



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:56 PM GMT

PDB ID : 1Z68
Title : Crystal Structure Of Human Fibroblast Activation Protein alpha
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Deposited on : 2005-03-21
Resolution : 2.60 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

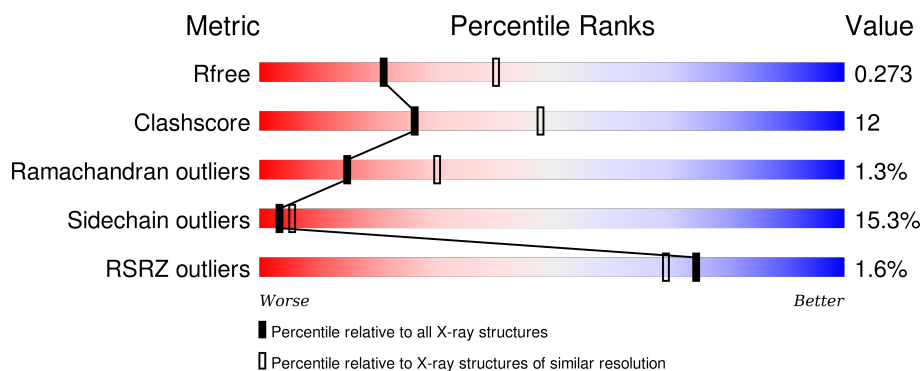
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	719	<div> <div>3%</div> <div>66%</div> <div>27%</div> <div>7%</div> </div>
1	B	719	<div> <div>63%</div> <div>30%</div> <div>6%</div> </div>

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	A	9201	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12600 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 fibroblast activation protein, alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	719	Total	C	N	O	S	0	0	0
			5889	3812	961	1094	22			
1	B	719	Total	C	N	O	S	0	6	0
			5915	3825	965	1103	22			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

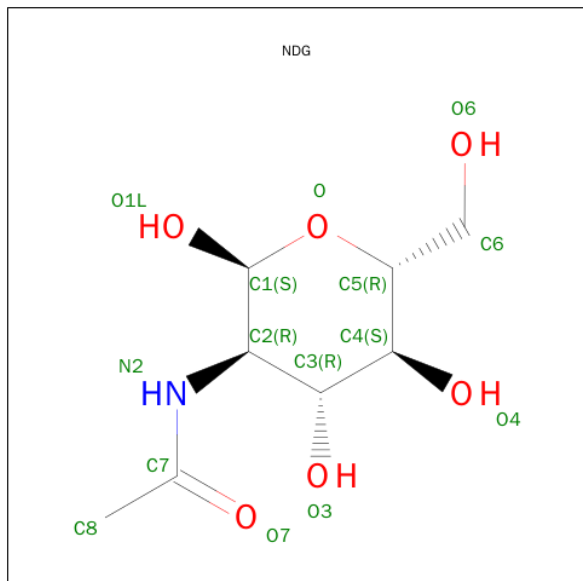
- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	B	2	Total	C	N	O	0	0
			28	16	2	10		

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is SUGAR (2-(ACETYLAMINO)-2-DEOXY-A-D-GLUCOPYRANOSE) (three-letter code: NDG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

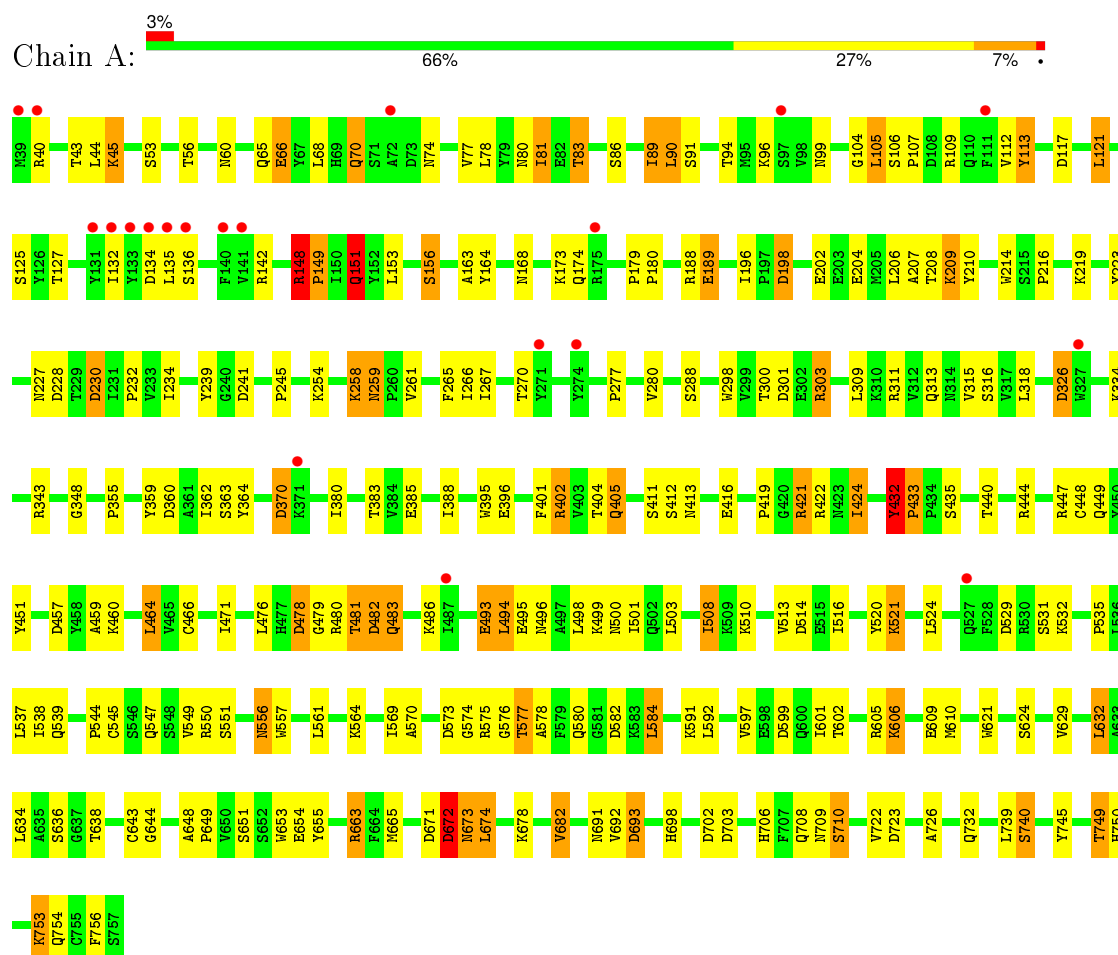
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	208	Total 208	O 208	0	0
6	B	420	Total 420	O 420	0	0

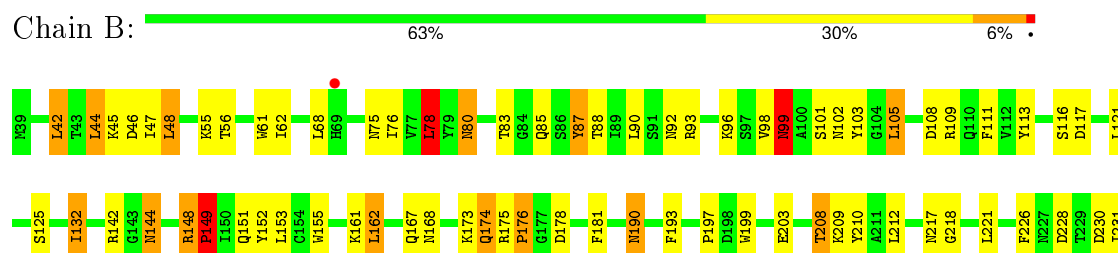
3 Residue-property plots

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: fibroblast activation protein, alpha subunit



- Molecule 1: fibroblast activation protein, alpha subunit



Y729	Y625	L524	T440	H338	A235
S730	Y628	P525	L443	F350	D241
Q732	V629	F528	L443	S353	Q243
N733	L632	S529	R447	V356	Y244
H734		R530	C446	Y356	P245
	S636	S531	Q449	Y359	R246
G738	G637	K532	T450	D360	T247
L739	T638	K533	Y451	A361	I248
S740	G639	K534	F455	I362	
	L640	P535	S456	S363	K254
H743	F641	C545		Y364	K258
T746	K642	S546	Y462	D370	V262
H747	C643	Q547	A463	K371	
M748	G644	L464	V465	D372	I266
	I645	R550	V465		T267
F751		S551	C466	K375	D268
L752	A648	V552		H376	T269
K753	P649	N556	I471	I380	T270
Q754	V650		S474	K381	Y271
G755	S651	S559	H477	D382	P272
F756	S652	Y560	D478	T383	
S757	K653	V568	G479	V384	P277
	E654		R480		
	V655	D573	T481	T391	V280
	V656	G574	D482	W395	P281
	V659	R575	Q483	E396	V282
	T660	G576	E484		
	T661	T577	T485	F401	D290
	L667	A578	K486	R402	Y291
		F579		V403	Y292
	K670	Q580	E490	D406	D301
D671	D672	K583	N491		E302
		L584	K492		R303
	T681	L585	L494	S411	L306
	R685	R590	E495	S412	
A686		K591	Y496	N413	R311
		L592	A497	E414	
	F689	D599	L498	R421	L318
			K499	R422	D322
	D693	G600	L503	N423	F323
	I704	I601		T424	R324
V705			B506	Y425	E325
H706		R605		K509	E326
F707		F612	K510	R426	D326
Q708				I427	
N709		K616	D514		W330
	I713	R617		S431	D331
			T517	Y432	C332
	V722	I620	L518	P433	P333
D723		W621		A434	K334
	T722	G622	K521	S435	T335
		H623	V522		Q336
	L728	S624	I523	C438	E337
				V439	

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.30Å 152.58Å 214.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 49.49 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.7 (50.00-2.60) 97.7 (49.49-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.223 , 0.283 0.220 , 0.273	Depositor DCC
R_{free} test set	3550 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 51.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 70534 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12600	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, NDG

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	0.43	0/6065	0.73	20/8250 (0.2%)
1	B	0.53	0/6119	0.81	24/8322 (0.3%)
All	All	0.48	0/12184	0.77	44/16572 (0.3%)

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	A	0	2
1	B	0	2
3	A	1	0
All	All	1	4

There are no bond length outliers.

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	ASP	CB-CG-OD2	7.81	125.33	118.30
1	B	301	ASP	CB-CG-OD2	7.50	125.05	118.30
1	B	108	ASP	CB-CG-OD2	7.06	124.65	118.30
1	B	78	LEU	CA-CB-CG	6.70	130.72	115.30
1	A	117	ASP	CB-CG-OD2	6.58	124.22	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	9201	NAG	C1

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	ARG	Peptide
1	A	432	TYR	Peptide
1	B	148	ARG	Peptide
1	B	432	TYR	Peptide

5.2 Too-close contacts

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	5889	0	5660	128	0
1	B	5915	0	5674	165	0
2	A	28	0	26	0	0
2	B	42	0	39	0	0
3	A	28	0	25	0	0
3	B	28	0	25	0	0
4	A	28	0	25	1	0
5	B	14	0	13	0	0
6	A	208	0	0	4	0
6	B	420	0	0	6	0
All	All	12600	0	11487	287	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 287 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:148:ARG:HB3	1:A:149:PRO:HD2	1.34	1.07
1:B:376:HIS:ND1	1:B:391:THR:HG22	1.72	1.05
1:B:254:LYS:NZ	1:B:706:HIS:HD2	1.65	0.93
1:B:651:SER:H	1:B:709:ASN:HD22	1.14	0.93
1:A:651:SER:H	1:A:709:ASN:HD22	0.97	0.92

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	717/719 (100%)	652 (91%)	58 (8%)	7 (1%)	19	39
1	B	723/719 (101%)	656 (91%)	56 (8%)	11 (2%)	13	26
All	All	1440/1438 (100%)	1308 (91%)	114 (8%)	18 (1%)	15	30

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	PRO
1	A	432	TYR
1	B	149	PRO
1	B	433	PRO
1	A	99	ASN

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	634/634 (100%)	528 (83%)	106 (17%)	3	4
1	B	640/634 (101%)	550 (86%)	90 (14%)	4	7
All	All	1274/1268 (100%)	1078 (85%)	196 (15%)	3	5

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	606	LYS

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Mol	Chain	Res	Type
1	B	48	LEU
1	B	616	LYS
1	A	624	SER
1	A	691	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	754	GLN
1	B	102	ASN
1	B	719	ASN
1	B	69	HIS
1	B	151	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 ⓘ

6 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	$\# Z > 2$
4	NDG	A	2271	1,4	14,14,15	0.64	0	15,19,21	1.34	2 (13%)
4	NAG	A	2272	4	14,14,15	0.60	0	15,19,21	0.97	1 (6%)
3	NAG	A	9201	1,3	14,14,15	0.45	0	15,19,21	0.98	1 (6%)
3	NAG	A	9202	3	14,14,15	0.48	0	15,19,21	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	9201	1,3	14,14,15	1.15	1 (7%)	15,19,21	1.18	2 (13%)
3	NAG	B	9202	3	14,14,15	0.74	1 (7%)	15,19,21	1.29	2 (13%)

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
4	NDG	A	2271	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	2272	4	-	0/6/23/26	0/1/1/1
3	NAG	A	9201	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	9202	3	-	0/6/23/26	0/1/1/1
3	NAG	B	9201	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	9202	3	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	9201	NAG	O5-C1	-3.80	1.37	1.43
3	B	9202	NAG	C1-C2	2.19	1.55	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2272	NAG	O5-C5-C6	2.12	111.93	107.35
3	B	9201	NAG	C2-N2-C7	2.12	125.77	123.04
3	B	9202	NAG	O5-C5-C6	2.47	112.69	107.35
3	A	9201	NAG	C1-O5-C5	2.62	115.57	112.25
3	B	9202	NAG	C4-C3-C2	2.77	115.53	111.23

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	9201	NAG	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2271	NDG	1	0

5.6 Ligand geometry

6 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	$\# Z > 2$
2	NAG	A	3141	1	14,14,15	0.61	0	15,19,21	1.31	2 (13%)
2	NAG	A	4901	1	14,14,15	0.83	1 (7%)	15,19,21	1.41	2 (13%)
2	NAG	B	2271	1	14,14,15	0.56	0	15,19,21	1.23	1 (6%)
5	NDG	B	3141	1	14,14,15	0.60	0	15,19,21	1.30	2 (13%)
2	NAG	B	4901	1	14,14,15	0.58	0	15,19,21	2.08	2 (13%)
2	NAG	B	6791	1	14,14,15	0.45	0	15,19,21	2.03	2 (13%)

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	3141	1	-	1/6/23/26	0/1/1/1
2	NAG	A	4901	1	-	0/6/23/26	0/1/1/1
2	NAG	B	2271	1	-	0/6/23/26	0/1/1/1
5	NDG	B	3141	1	-	0/6/23/26	0/1/1/1
2	NAG	B	4901	1	-	0/6/23/26	0/1/1/1
2	NAG	B	6791	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)
2	A	4901	NAG	C1-C2	2.46	1.55	1.52

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6791	NAG	C2-N2-C7	-2.34	120.03	123.04
5	B	3141	NDG	C1-O-C5	-2.29	109.34	112.25
2	A	3141	NAG	C3-C4-C5	2.00	113.69	110.20
2	A	4901	NAG	C1-O5-C5	2.54	115.48	112.25
5	B	3141	NDG	C2-N2-C7	2.82	126.66	123.04

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3141	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	719/719 (100%)	-0.10	20 (2%) 56 49	7, 27, 40, 67	0
1	B	719/719 (100%)	-0.31	3 (0%) 93 91	9, 23, 35, 47	0
All	All	1438/1438 (100%)	-0.21	23 (1%) 74 69	7, 25, 39, 67	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	ILE	4.8
1	A	133	TYR	4.8
1	A	274	TYR	4.5
1	A	141	VAL	4.5
1	A	135	LEU	4.0

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

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
4	NDG	A	2271	14/15	0.86	0.24	1.37	44,47,48,48	0
3	NAG	A	9201	14/15	0.85	0.26	-	55,56,57,57	0
3	NAG	B	9201	14/15	0.88	0.19	-	43,45,46,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	B	9202	14/15	0.88	0.30	-	50,51,51,52	0
3	NAG	A	9202	14/15	0.81	0.26	-	57,57,57,57	0
4	NAG	A	2272	14/15	0.82	0.43	-	50,51,52,52	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(\AA^2)	Q<0.9
2	NAG	A	3141	14/15	0.75	0.27	0.97	105,115,121,121	0
5	NDG	B	3141	14/15	0.90	0.17	0.77	47,51,53,53	0
2	NAG	B	2271	14/15	0.91	0.15	0.15	38,42,44,44	0
2	NAG	B	6791	14/15	0.81	0.42	-	53,56,59,59	0
2	NAG	A	4901	14/15	0.82	0.31	-	49,51,52,52	0
2	NAG	B	4901	14/15	0.86	0.28	-	36,38,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.