



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:44 PM UTC

PDB ID : 2DSZ / pdb_00002dsz
Title : Three dimensional structure of a goat signalling protein secreted during involution
Authors : Kumar, J.; Ethayathulla, A.S.; Singh, N.; Ujwal, R.; Srivastava, D.B.; Sharma, S.; Singh, T.P.
Deposited on : 2006-07-09
Resolution : 2.35 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

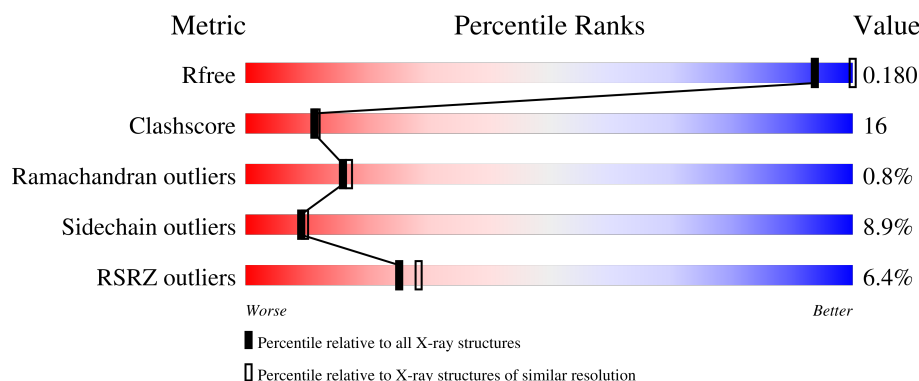
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	361	
2	B	5	

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	MAN	B	4	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3157 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.

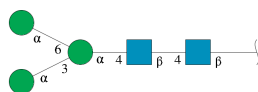
- Molecule 1 is a protein called Chitinase-3-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2877	1836	508	524	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	VAL	ILE	SEE REMARK 999	UNP Q8SPQ0
A	131	ALA	GLY	SEE REMARK 999	UNP Q8SPQ0
A	205	ASN	GLN	SEE REMARK 999	UNP Q8SPQ0
A	206	SER	GLU	SEE REMARK 999	UNP Q8SPQ0
A	?	-	ASP	SEE REMARK 999	UNP Q8SPQ0
A	361	ARG	GLU	SEE REMARK 999	UNP Q8SPQ0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	0	0	0
			61	34	2	25			

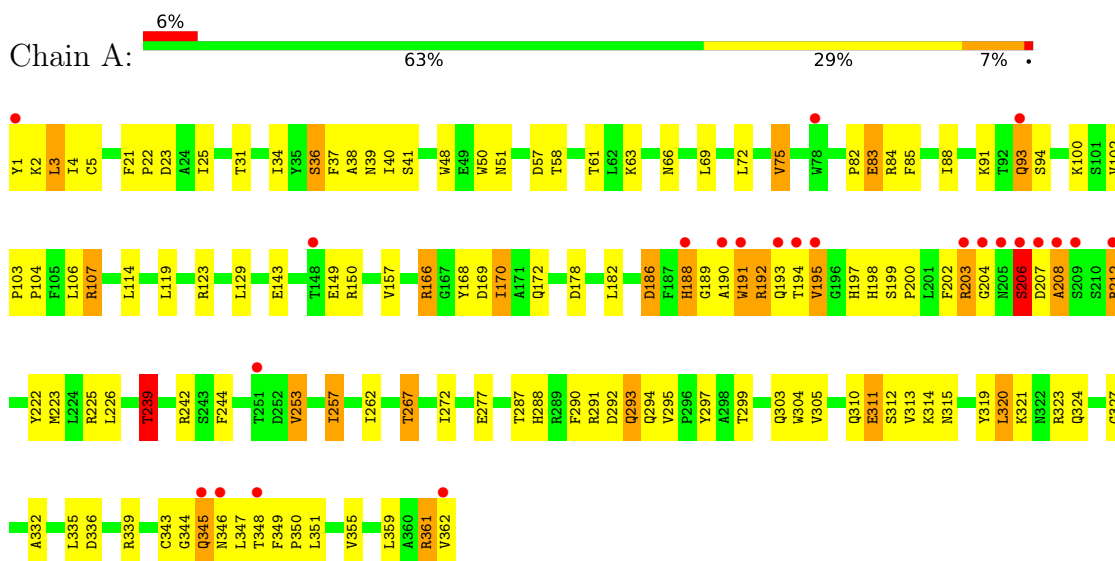
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	219	Total	O	0	0
			219	219		

3 Residue-property plots [i](#)

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: Chitinase-3-like protein 1



- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.12Å 66.21Å 108.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.00 – 2.35 56.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.6 (56.00-2.35) 95.4 (56.00-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.35Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.188 , 0.202 0.202 , 0.180	Depositor DCC
R_{free} test set	148 reflections (0.80%)	wwPDB-VP
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3157	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.54% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0/2953	1.01	20/4001 (0.5%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	206	SER	N-CA-C	9.40	125.13	111.87
1	A	192	ARG	N-CA-C	8.01	122.50	109.85
1	A	25	ILE	N-CA-C	6.82	117.84	108.84
1	A	66	ASN	CA-C-N	6.49	126.17	119.56
1	A	66	ASN	C-N-CA	6.49	126.17	119.56
1	A	361	ARG	N-CA-C	6.43	122.08	113.72
1	A	343	CYS	N-CA-C	6.12	118.33	109.71
1	A	305	VAL	N-CA-C	6.11	116.68	107.75
1	A	31	THR	N-CA-C	-6.01	106.07	113.41
1	A	188	HIS	N-CA-C	-6.00	102.61	110.53
1	A	166	ARG	N-CA-C	5.99	117.47	111.07
1	A	191	TRP	N-CA-C	5.91	118.96	111.69
1	A	212	ARG	N-CA-C	-5.83	106.13	113.18
1	A	203	ARG	N-CA-C	5.77	118.04	111.11
1	A	186	ASP	N-CA-C	-5.51	103.82	110.88
1	A	336	ASP	N-CA-C	-5.46	103.48	110.53
1	A	38	ALA	N-CA-C	-5.40	102.53	110.52
1	A	170	ILE	N-CA-C	5.32	115.94	110.36
1	A	239	THR	N-CA-C	-5.09	106.47	113.30
1	A	208	ALA	N-CA-C	5.07	121.61	110.80

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	2877	0	2817	94	0
2	B	61	0	52	2	0
3	A	219	0	0	10	0
All	All	3157	0	2869	94	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 16.

All (94) 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:203:ARG:HB3	1:A:212:ARG:HH11	1.34	0.92
1:A:262:ILE:H	1:A:303:GLN:HE22	1.31	0.75
1:A:200:PRO:HB3	1:A:293:GLN:HG2	1.72	0.72
1:A:212:ARG:O	1:A:212:ARG:HD2	1.89	0.71
1:A:83:GLU:H	1:A:83:GLU:CD	1.96	0.71
1:A:361:ARG:HG2	3:A:568:HOH:O	1.89	0.70
1:A:239:THR:HG21	1:A:332:ALA:O	1.91	0.70
1:A:203:ARG:HB3	1:A:212:ARG:NH1	2.07	0.69
1:A:182:LEU:HD21	1:A:223:MET:HG3	1.76	0.68
1:A:192:ARG:HA	1:A:192:ARG:HE	1.58	0.68
1:A:253:VAL:HG22	1:A:290:PHE:HE1	1.58	0.68
1:A:262:ILE:H	1:A:303:GLN:NE2	1.92	0.67
1:A:100:LYS:HD3	3:A:399:HOH:O	1.93	0.66
1:A:103:PRO:HB2	1:A:104:PRO:HD3	1.77	0.65
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.28	0.64
1:A:170:ILE:HD12	1:A:223:MET:HE1	1.79	0.63
1:A:311:GLU:HB2	3:A:503:HOH:O	1.98	0.62
1:A:57:ASP:O	1:A:61:THR:HG23	2.00	0.62
1:A:75:VAL:HG22	1:A:114:LEU:HD11	1.82	0.62
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.82	0.62
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.31	0.61
1:A:291:ARG:HG3	1:A:292:ASP:N	2.15	0.61
1:A:93:GLN:HG2	1:A:94:SER:N	2.14	0.60
1:A:40:ILE:O	2:B:1:NAG:H62	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:PHE:HB3	1:A:257:ILE:HD12	1.86	0.58
1:A:3:LEU:HD22	1:A:5:CYS:SG	2.44	0.57
1:A:287:THR:HB	3:A:507:HOH:O	2.03	0.57
1:A:361:ARG:O	1:A:362:VAL:HB	2.06	0.55
1:A:189:GLY:O	1:A:191:TRP:N	2.40	0.55
1:A:82:PRO:HG3	1:A:119:LEU:O	2.06	0.55
1:A:69:LEU:C	1:A:69:LEU:HD13	2.31	0.55
1:A:82:PRO:HD2	1:A:83:GLU:OE2	2.06	0.54
1:A:347:LEU:HD23	1:A:348:THR:N	2.23	0.54
1:A:189:GLY:C	1:A:191:TRP:H	2.17	0.53
1:A:150:ARG:NH2	1:A:178:ASP:OD1	2.42	0.53
1:A:323:ARG:NH1	3:A:442:HOH:O	2.41	0.53
1:A:107:ARG:HD3	1:A:143:GLU:OE2	2.09	0.52
1:A:48:TRP:HB3	3:A:447:HOH:O	2.08	0.52
1:A:4:ILE:HD12	1:A:4:ILE:N	2.25	0.51
1:A:323:ARG:NH1	1:A:323:ARG:HG2	2.26	0.51
1:A:345:GLN:C	1:A:347:LEU:H	2.19	0.51
1:A:324:GLN:HG2	3:A:560:HOH:O	2.10	0.50
1:A:361:ARG:HB2	3:A:567:HOH:O	2.10	0.50
1:A:323:ARG:HG2	1:A:323:ARG:HH11	1.76	0.49
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.93	0.49
1:A:189:GLY:C	1:A:191:TRP:N	2.71	0.48
1:A:202:PHE:HE2	1:A:294:GLN:NE2	2.11	0.48
1:A:313:VAL:CG1	1:A:355:VAL:CG2	2.91	0.48
1:A:41:SER:HA	2:B:1:NAG:H62	1.94	0.48
1:A:344:GLY:O	1:A:345:GLN:C	2.56	0.47
1:A:34:ILE:HG12	1:A:72:LEU:HB2	1.95	0.47
1:A:204:GLY:C	1:A:206:SER:H	2.21	0.47
1:A:202:PHE:CE2	1:A:294:GLN:NE2	2.83	0.47
1:A:267:THR:HB	1:A:277:GLU:OE1	2.14	0.47
1:A:36:SER:HA	1:A:37:PHE:HA	1.71	0.47
1:A:319:TYR:CZ	1:A:323:ARG:HD2	2.50	0.47
1:A:195:VAL:HG13	1:A:304:TRP:CZ2	2.50	0.46
1:A:222:TYR:CE2	1:A:226:LEU:HD11	2.50	0.46
1:A:199:SER:N	1:A:200:PRO:HD3	2.31	0.46
1:A:310:GLN:O	1:A:314:LYS:HG3	2.16	0.46
1:A:192:ARG:CZ	1:A:193:GLN:HG2	2.45	0.45
1:A:212:ARG:O	1:A:212:ARG:CD	2.61	0.45
1:A:339:ARG:HH11	1:A:339:ARG:HG2	1.80	0.45
1:A:262:ILE:HG12	1:A:303:GLN:NE2	2.32	0.45
1:A:313:VAL:CG1	1:A:355:VAL:HG22	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LYS:HB3	1:A:93:GLN:NE2	2.32	0.44
1:A:197:HIS:NE2	1:A:295:VAL:HB	2.32	0.44
1:A:311:GLU:HG3	1:A:312:SER:N	2.31	0.44
1:A:320:LEU:HD11	1:A:327:GLY:C	2.42	0.44
1:A:1:TYR:CZ	1:A:321:LYS:HG2	2.53	0.44
1:A:63:LYS:HG3	1:A:69:LEU:HD12	1.98	0.44
1:A:169:ASP:OD2	1:A:172:GLN:HG3	2.18	0.44
1:A:2:LYS:HB3	1:A:4:ILE:CD1	2.48	0.44
1:A:186:ASP:HA	1:A:242:ARG:HH12	1.83	0.44
1:A:288:HIS:HB2	1:A:297:TYR:CE1	2.53	0.44
1:A:313:VAL:HG13	1:A:355:VAL:HG22	2.00	0.43
1:A:157:VAL:HG13	1:A:168:TYR:CE1	2.52	0.43
1:A:349:PHE:N	1:A:350:PRO:HD3	2.33	0.43
1:A:39:ASN:HB2	1:A:48:TRP:CE3	2.54	0.43
1:A:204:GLY:C	1:A:206:SER:N	2.76	0.42
1:A:203:ARG:HB3	1:A:212:ARG:CD	2.48	0.42
1:A:361:ARG:CB	3:A:567:HOH:O	2.66	0.42
1:A:91:LYS:HB2	1:A:94:SER:OG	2.20	0.41
1:A:50:TRP:CD1	1:A:50:TRP:H	2.38	0.41
1:A:51:ASN:HA	3:A:527:HOH:O	2.18	0.41
1:A:84:ARG:O	1:A:88:ILE:HG12	2.19	0.41
1:A:239:THR:O	1:A:239:THR:HG23	2.20	0.41
1:A:123:ARG:HA	1:A:166:ARG:O	2.19	0.41
1:A:21:PHE:C	1:A:23:ASP:N	2.77	0.41
1:A:188:HIS:H	1:A:198:HIS:HA	1.84	0.41
1:A:188:HIS:HE1	1:A:194:THR:O	2.04	0.40
1:A:22:PRO:HB2	1:A:58:THR:HG22	2.04	0.40
1:A:192:ARG:NE	1:A:193:GLN:H	2.19	0.40
1:A:198:HIS:C	1:A:200:PRO:HD3	2.45	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	359/361 (99%)	340 (95%)	16 (4%)	3 (1%)	16 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	ALA
1	A	346	ASN
1	A	208	ALA

5.3.2 Protein sidechains [i](#)

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	302/302 (100%)	275 (91%)	27 (9%)	9 10

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	36	SER
1	A	75	VAL
1	A	83	GLU
1	A	85	PHE
1	A	93	GLN
1	A	106	LEU
1	A	107	ARG
1	A	129	LEU
1	A	149	GLU
1	A	195	VAL
1	A	206	SER
1	A	207	ASP
1	A	225	ARG
1	A	239	THR
1	A	253	VAL
1	A	257	ILE
1	A	267	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	272	ILE
1	A	293	GLN
1	A	299	THR
1	A	311	GLU
1	A	315	ASN
1	A	320	LEU
1	A	345	GLN
1	A	351	LEU
1	A	359	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	A	188	HIS
1	A	198	HIS
1	A	294	GLN
1	A	303	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 ⓘ

5 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1	2,1	14,14,15	0.71	1 (7%)	17,19,21	1.16	2 (11%)
2	NAG	B	2	2	14,14,15	1.10	1 (7%)	17,19,21	1.95	4 (23%)
2	MAN	B	3	2	11,11,12	1.95	5 (45%)	15,15,17	1.78	5 (33%)
2	MAN	B	4	2	11,11,12	1.03	1 (9%)	15,15,17	1.26	1 (6%)
2	MAN	B	5	2	11,11,12	0.65	0	15,15,17	0.73	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	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	3/6/23/26	0/1/1/1
2	MAN	B	3	2	-	1/2/19/22	0/1/1/1
2	MAN	B	4	2	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	B	5	2	-	0/2/19/22	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	MAN	C4-C5	-3.22	1.46	1.53
2	B	3	MAN	O5-C5	2.72	1.48	1.43
2	B	3	MAN	O5-C1	2.70	1.48	1.43
2	B	2	NAG	O5-C1	2.46	1.47	1.43
2	B	1	NAG	C1-C2	2.30	1.55	1.52
2	B	3	MAN	C4-C3	-2.24	1.46	1.52
2	B	3	MAN	C1-C2	2.23	1.57	1.52
2	B	4	MAN	O5-C5	-2.15	1.39	1.43

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C4-C3-C2	4.20	117.17	111.02
2	B	2	NAG	C3-C4-C5	3.92	117.34	110.23
2	B	3	MAN	O3-C3-C4	-3.79	101.44	110.38
2	B	2	NAG	O4-C4-C3	-3.32	102.56	110.38
2	B	4	MAN	C3-C4-C5	2.56	114.87	110.23
2	B	1	NAG	O4-C4-C3	-2.48	104.53	110.38
2	B	3	MAN	O4-C4-C3	-2.43	104.66	110.38
2	B	1	NAG	C4-C3-C2	2.35	114.47	111.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	MAN	O6-C6-C5	-2.31	103.48	111.33
2	B	3	MAN	C2-C3-C4	2.28	114.87	110.86
2	B	3	MAN	C1-O5-C5	2.04	114.92	112.19
2	B	2	NAG	O4-C4-C5	-2.04	104.29	109.32

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	4	MAN	C1

All (6) torsion outliers are listed below:

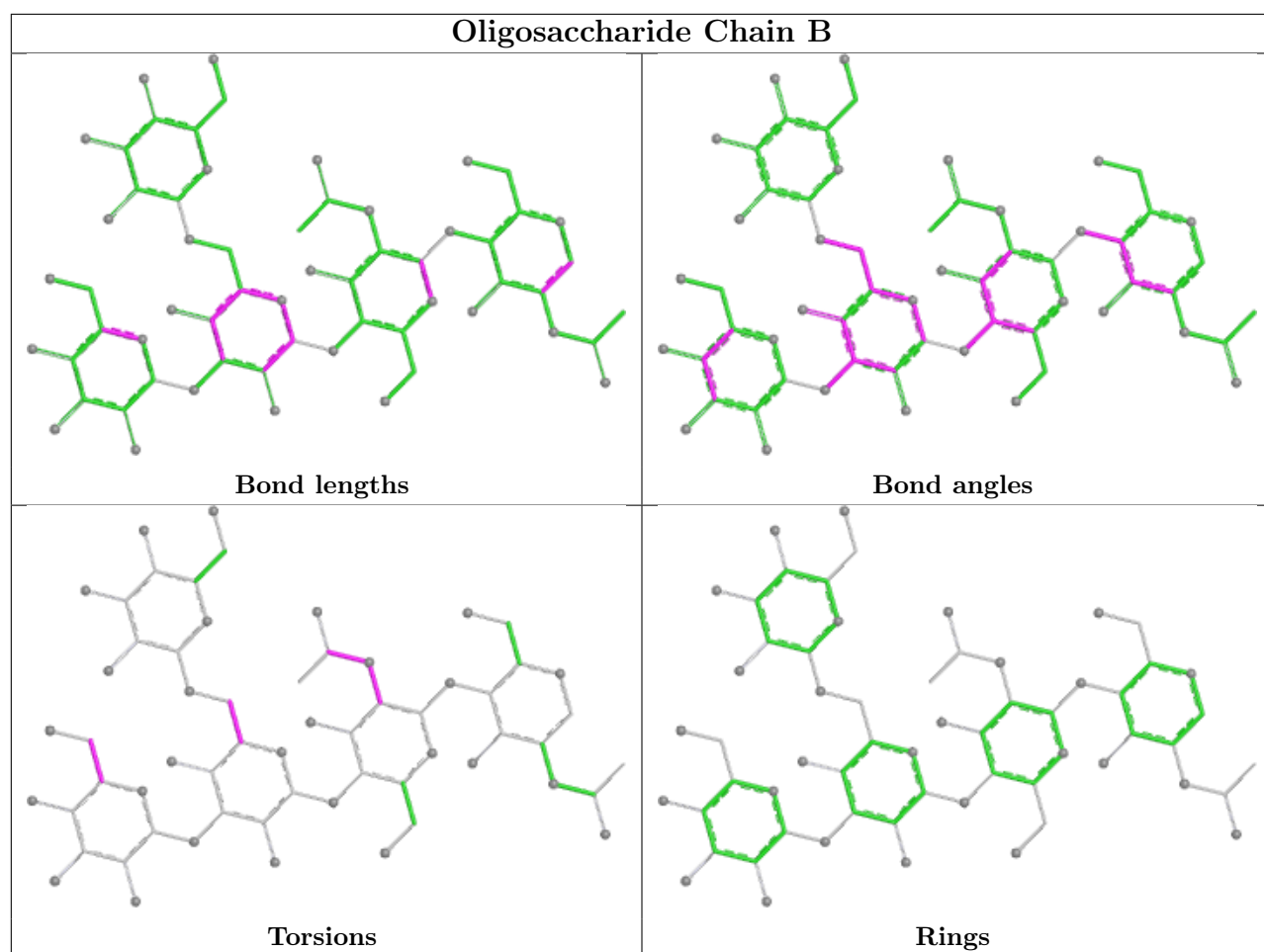
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C3-C2-N2-C7
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	B	4	MAN	C4-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
2	B	3	MAN	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	361/361 (100%)	0.52	23 (6%)	25 28	15, 36, 67, 92	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	362	VAL	5.8
1	A	208	ALA	5.0
1	A	191	TRP	3.8
1	A	203	ARG	3.6
1	A	204	GLY	3.3
1	A	207	ASP	3.2
1	A	212	ARG	3.0
1	A	93	GLN	2.7
1	A	78	TRP	2.5
1	A	209	SER	2.4
1	A	205	ASN	2.4
1	A	348	THR	2.4
1	A	206	SER	2.4
1	A	346	ASN	2.3
1	A	195	VAL	2.3
1	A	188	HIS	2.2
1	A	193	GLN	2.1
1	A	190	ALA	2.1
1	A	194	THR	2.1
1	A	148	THR	2.1
1	A	251	THR	2.0
1	A	1	TYR	2.0
1	A	345	GLN	2.0

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

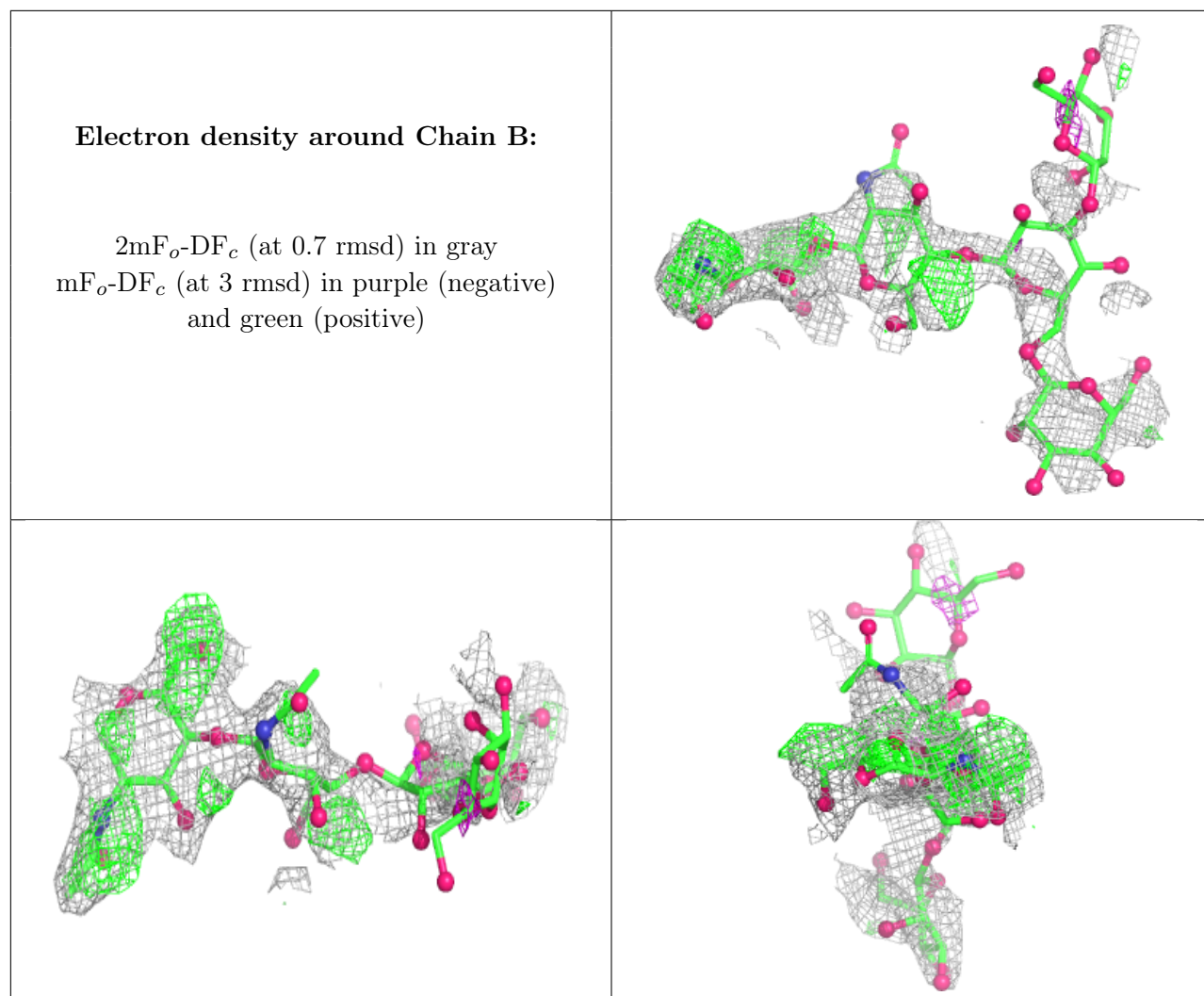
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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
2	MAN	B	4	11/12	0.18	0.27	51,51,53,55	11
2	MAN	B	3	11/12	0.30	0.21	55,55,56,57	11
2	NAG	B	2	14/15	0.33	0.25	54,56,59,59	14
2	MAN	B	5	11/12	0.36	0.17	51,52,54,55	11
2	NAG	B	1	14/15	0.54	0.31	40,43,46,51	14

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.