



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 07:02 PM BST

PDB ID : 6BYK
Title : Structure of 14-3-3 beta/alpha bound to O-ClcNAc peptide
Authors : Schumacher, M.A.
Deposited on : 2017-12-20
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

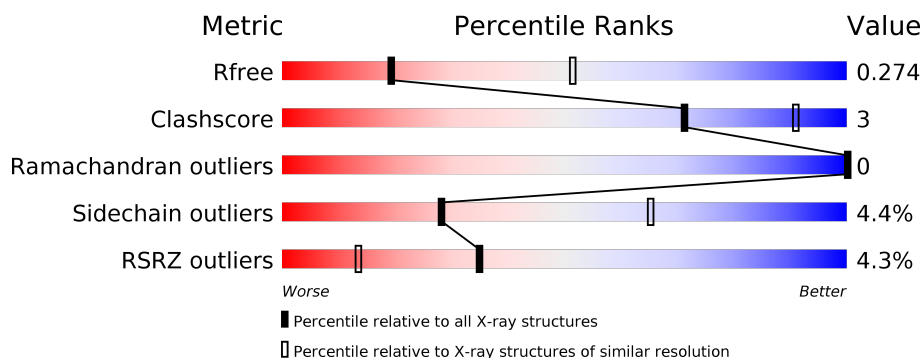
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
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 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 $\leq 5\%$. 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	230	<div> <div>2%</div> <div>89%</div> <div>11%</div> </div>
1	B	230	<div> <div>2%</div> <div>91%</div> <div>8%</div> </div>
1	C	230	<div> <div>2%</div> <div>88%</div> <div>11%</div> </div>
1	D	230	<div> <div>5%</div> <div>87%</div> <div>13%</div> </div>
2	G	12	<div> <div>8%</div> <div>58%</div> <div>17%</div> <div>25%</div> </div>
2	J	12	<div> <div>58%</div> <div>50%</div> <div>17%</div> <div>8%</div> <div>25%</div> </div>

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Mol	Chain	Length	Quality of chain
2	K	12	
2	R	12	

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
3	NAG	G	601	-	-	-	X
3	NAG	J	601	-	-	-	X
3	NAG	K	601	-	-	-	X
3	NAG	R	601	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14704 atoms, of which 7139 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 14-3-3 protein beta/alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	230	Total	C	H	N	O	S	0	0	0
			3617	1149	1783	305	371	9			
1	B	230	Total	C	H	N	O	S	0	0	0
			3629	1148	1799	309	364	9			
1	C	230	Total	C	H	N	O	S	0	0	0
			3637	1152	1800	307	369	9			
1	D	230	Total	C	H	N	O	S	0	0	0
			3578	1143	1757	304	365	9			

- Molecule 2 is a protein called ATPVVSQASSTT O-GlcNac peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	9	Total	C	N	O	0	0	0
			60	36	10	14			
2	J	9	Total	C	N	O	0	0	0
			60	36	10	14			
2	K	5	Total	C	N	O	0	0	0
			34	21	6	7			
2	R	5	Total	C	N	O	0	0	0
			33	19	6	8			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

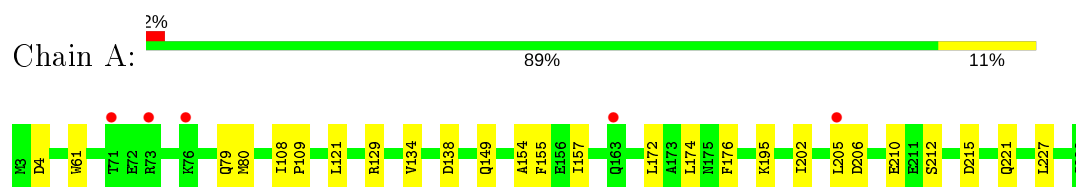


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	J	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	R	1	Total	C	N	O	0	0
			14	8	1	5		

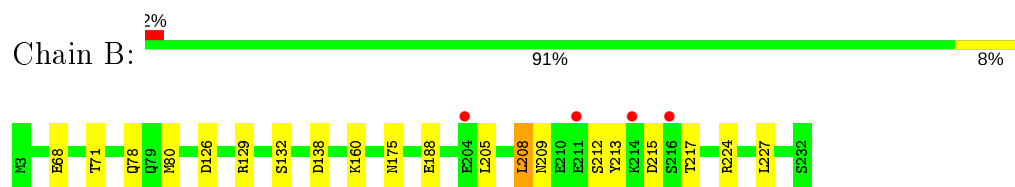
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

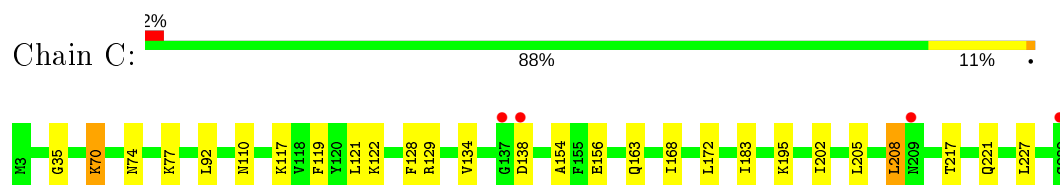
- Molecule 1: 14-3-3 protein beta/alpha



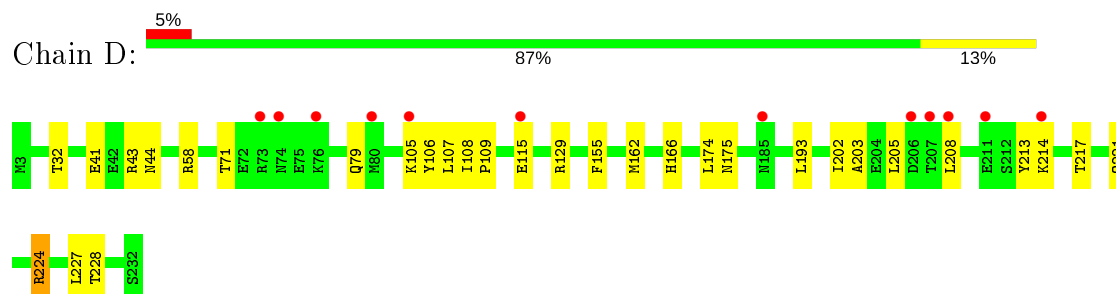
- Molecule 1: 14-3-3 protein beta/alpha



- Molecule 1: 14-3-3 protein beta/alpha

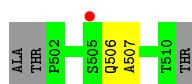


- Molecule 1: 14-3-3 protein beta/alpha

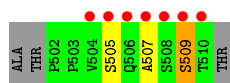


- Molecule 2: ATPVVSQASSTT O-GlcNAc peptide

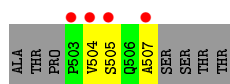




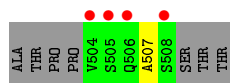
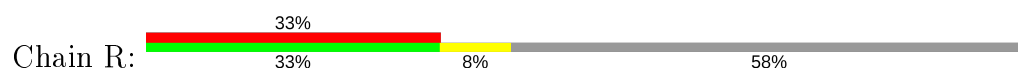
- Molecule 2: ATPPVSQASSTT O-GlcNac peptide



- Molecule 2: ATPPVSQASSTT O-GlcNac peptide



- Molecule 2: ATPPVSQASSTT O-GlcNac peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.67Å 71.45Å 95.76Å 90.00° 111.61° 90.00°	Depositor
Resolution (Å)	89.03 – 3.00 89.03 – 3.00	Depositor EDS
% Data completeness (in resolution range)	89.3 (89.03-3.00) 90.2 (89.03-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.215 , 0.268 0.223 , 0.274	Depositor DCC
R_{free} test set	1852 reflections (9.76%)	wwPDB-VP
Wilson B-factor (Å ²)	66.5	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 79.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14704	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.25	0/1861	0.42	0/2510
1	B	0.26	0/1857	0.43	0/2502
1	C	0.24	0/1864	0.42	0/2512
1	D	0.25	0/1848	0.40	0/2494
2	G	0.38	0/61	0.65	0/83
2	J	0.38	0/61	0.57	0/83
2	K	0.37	0/34	0.70	0/45
2	R	0.21	0/32	0.45	0/42
All	All	0.25	0/7618	0.42	0/10271

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	A	1834	1783	1786	10	0
1	B	1830	1799	1798	10	0
1	C	1837	1800	1802	14	0
1	D	1821	1757	1769	16	0
2	G	60	0	57	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	60	0	57	3	0
2	K	34	0	33	2	0
2	R	33	0	30	1	0
3	G	14	0	13	2	0
3	J	14	0	13	4	0
3	K	14	0	13	2	0
3	R	14	0	13	2	0
All	All	7565	7139	7384	52	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 3.

All (52) 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:D:129:ARG:NH2	3:J:601:NAG:O3	2.18	0.76
1:B:175:ASN:ND2	3:G:601:NAG:O7	2.30	0.65
1:D:175:ASN:ND2	3:J:601:NAG:O7	2.31	0.63
2:G:507:ALA:HB2	3:G:601:NAG:H82	1.87	0.57
1:B:68:GLU:O	1:B:78:GLN:NE2	2.36	0.56
1:C:129:ARG:NH2	3:R:601:NAG:O3	2.38	0.56
1:C:202:ILE:HA	1:C:205:LEU:HD11	1.89	0.55
2:R:507:ALA:HB2	3:R:601:NAG:H82	1.90	0.54
1:D:205:LEU:HD22	1:D:208:LEU:HD12	1.93	0.50
1:D:115:GLU:HA	1:D:162:MET:CE	2.43	0.49
1:D:43:ARG:NH2	2:J:509:SER:OG	2.42	0.48
1:D:58:ARG:NH1	3:J:601:NAG:O4	2.48	0.47
2:J:507:ALA:HB2	3:J:601:NAG:H82	1.97	0.47
1:C:129:ARG:HG3	1:C:183:ILE:HG13	1.96	0.46
1:B:213:TYR:CE2	1:B:217:THR:HG21	2.52	0.45
1:C:121:LEU:CB	1:C:154:ALA:HB2	2.46	0.44
1:B:126:ASP:OD1	1:B:129:ARG:NH2	2.49	0.44
1:D:224:ARG:O	1:D:228:THR:HG23	2.17	0.44
1:D:155:PHE:CZ	1:D:193:LEU:HD11	2.53	0.44
1:C:205:LEU:HD23	1:C:208:LEU:HD12	2.00	0.44
1:A:155:PHE:HA	1:A:172:LEU:HD21	2.00	0.43
1:C:122:LYS:HD2	1:C:172:LEU:HA	2.00	0.43
1:A:174:LEU:HD21	2:K:505:SER:HA	1.99	0.43
1:B:208:LEU:HD22	1:B:209:ASN:HD22	1.83	0.43
1:D:105:LYS:HD2	1:D:106:TYR:CE2	2.53	0.43
1:B:129:ARG:O	1:B:132:SER:OG	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:LYS:HA	1:C:227:LEU:HD11	1.99	0.43
1:C:92:LEU:HD23	1:C:134:VAL:HG11	2.01	0.43
1:D:108:ILE:N	1:D:109:PRO:HD2	2.34	0.42
1:D:174:LEU:HD21	2:J:505:SER:HA	2.01	0.42
1:A:202:ILE:HA	1:A:205:LEU:HB2	2.00	0.42
1:A:157:ILE:HG12	1:B:188:GLU:HG2	2.00	0.42
1:B:209:ASN:O	1:B:213:TYR:HB2	2.20	0.42
1:C:119:PHE:HD2	1:C:168:ILE:HD12	1.84	0.42
1:A:129:ARG:NH2	3:K:601:NAG:O3	2.53	0.42
1:C:121:LEU:HB2	1:C:154:ALA:HB2	2.02	0.42
1:C:217:THR:O	1:C:221:GLN:N	2.52	0.42
1:D:205:LEU:O	1:D:205:LEU:HD13	2.20	0.42
1:D:32:THR:HG23	1:D:107:LEU:HD21	2.02	0.42
1:C:35:GLY:O	1:C:110:ASN:ND2	2.53	0.42
1:D:213:TYR:CE2	1:D:217:THR:HG21	2.55	0.42
1:C:74:ASN:HB3	1:C:77:LYS:HB3	2.01	0.41
1:D:217:THR:O	1:D:221:GLN:N	2.52	0.41
1:A:138:ASP:HB3	1:B:160:LYS:HG3	2.02	0.41
1:A:121:LEU:CB	1:A:154:ALA:HB2	2.51	0.41
1:A:61:TRP:CE2	1:A:134:VAL:HG12	2.56	0.41
1:D:202:ILE:HG13	1:D:203:ALA:N	2.36	0.41
1:C:70:LYS:HD2	1:C:70:LYS:N	2.35	0.41
1:B:209:ASN:OD1	1:B:212:SER:N	2.43	0.41
2:K:507:ALA:HB2	3:K:601:NAG:H82	2.03	0.41
1:A:195:LYS:HA	1:A:227:LEU:HD11	2.03	0.41
1:A:108:ILE:N	1:A:109:PRO:HD2	2.36	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/230 (99%)	223 (98%)	5 (2%)	0	100	100
1	B	228/230 (99%)	219 (96%)	9 (4%)	0	100	100
1	C	228/230 (99%)	220 (96%)	8 (4%)	0	100	100
1	D	228/230 (99%)	218 (96%)	10 (4%)	0	100	100
2	G	7/12 (58%)	4 (57%)	3 (43%)	0	100	100
2	J	7/12 (58%)	4 (57%)	3 (43%)	0	100	100
2	K	3/12 (25%)	1 (33%)	2 (67%)	0	100	100
2	R	3/12 (25%)	3 (100%)	0	0	100	100
All	All	932/968 (96%)	892 (96%)	40 (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	198/204 (97%)	188 (95%)	10 (5%)	24	60
1	B	197/204 (97%)	189 (96%)	8 (4%)	30	67
1	C	199/204 (98%)	192 (96%)	7 (4%)	36	71
1	D	194/204 (95%)	186 (96%)	8 (4%)	30	67
2	G	8/10 (80%)	7 (88%)	1 (12%)	4	20
2	J	8/10 (80%)	7 (88%)	1 (12%)	4	20
2	K	4/10 (40%)	3 (75%)	1 (25%)	0	3
2	R	4/10 (40%)	4 (100%)	0	100	100
All	All	812/856 (95%)	776 (96%)	36 (4%)	28	65

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	79	GLN

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Mol	Chain	Res	Type
1	A	80	MET
1	A	149	GLN
1	A	176	PHE
1	A	206	ASP
1	A	210	GLU
1	A	212	SER
1	A	215	ASP
1	A	221	GLN
1	B	71	THR
1	B	80	MET
1	B	138	ASP
1	B	205	LEU
1	B	208	LEU
1	B	215	ASP
1	B	224	ARG
1	B	227	LEU
1	C	70	LYS
1	C	117	LYS
1	C	128	PHE
1	C	138	ASP
1	C	156	GLU
1	C	163	GLN
1	C	208	LEU
1	D	41	GLU
1	D	44	ASN
1	D	71	THR
1	D	79	GLN
1	D	166	HIS
1	D	214	LYS
1	D	224	ARG
1	D	227	LEU
2	G	506	GLN
2	J	509	SER
2	K	504	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	79	GLN
1	B	221	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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	R	601	2	14,14,15	0.33	0	17,19,21	0.51	0
3	NAG	G	601	2	14,14,15	0.65	0	17,19,21	0.93	1 (5%)
3	NAG	J	601	2	14,14,15	0.91	1 (7%)	17,19,21	1.07	1 (5%)
3	NAG	K	601	2	14,14,15	0.41	0	17,19,21	0.53	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	R	601	2	-	0/6/23/26	0/1/1/1
3	NAG	G	601	2	-	0/6/23/26	0/1/1/1
3	NAG	J	601	2	-	0/6/23/26	0/1/1/1
3	NAG	K	601	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	601	NAG	O5-C1	3.08	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	601	NAG	C1-O5-C5	3.93	117.52	112.19
3	G	601	NAG	C1-O5-C5	3.15	116.46	112.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	R	601	NAG	2	0
3	G	601	NAG	2	0
3	J	601	NAG	4	0
3	K	601	NAG	2	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	230/230 (100%)	0.05	5 (2%) 62 33	39, 68, 175, 257	0
1	B	230/230 (100%)	0.02	4 (1%) 70 41	32, 62, 166, 253	0
1	C	230/230 (100%)	0.08	4 (1%) 70 41	47, 73, 196, 289	0
1	D	230/230 (100%)	0.21	12 (5%) 27 10	48, 75, 224, 303	0
2	G	9/12 (75%)	1.42	1 (11%) 5 1	115, 128, 157, 168	0
2	J	9/12 (75%)	4.23	7 (77%) 0 0	156, 224, 315, 335	0
2	K	5/12 (41%)	2.92	4 (80%) 0 0	206, 212, 238, 263	0
2	R	5/12 (41%)	2.67	4 (80%) 0 0	147, 157, 203, 245	0
All	All	948/968 (97%)	0.17	41 (4%) 35 13	32, 71, 204, 335	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	508	SER	7.4
2	J	507	ALA	7.2
2	J	505	SER	6.7
1	C	138	ASP	5.7
2	K	507	ALA	4.8
2	R	505	SER	4.6
2	J	510	THR	4.3
1	D	74	ASN	4.2
2	J	504	VAL	3.9
1	D	211	GLU	3.8
2	J	509	SER	3.7
1	D	73	ARG	3.4
2	J	506	GLN	3.2
1	D	214	LYS	3.2
1	D	207	THR	3.2
2	K	503	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
2	G	505	SER	3.1
2	R	508	SER	3.1
1	A	71	THR	3.0
2	K	504	VAL	3.0
1	D	206	ASP	3.0
2	R	504	VAL	2.9
1	D	115	GLU	2.9
1	B	211	GLU	2.9
1	A	76	LYS	2.9
1	A	73	ARG	2.8
1	A	205	LEU	2.6
1	D	105	LYS	2.5
1	D	185	ASN	2.4
1	B	204	GLU	2.4
1	B	216	SER	2.3
2	R	506	GLN	2.3
1	D	80	MET	2.2
1	D	76	LYS	2.2
1	B	214	LYS	2.2
1	C	232	SER	2.1
1	D	208	LEU	2.1
1	C	137	GLY	2.1
1	A	163	GLN	2.1
1	C	209	ASN	2.0
2	K	505	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

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. 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(\AA^2)	Q<0.9
3	NAG	J	601	14/15	0.48	0.81	213,216,217,218	0
3	NAG	G	601	14/15	0.54	0.79	168,173,185,186	0
3	NAG	R	601	14/15	0.60	0.76	185,187,189,191	0
3	NAG	K	601	14/15	0.70	0.62	225,228,232,232	0

6.5 Other polymers [i](#)

There are no such residues in this entry.