

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 20, 2020 – 10:27 PM BST

PDB ID	:	4KQA
$\operatorname{Title}$	:	Crystal structure of the golgi casein kinase
Authors	:	Xiao, J.
Deposited on	:	2013-05-14
$\operatorname{Resolution}$	:	2.60  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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	7.0.044  (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	$3455\ (2.60-2.60)$
Sidechain outliers	138945	3455(2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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 <=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	А	453	<sup>2%</sup> <b>7</b> 9%	13%	8%
1	В	453	9%	13%	• 6%
1	С	453	% 	11%	• 8%
1	D	453	11%	17%	• 8%
2	Е	3	67%	33%	
2	G	3	67%	33%	



Conti	Continued from previous page							
Mol	Chain	Length	Quality of chain					
2	Ι	3	67% 33%					
2	К	3	33%	67%				
3	F	2	50%	50%				
3	Н	2	50%	50%				
3	J	2		00%				
3	L	2	50%	50%				

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	BMA	G	3	X	_	-	-



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 14391 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.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Δ	418	Total	С	Ν	Ο	$\mathbf{S}$	Se	0	0	0
	A	410	3453	2198	604	632	10	9	0		0
1	В	426	Total	С	Ν	Ο	S	Se	0	0	0
	D		3516	2234	618	645	10	9			U
1	С	C 419	Total	С	Ν	Ο	S	Se	0	0	0
			3454	2198	605	632	10	9	0	0	0
1	1 D	416	Total	С	Ν	Ο	S	Se	0	0	0
	410	3427	2181	601	626	10	9	0	U		

• Molecule 1 is a protein called Protein H03A11.1.

• Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
9	F	3	Total C N O	0	0	0
2	Ľ	5	39 $22$ $2$ $15$	0	0	0
9	С	2	Total C N O	0	0	0
	G	5	39 $22$ $2$ $15$	0	0	0
0	Т	2	Total C N O	0	0	0
	1		39 $22$ $2$ $15$	0		0
0		9	Total C N O	0	0	0
2	IX I	A 3	39  22  2  15			0

• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	F	2	Total         C         N         O           28         16         2         10	0	0	0
3	Н	2	Total         C         N         O           28         16         2         10	0	0	0
3	J	2	Total         C         N         O           28         16         2         10	0	0	0
3	L	2	Total         C         N         O           28         16         2         10	0	0	0

• Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Ni 1 1	0	0
4	А	1	Total Ni 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	76	Total O 76 76	0	0
5	В	54	$\begin{array}{cc} \text{Total} & \text{O} \\ 54 & 54 \end{array}$	0	0
5	С	99	Total O 99 99	0	0
5	D	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0



# 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: Protein H03A11.1



# 

#### ASN ASP GLU GLU GLU GLU GLU GLU HIS GLU HIS GLU ASP LYS LYS LYS ILYS VAL

• Molecule 1: Protein H03A11.1



• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:	67%	33%	I
NAG1 NAG2 EMA3			
• Molecule 2: bet	a D mannopyranoso (1.4) $2$	acatamida 2 daavy bata D gl	$u_{convranceo}(1,4)$ ?

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-ac etamido-2-deoxy-beta-D-glucopyranose

Chain G:	67%	33%
NAG1 NAG2 BMA3		

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-ac etamido-2-deoxy-beta-D-glucopyranose

Chain I:	67%	33%

NAG1 NAG2 BMA3

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



Chain K:	33%	67%	
• Molecule 3: opyranose	2-acetamido-2-de	oxy-beta-D-glucopyranose-(1-4)-2-acetamid	o-2-deoxy-beta-D-gluc
Chain F:	50%	50%	
NAG 2 NAG 2			
• Molecule 3: opyranose	2-acetamido-2-deo	oxy-beta-D-glucopyranose-(1-4)-2-acetamid	o-2-deoxy-beta-D-gluc
Chain H:	50%	50%	
NAG 1 NAG 2			
• Molecule 3: opyranose	2-acetamido-2-deo	oxy-beta-D-glucopyranose-(1-4)-2-acetamid	o-2-deoxy-beta-D-gluc
Chain J:		100%	
NAG 1 NAG 2			
• Molecule 3: opyranose	2-acetamido-2-deo	oxy-beta-D-glucopyranose-(1-4)-2-acetamid	o-2-deoxy-beta-D-gluc
Chain L:	50%	50%	
NAG1 NAG2			



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	78.79Å 157.31Å 168.76Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Posolution(A)	46.46 - 2.60	Depositor
Resolution (A)	46.46 - 2.60	EDS
% Data completeness	98.4 (46.46-2.60)	Depositor
(in resolution range)	$94.1 \ (46.46 - 2.60)$	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.36 (at 2.61 \text{\AA})$	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
D D.	0.217 , $0.254$	Depositor
10, 10 free	0.217 , $0.254$	DCC
$R_{free}$ test set	3202 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	47.0	Xtriage
Anisotropy	0.566	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , $37.7$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14391	wwPDB-VP
Average B, all atoms $(Å^2)$	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: NI, BMA, 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).

Mal	l Chain	Bond lengths		Bond angles	
		RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.22	0/3538	0.40	0/4762
1	В	0.22	0/3603	0.41	0/4852
1	С	0.22	0/3539	0.40	0/4765
1	D	0.22	0/3510	0.40	0/4725
All	All	0.22	0/14190	0.40	0/19104

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

#### 5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	3453	0	3331	31	0
1	В	3516	0	3395	32	0
1	С	3454	0	3335	31	0
1	D	3427	0	3315	47	0
2	Е	39	0	34	0	0
2	G	39	0	34	0	0
2	Ι	39	0	34	0	0
2	K	39	0	34	1	0
3	F	28	0	25	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Н	28	0	25	1	0
3	J	28	0	25	0	0
3	L	28	0	25	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
5	А	76	0	0	1	0
5	В	54	0	0	3	0
5	С	99	0	0	3	0
5	D	42	0	0	2	0
All	All	14391	0	13612	140	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 5.

All (140) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:B:150:ASP:OD1	1:B:231:ARG:NH1	2.12	0.82
1:B:419:THR:O	5:B:722:HOH:O	1.97	0.81
1:B:306:ARG:NH1	1:B:371:GLU:OE2	2.15	0.80
1:D:306:ARG:NH1	1:D:371:GLU:OE2	2.16	0.78
1:A:306:ARG:NH1	1:A:371:GLU:OE1	2.18	0.77
1:B:120:TRP:O	1:B:122:LYS:N	2.24	0.70
1:A:274:ASP:OD1	1:C:272:ARG:NH1	2.27	0.68
1:D:77:ASP:HB3	1:D:80:ASN:HB2	1.77	0.67
1:B:124:GLU:HG2	1:B:125:GLN:HG2	1.77	0.65
1:B:234:ILE:HD12	1:B:386:LEU:HD13	1.78	0.65
1:B:133:ASN:HA	1:B:136:ARG:HG2	1.79	0.65
1:A:129:PRO:O	1:A:131:ASP:N	2.30	0.64
1:C:137:PHE:HA	1:C:152:MSE:HE1	1.78	0.64
1:B:137:PHE:HA	1:B:152:MSE:HE1	1.80	0.63
1:C:112:LYS:HB2	1:C:379:LEU:HD21	1.80	0.63
1:A:211:ASP:OD2	1:A:214:ARG:NH2	2.32	0.63
1:B:66:ILE:HG23	1:B:286:LEU:HD23	1.80	0.63
1:C:66:ILE:HG23	1:C:286:LEU:HD23	1.81	0.62
1:A:325:GLU:OE2	1:A:336:LYS:NZ	2.33	0.62
1:C:316:THR:HG21	1:C:321:ASN:O	2.00	0.61
1:D:137:PHE:HA	1:D:152:MSE:HE1	1.81	0.60
1:D:307:LYS:HG3	1:D:374:ASN:HB2	1.83	0.59
1:B:81:PHE:O	1:B:428:LYS:NZ	2.31	0.58
1:B:407:ARG:NH1	1:B:407:ARG:O	2.37	0.58



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:C:325:GLU:OE2	1:C:336:LYS:NZ	2.36	0.58	
1:B:325:GLU:OE2	1:B:336:LYS:NZ	2.36	0.57	
1:D:410:CYS:SG	5:D:730:HOH:O	2.57	0.57	
1:B:315:ARG:NH2	1:B:399:ASP:OD2	2.37	0.57	
1:A:93:LEU:HD22	1:A:467:LEU:HD13	1.87	0.56	
1:D:171:MSE:HE1	1:D:190:VAL:HG13	1.87	0.56	
1:A:214:ARG:NH1	1:A:391:ALA:O	2.39	0.55	
1:A:274:ASP:CG	1:C:272:ARG:HH12	2.09	0.55	
1:D:305:PRO:HG2	1:D:374:ASN:O	2.07	0.54	
1:A:315:ARG:NH2	1:A:399:ASP:OD2	2.41	0.54	
1:B:423:PHE:N	5:B:722:HOH:O	2.12	0.54	
1:C:147:TYR:CZ	1:C:231:ARG:HG2	2.43	0.54	
1:D:146:VAL:HG23	1:D:147:TYR:HD1	1.73	0.54	
1:C:80:ASN:O	1:C:80:ASN:ND2	2.31	0.54	
1:A:66:ILE:HG23	1:A:286:LEU:HD23	1.89	0.53	
1:C:314:ARG:NH1	1:C:368:HIS:HB2	2.24	0.53	
1:D:325:GLU:OE2	1:D:336:LYS:NZ	2.41	0.52	
1:D:83:PHE:CE2	1:D:456:GLU:HB3	2.44	0.52	
1:D:333:CYS:HA	1:D:337:VAL:HG13	1.89	0.52	
1:C:314:ARG:NH2	5:C:716:HOH:O	2.42	0.52	
1:B:437:SER:O	1:B:440:LYS:HG2	2.10	0.52	
1:C:192:LYS:NZ	1:C:218:GLU:OE2	2.32	0.52	
1:A:147:TYR:CD2	1:A:153:ILE:HG13	2.44	0.52	
1:D:135:GLU:HG3	1:D:187:LYS:NZ	2.26	0.51	
1:B:407:ARG:NH1	1:B:410:CYS:SG	2.83	0.51	
1:D:132:ASP:OD1	1:D:187:LYS:NZ	2.43	0.51	
1:D:336:LYS:O	1:D:340:LYS:NZ	2.30	0.51	
1:A:424:TYR:CG	1:A:463:MSE:HG3	2.46	0.51	
1:A:147:TYR:CZ	1:A:231:ARG:HG2	2.45	0.51	
1:A:166:LYS:NZ	1:A:186:ASP:OD1	2.42	0.50	
1:B:147:TYR:CD1	1:B:153:ILE:HG13	2.47	0.50	
1:D:111:LYS:HE2	1:D:380:PRO:HD3	1.93	0.50	
1:D:154:ASP:HA	1:D:157:LEU:HD22	1.94	0.50	
1:D:343:TYR:HB3	1:D:349:LEU:HG	1.93	0.50	
1:D:315:ARG:NH2	1:D:399:ASP:OD2	2.45	0.50	
1:D:146:VAL:HG22	1:D:232:ARG:HA	1.94	0.50	
1:B:92:LYS:HG2	1:B:467:LEU:HD11	1.94	0.49	
1:D:81:PHE:O	1:D:428:LYS:NZ	2.30	0.49	
1:B:251:ALA:O	1:B:256:LYS:NZ	2.46	0.49	
1:B:89:THR:HG23	1:B:467:LEU:HD22	1.95	0.49	
1:A:225:ASP:OD2	1:A:385:HIS:ND1	2.34	0.49	



Interstomic Clash						
Atom-1	Atom-2	distance $(Å)$	overlan (Å)			
1:C:379:LEU:H	1:C:379:LEU:HD12	1 78	0.48			
1:D:367:ARG:HH22	1:D:388:HIS:CE1	2.32	0.48			
1:D:148:SEB:O	2:K:2:NAG:H2	2 13	0.48			
$1 \cdot D \cdot 410 \cdot CYS \cdot O$	1.D.478.VAL.HG12	2.13	0.10			
1:A:177:VAL:HG11	1:A:283:ILE:HD11	1.97	0.47			
1:D:117:SEB:HB3	1:D:139:SER:HB3	1.97	0.47			
1:D:349:LEU:HB3	1:D:411:ILE:HD11	1.97	0.46			
1:D:171:MSE:HB2	1:D:180:VAL:HG23	1.97	0.46			
1:C:421:MSE:HE3	1:C:421:MSE:HA	1.97	0.46			
1:C:147:TYR:CD2	1:C:153:ILE:HG13	2.51	0.46			
1:C:315:ARG:NH1	5:C:734:HOH:O	2.48	0.46			
1:A:93:LEU:HD21	1:A:467:LEU:HB2	1.96	0.46			
1:A:104:GLN:O	1:A:107:GLN:HG2	2.16	0.46			
1:C:169:HIS:HB2	1:C:180:VAL:HG13	1.98	0.45			
1:C:87:LYS:HD2	1:C:90:LEU:HD23	1.97	0.45			
1:D:112:LYS:HB3	1:D:379:LEU:HD11	1.99	0.45			
1:A:357:ILE:HD13	1:A:420:LEU:HD11	1.98	0.45			
1:D:258:THR:HB	1:D:270:VAL:HB	1.98	0.45			
1:A:211:ASP:HB3	1:A:390:ARG:HG2	1.99	0.45			
1:B:211:ASP:HB3	1:B:390:ARG:HG2	1.98	0.44			
1:D:420:LEU:HB3	1:D:463:MSE:HE1	1.98	0.44			
1:B:436:GLU:O	1:B:439:SER:OG	2.32	0.44			
1:B:116:LEU:HD12	1:B:141:ILE:HB	1.99	0.44			
1:D:320:LYS:HD2	1:D:320:LYS:N	2.33	0.44			
1:B:112:LYS:O	1:B:143:SER:OG	2.32	0.44			
1:D:441:ASP:HA	1:D:442:PRO:HD3	1.88	0.44			
1:D:146:VAL:HG23	1:D:147:TYR:CD1	2.52	0.43			
1:D:403:ILE:HD12	1:D:465:HIS:CD2	2.53	0.43			
1:D:147:TYR:CD2	1:D:153:ILE:HG13	2.54	0.43			
1:D:167:HIS:HB2	1:D:182:THR:HB	2.00	0.43			
1:D:478:VAL:HG23	1:D:479:LEU:N	2.33	0.43			
1:D:195:ARG:NH2	5:D:711:HOH:O	2.44	0.43			
1:C:191:PHE:CE1	1:C:292:GLY:HA3	2.54	0.43			
1:A:191:PHE:CE1	1:A:292:GLY:HA3	2.53	0.43			
1:B:93:LEU:HD13	1:B:421:MSE:HE1	2.01	0.43			
1:D:220:ALA:HA	1:D:438:LEU:HD21	2.00	0.43			
1:A:69:SER:HA	1:A:73:LYS:NZ	2.34	0.43			
1:C:179:PHE:HB2	1:C:191:PHE:HB3	2.01	0.43			
1:D:103:ASP:O	1:D:107:GLN:HG2	2.19	0.43			
1:A:220:ALA:HA	1:A:438:LEU:HD21	2.00	0.42			
1:B:232:ARG:HD2	1:B:382:TYR:CD1	2.53	0.42			



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:114:ILE:HG13	1:A:118:LYS:HE3	2.01	0.42
1:A:163:SER:HA	1:A:164:PRO:HD3	1.92	0.42
1:A:63:HIS:N	5:A:713:HOH:O	2.49	0.42
1:C:203:ASP:HB3	1:C:206:HIS:CG	2.55	0.42
1:C:424:TYR:CG	1:C:463:MSE:HG3	2.55	0.42
1:D:171:MSE:HE3	1:D:178:LYS:HB3	2.02	0.42
1:D:360:TYR:CD1	1:D:403:ILE:HG12	2.55	0.42
1:B:117:SER:HB2	1:B:139:SER:HB2	2.01	0.42
1:C:178:LYS:HG2	1:C:192:LYS:HG2	2.01	0.42
1:C:166:LYS:HE3	1:C:184:LYS:HA	2.01	0.41
1:D:135:GLU:HG3	1:D:187:LYS:HZ1	1.85	0.41
1:A:171:MSE:HB2	1:A:180:VAL:HG23	2.02	0.41
1:D:146:VAL:HG21	1:D:233:ALA:O	2.20	0.41
1:C:167:HIS:HB2	1:C:182:THR:HB	2.03	0.41
1:D:475:VAL:HA	1:D:478:VAL:HG22	2.02	0.41
1:A:147:TYR:CE2	1:A:231:ARG:HG2	2.55	0.41
1:A:413:ARG:HA	1:A:414:PRO:HD3	1.89	0.41
1:C:153:ILE:HA	1:C:153:ILE:HD13	1.95	0.41
1:D:166:LYS:HE3	1:D:167:HIS:CD2	2.55	0.41
1:A:83:PHE:O	1:A:84:SER:HB3	2.21	0.41
1:B:305:PRO:HG2	1:B:374:ASN:O	2.20	0.41
1:C:253:LYS:HB3	1:C:253:LYS:HE2	1.93	0.41
1:D:307:LYS:N	1:D:372:SER:O	2.43	0.41
1:A:307:LYS:HG3	1:A:374:ASN:HB2	2.03	0.41
1:C:367:ARG:HH22	1:C:388:HIS:CD2	2.39	0.41
1:C:63:HIS:N	5:C:733:HOH:O	2.53	0.41
1:C:485:ASN:HA	1:C:486:PRO:HD2	1.88	0.40
1:B:407:ARG:HA	1:B:407:ARG:HD2	1.77	0.40
1:B:422:ASN:N	5:B:722:HOH:O	2.55	0.40
1:B:188:GLN:O	1:B:297:PHE:HB2	2.21	0.40
1:C:441:ASP:HA	1:C:442:PRO:HD3	1.90	0.40
1:B:103:ASP:O	1:B:107:GLN:HG3	2.21	0.40
1:D:337:VAL:HG23	1:D:349:LEU:HD21	2.04	0.40
3:H:1:NAG:H61	3:H:2:NAG:HN2	1.87	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	Perce	$\mathbf{ntiles}$
1	А	412/453~(91%)	393~(95%)	17 (4%)	2(0%)	29	52
1	В	424/453~(94%)	405~(96%)	15~(4%)	4 (1%)	17	35
1	С	415/453~(92%)	398~(96%)	14 (3%)	3 (1%)	22	43
1	D	412/453~(91%)	394~(96%)	18 (4%)	0	100	100
All	All	1663/1812~(92%)	1590 (96%)	64 (4%)	9 (0%)	29	52

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	130	GLU
1	В	121	GLU
1	В	122	LYS
1	С	377	ASN
1	С	378	ASP
1	В	124	GLU
1	С	379	LEU
1	В	149	ASP
1	А	378	ASP

#### 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	А	386/410~(94%)	380~(98%)	6~(2%)	62 82
1	В	393/410~(96%)	383~(98%)	10 (2%)	47 73



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	С	386/410~(94%)	375~(97%)	11 (3%)	43	69
1	D	383/410~(93%)	366~(96%)	17~(4%)	28	53
All	All	1548/1640~(94%)	1504 (97%)	44 (3%)	43	69

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

Mol	Chain	$\mathbf{Res}$	Type
1	А	130	GLU
1	А	212	PHE
1	А	265	LYS
1	А	297	PHE
1	А	330	MSE
1	А	475	VAL
1	В	114	ILE
1	В	118	LYS
1	В	124	GLU
1	В	126	ARG
1	В	128	VAL
1	В	152	MSE
1	В	212	PHE
1	В	297	PHE
1	В	337	VAL
1	В	487	ASP
1	С	80	ASN
1	С	131	ASP
1	С	152	MSE
1	С	171	MSE
1	С	175	THR
1	С	212	PHE
1	С	297	PHE
1	С	316	THR
1	С	348	ARG
1	С	386	LEU
1	С	487	ASP
1	D	75	LEU
1	D	88	ILE
1	D	94	TYR
1	D	96	LEU
1	D	118	LYS
1	D	119	PHE
1	D	152	MSE



Mol	Chain	Res	Type
1	D	157	LEU
1	D	212	PHE
1	D	244	THR
1	D	297	PHE
1	D	298	LEU
1	D	337	VAL
1	D	394	ARG
1	D	403	ILE
1	D	473	ARG
1	D	484	ASN

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

#### 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)

20 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).

Mal	Mol Tuno Chain Bog		Dog	Timle	Bo	Bond lengths			Bond angles		
NIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
2	NAG	Е	1	1,2	14,14,15	0.57	0	$17,\!19,\!21$	1.21	1 (5%)	
2	NAG	Е	2	2	14,14,15	0.22	0	17,19,21	0.35	0	
2	BMA	Е	3	2	11,11,12	0.61	0	$15,\!15,\!17$	0.78	0	
3	NAG	F	1	1,3	14,14,15	0.31	0	$17,\!19,\!21$	0.84	1 (5%)	
3	NAG	F	2	3	14,14,15	0.20	0	17,19,21	0.40	0	



Mal	Tune	Chain	Dog	Tink	Bond lengths		$_{\rm ths}$	B	ond ang	les
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	#  Z  > 2
2	NAG	G	1	1,2	14,14,15	0.32	0	17,19,21	1.35	2 (11%)
2	NAG	G	2	2	14,14,15	0.35	0	17,19,21	0.35	0
2	BMA	G	3	2	11,11,12	0.56	0	$15,\!15,\!17$	0.79	0
3	NAG	Н	1	1,3	14, 14, 15	0.20	0	$17,\!19,\!21$	2.08	1(5%)
3	NAG	Н	2	3	14, 14, 15	0.27	0	17,19,21	0.38	0
2	NAG	Ι	1	1,2	14,14,15	0.68	1 (7%)	17,19,21	1.66	2 (11%)
2	NAG	Ι	2	2	14,14,15	0.30	0	17,19,21	0.30	0
2	BMA	Ι	3	2	11,11,12	0.61	0	$15,\!15,\!17$	0.84	0
3	NAG	J	1	1,3	14, 14, 15	0.34	0	17,19,21	0.52	0
3	NAG	J	2	3	14, 14, 15	0.27	0	17,19,21	0.32	0
2	NAG	K	1	1,2	14,14,15	0.22	0	17,19,21	1.87	2 (11%)
2	NAG	K	2	2	14,14,15	0.20	0	17,19,21	0.44	0
2	BMA	K	3	2	11,11,12	0.60	0	$15,\!15,\!17$	0.79	0
3	NAG	L	1	1,3	14,14,15	0.31	0	17,19,21	1.56	1 (5%)
3	NAG	L	2	3	14,14,15	0.22	0	17,19,21	0.40	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	Е	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	Е	2	2	-	0/6/23/26	0/1/1/1
2	BMA	Е	3	2	-	0/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	G	2	2	-	1/6/23/26	0/1/1/1
2	BMA	G	3	2	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	Н	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	Н	2	3	-	4/6/23/26	0/1/1/1
2	NAG	Ι	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	Ι	2	2	-	1/6/23/26	0/1/1/1
2	BMA	Ι	3	2	-	2/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	1/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1



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Mol	Type	Chain	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
2	BMA	K	3	2	-	0/2/19/22	0/1/1/1
3	NAG	L	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	Ι	1	NAG	O5-C1	-2.14	1.40	1.43

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
3	Η	1	NAG	O4-C4-C5	8.27	129.84	109.30
2	Ι	1	NAG	O4-C4-C3	-6.17	96.09	110.35
3	L	1	NAG	O4-C4-C3	5.91	124.00	110.35
2	Κ	1	NAG	O4-C4-C3	5.68	123.49	110.35
2	Κ	1	NAG	O4-C4-C5	4.93	121.53	109.30
2	Ε	1	NAG	O4-C4-C5	4.35	120.11	109.30
2	G	1	NAG	O4-C4-C3	3.69	118.88	110.35
2	G	1	NAG	O4-C4-C5	3.66	118.39	109.30
2	Ι	1	NAG	O4-C4-C5	-2.53	103.02	109.30
3	F	1	NAG	O4-C4-C3	-2.23	105.19	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	G	3	BMA	C1

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	1	NAG	C4-C5-C6-O6
3	Н	1	NAG	O5-C5-C6-O6
2	Е	1	NAG	C4-C5-C6-O6
2	Е	1	NAG	O5-C5-C6-O6
2	G	1	NAG	O5-C5-C6-O6
3	Н	2	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	Н	1	NAG	C4-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6



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Conti	Continucu from pretious paye							
Mol	Chain	$\mathbf{Res}$	Type	Atoms				
2	Ι	1	NAG	C8-C7-N2-C2				
2	Ι	1	NAG	O7-C7-N2-C2				
2	K	1	NAG	C8-C7-N2-C2				
2	K	1	NAG	O7-C7-N2-C2				
3	Н	2	NAG	C8-C7-N2-C2				
3	Н	2	NAG	O7-C7-N2-C2				
3	Н	2	NAG	C4-C5-C6-O6				
2	Ι	1	NAG	O5-C5-C6-O6				
2	G	2	NAG	O5-C5-C6-O6				
3	J	2	NAG	O5-C5-C6-O6				
2	Ι	2	NAG	O5-C5-C6-O6				
2	K	1	NAG	O5-C5-C6-O6				
3	F	2	NAG	C4-C5-C6-O6				
2	Ι	3	BMA	C4-C5-C6-O6				
2	G	1	NAG	C3-C2-N2-C7				
2	Ι	3	BMA	O5-C5-C6-O6				
3	L	1	NAG	C4-C5-C6-O6				
2	Е	1	NAG	C3-C2-N2-C7				
2	Е	1	NAG	C1-C2-N2-C7				

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	2	NAG	1	0
3	Н	1	NAG	1	0
3	Н	2	NAG	1	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)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 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 (i)

#### 6.1 Protein, DNA and RNA chains (i)

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,  $95^{th}$  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	< <b>RSRZ</b> >	#RSRZ $>$ 2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	$Q{<}0.9$
1	А	409/453~(90%)	0.10	8 (1%) 65 60	31, 47, 82, 118	0
1	В	417/453~(92%)	0.45	39 (9%) 8 5	33, 53, 88, 164	0
1	С	410/453~(90%)	0.10	6 (1%) 73 70	31, 47, 81, 119	0
1	D	407/453~(89%)	0.51	51 (12%) 3 2	36, 54, 83, 118	0
All	All	1643/1812~(90%)	0.29	104 (6%) 20 15	31, 51, 83, 164	0

All (104) RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	D	344	ALA	7.5
1	В	123	SER	5.3
1	D	424	TYR	5.2
1	А	85	SER	4.8
1	D	414	PRO	4.8
1	В	71	GLY	4.7
1	D	479	LEU	4.5
1	D	474	GLY	4.5
1	D	483	TYR	4.4
1	В	378	ASP	4.4
1	D	484	ASN	4.3
1	В	75	LEU	4.3
1	В	66	ILE	4.2
1	D	412	LEU	4.2
1	В	67	PRO	4.2
1	D	94	TYR	4.1
1	D	93	LEU	4.0
1	В	94	TYR	3.9
1	В	344	ALA	3.8
1	В	124	GLU	3.8
1	D	102	PHE	3.7



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Mol	Chain	Res	Type	RSRZ
1	D	91	ARG	3.6
1	В	70	LEU	3.6
1	D	417	PHE	3.5
1	D	345	HIS	3.5
1	D	470	PHE	3.4
1	D	476	ALA	3.4
1	В	72	GLU	3.3
1	D	341	ARG	3.3
1	D	379	LEU	3.3
1	D	377	ASN	3.2
1	В	379	LEU	3.2
1	D	475	VAL	3.1
1	В	174	GLY	3.1
1	D	485	ASN	3.0
1	D	105	LEU	3.0
1	D	228	LEU	3.0
1	В	103	ASP	3.0
1	D	478	VAL	2.9
1	В	412	LEU	2.8
1	В	112	LYS	2.8
1	В	483	TYR	2.8
1	В	102	PHE	2.8
1	D	420	LEU	2.8
1	А	71	GLY	2.8
1	А	378	ASP	2.7
1	В	82	LEU	2.7
1	D	375	VAL	2.7
1	D	382	TYR	2.7
1	D	84	SER	2.7
1	B	341	ARG	2.7
1	В	484	ASN	2.7
1	В	107	GLN	2.7
1	D	466	ILE	2.7
1	В	380	PRO	2.7
1	D	411	ILE	2.7
1	С	119	PHE	2.6
1	В	69	SER	2.6
1	D	452	TYR	2.6
1	D	480	VAL	2.6
1	A	172	ASP	2.6
1	D	88	ILE	2.6
1	D	378	ASP	2.5



Mol	Chain	Res	Type	RSRZ
1	В	481	ALA	2.5
1	D	347	ARG	2.5
1	А	75	LEU	2.5
1	А	84	SER	2.5
1	D	343	TYR	2.5
1	В	114	ILE	2.4
1	В	125	GLN	2.4
1	С	131	ASP	2.4
1	D	340	LYS	2.4
1	D	464	SER	2.4
1	D	380	PRO	2.4
1	D	173	GLY	2.4
1	D	349	LEU	2.3
1	В	431	THR	2.3
1	D	97	THR	2.3
1	В	375	VAL	2.3
1	D	427	PRO	2.3
1	С	376	PHE	2.3
1	D	481	ALA	2.2
1	D	230	PHE	2.2
1	С	487	ASP	2.2
1	В	305	PRO	2.2
1	А	484	ASN	2.2
1	С	488	VAL	2.2
1	D	369	HIS	2.2
1	D	107	GLN	2.2
1	В	73	LYS	2.2
1	В	142	GLY	2.2
1	В	88	ILE	2.2
1	D	87	LYS	2.2
1	В	474	GLY	2.2
1	В	120	TRP	2.1
1	D	110	CYS	2.1
1	А	173	GLY	2.1
1	В	345	HIS	2.1
1	В	308	HIS	2.1
1	D	98	LYS	2.1
1	С	341	ARG	2.0
1	В	377	ASN	2.0
1	В	180	VAL	2.0
1	D	96	LEU	2.0

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#### 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	BMA	K	3	11/12	0.67	0.27	$97,\!125,\!139,\!147$	0
2	BMA	G	3	11/12	0.72	0.27	$106,\!122,\!135,\!136$	0
3	NAG	Н	2	14/15	0.74	0.30	86,102,125,127	0
2	BMA	Е	3	11/12	0.80	0.16	60,72,100,103	0
2	BMA	Ι	3	11/12	0.84	0.13	60,80,92,97	0
3	NAG	L	2	14/15	0.85	0.20	64,97,115,115	0
3	NAG	F	2	14/15	0.86	0.19	$78,\!106,\!131,\!143$	0
3	NAG	J	2	14/15	0.87	0.25	51,68,83,88	0
2	NAG	G	2	14/15	0.90	0.17	$55,\!75,\!95,\!101$	0
2	NAG	K	2	14/15	0.91	0.15	46,69,77,81	0
2	NAG	G	1	14/15	0.91	0.20	53,72,93,97	0
3	NAG	Н	1	14/15	0.92	0.22	$45,\!54,\!71,\!94$	0
3	NAG	F	1	14/15	0.92	0.17	40,51,74,82	0
2	NAG	K	1	14/15	0.92	0.14	$54,\!68,\!103,\!103$	0
3	NAG	J	1	14/15	0.93	0.14	$31,\!47,\!56,\!72$	0
2	NAG	Ι	1	14/15	0.93	0.15	$46,\!66,\!93,\!103$	0
2	NAG	Е	1	14/15	0.94	0.13	$29,\!55,\!102,\!107$	0
2	NAG	I	2	14/15	0.95	0.14	48,70,90,98	0
3	NAG	L	1	14/15	0.96	0.15	32,54,84,85	0
2	NAG	E	2	14/15	0.97	0.11	$\overline{38,54,65,69}$	0

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.



















![](_page_35_Figure_3.jpeg)

![](_page_35_Picture_4.jpeg)

![](_page_36_Figure_3.jpeg)

![](_page_36_Picture_4.jpeg)

#### 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	NI	В	606	1/1	0.98	0.19	42,42,42,42	0
4	NI	А	606	1/1	0.98	0.16	$47,\!47,\!47,\!47$	0

#### 6.5 Other polymers (i)

There are no such residues in this entry.

![](_page_37_Picture_8.jpeg)