

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	6KBI
Title	:	Crystal structure of ErbB3 N418Q mutant
Authors	:	Kato, K.; Yao, M.
Deposited on	:	2019-06-25
Resolution	:	3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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 as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	620	3% 60%	25%	•	11%		
1	В	620	73%		20%	• 5%		
2	С	2	50%	50%				
2	D	2	100%					

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 crite-



ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	А	707	-	-	-	Х



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8967 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 Receptor tyrosine-protein kinase erbB-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	550	Total 4212	C 2607	N 766	0 785	$\begin{array}{c} \mathrm{S} \\ 54 \end{array}$	0	0	0
1	В	588	Total 4517	C 2792	N 818	0 848	${ m S}{ m 59}$	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	418	GLN	ASN	engineered mutation	UNP P21860
В	418	GLN	ASN	engineered mutation	UNP P21860

• Molecule 2 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
2	С	9	Total	С	Ν	0	0	0	0
2	C		28	16	2	10	0	0	0
0	П	2	Total	С	Ν	0	0	0	0
			28	16	2	10			U

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf
2	٨	1	Total	С	Ν	0	0	0
3	A	1	14	8	1	5	0	0
9	Δ	1	Total	С	Ν	0	0	0
5	A	L	14	8	1	5	0	0
2	Δ	1	Total	С	Ν	0	0	0
0	A	L	14	8	1	5	0	0
3	Λ	1	Total	С	Ν	0	0	0
0	Π	T	14	8	1	5	0	0
ગ	Δ	1	Total	С	Ν	0	0	0
0	Π	T	14	8	1	5	0	0
ગ	Δ	1	Total	С	Ν	0	0	0
0	Π	T	14	8	1	5	0	0
3	В	1	Total	С	Ν	Ο	0	0
0	D	T	14	8	1	5	0	0
3	В	1	Total	С	Ν	Ο	0	0
0	D	T	14	8	1	5	0	0
3	В	1	Total	С	Ν	Ο	0	0
0	D	T	14	8	1	5	0	0
3	В	1	Total	С	Ν	Ο	0	0
0	D	T	14	8	1	5	0	0
3	В	1	Total	С	Ν	Ο	0	0
		1	14	8	1	5		0
3	В	1	Total	С	Ν	Ο	0	0
		1	14	8	1	5		U
3	В	1	Total	С	Ν	Ο	0	0
0		1	14	8	1	5		U



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: Receptor tyrosine-protein kinase erbB-3

• Molecule 1: Receptor tyrosine-protein kinase erbB-3





C236 C236 1376 C236 1376 C236 1376 C236 1376 C236 1388 C236 1388 C236 1388 C236 1388 C236 1388 C236 1388 C235 1388 C235 1388 C252 1388 C252 1389 C256 1389 C256 1402 C296 R407 C296 R41 C312 R421 C312 R441 C312 R441 C316 R441 C315 R441 C316 R441 C315 R441 C316 R441 C315 R441 C316 R441 C316 R441 C316 R441 C316 R441 C316 <tr

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

Chain C: 50% 50%

NAG1 NAG2

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

Chain D:

100%

NAG1 NAG2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	236.10Å 49.46Å 190.92Å	Deperitor
a, b, c, α , β , γ	90.00° 125.62° 90.00°	Depositor
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	46.62 - 3.00	Depositor
Resolution (A)	48.16 - 3.00	EDS
% Data completeness	99.3 (46.62-3.00)	Depositor
(in resolution range)	99.4 (48.16-3.00)	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.77 (at 3.01 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
D D.	0.221 , 0.278	Depositor
Π, Π_{free}	0.225 , 0.280	DCC
R_{free} test set	1832 reflections (5.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	60.5	Xtriage
Anisotropy	0.956	Xtriage
Bulk solvent $k_{sol}(e/A^3)$, $B_{sol}(A^2)$	0.28 , 40.5	EDS
L-test for twinning ²	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	0.003 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8967	wwPDB-VP
Average B, all atoms $(Å^2)$	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities 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: 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 Chain		Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.53	1/4314~(0.0%)	0.85	6/5852~(0.1%)	
1	В	0.50	0/4626	0.74	4/6276~(0.1%)	
All	All	0.52	1/8940~(0.0%)	0.79	10/12128~(0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	2
1	В	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	254	GLU	CG-CD	-5.79	1.43	1.51

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	248	LYS	CD-CE-NZ	-9.26	90.40	111.70
1	А	246	TYR	CA-CB-CG	6.99	126.67	113.40
1	В	441	ARG	NE-CZ-NH2	-6.85	116.88	120.30
1	А	557	CYS	CA-CB-SG	-5.89	103.40	114.00
1	А	457	GLY	N-CA-C	-5.74	98.74	113.10

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	А	248	LYS	Peptide
1	А	540	MET	Peptide
1	В	320	ARG	Peptide
1	В	355	HIS	Peptide

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	4212	0	4006	121	0
1	В	4517	0	4277	82	0
2	С	28	0	25	0	0
2	D	28	0	25	0	0
3	А	84	0	78	5	0
3	В	98	0	91	4	0
All	All	8967	0	8502	202	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 12.

The worst 5 of 202 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:248:LYS:HE3	1:A:251:PHE:HA	1.36	1.05
1:A:557:CYS:SG	1:A:561:ARG:NH1	2.36	0.97
1:A:276:VAL:HG13	1:A:299:LYS:HB2	1.49	0.95
1:A:534:HIS:CE1	1:A:551:SER:HB2	2.03	0.94
1:A:295:LYS:O	1:A:297:GLY:N	2.01	0.94

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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



of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	А	546/620~(88%)	497 (91%)	44 (8%)	5 (1%)	17 55
1	В	584/620~(94%)	534 (91%)	45 (8%)	5 (1%)	17 55
All	All	1130/1240 (91%)	1031 (91%)	89~(8%)	10 (1%)	17 55

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	296	ASN
1	А	552	ASP
1	В	35	GLU
1	В	187	THR
1	А	577	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	А	474/536~(88%)	448 (94%)	26~(6%)	21 57	
1	В	510/536~(95%)	490 (96%)	20 (4%)	32 69	
All	All	984/1072~(92%)	938~(95%)	46 (5%)	26 63	

5 of 46 residues with a non-rotameric side chain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	38	GLU
1	В	280	THR
1	В	107	ASN
1	В	151	ARG
1	В	375	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such



sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	252	GLN
1	В	160	ASN
1	В	341	ASN
1	В	205	ASN
1	А	242	GLN

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)

4 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	al Type Chain Beg I		Tinle	Bond lengths			Bond angles			
IVIOI	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	2,1	14,14,15	0.27	0	17,19,21	1.49	3 (17%)
2	NAG	С	2	2	14,14,15	0.39	0	17,19,21	0.56	0
2	NAG	D	1	2,1	14,14,15	1.08	1 (7%)	17,19,21	1.23	2 (11%)
2	NAG	D	2	2	14,14,15	0.44	0	17,19,21	0.75	1 (5%)

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	С	1	2,1	-	6/6/23/26	0/1/1/1		
	Continued on next page								

Continued from previous page...MolTypeChainResLinkChirals

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	С	2	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
2	D	1	NAG	C2-N2	3.37	1.52	1.46

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
2	С	1	NAG	C2-N2-C7	4.24	128.94	122.90
2	D	1	NAG	O5-C1-C2	-3.55	105.68	111.29
2	С	1	NAG	C1-C2-N2	2.93	115.49	110.49
2	D	1	NAG	C1-O5-C5	2.35	115.37	112.19
2	D	2	NAG	C3-C4-C5	2.24	114.23	110.24

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	O5-C5-C6-O6
2	С	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	С	1	NAG	C4-C5-C6-O6
2	С	1	NAG	C8-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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)

13 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).

Mal	Turne	Chain	Dec	Tink	Bo	ond leng	Bond angles			
MOI	туре	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	А	706	1	14,14,15	0.76	1 (7%)	17,19,21	0.88	0
3	NAG	В	701	1	14,14,15	0.89	1 (7%)	17,19,21	1.07	2 (11%)
3	NAG	А	708	1	14,14,15	0.23	0	17,19,21	0.70	0



Mal	Tuno	Chain	Dog	Link	Bo	ond leng	$_{\rm ths}$	B	ond ang	les
WIOI	Type	Ullalli	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	В	706	1	14,14,15	0.31	0	17,19,21	0.38	0
3	NAG	В	707	1	14,14,15	1.62	1 (7%)	17,19,21	1.07	1 (5%)
3	NAG	А	701	1	14,14,15	0.84	1 (7%)	17,19,21	0.80	0
3	NAG	В	702	1	14,14,15	0.31	0	17,19,21	0.54	0
3	NAG	В	705	1	14,14,15	0.87	1 (7%)	17,19,21	1.11	2 (11%)
3	NAG	А	705	1	14,14,15	0.94	1 (7%)	17,19,21	0.99	2 (11%)
3	NAG	В	709	1	14,14,15	0.72	1 (7%)	17,19,21	1.21	2 (11%)
3	NAG	А	702	1	14,14,15	0.37	0	17,19,21	0.40	0
3	NAG	В	708	1	14,14,15	1.56	1 (7%)	17,19,21	0.76	0
3	NAG	А	707	1	14,14,15	1.04	1 (7%)	17,19,21	0.62	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
3	NAG	А	706	1	-	2/6/23/26	0/1/1/1
3	NAG	В	701	1	-	2/6/23/26	0/1/1/1
3	NAG	А	708	1	-	2/6/23/26	0/1/1/1
3	NAG	В	706	1	-	2/6/23/26	0/1/1/1
3	NAG	В	707	1	-	2/6/23/26	0/1/1/1
3	NAG	А	701	1	-	3/6/23/26	0/1/1/1
3	NAG	В	702	1	-	2/6/23/26	0/1/1/1
3	NAG	В	705	1	-	1/6/23/26	0/1/1/1
3	NAG	А	705	1	-	1/6/23/26	0/1/1/1
3	NAG	В	709	1	-	4/6/23/26	0/1/1/1
3	NAG	А	702	1	-	0/6/23/26	0/1/1/1
3	NAG	В	708	1	-	4/6/23/26	0/1/1/1
3	NAG	А	707	1	-	2/6/23/26	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(\text{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
3	В	707	NAG	O5-C1	-5.95	1.34	1.43
3	В	708	NAG	C1-C2	5.11	1.60	1.52
3	В	701	NAG	O5-C1	-2.93	1.39	1.43
3	А	707	NAG	O5-C1	2.71	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	705	NAG	O5-C1	-2.68	1.39	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	709	NAG	C1-O5-C5	3.85	117.40	112.19
3	В	707	NAG	C1-O5-C5	-3.33	107.68	112.19
3	В	705	NAG	O5-C1-C2	-3.06	106.46	111.29
3	В	701	NAG	C1-O5-C5	-2.94	108.21	112.19
3	В	709	NAG	C2-N2-C7	2.43	126.36	122.90

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	706	NAG	O5-C5-C6-O6
3	В	707	NAG	O5-C5-C6-O6
3	В	708	NAG	O5-C5-C6-O6
3	В	702	NAG	O5-C5-C6-O6
3	В	709	NAG	O5-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	706	NAG	2	0
3	А	701	NAG	2	0
3	В	702	NAG	1	0
3	В	709	NAG	1	0
3	В	708	NAG	2	0
3	А	707	NAG	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (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	<RSRZ $>$	#RSRZ>2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	А	550/620~(88%)	0.08	19 (3%) 44 18	40, 70, 108, 133	0
1	В	588/620~(94%)	-0.16	0 100 100	31, 56, 87, 110	0
All	All	1138/1240 (91%)	-0.04	19 (1%) 70 41	31, 62, 102, 133	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	573	GLY	4.3
1	А	572	HIS	4.1
1	А	550	GLY	3.7
1	А	246	TYR	3.5
1	А	551	SER	3.2

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	$B-factors(Å^2)$	Q<0.9
2	NAG	D	2	14/15	0.85	0.20	98,112,117,123	0
2	NAG	С	2	14/15	0.86	0.16	88,104,110,112	0
2	NAG	С	1	14/15	0.94	0.17	58,72,86,93	0
2	NAG	D	1	14/15	0.95	0.14	64,73,86,94	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.





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	B-factors(Å ²)	Q<0.9
3	NAG	А	707	14/15	0.68	0.69	81,109,117,122	0
3	NAG	В	709	14/15	0.68	0.24	81,95,104,107	14
3	NAG	В	705	14/15	0.69	0.37	86,106,128,132	0
3	NAG	В	708	14/15	0.77	0.34	79,87,92,95	0
3	NAG	А	708	14/15	0.82	0.34	91,110,123,125	0
3	NAG	А	706	14/15	0.84	0.24	96,110,116,120	0
3	NAG	В	701	14/15	0.85	0.22	54,79,89,94	0
3	NAG	А	705	14/15	0.85	0.40	110,120,127,132	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
3	NAG	А	702	14/15	0.88	0.14	84,106,114,116	0
3	NAG	В	706	14/15	0.89	0.22	75,90,101,106	0
3	NAG	В	702	14/15	0.89	0.14	86,95,102,105	0
3	NAG	А	701	14/15	0.89	0.17	56,64,72,74	0
3	NAG	В	707	14/15	0.90	0.22	66,70,85,91	0

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6.5 Other polymers (i)

There are no such residues in this entry.

