



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2017 – 04:45 AM EDT

PDB ID : 5V4N
Title : Structure of HLA-DR1 with bound alpha3(135-145) peptide
Authors : Petersen, J.; Rossjohn, J.
Deposited on : 2017-03-10
Resolution : 3.40 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

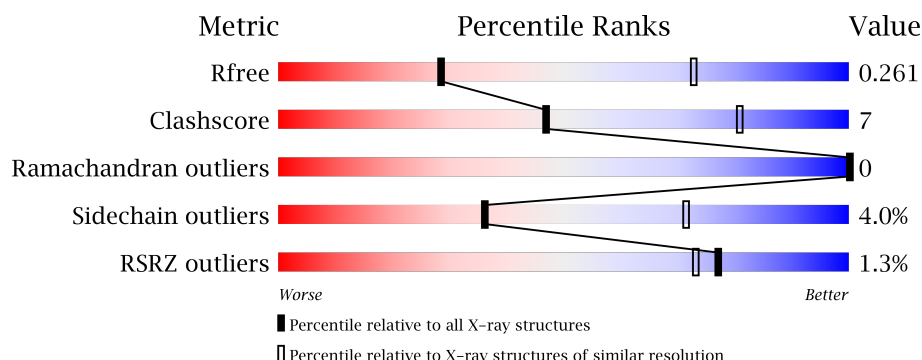
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	100719	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)

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 $\leq 5\%$. 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	189	<div> <div>3%</div> <div>75%</div> <div>20%</div> <div>5%</div> </div>
1	D	189	<div> <div>%</div> <div>78%</div> <div>15%</div> <div>5%</div> </div>
2	C	216	<div> <div>2%</div> <div>73%</div> <div>19%</div> <div>7%</div> </div>
2	F	216	<div> <div>70%</div> <div>20%</div> <div>9%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6193 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 HLA-DRA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1459	946	235	273	5			
1	D	179	Total	C	N	O	S	0	0	0
			1459	946	235	273	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	THR	-	expression tag	UNP P01903
A	183	SER	-	expression tag	UNP P01903
A	184	GLY	-	expression tag	UNP P01903
A	185	ASP	-	expression tag	UNP P01903
A	186	ASP	-	expression tag	UNP P01903
A	187	ASP	-	expression tag	UNP P01903
A	188	ASP	-	expression tag	UNP P01903
A	189	LYS	-	expression tag	UNP P01903
D	182	THR	-	expression tag	UNP P01903
D	183	SER	-	expression tag	UNP P01903
D	184	GLY	-	expression tag	UNP P01903
D	185	ASP	-	expression tag	UNP P01903
D	186	ASP	-	expression tag	UNP P01903
D	187	ASP	-	expression tag	UNP P01903
D	188	ASP	-	expression tag	UNP P01903
D	189	LYS	-	expression tag	UNP P01903

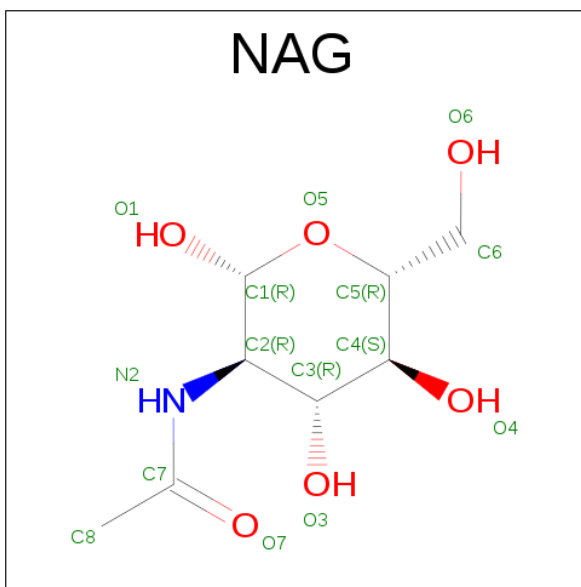
- Molecule 2 is a protein called alpha3(135-145)-HLA-DRB1*01:01.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	200	Total	C	N	O	S	0	0	0
			1627	1034	287	300	6			
2	F	197	Total	C	N	O	S	0	0	0
			1606	1020	283	297	6			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	11	GLY	-	linker	PDB ?
C	12	SER	-	linker	PDB ?
C	237	GLY	-	linker	PDB ?
C	238	GLY	-	linker	PDB ?
C	239	SER	-	linker	PDB ?
C	240	ILE	-	linker	PDB ?
C	241	GLU	-	linker	PDB ?
C	242	GLY	-	linker	PDB ?
C	243	ARG	-	linker	PDB ?
C	244	GLY	-	linker	PDB ?
C	245	GLY	-	linker	PDB ?
C	246	SER	-	linker	PDB ?
C	247	GLY	-	linker	PDB ?
C	248	ALA	-	linker	PDB ?
C	249	SER	ALA	linker	UNP P04229
F	11	GLY	-	linker	PDB ?
F	12	SER	-	linker	PDB ?
F	237	GLY	-	linker	PDB ?
F	238	GLY	-	linker	PDB ?
F	239	SER	-	linker	PDB ?
F	240	ILE	-	linker	PDB ?
F	241	GLU	-	linker	PDB ?
F	242	GLY	-	linker	PDB ?
F	243	ARG	-	linker	PDB ?
F	244	GLY	-	linker	PDB ?
F	245	GLY	-	linker	PDB ?
F	246	SER	-	linker	PDB ?
F	247	GLY	-	linker	PDB ?
F	248	ALA	-	linker	PDB ?
F	249	SER	ALA	linker	UNP P04229

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		

T355	GLN	PRO	LEU	D359	H360	H361	H362	I363	I364	V365	C366	F371	Y378	R379	K380	F381	R382	E386	D401	K402	T403	Y408	T412	K413	P414	R415	E418	T421	Y429	L433	K439
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.09 Å 118.41 Å 120.88 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.83 – 3.40 53.83 – 3.41	Depositor EDS
% Data completeness (in resolution range)	99.3 (53.83-3.40) 99.3 (53.83-3.41)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.40 Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.212 , 0.263 0.210 , 0.261	Depositor DCC
R_{free} test set	836 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	63.4	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 30.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.038 for -h,l,k	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6193	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 4.59% 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	0.29	0/1504	0.47	0/2054
1	D	0.30	1/1504 (0.1%)	0.46	0/2054
2	C	0.25	0/1672	0.45	0/2272
2	F	0.25	0/1649	0.47	0/2239
All	All	0.27	1/6329 (0.0%)	0.46	0/8619

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	114	PRO	C-N	6.13	1.46	1.34

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	1459	0	1380	22	0
1	D	1459	0	1380	23	0
2	C	1627	0	1539	27	0
2	F	1606	0	1515	26	0
3	A	14	0	13	2	0
3	D	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	14	0	13	0	0
All	All	6193	0	5853	86	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 7.

All (86) 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:73:MET:SD	1:A:76:ARG:NH1	2.50	0.85
2:F:346:PRO:HB3	2:F:371:PHE:HB3	1.66	0.76
1:A:123:ARG:NE	1:A:124:ASN:OD1	2.23	0.71
1:A:22:PHE:HB2	1:A:63:ILE:HD11	1.75	0.69
1:A:28:GLY:O	1:A:146:ARG:NH2	2.26	0.68
2:C:290:ASP:HB3	2:C:293:VAL:HG12	1.75	0.67
2:F:382:ARG:NH1	2:F:418:GLU:OE2	2.26	0.67
2:C:346:PRO:HB3	2:C:371:PHE:HB3	1.77	0.67
2:F:429:VAL:HG11	2:F:433:LEU:HD11	1.77	0.67
2:C:429:VAL:HG11	2:C:433:LEU:HD11	1.77	0.67
1:A:16:PRO:HD2	2:C:255:ARG:HD3	1.76	0.66
2:F:290:ASP:HB3	2:F:293:VAL:HG12	1.78	0.65
1:D:70:LEU:O	1:D:74:THR:OG1	2.16	0.63
2:C:253:ARG:O	2:C:255:ARG:NH1	2.32	0.62
1:A:70:LEU:O	1:A:74:THR:OG1	2.16	0.60
2:F:319:GLN:HE22	2:F:320:ARG:HH21	1.48	0.60
2:C:274:ARG:NH2	2:C:290:ASP:OD2	2.34	0.60
1:D:76:ARG:NH2	2:F:10:PHE:O	2.36	0.59
2:F:274:ARG:NH2	2:F:290:ASP:OD2	2.36	0.59
1:A:166:GLU:HB3	3:A:1000:NAG:H61	1.84	0.58
1:D:92:LEU:HD12	1:D:106:ILE:HB	1.86	0.57
2:C:425:GLU:HG2	2:C:432:PRO:HB3	1.88	0.56
1:D:123:ARG:NH1	1:D:161:TYR:OH	2.39	0.55
1:D:110:ASP:OD1	1:D:111:LYS:N	2.39	0.55
1:D:22:PHE:HB2	1:D:63:ILE:HD11	1.89	0.54
1:A:110:ASP:OD1	1:A:111:LYS:N	2.41	0.53
2:F:335:GLY:O	2:F:339:THR:OG1	2.20	0.52
3:A:1000:NAG:H3	3:A:1000:NAG:H83	1.92	0.52
1:A:132:VAL:HG12	1:A:151:LEU:HD13	1.92	0.51
2:F:295:GLU:OE1	2:F:297:ARG:NH2	2.41	0.51
2:C:401:ASP:OD1	2:C:403:THR:OG1	2.27	0.51
2:C:317:LEU:O	2:C:321:ARG:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:ILE:HG22	1:D:32:PHE:HD2	1.76	0.51
2:F:319:GLN:HE22	2:F:320:ARG:NH2	2.10	0.50
1:D:140:ARG:O	2:F:261:LYS:NZ	2.45	0.50
1:D:5:HIS:NE2	2:F:340:VAL:HG13	2.27	0.49
2:C:6:LYS:HD3	2:C:7:GLY:N	2.28	0.49
1:A:31:ILE:HG22	1:A:32:PHE:HD2	1.77	0.49
1:D:151:LEU:HD23	1:D:153:PHE:HB3	1.94	0.48
2:F:381:PHE:HD2	2:F:386:GLU:HA	1.78	0.48
2:C:259:GLN:HG3	2:C:280:ILE:HB	1.96	0.47
2:F:277:GLU:HB3	2:F:289:PHE:HB3	1.97	0.47
1:D:160:VAL:HB	1:D:177:HIS:HE1	1.78	0.47
1:D:9:GLN:HB3	2:F:262:PHE:HB2	1.97	0.47
1:A:89:VAL:HG23	1:A:174:LEU:HD23	1.97	0.46
2:C:335:GLY:O	2:C:339:THR:OG1	2.25	0.46
1:D:26:PHE:HB2	1:D:31:ILE:HD11	1.97	0.46
1:D:151:LEU:CD2	1:D:153:PHE:HB3	2.46	0.46
2:F:378:VAL:HB	2:F:408:VAL:HG21	1.96	0.46
1:A:142:ASP:OD2	1:A:144:LEU:HD12	2.16	0.45
1:A:12:PHE:CE2	1:A:21:GLU:HB3	2.52	0.45
2:C:419:VAL:HG22	2:C:438:ARG:HG2	1.99	0.45
1:D:160:VAL:HB	1:D:177:HIS:CE1	2.51	0.45
1:D:38:LYS:HB2	1:D:40:GLU:HG2	1.98	0.45
2:C:381:PHE:HB2	2:C:421:THR:HB	1.99	0.45
2:C:356:GLN:O	2:C:358:LEU:N	2.47	0.44
1:D:12:PHE:CB	2:F:259:GLN:HB3	2.47	0.44
1:D:76:ARG:HH12	2:F:306:ASP:CG	2.20	0.44
2:C:293:VAL:HG13	2:C:295:GLU:H	1.82	0.44
1:D:12:PHE:CE2	1:D:21:GLU:HB3	2.52	0.44
1:D:142:ASP:OD1	1:D:142:ASP:N	2.50	0.44
2:F:335:GLY:HA2	2:F:338:PHE:CE1	2.53	0.44
2:F:401:ASP:OD1	2:F:403:THR:OG1	2.30	0.43
1:A:143:HIS:CD2	2:C:280:ILE:HD13	2.53	0.43
1:A:160:VAL:HB	1:A:177:HIS:CE1	2.52	0.43
1:A:73:MET:HG3	2:C:258:TRP:CZ3	2.53	0.43
1:D:17:ASP:OD1	2:F:255:ARG:NE	2.51	0.43
2:C:366:CYS:HB2	2:C:380:TRP:CZ2	2.54	0.43
1:A:142:ASP:N	1:A:142:ASP:OD1	2.52	0.43
2:C:387:GLU:HG2	2:C:410:LEU:HD11	2.01	0.42
2:F:317:LEU:O	2:F:321:ARG:HG3	2.19	0.42
2:C:314:LYS:HD3	2:C:314:LYS:HA	1.85	0.42
1:A:143:HIS:CG	2:C:280:ILE:HD13	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:366:CYS:HB2	2:F:380:TRP:CZ2	2.54	0.42
2:C:258:TRP:CH2	2:C:279:CYS:HB3	2.55	0.41
1:A:9:GLN:HB3	2:C:262:PHE:HB2	2.01	0.41
1:A:12:PHE:CB	2:C:259:GLN:HB3	2.51	0.41
2:F:277:GLU:OE1	2:F:320:ARG:NE	2.54	0.41
1:A:172:GLU:OE1	1:A:172:GLU:N	2.53	0.41
2:F:259:GLN:HG3	2:F:280:ILE:HB	2.03	0.41
1:D:142:ASP:OD2	1:D:144:LEU:HD12	2.20	0.40
2:F:412:THR:O	2:F:414:PRO:HD3	2.22	0.40
1:A:123:ARG:HA	1:A:161:TYR:HA	2.02	0.40
2:C:279:CYS:HB2	2:C:287:VAL:HG12	2.03	0.40
2:C:374:GLY:O	2:C:396:LEU:HD21	2.22	0.40
1:D:105:LEU:HA	1:D:105:LEU:HD23	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	177/189 (94%)	171 (97%)	6 (3%)	0	100	100
1	D	177/189 (94%)	172 (97%)	5 (3%)	0	100	100
2	C	196/216 (91%)	189 (96%)	7 (4%)	0	100	100
2	F	191/216 (88%)	184 (96%)	7 (4%)	0	100	100
All	All	741/810 (92%)	716 (97%)	25 (3%)	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	161/173 (93%)	152 (94%)	9 (6%)	25	62
1	D	161/173 (93%)	156 (97%)	5 (3%)	45	77
2	C	175/187 (94%)	170 (97%)	5 (3%)	48	78
2	F	173/187 (92%)	165 (95%)	8 (5%)	31	68
All	All	670/720 (93%)	643 (96%)	27 (4%)	36	71

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

Mol	Chain	Res	Type
1	A	11	GLU
1	A	41	THR
1	A	47	GLU
1	A	74	THR
1	A	138	LEU
1	A	153	PHE
1	A	162	ASP
1	A	164	ARG
1	A	180	PHE
2	C	260	LEU
2	C	354	LYS
2	C	360	HIS
2	C	364	LEU
2	C	396	LEU
1	D	57	GLN
1	D	74	THR
1	D	92	LEU
1	D	153	PHE
1	D	164	ARG
2	F	260	LEU
2	F	319	GLN
2	F	360	HIS
2	F	362	ASN
2	F	363	LEU

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Mol	Chain	Res	Type
2	F	364	LEU
2	F	415	ARG
2	F	421	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	330	HIS
2	F	319	GLN
2	F	405	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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	A	1000	1	14,14,15	0.37	0	15,19,21	1.43	2 (13%)
3	NAG	D	1000	1	14,14,15	0.37	0	15,19,21	0.59	0
3	NAG	F	1000	2	14,14,15	0.18	0	15,19,21	0.52	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	A	1000	1	-	0/6/23/26	0/1/1/1
3	NAG	D	1000	1	-	0/6/23/26	0/1/1/1
3	NAG	F	1000	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1000	NAG	C1-C2-N2	2.59	114.91	110.49
3	A	1000	NAG	C2-N2-C7	4.22	129.10	122.94

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	A	1000	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	179/189 (94%)	0.16	5 (2%) 53 50	40, 75, 120, 147	0
1	D	179/189 (94%)	-0.00	1 (0%) 89 86	33, 59, 95, 108	0
2	C	200/216 (92%)	-0.14	4 (2%) 65 61	33, 57, 107, 157	0
2	F	197/216 (91%)	-0.14	0 100 100	34, 58, 114, 159	0
All	All	755/810 (93%)	-0.04	10 (1%) 77 73	33, 60, 115, 159	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	128	VAL	2.9
2	C	417	GLY	2.5
1	D	182	THR	2.4
1	A	161	TYR	2.3
1	A	129	THR	2.3
2	C	415	ARG	2.2
1	A	165	VAL	2.2
2	C	357	PRO	2.1
2	C	355	THR	2.1
1	A	120	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](#)

There are no carbohydrates in this entry.

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(\AA^2)	Q<0.9
3	NAG	D	1000	14/15	0.84	0.25	1.01	88,95,101,101	0
3	NAG	A	1000	14/15	0.76	0.35	-	128,147,162,165	0
3	NAG	F	1000	14/15	0.88	0.15	-	84,106,117,122	0

6.5 Other polymers [i](#)

There are no such residues in this entry.