W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:38 PM GMT

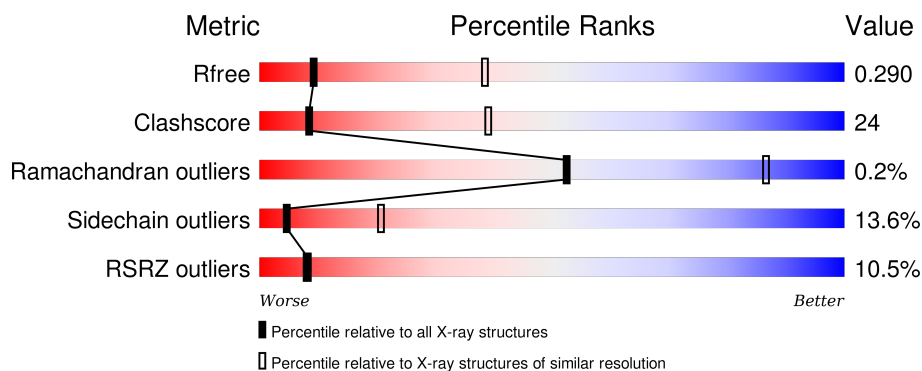|		
PDB ID	:	4FN0
Title	:	Crystal structure of mouse nectin-2 extracellular fragment D1-D2, 2nd crystal form
Authors	:	Harrison, O.J.; Brasch, J.; Shapiro, L.
Deposited on	:	2012-06-18
Resolution	:	3.35 Å(reported)

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 3.35 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	Percentile Ranks	Value
Rfree		0.290
Clashscore		24
Ramachandran outliers		0.2%
Sidechain outliers		13.6%
RSRZ outliers		10.5%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1005 (3.42-3.30)
Clashscore	102246	1076 (3.42-3.30)
Ramachandran outliers	100387	1059 (3.42-3.30)
Sidechain outliers	100360	1058 (3.42-3.30)
RSRZ outliers	91569	1010 (3.42-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	225	11% / 54% / 37% / 6% ·
1	B	225	% / 51% / 40% / 6% ··
1	C	225	19% / 61% / 32% · ·

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	302	-	-	X	-
2	FUC	B	304	-	-	X	-
3	NAG	C	305	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5383 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 Poliovirus receptor-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1706	1067	316	319	4			
1	B	220	Total	C	N	O	S	0	0	0
			1706	1067	316	319	4			
1	C	219	Total	C	N	O	S	0	0	0
			1696	1061	313	318	4			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	HIS	-	EXPRESSION TAG	UNP P32507
A	252	HIS	-	EXPRESSION TAG	UNP P32507
A	253	HIS	-	EXPRESSION TAG	UNP P32507
A	254	HIS	-	EXPRESSION TAG	UNP P32507
A	255	HIS	-	EXPRESSION TAG	UNP P32507
A	256	HIS	-	EXPRESSION TAG	UNP P32507
B	251	HIS	-	EXPRESSION TAG	UNP P32507
B	252	HIS	-	EXPRESSION TAG	UNP P32507
B	253	HIS	-	EXPRESSION TAG	UNP P32507
B	254	HIS	-	EXPRESSION TAG	UNP P32507
B	255	HIS	-	EXPRESSION TAG	UNP P32507
B	256	HIS	-	EXPRESSION TAG	UNP P32507
C	251	HIS	-	EXPRESSION TAG	UNP P32507
C	252	HIS	-	EXPRESSION TAG	UNP P32507
C	253	HIS	-	EXPRESSION TAG	UNP P32507
C	254	HIS	-	EXPRESSION TAG	UNP P32507
C	255	HIS	-	EXPRESSION TAG	UNP P32507
C	256	HIS	-	EXPRESSION TAG	UNP P32507

- Molecule 2 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	4	Total 49	C 28	N 2	O 19	0	0
2	A	4	Total 49	C 28	N 2	O 19	0	0
2	B	4	Total 49	C 28	N 2	O 19	0	0
2	B	4	Total 49	C 28	N 2	O 19	0	0
2	C	4	Total 49	C 28	N 2	O 19	0	0

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).
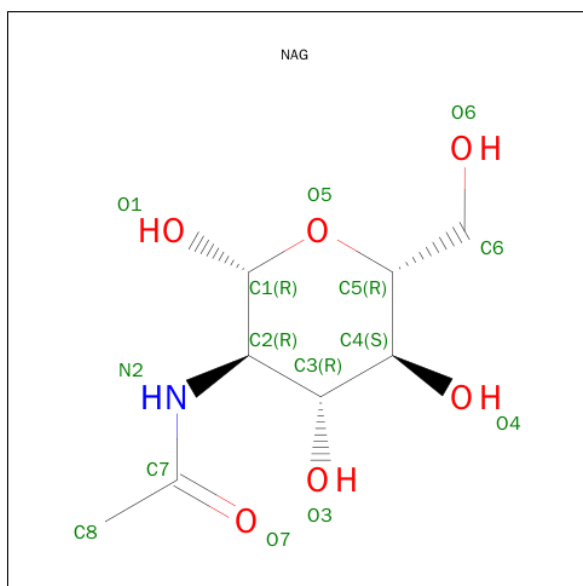
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total 6	O 6	0	0
4	B	8	Total 8	O 8	0	0
4	C	2	Total 2	O 2	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Poliovirus receptor-related protein 2
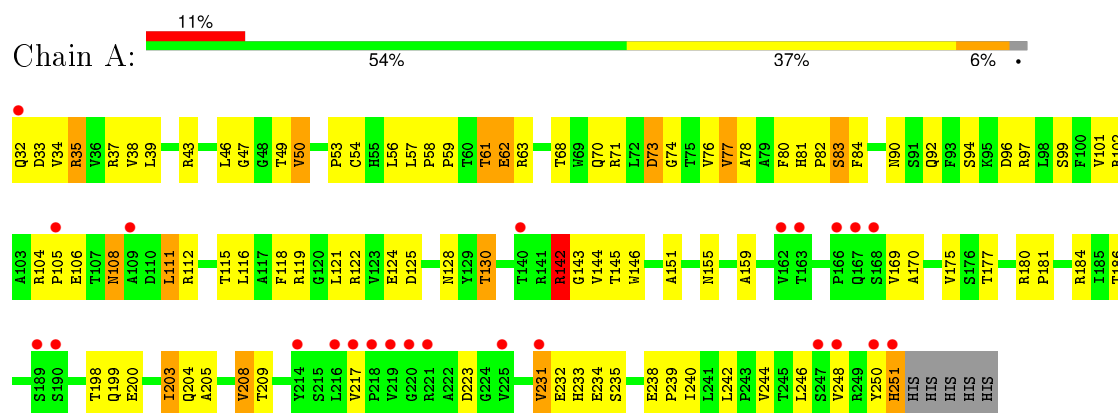
• Molecule 1: Poliovirus receptor-related protein 2
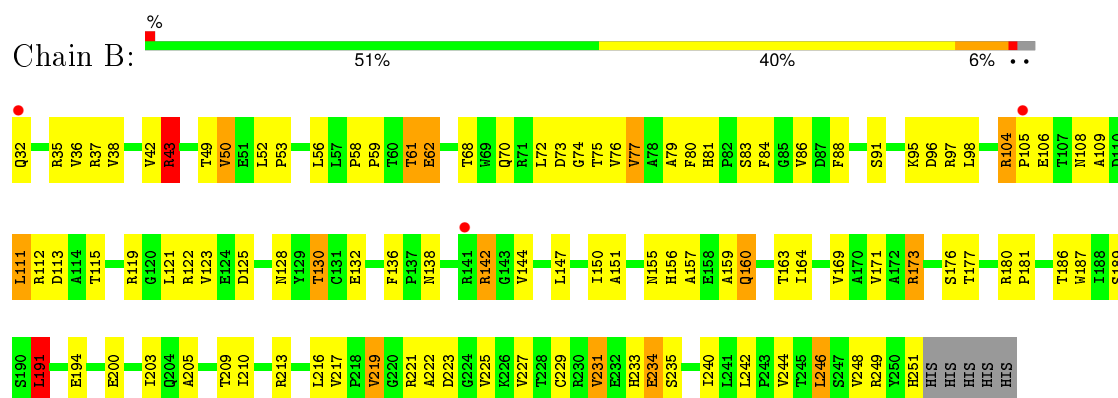
• Molecule 1: Poliovirus receptor-related protein 2
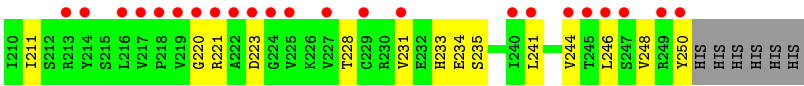
4 Data and refinement statistics (i)

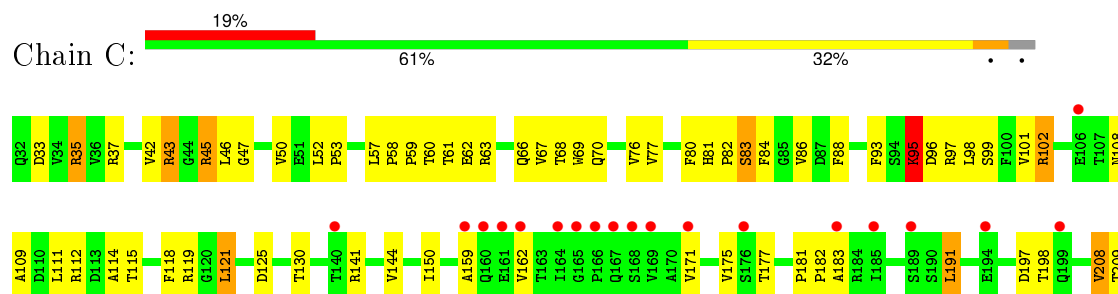| Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	117.02Å 117.02Å 158.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.35 29.26 – 3.35	Depositor EDS
% Data completeness (in resolution range)	99.3 (20.00-3.35) 99.5 (29.26-3.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.94 (at 3.39Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.247 , 0.293 0.246 , 0.290	Depositor DCC
R_{free} test set	937 reflections (5.38%)	DCC
Wilson B-factor (Å^2)	78.5	Xtriage
Anisotropy	0.786	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 78.9	EDS
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
L-test for twinning [2]	$< |L| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Outliers	2 of 18430 reflections (0.011%)	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5383	wwPDB-VP
Average B, all atoms (Å^2)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.88% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

Full wwPDB X-ray Structure Validation Report

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: BMA, NAG, FUC

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	0.78	0/1744	0.87	1/2378 (0.0%)
1	B	0.75	1/1744 (0.1%)	0.86	2/2378 (0.1%)
1	C	0.67	1/1733 (0.1%)	0.77	0/2363
All	All	0.74	2/5221 (0.0%)	0.84	3/7119 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	69	TRP	CD2-CE2	5.63	1.48	1.41
1	B	187	TRP	CD2-CE2	5.29	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	LEU	CB-CG-CD1	6.12	121.41	111.00
1	A	142	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	B	43	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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	1706	0	1687	93	0
1	B	1706	0	1687	83	0
1	C	1696	0	1680	71	0
2	A	98	0	86	6	0
2	B	98	0	86	16	0
2	C	49	0	43	0	0
3	C	14	0	13	2	0
4	A	6	0	0	0	0
4	B	8	0	0	0	0
4	C	2	0	0	0	0
All	All	5383	0	5282	256	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 24.

All (256) 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:223:ASP:HB3	1:A:248:VAL:HG22	1.22	1.21
2:B:302:NAG:N2	2:B:304:FUC:H61	1.62	1.15
1:B:106:GLU:HA	1:B:109:ALA:HB2	1.21	1.15
1:A:104:ARG:HD3	1:A:105:PRO:HD2	1.35	1.07
1:B:219:VAL:HG22	1:B:221:ARG:H	1.17	1.06
1:B:189:SER:HB2	1:B:227:VAL:HG13	1.40	1.04
2:B:302:NAG:C2	2:B:304:FUC:H61	1.90	1.00
1:B:106:GLU:HA	1:B:109:ALA:CB	1.93	0.98
1:B:111:LEU:H	1:B:111:LEU:HD23	1.29	0.97
1:B:177:THR:HA	1:B:209:THR:HG23	1.47	0.96
2:A:301:NAG:H4	2:A:304:FUC:O2	1.65	0.96
1:A:231:VAL:HG13	1:A:240:ILE:CG2	1.97	0.95
1:C:80:PHE:CD2	1:C:111:LEU:HD22	2.04	0.92
2:B:302:NAG:H3	2:B:304:FUC:C6	2.00	0.91
2:B:302:NAG:HN2	2:B:304:FUC:H61	1.22	0.91
1:C:62:GLU:OE1	3:C:305:NAG:H83	1.71	0.90
1:A:104:ARG:HG2	1:A:108:ASN:N	1.92	0.85
1:B:43:ARG:HB3	1:B:150:ILE:HD11	1.57	0.84
1:B:80:PHE:CE2	1:B:111:LEU:HD13	2.12	0.83
1:A:128:ASN:ND2	2:A:301:NAG:O7	2.13	0.81
1:A:71:ARG:NH1	1:B:219:VAL:HG21	1.95	0.81
2:B:302:NAG:HN2	2:B:304:FUC:C6	1.94	0.80
2:B:302:NAG:C1	2:B:304:FUC:H61	2.10	0.80
1:C:101:VAL:HG12	1:C:102:ARG:CZ	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ARG:NH1	1:A:108:ASN:HA	1.99	0.77
1:B:191:LEU:HD22	1:B:216:LEU:HD22	1.67	0.77
1:A:80:PHE:CE2	1:A:111:LEU:HD13	2.21	0.76
2:B:302:NAG:H3	2:B:304:FUC:H63	1.67	0.75
1:B:80:PHE:CD2	1:B:111:LEU:HD13	2.22	0.74
1:A:231:VAL:HG13	1:A:240:ILE:HG22	1.69	0.73
1:A:231:VAL:HG13	1:A:240:ILE:HG23	1.69	0.73
1:B:50:VAL:HG22	1:B:121:LEU:HD11	1.70	0.73
1:B:104:ARG:HG2	1:B:108:ASN:HD22	1.53	0.73
1:B:219:VAL:HG22	1:B:221:ARG:N	1.98	0.72
1:A:81:HIS:CD2	1:A:84:PHE:CD2	2.77	0.72
1:A:130:THR:O	1:A:130:THR:HG22	1.88	0.72
1:B:53:PRO:HA	1:B:115:THR:HG23	1.71	0.72
1:A:46:LEU:HD23	1:A:47:GLY:N	2.06	0.71
1:C:58:PRO:HA	1:C:59:PRO:C	2.11	0.70
1:B:96:ASP:OD1	1:B:97:ARG:HG3	1.92	0.70
1:A:104:ARG:HG2	1:A:108:ASN:CA	2.21	0.70
1:B:106:GLU:CA	1:B:109:ALA:HB2	2.12	0.69
1:C:182:PRO:HG3	1:C:208:VAL:HG21	1.74	0.69
2:B:302:NAG:C3	2:B:304:FUC:C6	2.71	0.68
1:A:33:ASP:HB3	1:A:35:ARG:HE	1.57	0.68
1:B:122:ARG:NH1	1:B:125:ASP:OD1	2.26	0.68
1:A:104:ARG:HD3	1:A:105:PRO:CD	2.21	0.67
1:A:97:ARG:NH2	1:A:125:ASP:OD2	2.28	0.66
1:A:80:PHE:CD2	1:A:111:LEU:HD13	2.31	0.66
1:A:104:ARG:HG2	1:A:108:ASN:CB	2.26	0.66
1:A:53:PRO:HA	1:A:115:THR:HG23	1.78	0.66
1:A:90:ASN:OD1	1:A:92:GLN:HB2	1.96	0.65
1:A:58:PRO:HA	1:A:59:PRO:C	2.17	0.65
1:A:177:THR:HA	1:A:209:THR:HG23	1.78	0.65
2:B:302:NAG:C1	2:B:304:FUC:C6	2.76	0.64
1:A:238:GLU:HB3	1:A:239:PRO:CD	2.28	0.64
1:A:104:ARG:HG2	1:A:108:ASN:HB3	1.78	0.63
2:B:302:NAG:C2	2:B:304:FUC:C6	2.73	0.63
1:C:159:ALA:HB2	1:C:244:VAL:CG1	2.28	0.63
1:C:101:VAL:CG1	1:C:102:ARG:NH2	2.62	0.63
1:B:73:ASP:OD1	1:B:75:THR:HG23	1.99	0.63
1:C:70:GLN:HG2	1:C:76:VAL:HG22	1.80	0.63
1:A:146:TRP:NE1	2:A:301:NAG:H82	2.15	0.62
1:A:81:HIS:HD2	1:A:84:PHE:H	1.48	0.61
1:A:159:ALA:N	1:A:244:VAL:HG11	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:VAL:HG21	1:B:147:LEU:HD11	1.81	0.61
1:B:231:VAL:HG13	1:B:240:ILE:HB	1.83	0.61
1:A:37:ARG:HB2	1:A:57:LEU:HD11	1.81	0.61
1:B:223:ASP:HB2	1:B:248:VAL:HG22	1.83	0.60
1:A:142:ARG:HH11	1:A:142:ARG:CG	2.15	0.60
1:A:32:GLN:HE22	1:A:143:GLY:HA2	1.65	0.60
1:B:97:ARG:NH2	1:B:125:ASP:OD2	2.35	0.59
1:B:132:GLU:OE2	1:B:142:ARG:NH2	2.35	0.59
1:C:102:ARG:HH11	1:C:102:ARG:CG	2.14	0.59
1:B:128:ASN:ND2	2:B:301:NAG:O7	2.32	0.59
1:C:97:ARG:NH2	1:C:125:ASP:OD2	2.34	0.59
1:A:238:GLU:HB3	1:A:239:PRO:HD2	1.86	0.58
1:A:32:GLN:NE2	1:A:144:VAL:HG12	2.18	0.58
1:C:101:VAL:HG11	1:C:102:ARG:NH2	2.19	0.58
1:A:56:LEU:HD23	1:A:112:ARG:NH2	2.18	0.58
1:A:71:ARG:HH12	1:B:219:VAL:HG21	1.67	0.58
1:B:80:PHE:HE2	1:B:111:LEU:HD13	1.68	0.57
1:A:223:ASP:HB3	1:A:248:VAL:CG2	2.16	0.57
1:C:60:THR:HA	1:C:112:ARG:CZ	2.34	0.57
1:B:62:GLU:CD	1:B:62:GLU:N	2.58	0.57
1:A:73:ASP:OD1	1:B:219:VAL:HG23	2.04	0.57
1:C:102:ARG:HG2	1:C:102:ARG:HH11	1.70	0.57
1:B:70:GLN:HG2	1:B:76:VAL:HG22	1.87	0.57
1:B:77:VAL:HG13	1:B:98:LEU:HD12	1.86	0.56
1:C:228:THR:HG21	1:C:241:LEU:HB3	1.87	0.56
1:A:77:VAL:HG12	1:A:78:ALA:N	2.20	0.56
1:C:223:ASP:HB2	1:C:248:VAL:HG22	1.88	0.56
1:C:183:ALA:HB1	1:C:231:VAL:HG23	1.88	0.56
1:C:62:GLU:CD	3:C:305:NAG:H83	2.26	0.56
1:B:58:PRO:HA	1:B:59:PRO:C	2.26	0.56
1:C:102:ARG:HH11	1:C:102:ARG:HB2	1.70	0.56
1:A:70:GLN:HG2	1:A:74:GLY:O	2.06	0.55
1:B:111:LEU:HD23	1:B:111:LEU:N	2.11	0.55
1:A:50:VAL:HG23	1:A:118:PHE:HB2	1.88	0.55
2:B:302:NAG:N2	2:B:304:FUC:C6	2.52	0.55
1:A:104:ARG:CG	1:A:108:ASN:HB3	2.37	0.55
1:C:101:VAL:HG12	1:C:102:ARG:NH2	2.22	0.55
1:C:162:VAL:HG21	1:C:171:VAL:HG12	1.87	0.54
1:B:233:HIS:HD2	1:B:235:SER:H	1.56	0.54
1:A:199:GLN:O	1:A:200:GLU:HB3	2.07	0.54
1:A:250:TYR:O	1:A:250:TYR:CG	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:HIS:CD2	1:B:83:SER:H	2.26	0.54
1:C:228:THR:CG2	1:C:241:LEU:HB3	2.37	0.54
1:C:175:VAL:HG12	1:C:211:ILE:HG23	1.90	0.54
1:B:181:PRO:O	1:B:233:HIS:HE1	1.91	0.53
1:B:68:THR:HG22	1:B:79:ALA:HB2	1.90	0.53
1:C:177:THR:HA	1:C:209:THR:HG23	1.90	0.53
1:A:80:PHE:CD2	1:A:111:LEU:CD1	2.91	0.53
1:B:61:THR:OG1	1:B:62:GLU:OE1	2.17	0.53
2:B:302:NAG:C3	2:B:304:FUC:H61	2.33	0.53
1:C:81:HIS:HD2	1:C:84:PHE:H	1.57	0.53
1:C:233:HIS:CD2	1:C:235:SER:H	2.26	0.53
1:B:171:VAL:HG23	1:B:246:LEU:HD11	1.90	0.53
1:A:81:HIS:CD2	1:A:83:SER:H	2.27	0.53
1:A:151:ALA:HB3	1:A:180:ARG:HB3	1.89	0.53
2:A:301:NAG:O3	2:A:302:NAG:O5	2.22	0.53
1:B:81:HIS:HD2	1:B:84:PHE:H	1.57	0.53
2:A:301:NAG:C1	2:A:301:NAG:O7	2.55	0.52
1:B:163:THR:HG22	1:B:164:ILE:N	2.23	0.52
1:B:233:HIS:CD2	1:B:235:SER:H	2.28	0.52
1:B:43:ARG:HH22	1:B:234:GLU:HG2	1.74	0.52
1:C:81:HIS:CD2	1:C:84:PHE:CD1	2.97	0.52
1:C:60:THR:HA	1:C:112:ARG:NH2	2.25	0.52
1:A:142:ARG:HH11	1:A:142:ARG:HG2	1.74	0.52
1:C:77:VAL:HG22	1:C:93:PHE:CG	2.45	0.51
1:B:49:THR:HG22	1:B:119:ARG:HB2	1.90	0.51
1:A:38:VAL:HG12	1:A:54:CYS:HA	1.93	0.51
1:C:98:LEU:HD21	1:C:118:PHE:CD1	2.45	0.51
1:A:124:GLU:N	1:A:124:GLU:OE2	2.43	0.51
1:A:122:ARG:NH1	1:A:124:GLU:HB2	2.25	0.51
1:A:71:ARG:HH11	1:B:219:VAL:HG21	1.73	0.51
1:C:86:VAL:CG1	1:C:88:PHE:CE2	2.94	0.51
1:B:181:PRO:O	1:B:233:HIS:CE1	2.64	0.51
1:A:73:ASP:CG	1:B:219:VAL:HG23	2.31	0.51
1:C:60:THR:HA	1:C:112:ARG:NH1	2.26	0.51
1:B:43:ARG:NH2	1:B:234:GLU:HG2	2.26	0.50
1:B:151:ALA:HB3	1:B:180:ARG:HB3	1.93	0.50
1:B:123:VAL:HG21	1:B:205:ALA:O	2.10	0.50
1:C:50:VAL:HG22	1:C:121:LEU:HD11	1.93	0.50
1:A:181:PRO:O	1:A:233:HIS:HE1	1.94	0.50
1:A:58:PRO:HA	1:A:59:PRO:O	2.11	0.50
1:B:49:THR:HG22	1:B:119:ARG:CB	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:ASN:OD1	1:C:109:ALA:N	2.43	0.50
2:B:301:NAG:H4	2:B:304:FUC:O5	2.12	0.50
1:B:81:HIS:HD2	1:B:83:SER:H	1.59	0.50
1:C:81:HIS:CD2	1:C:83:SER:H	2.29	0.50
1:C:66:GLN:NE2	1:C:68:THR:HG23	2.27	0.50
1:B:72:LEU:C	1:B:74:GLY:H	2.14	0.49
1:C:46:LEU:HD23	1:C:47:GLY:N	2.27	0.49
1:C:181:PRO:O	1:C:233:HIS:HE1	1.95	0.49
1:A:101:VAL:O	1:A:102:ARG:C	2.50	0.49
1:C:80:PHE:CE2	1:C:111:LEU:HD22	2.45	0.49
1:C:182:PRO:HG3	1:C:208:VAL:CG2	2.42	0.49
1:C:159:ALA:HB2	1:C:244:VAL:HG13	1.93	0.49
1:B:125:ASP:O	1:B:147:LEU:HD23	2.12	0.49
1:A:233:HIS:CD2	1:A:235:SER:H	2.30	0.49
1:A:99:SER:O	1:A:116:LEU:HD12	2.13	0.49
1:A:146:TRP:HE1	2:A:301:NAG:H82	1.78	0.49
1:A:181:PRO:O	1:A:233:HIS:CE1	2.65	0.49
1:A:142:ARG:NH1	1:A:142:ARG:HG2	2.28	0.49
1:B:111:LEU:H	1:B:111:LEU:CD2	2.07	0.48
1:A:144:VAL:O	1:A:144:VAL:HG13	2.13	0.48
1:A:56:LEU:HD23	1:A:112:ARG:CZ	2.43	0.48
1:B:77:VAL:HG13	1:B:98:LEU:CD1	2.44	0.48
1:C:45:ARG:HA	1:C:150:ILE:O	2.13	0.48
1:A:80:PHE:C	1:A:80:PHE:CD2	2.88	0.47
1:B:97:ARG:HH12	1:B:122:ARG:NH1	2.12	0.47
1:A:155:ASN:HB3	1:A:242:LEU:HD11	1.97	0.47
1:B:171:VAL:HG23	1:B:246:LEU:CD1	2.45	0.47
1:C:102:ARG:HH11	1:C:102:ARG:CB	2.27	0.47
1:C:181:PRO:O	1:C:233:HIS:CE1	2.68	0.47
1:C:144:VAL:O	1:C:144:VAL:HG13	2.13	0.47
1:B:138:ASN:HD22	2:B:305:NAG:C7	2.28	0.47
1:A:49:THR:HG22	1:A:119:ARG:CB	2.45	0.47
1:C:233:HIS:HD2	1:C:235:SER:H	1.62	0.47
1:B:159:ALA:HB2	1:B:244:VAL:CG1	2.45	0.47
1:A:142:ARG:NH1	1:A:142:ARG:CG	2.78	0.47
1:B:43:ARG:HB3	1:B:150:ILE:CD1	2.38	0.46
1:B:104:ARG:NH2	1:B:113:ASP:OD2	2.47	0.46
1:B:49:THR:HG22	1:B:119:ARG:HA	1.98	0.46
1:A:102:ARG:HH22	1:A:106:GLU:C	2.19	0.46
1:A:58:PRO:CA	1:A:59:PRO:C	2.83	0.46
1:A:198:THR:HG22	1:A:199:GLN:N	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:VAL:CG2	1:C:111:LEU:HD23	2.46	0.46
1:A:233:HIS:HD2	1:A:235:SER:OG	1.98	0.46
1:B:104:ARG:HD3	1:B:108:ASN:HB2	1.97	0.46
1:A:203:ILE:HD12	1:A:204:GLN:H	1.81	0.46
1:B:52:LEU:N	1:B:52:LEU:HD12	2.31	0.46
1:C:86:VAL:HG11	1:C:88:PHE:CE2	2.52	0.45
1:C:183:ALA:HB1	1:C:231:VAL:CG2	2.46	0.45
1:C:141:ARG:HG2	1:C:141:ARG:HH11	1.82	0.45
1:A:70:GLN:HG3	1:A:76:VAL:HG22	1.98	0.45
1:A:104:ARG:CG	1:A:108:ASN:N	2.75	0.45
1:B:130:THR:HG22	1:B:130:THR:O	2.17	0.45
1:B:36:VAL:HG12	1:B:38:VAL:HG13	1.98	0.45
1:A:81:HIS:CD2	1:A:84:PHE:H	2.31	0.45
1:C:57:LEU:HA	1:C:57:LEU:HD12	1.82	0.45
1:C:95:LYS:HE3	1:C:95:LYS:HB3	1.80	0.45
1:A:73:ASP:OD2	1:B:219:VAL:HG23	2.16	0.45
1:B:160:GLN:HE22	1:B:173:ARG:HB3	1.82	0.45
1:A:77:VAL:CG1	1:A:78:ALA:N	2.80	0.45
1:B:222:ALA:O	1:B:225:VAL:HG23	2.17	0.45
1:A:169:VAL:HG22	1:A:170:ALA:N	2.32	0.45
1:B:156:HIS:CD2	1:B:157:ALA:H	2.35	0.44
1:B:43:ARG:HH22	1:B:234:GLU:CG	2.31	0.44
1:B:56:LEU:HB3	1:B:112:ARG:HB3	2.00	0.44
1:A:251:HIS:H	1:A:251:HIS:CD2	2.35	0.44
1:A:175:VAL:HG12	1:A:177:THR:CG2	2.47	0.44
1:C:220:GLY:HA2	1:C:248:VAL:HG21	2.00	0.44
1:A:200:GLU:O	1:A:208:VAL:HG22	2.18	0.44
1:C:191:LEU:HD23	1:C:221:ARG:NH2	2.33	0.44
1:C:62:GLU:OE2	1:C:62:GLU:N	2.50	0.44
1:B:144:VAL:HG13	1:B:144:VAL:O	2.18	0.44
1:A:61:THR:N	1:A:62:GLU:OE2	2.44	0.44
1:C:67:VAL:HG23	1:C:111:LEU:HD23	2.00	0.43
1:C:67:VAL:HG11	1:C:114:ALA:CB	2.47	0.43
1:C:80:PHE:CD2	1:C:80:PHE:C	2.90	0.43
1:A:32:GLN:NE2	1:A:143:GLY:HA2	2.32	0.43
1:A:73:ASP:OD2	1:A:73:ASP:N	2.49	0.43
1:B:136:PHE:HB2	1:C:66:GLN:OE1	2.18	0.43
1:A:104:ARG:HH11	1:A:108:ASN:HA	1.82	0.43
1:A:39:LEU:O	1:A:145:THR:HG23	2.18	0.43
1:B:229:CYS:HB3	1:B:242:LEU:HB2	2.00	0.43
1:C:33:ASP:HB3	1:C:35:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:PRO:O	1:B:106:GLU:HB2	2.19	0.43
1:C:60:THR:HG22	1:C:112:ARG:HD2	2.01	0.43
1:C:88:PHE:CZ	1:C:99:SER:HA	2.54	0.43
1:C:58:PRO:HB2	1:C:59:PRO:HA	2.01	0.43
1:B:81:HIS:CD2	1:B:84:PHE:H	2.35	0.43
1:B:68:THR:HG22	1:B:79:ALA:CB	2.48	0.43
1:C:197:ASP:O	1:C:198:THR:HG23	2.18	0.43
1:C:52:LEU:O	1:C:115:THR:HG23	2.18	0.43
1:C:101:VAL:CG1	1:C:102:ARG:CZ	2.89	0.43
1:C:81:HIS:HA	1:C:82:PRO:HD3	1.93	0.43
1:B:86:VAL:HG11	1:B:88:PHE:CE2	2.54	0.43
1:B:128:ASN:ND2	2:B:301:NAG:C7	2.82	0.42
1:C:53:PRO:HA	1:C:115:THR:HG23	2.00	0.42
1:A:104:ARG:CZ	1:A:108:ASN:HA	2.48	0.42
1:C:67:VAL:HG11	1:C:114:ALA:HB1	2.02	0.42
1:A:217:VAL:O	1:A:217:VAL:HG23	2.20	0.42
1:C:80:PHE:HD2	1:C:111:LEU:HD22	1.76	0.42
1:A:81:HIS:HA	1:A:82:PRO:HD3	1.82	0.41
1:A:46:LEU:C	1:A:46:LEU:HD23	2.41	0.41
1:B:62:GLU:H	1:B:62:GLU:CD	2.21	0.41
1:A:204:GLN:O	1:A:205:ALA:C	2.59	0.41
1:A:50:VAL:HG22	1:A:121:LEU:HD11	2.03	0.41
1:A:121:LEU:HA	1:A:121:LEU:HD23	1.86	0.41
1:A:232:GLU:HG2	1:A:239:PRO:HG3	2.03	0.40
1:C:60:THR:HG22	1:C:112:ARG:NH1	2.36	0.40
1:B:155:ASN:HD22	1:B:176:SER:HA	1.85	0.40
1:C:43:ARG:HB3	1:C:150:ILE:HD12	2.04	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	Percentiles	
1	A	218/225 (97%)	204 (94%)	14 (6%)	0	100	100
1	B	218/225 (97%)	208 (95%)	10 (5%)	0	100	100
1	C	217/225 (96%)	204 (94%)	12 (6%)	1 (0%)	34	74
All	All	653/675 (97%)	616 (94%)	36 (6%)	1 (0%)	52	86

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	95	LYS

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	186/191 (97%)	161 (87%)	25 (13%)	5	21
1	B	186/191 (97%)	154 (83%)	32 (17%)	2	12
1	C	185/191 (97%)	166 (90%)	19 (10%)	9	34
All	All	557/573 (97%)	481 (86%)	76 (14%)	5	21

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	VAL
1	A	35	ARG
1	A	43	ARG
1	A	50	VAL
1	A	61	THR
1	A	62	GLU
1	A	63	ARG
1	A	68	THR
1	A	73	ASP
1	A	77	VAL
1	A	83	SER
1	A	94	SER

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Mol	Chain	Res	Type
1	A	96	ASP
1	A	108	ASN
1	A	111	LEU
1	A	130	THR
1	A	142	ARG
1	A	184	ARG
1	A	186	THR
1	A	203	ILE
1	A	208	VAL
1	A	231	VAL
1	A	234	GLU
1	A	246	LEU
1	A	251	HIS
1	B	32	GLN
1	B	35	ARG
1	B	37	ARG
1	B	42	VAL
1	B	43	ARG
1	B	50	VAL
1	B	61	THR
1	B	62	GLU
1	B	77	VAL
1	B	91	SER
1	B	95	LYS
1	B	104	ARG
1	B	111	LEU
1	B	130	THR
1	B	142	ARG
1	B	160	GLN
1	B	169	VAL
1	B	173	ARG
1	B	186	THR
1	B	191	LEU
1	B	194	GLU
1	B	200	GLU
1	B	203	ILE
1	B	210	ILE
1	B	213	ARG
1	B	217	VAL
1	B	219	VAL
1	B	231	VAL
1	B	234	GLU

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Mol	Chain	Res	Type
1	B	246	LEU
1	B	249	ARG
1	B	251	HIS
1	C	35	ARG
1	C	37	ARG
1	C	42	VAL
1	C	43	ARG
1	C	45	ARG
1	C	61	THR
1	C	63	ARG
1	C	83	SER
1	C	95	LYS
1	C	96	ASP
1	C	102	ARG
1	C	119	ARG
1	C	121	LEU
1	C	130	THR
1	C	191	LEU
1	C	208	VAL
1	C	234	GLU
1	C	246	LEU
1	C	250	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	55	HIS
1	A	81	HIS
1	A	108	ASN
1	A	152	GLN
1	A	155	ASN
1	A	233	HIS
1	A	251	HIS
1	B	81	HIS
1	B	108	ASN
1	B	155	ASN
1	B	156	HIS
1	B	160	GLN
1	B	233	HIS
1	C	55	HIS
1	C	81	HIS

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Mol	Chain	Res	Type
1	C	155	ASN
1	C	233	HIS

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 carbohydrates are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	NAG	A	301	1,2	14,14,15	0.79	0	15,19,21	1.65	3 (20%)
2	NAG	A	302	2	14,14,15	0.61	0	15,19,21	0.89	1 (6%)
2	BMA	A	303	2	11,11,12	0.59	0	14,15,17	1.37	1 (7%)
2	FUC	A	304	2	10,10,11	1.27	2 (20%)	14,14,16	1.90	3 (21%)
2	NAG	A	305	1,2	14,14,15	0.81	1 (7%)	15,19,21	1.28	2 (13%)
2	NAG	A	306	2	14,14,15	0.54	0	15,19,21	1.24	2 (13%)
2	BMA	A	307	2	11,11,12	0.65	0	14,15,17	0.72	0
2	FUC	A	308	2	10,10,11	0.69	0	14,14,16	1.69	3 (21%)
2	NAG	B	301	1,2	14,14,15	0.85	1 (7%)	15,19,21	0.98	1 (6%)
2	NAG	B	302	2	14,14,15	0.52	0	15,19,21	0.62	0
2	BMA	B	303	2	11,11,12	0.43	0	14,15,17	0.67	0
2	FUC	B	304	2	10,10,11	0.86	0	14,14,16	1.53	5 (35%)
2	NAG	B	305	1,2	14,14,15	0.86	1 (7%)	15,19,21	1.00	0
2	NAG	B	306	2	14,14,15	0.65	0	15,19,21	0.93	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$\|Z\|>2$	Counts	RMSZ	#$\|Z\|>2$
2	BMA	B	307	2	11,11,12	0.60	0	14,15,17	1.34	2 (14%)
2	FUC	B	308	2	10,10,11	0.71	0	14,14,16	1.08	2 (14%)
2	NAG	C	301	1,2	14,14,15	0.62	0	15,19,21	1.12	2 (13%)
2	NAG	C	302	2	14,14,15	0.60	0	15,19,21	1.07	1 (6%)
2	BMA	C	303	2	11,11,12	0.76	1 (9%)	14,15,17	1.53	3 (21%)
2	FUC	C	304	2	10,10,11	0.75	0	14,14,16	1.92	3 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	301	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	302	2	-	0/6/23/26	0/1/1/1
2	BMA	A	303	2	-	0/2/19/22	0/1/1/1
2	FUC	A	304	2	-	0/0/17/20	0/1/1/1
2	NAG	A	305	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	306	2	-	0/6/23/26	0/1/1/1
2	BMA	A	307	2	-	0/2/19/22	0/1/1/1
2	FUC	A	308	2	-	0/0/17/20	0/1/1/1
2	NAG	B	301	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	302	2	-	0/6/23/26	0/1/1/1
2	BMA	B	303	2	-	0/2/19/22	0/1/1/1
2	FUC	B	304	2	-	0/0/17/20	0/1/1/1
2	NAG	B	305	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	306	2	-	0/6/23/26	0/1/1/1
2	BMA	B	307	2	-	0/2/19/22	0/1/1/1
2	FUC	B	308	2	-	0/0/17/20	0/1/1/1
2	NAG	C	301	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	302	2	-	0/6/23/26	0/1/1/1
2	BMA	C	303	2	-	0/2/19/22	0/1/1/1
2	FUC	C	304	2	-	0/0/17/20	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	305	NAG	O5-C1	-2.45	1.39	1.43
2	A	305	NAG	O5-C1	-2.36	1.39	1.43
2	B	301	NAG	O5-C1	-2.18	1.40	1.43
2	C	303	BMA	C2-C3	2.04	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	304	FUC	C1-C2	2.21	1.57	1.52
2	A	304	FUC	C2-C3	3.03	1.56	1.52

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	NAG	C3-C2-N2	-3.96	101.08	110.56
2	A	308	FUC	O5-C1-C2	-3.61	104.99	110.86
2	A	305	NAG	C1-O5-C5	-3.57	107.72	112.25
2	B	304	FUC	O5-C1-C2	-2.94	106.08	110.86
2	A	304	FUC	O5-C1-C2	-2.79	106.34	110.86
2	A	305	NAG	O6-C6-C5	-2.45	103.23	111.33
2	B	301	NAG	O7-C7-C8	-2.43	117.61	122.06
2	C	302	NAG	C4-C3-C2	-2.39	107.51	111.23
2	B	307	BMA	C1-C2-C3	-2.37	106.74	109.54
2	A	306	NAG	O7-C7-C8	-2.31	117.83	122.06
2	C	304	FUC	O5-C5-C4	-2.14	105.81	109.53
2	B	308	FUC	C1-O5-C5	-2.14	109.07	112.38
2	B	304	FUC	O5-C5-C4	-2.06	105.96	109.53
2	C	301	NAG	C4-C3-C2	2.09	114.47	111.23
2	A	301	NAG	O7-C7-N2	2.09	126.12	121.86
2	B	304	FUC	C1-O5-C5	2.16	115.71	112.38
2	C	303	BMA	O5-C1-C2	2.20	114.43	110.86
2	B	304	FUC	O5-C5-C6	2.21	109.78	106.13
2	A	304	FUC	C2-C3-C4	2.21	114.80	111.04
2	B	306	NAG	C4-C3-C2	2.38	114.93	111.23
2	C	301	NAG	O5-C5-C6	2.40	112.55	107.35
2	C	304	FUC	O5-C5-C6	2.44	110.17	106.13
2	A	308	FUC	C1-O5-C5	2.55	116.31	112.38
2	A	302	NAG	C4-C3-C2	2.62	115.31	111.23
2	B	304	FUC	C1-C2-C3	2.69	112.72	109.54
2	B	308	FUC	O5-C5-C6	2.71	110.61	106.13
2	A	306	NAG	C1-O5-C5	2.75	115.74	112.25
2	A	301	NAG	O6-C6-C5	2.84	120.72	111.33
2	B	307	BMA	C3-C4-C5	2.85	115.16	110.20
2	C	303	BMA	C1-O5-C5	3.33	116.47	112.25
2	C	303	BMA	C1-C2-C3	3.36	113.51	109.54
2	A	303	BMA	C1-C2-C3	3.43	113.59	109.54
2	A	308	FUC	O5-C5-C6	3.50	111.92	106.13
2	A	304	FUC	C1-C2-C3	5.14	115.62	109.54
2	C	304	FUC	C1-C2-C3	5.75	116.35	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NAG	6	0
2	A	302	NAG	1	0
2	A	304	FUC	1	0
2	B	301	NAG	3	0
2	B	302	NAG	12	0
2	B	304	FUC	13	0
2	B	305	NAG	1	0

5.6 Ligand geometry (i)

1 ligand is 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	C	305	1	14,14,15	1.37	1 (7%)	15,19,21	3.00	5 (33%)

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	C	305	1	-	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	C	305	NAG	C1-C2	3.81	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	305	NAG	C4-C3-C2	-2.81	106.86	111.23
3	C	305	NAG	O7-C7-C8	-2.27	117.91	122.06
3	C	305	NAG	O3-C3-C2	2.45	113.97	109.11
3	C	305	NAG	O5-C5-C6	2.93	113.70	107.35
3	C	305	NAG	C1-O5-C5	9.75	124.62	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	305	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 (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, 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	220/225 (97%)	0.42	24 (10%)	7	7	44, 96, 303, 370	0
1	B	220/225 (97%)	-0.18	3 (1%)	78	79	65, 90, 146, 246	0
1	C	219/225 (97%)	0.75	42 (19%)	2	2	75, 145, 325, 384	0
All	All	659/675 (97%)	0.33	69 (10%)	8	8	44, 102, 301, 384	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	159	ALA	8.9
1	A	216	LEU	8.9
1	C	162	VAL	8.6
1	C	222	ALA	8.4
1	C	165	GLY	7.7
1	A	247	SER	7.5
1	C	221	ARG	7.5
1	C	189	SER	7.3
1	A	166	PRO	6.4
1	C	250	TYR	6.4
1	C	225	VAL	6.1
1	A	250	TYR	5.6
1	C	245	THR	5.4
1	A	220	GLY	5.1
1	A	167	GLN	4.7
1	A	217	VAL	4.5
1	C	164	ILE	4.5
1	C	219	VAL	4.0
1	B	105	PRO	4.0
1	C	168	SER	3.9
1	C	216	LEU	3.9
1	C	247	SER	3.8
1	C	240	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	231	VAL	3.7
1	C	169	VAL	3.7
1	C	224	GLY	3.6
1	A	219	VAL	3.6
1	C	220	GLY	3.5
1	C	217	VAL	3.5
1	A	32	GLN	3.4
1	A	221	ARG	3.3
1	A	105	PRO	3.2
1	C	167	GLN	3.2
1	A	214	TYR	3.1
1	C	218	PRO	3.0
1	C	185	ILE	3.0
1	C	229	CYS	2.9
1	A	189	SER	2.9
1	A	190	SER	2.9
1	C	214	TYR	2.9
1	A	162	VAL	2.8
1	A	218	PRO	2.8
1	C	241	LEU	2.7
1	C	246	LEU	2.7
1	A	163	THR	2.7
1	C	223	ASP	2.7
1	C	166	PRO	2.5
1	A	109	ALA	2.5
1	C	161	GLU	2.5
1	C	244	VAL	2.5
1	A	168	SER	2.4
1	A	248	VAL	2.4
1	C	140	THR	2.4
1	B	32	GLN	2.4
1	A	225	VAL	2.4
1	C	227	VAL	2.3
1	C	194	GLU	2.3
1	C	176	SER	2.3
1	C	213	ARG	2.2
1	B	141	ARG	2.2
1	C	106	GLU	2.1
1	C	160	GLN	2.1
1	C	183	ALA	2.1
1	C	249	ARG	2.1
1	C	171	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	231	VAL	2.1
1	A	251	HIS	2.0
1	C	199	GLN	2.0
1	A	140	THR	2.0

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

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

6.3 Carbohydrates (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	NAG	A	301	14/15	0.88	0.13	-2.20	70,104,145,151	0
2	BMA	B	307	11/12	0.35	0.27	-	159,200,215,218	0
2	NAG	A	306	14/15	0.82	0.35	-	129,138,158,183	0
2	NAG	C	302	14/15	0.88	0.28	-	120,158,179,182	0
2	FUC	C	304	10/11	0.91	0.20	-	155,164,171,185	0
2	FUC	A	304	10/11	0.78	0.31	-	141,169,181,181	0
2	BMA	B	303	11/12	0.62	0.17	-	141,198,207,212	0
2	NAG	B	305	14/15	0.87	0.51	-	107,156,191,192	0
2	FUC	B	308	10/11	0.80	0.43	-	159,170,186,189	0
2	FUC	A	308	10/11	0.82	0.30	-	136,143,154,163	0
2	BMA	A	303	11/12	0.51	0.18	-	165,194,205,209	0
2	NAG	A	302	14/15	0.91	0.20	-	114,149,173,185	0
2	BMA	C	303	11/12	0.86	0.30	-	162,184,193,200	0
2	BMA	A	307	11/12	0.64	0.34	-	163,182,188,191	0
2	NAG	B	302	14/15	0.90	0.23	-	113,158,178,193	0
2	NAG	C	301	14/15	0.95	0.15	-	85,108,126,143	0
2	NAG	B	306	14/15	0.84	0.62	-	193,211,228,249	0
2	NAG	B	301	14/15	0.89	0.16	-	90,115,144,149	0
2	FUC	B	304	10/11	0.91	0.33	-	148,156,165,165	0
2	NAG	A	305	14/15	0.84	0.24	-	76,104,136,137	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	NAG	C	305	14/15	0.48	0.39	3.59	116,135,154,159	0

6.5 Other polymers (i)

There are no such residues in this entry.