A	812	NAG	1	0
2	B	807	NAG	1	0
5	B	808	NAG	1	0

5.6 Ligand geometry ⓘ

6 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
3	NAG	A	803	1	14,14,15	0.52	0	15,19,21	1.40	2 (13%)
4	BLD	A	804	-	36,37,37	1.96	7 (19%)	45,59,59	2.58	16 (35%)
3	NAG	A	815	1	14,14,15	0.51	0	15,19,21	1.39	2 (13%)
4	BLD	B	801	-	36,37,37	2.02	9 (25%)	45,59,59	2.57	15 (33%)
3	NAG	B	802	1	14,14,15	0.44	0	15,19,21	0.94	1 (6%)
3	NAG	B	805	1	14,14,15	0.59	0	15,19,21	1.06	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
3	NAG	A	803	1	-	0/6/23/26	0/1/1/1
4	BLD	A	804	-	-	0/20/85/85	0/4/4/4
3	NAG	A	815	1	-	0/6/23/26	0/1/1/1
4	BLD	B	801	-	-	0/20/85/85	0/4/4/4
3	NAG	B	802	1	-	0/6/23/26	0/1/1/1
3	NAG	B	805	1	-	0/6/23/26	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	801	BLD	O07-C07	-5.68	1.37	1.45
4	A	804	BLD	O07-C07	-5.61	1.37	1.45
4	B	801	BLD	C20-C17	-3.07	1.49	1.54
4	A	804	BLD	C19-C10	-2.80	1.49	1.54
4	B	801	BLD	C19-C10	-2.80	1.49	1.54
4	A	804	BLD	C20-C17	-2.67	1.50	1.54
4	A	804	BLD	C10-C05	-2.32	1.52	1.56
4	A	804	BLD	O22-C22	-2.20	1.37	1.43
4	A	804	BLD	C13-C14	-2.20	1.50	1.55
4	B	801	BLD	C10-C05	-2.08	1.52	1.56
4	B	801	BLD	O22-C22	-2.06	1.38	1.43
4	B	801	BLD	C13-C14	-2.01	1.50	1.55
4	B	801	BLD	O07-C06	2.36	1.37	1.34
4	B	801	BLD	C08-C14	2.40	1.58	1.53
4	A	804	BLD	O06-C06	6.61	1.37	1.21
4	B	801	BLD	O06-C06	6.72	1.38	1.21

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	801	BLD	C13-C17-C20	-6.47	111.24	118.91
4	A	804	BLD	C19-C10-C05	-6.06	99.36	109.96
4	A	804	BLD	O07-C06-O06	-5.89	106.74	116.53
4	B	801	BLD	C19-C10-C05	-5.83	99.76	109.96
4	B	801	BLD	C18-C13-C12	-5.38	101.37	110.54
4	A	804	BLD	C18-C13-C12	-5.26	101.57	110.54
4	A	804	BLD	C13-C17-C20	-4.86	113.15	118.91
4	B	801	BLD	O07-C06-O06	-4.01	109.87	116.53
3	A	815	NAG	C2-N2-C7	-3.07	119.09	123.04
4	B	801	BLD	C21-C20-C17	-3.06	107.42	112.66
3	B	802	NAG	C2-N2-C7	-2.10	120.34	123.04
4	A	804	BLD	C21-C20-C17	-2.05	109.16	112.66
3	B	805	NAG	C2-N2-C7	-2.02	120.44	123.04
4	A	804	BLD	C15-C14-C13	2.09	106.53	103.82
4	B	801	BLD	C26-C25-C27	2.14	116.96	110.67
4	B	801	BLD	C13-C14-C08	2.15	117.73	114.37
4	A	804	BLD	C14-C08-C09	2.15	111.89	109.06
3	A	803	NAG	C4-C3-C2	2.16	114.58	111.23
4	A	804	BLD	C11-C12-C13	2.17	116.70	112.84
4	A	804	BLD	C12-C13-C14	2.26	110.98	107.31
4	B	801	BLD	C04-C03-C02	2.63	113.72	110.23
4	B	801	BLD	C14-C08-C09	2.70	112.60	109.06
4	A	804	BLD	C16-C17-C13	2.94	107.64	103.82
4	B	801	BLD	C16-C17-C20	3.17	116.92	112.59
4	B	801	BLD	C16-C17-C13	3.50	108.37	103.82
4	A	804	BLD	C04-C03-C02	3.50	114.87	110.23
3	A	803	NAG	C1-O5-C5	3.63	116.86	112.25
3	A	815	NAG	C1-O5-C5	3.79	117.06	112.25
4	A	804	BLD	C16-C17-C20	3.93	117.95	112.59
4	A	804	BLD	C12-C13-C17	4.08	123.80	116.56
4	B	801	BLD	C01-C10-C05	4.33	113.92	107.16
4	B	801	BLD	C01-C02-C03	4.40	116.53	111.31
4	A	804	BLD	C10-C01-C02	4.49	121.50	114.05
4	A	804	BLD	C01-C02-C03	4.64	116.80	111.31
4	B	801	BLD	C10-C01-C02	5.05	122.43	114.05
4	B	801	BLD	C12-C13-C17	5.20	125.79	116.56
4	A	804	BLD	C01-C10-C05	5.50	115.76	107.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	804	BLD	5	0
3	A	815	NAG	2	0
4	B	801	BLD	5	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	724/740 (97%)	-0.21	28 (3%)	43 48	11, 22, 48, 88	0
1	B	724/740 (97%)	-0.21	24 (3%)	50 55	12, 23, 50, 97	0
All	All	1448/1480 (97%)	-0.21	52 (3%)	46 51	11, 22, 49, 97	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	400	SER	10.7
1	A	400	SER	6.8
1	B	31	ASP	4.9
1	B	617	MET	4.9
1	A	619	HIS	4.6
1	A	59	TYR	4.5
1	B	619	HIS	4.4
1	B	59	TYR	4.4
1	B	618	VAL	4.4
1	A	64	GLY	4.4
1	B	119	ASP	4.3
1	A	32	PHE	4.3
1	A	399	GLN	4.3
1	A	617	MET	3.9
1	A	620	SER	3.6
1	B	76	ASP	3.6
1	B	32	PHE	3.6
1	B	757	SER	3.5
1	A	120	SER	3.4
1	B	120	SER	3.3
1	A	393	SER	3.2
1	A	756	GLY	3.1
1	A	618	VAL	3.1
1	A	757	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	31	ASP	3.1
1	B	121	SER	3.0
1	B	64	GLY	3.0
1	B	75	ASP	2.8
1	B	399	GLN	2.7
1	B	590	GLU	2.6
1	A	593	THR	2.5
1	B	393	SER	2.5
1	A	118	GLY	2.5
1	B	401	SER	2.5
1	A	473	LYS	2.4
1	A	397	SER	2.4
1	B	620	SER	2.4
1	B	594	ASP	2.3
1	A	614	ARG	2.3
1	A	481	ILE	2.3
1	B	60	GLU	2.3
1	A	472	VAL	2.3
1	B	623	ALA	2.2
1	A	119	ASP	2.2
1	A	60	GLU	2.2
1	B	369	ILE	2.1
1	A	456	VAL	2.1
1	B	621	CYS	2.1
1	A	590	GLU	2.1
1	A	630	MET	2.0
1	A	398	LEU	2.0
1	A	497	ARG	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(\AA^2)	Q<0.9
2	NAG	A	801	14/15	0.86	0.30	8.64	25,41,51,52	0
2	NAG	B	803	14/15	0.86	0.23	6.01	28,41,47,52	0
2	NAG	B	814	14/15	0.96	0.14	1.02	16,23,29,31	0
2	NAG	A	811	14/15	0.96	0.10	-0.19	16,24,33,33	0
5	MAN	A	809	11/12	0.94	0.13	-1.17	16,20,24,42	0
5	NAG	A	805	14/15	0.97	0.11	-1.27	17,22,25,33	0
5	NAG	B	808	14/15	0.97	0.09	-1.40	18,23,32,32	0
5	MAN	B	812	11/12	0.96	0.09	-1.60	16,22,26,33	0
5	MAN	B	813	11/12	0.97	0.10	-	15,20,24,32	0
5	NAG	A	806	14/15	0.95	0.16	-	16,26,32,32	0
2	NAG	B	815	14/15	0.94	0.27	-	22,35,43,46	0
2	NAG	B	817	14/15	0.87	0.36	-	44,60,63,64	0
5	NAG	B	809	14/15	0.97	0.13	-	19,25,30,31	0
2	NAG	A	814	14/15	0.90	0.42	-	31,52,62,66	0
2	NAG	B	806	14/15	0.85	0.25	-	40,50,57,58	0
2	NAG	A	802	14/15	0.90	0.38	-	38,54,62,63	0
2	NAG	B	816	14/15	0.95	0.27	-	29,42,54,54	0
2	NAG	B	807	14/15	0.83	0.39	-	49,68,74,77	0
2	NAG	A	812	14/15	0.94	0.27	-	28,34,44,45	0
2	NAG	A	813	14/15	0.94	0.24	-	28,38,46,46	0
2	NAG	B	804	14/15	0.90	0.35	-	35,44,48,49	0
5	MAN	A	808	11/12	0.86	0.17	-	18,23,25,27	0
5	MAN	A	810	11/12	0.96	0.12	-	16,19,23,29	0
5	MAN	B	811	11/12	0.92	0.14	-	16,22,24,25	0
5	BMA	A	807	11/12	0.94	0.24	-	28,34,41,43	0
5	BMA	B	810	11/12	0.93	0.21	-	25,29,36,38	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(\AA^2)	Q<0.9
3	NAG	B	802	14/15	0.86	0.26	9.18	37,48,54,59	0
3	NAG	B	805	14/15	0.91	0.22	0.31	30,39,48,52	0
4	BLD	B	801	34/34	0.94	0.15	0.10	17,23,28,29	23
4	BLD	A	804	34/34	0.93	0.15	-0.08	15,22,30,35	23
3	NAG	A	803	14/15	0.89	0.16	-0.49	30,40,48,48	0
3	NAG	A	815	14/15	0.80	0.31	-	33,49,60,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.