



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:34 PM GMT

PDB ID : 1G82  
Title : STRUCTURE OF FIBROBLAST GROWTH FACTOR 9  
Authors : Hecht, H.J.; Adar, R.; Hofmann, B.; Bogin, O.; Weich, H.; Yayon, A.  
Deposited on : 2000-11-16  
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](mailto: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.

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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

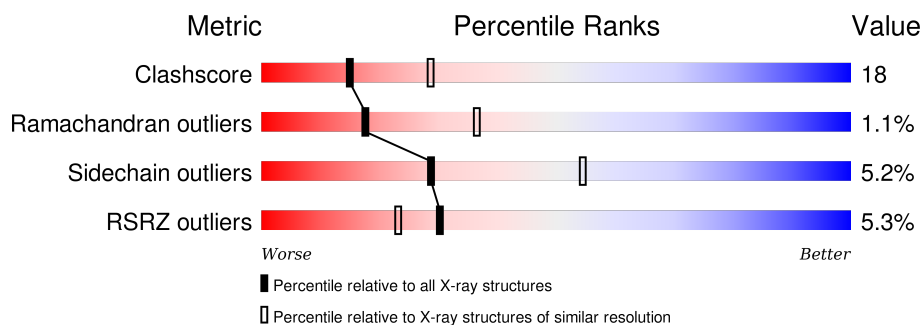
# 1 Overall quality at a glance ⓘ

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))
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  $\geq 3$ , 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	160	<div> <div>3%</div> <div>63%</div> <div>25%</div> <div>9%</div> <div>..</div> </div>
1	B	160	<div> <div>17%</div> <div>41%</div> <div>51%</div> <div>5%</div> <div>..</div> </div>
1	C	160	<div> <div>67%</div> <div>24%</div> <div>5%</div> <div>..</div> </div>
1	D	160	<div> <div>%</div> <div>59%</div> <div>33%</div> <div>..</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
2	NAG	A	652	X	-	-	-
2	NAG	D	652	X	-	-	-
2	FUC	D	653	X	-	-	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5480 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 GROWTH FACTOR 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1295	819	234	239	3			
1	B	157	Total	C	N	O	S	0	0	0
			1295	821	234	237	3			
1	C	155	Total	C	N	O	S	0	0	0
			1279	811	231	234	3			
1	D	155	Total	C	N	O	S	0	0	0
			1276	809	231	233	3			

- Molecule 2 is a polymer of unknown type called SUGAR (BRANCHED NAG-NAG-FUC).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			38	22	2	14		
2	C	3	Total	C	N	O	0	0
			38	22	2	14		
2	D	3	Total	C	N	O	0	0
			38	22	2	14		

- 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	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

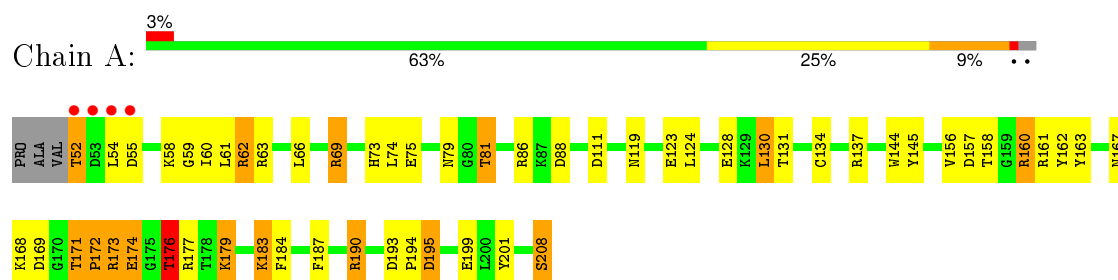
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	59	Total	O	0	0
			59	59		
5	B	4	Total	O	0	0
			4	4		
5	C	35	Total	O	0	0
			35	35		
5	D	49	Total	O	0	0
			49	49		

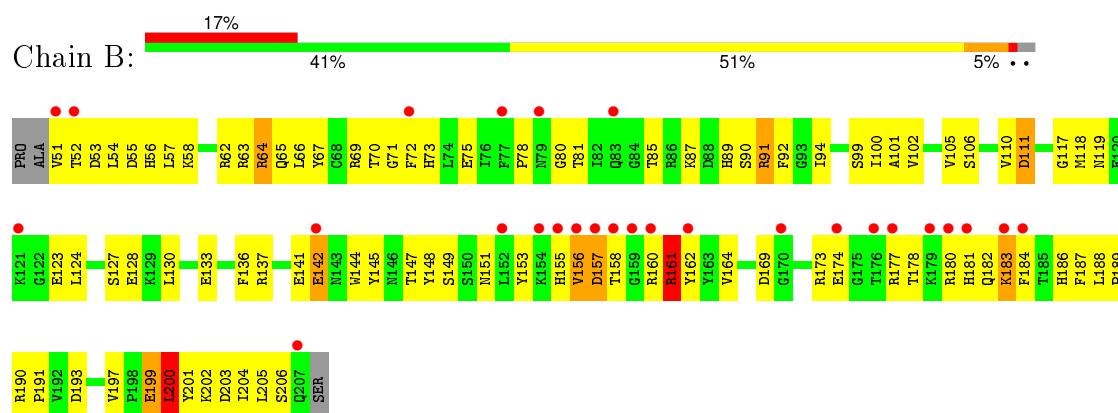
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

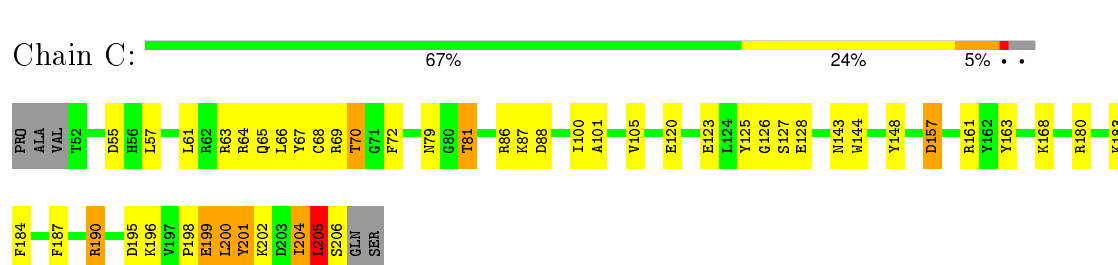
#### • Molecule 1: FIBROBLAST GROWTH FACTOR 9



#### • Molecule 1: FIBROBLAST GROWTH FACTOR 9

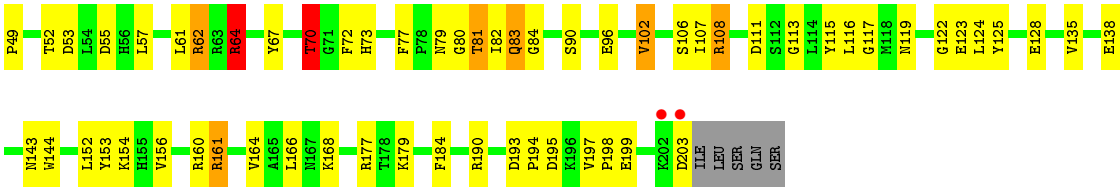


#### • Molecule 1: FIBROBLAST GROWTH FACTOR 9



#### • Molecule 1: FIBROBLAST GROWTH FACTOR 9







## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.95Å 151.95Å 117.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 39.66 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.60) 100.0 (39.66-2.60)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.52 (at 2.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.208 , 0.248 0.211 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	52.4	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 58.1	EDS
Estimated twinning fraction	0.018 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 40975 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5480	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: FUC, SO4, 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	1.80	22/1325 (1.7%)	1.54	18/1783 (1.0%)
1	B	1.25	3/1325 (0.2%)	1.21	12/1785 (0.7%)
1	C	1.66	9/1309 (0.7%)	1.36	14/1763 (0.8%)
1	D	1.86	28/1307 (2.1%)	1.48	15/1761 (0.9%)
All	All	1.66	62/5266 (1.2%)	1.40	59/7092 (0.8%)

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
2	A	1	0
2	D	2	0
All	All	3	0

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	120	GLU	CD-OE2	8.82	1.35	1.25
1	A	195	ASP	CB-CG	8.26	1.69	1.51
1	A	179	LYS	CE-NZ	8.12	1.69	1.49
1	A	162	TYR	CD2-CE2	-8.07	1.27	1.39
1	D	123	GLU	CD-OE1	7.68	1.34	1.25

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	64	ARG	NE-CZ-NH2	-12.57	114.01	120.30
1	A	62	ARG	NE-CZ-NH2	-12.02	114.29	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ARG	NE-CZ-NH2	-11.65	114.48	120.30
1	A	62	ARG	NE-CZ-NH1	11.48	126.04	120.30
1	A	195	ASP	CB-CG-OD2	10.39	127.65	118.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	652	NAG	C1
2	D	652	NAG	C1
2	D	653	FUC	C1

There are no planarity outliers.

## 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	1295	0	1272	31	0
1	B	1295	0	1275	96	0
1	C	1279	0	1259	29	0
1	D	1276	0	1254	32	0
2	A	38	0	34	0	0
2	C	38	0	34	4	0
2	D	38	0	34	1	0
3	B	14	0	13	0	0
4	A	15	0	0	1	0
4	B	10	0	0	1	0
4	C	20	0	0	0	0
4	D	15	0	0	1	0
5	A	59	0	0	2	0
5	B	4	0	0	0	0
5	C	35	0	0	0	0
5	D	49	0	0	3	0
All	All	5480	0	5175	185	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 18.

The worst 5 of 185 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:179:LYS:CE	1:A:179:LYS:NZ	1.69	1.49
1:B:158:THR:CG2	1:B:160:ARG:HG2	1.61	1.30
1:B:64:ARG:HH11	1:B:64:ARG:CG	1.43	1.27
1:B:155:HIS:HD2	1:B:162:TYR:CE1	1.62	1.16
1:B:158:THR:HG21	1:B:160:ARG:HG2	1.19	1.09

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	155/160 (97%)	149 (96%)	6 (4%)	0	100	100
1	B	155/160 (97%)	136 (88%)	16 (10%)	3 (2%)	10	19
1	C	153/160 (96%)	142 (93%)	7 (5%)	4 (3%)	7	11
1	D	153/160 (96%)	147 (96%)	6 (4%)	0	100	100
All	All	616/640 (96%)	574 (93%)	35 (6%)	7 (1%)	17	36

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	ASP
1	B	156	VAL
1	C	200	LEU
1	B	183	LYS
1	C	202	LYS

### 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	141/143 (99%)	133 (94%)	8 (6%)	25	49
1	B	141/143 (99%)	131 (93%)	10 (7%)	18	36
1	C	139/143 (97%)	136 (98%)	3 (2%)	60	83
1	D	138/143 (96%)	130 (94%)	8 (6%)	25	49
All	All	559/572 (98%)	530 (95%)	29 (5%)	29	54

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	142	GLU
1	B	200	LEU
1	D	108	ARG
1	B	161	ARG
1	B	206	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	151	ASN
1	C	186	HIS
1	B	181	HIS
1	B	139	GLN
1	B	155	HIS

### 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 ⓘ

9 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	651	1,2	14,14,15	2.58	5 (35%)	15,19,21	5.00	11 (73%)
2	NAG	A	652	2	14,14,15	0.94	0	15,19,21	2.07	3 (20%)
2	FUC	A	653	2	10,10,11	1.31	2 (20%)	14,14,16	1.97	4 (28%)
2	NAG	C	651	1,2	14,14,15	1.19	1 (7%)	15,19,21	2.87	8 (53%)
2	NAG	C	652	2	14,14,15	1.36	1 (7%)	15,19,21	3.03	9 (60%)
2	FUC	C	653	2	10,10,11	1.35	1 (10%)	14,14,16	3.09	6 (42%)
2	NAG	D	651	1,2	14,14,15	1.76	2 (14%)	15,19,21	3.03	6 (40%)
2	NAG	D	652	2	14,14,15	1.13	1 (7%)	15,19,21	1.81	4 (26%)
2	FUC	D	653	2	10,10,11	0.92	1 (10%)	14,14,16	2.49	7 (50%)

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	651	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	652	2	1/1/5/7	0/6/23/26	0/1/1/1
2	FUC	A	653	2	-	0/0/17/20	0/1/1/1
2	NAG	C	651	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	652	2	-	0/6/23/26	0/1/1/1
2	FUC	C	653	2	-	0/0/17/20	0/1/1/1
2	NAG	D	651	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	652	2	1/1/5/7	0/6/23/26	0/1/1/1
2	FUC	D	653	2	1/1/4/5	0/0/17/20	0/1/1/1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	651	NAG	C2-N2	-6.99	1.33	1.46
2	A	651	NAG	C4-C5	-4.16	1.44	1.53
2	A	651	NAG	C4-C3	-3.41	1.43	1.52
2	C	653	FUC	O5-C1	-3.25	1.38	1.43
2	A	653	FUC	C2-C3	-2.84	1.48	1.52

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	651	NAG	C3-C2-N2	-8.92	89.19	110.56
2	C	653	FUC	C2-C3-C4	-8.26	97.02	111.04
2	A	651	NAG	C3-C4-C5	-7.70	96.78	110.20
2	C	651	NAG	C2-N2-C7	-6.53	114.65	123.04
2	D	651	NAG	C8-C7-N2	-6.26	104.13	116.11

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	652	NAG	C1
2	A	652	NAG	C1
2	D	653	FUC	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	651	NAG	C8-C7-N2-C2
2	C	651	NAG	O7-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	651	NAG	2	0
2	C	652	NAG	2	0
2	D	651	NAG	1	0
2	D	652	NAG	1	0

## 5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	SO4	A	290	-	4,4,4	1.49	1 (25%)	6,6,6	1.01	0
4	SO4	A	294	-	4,4,4	0.80	0	6,6,6	1.20	1 (16%)
4	SO4	A	299	-	4,4,4	0.46	0	6,6,6	0.79	0
4	SO4	B	291	-	4,4,4	0.58	0	6,6,6	0.88	0
4	SO4	B	295	-	4,4,4	0.70	0	6,6,6	1.24	1 (16%)
3	NAG	B	651	1	14,14,15	1.10	1 (7%)	15,19,21	1.68	3 (20%)
4	SO4	C	292	-	4,4,4	1.63	1 (25%)	6,6,6	0.47	0
4	SO4	C	296	-	4,4,4	0.58	0	6,6,6	0.54	0
4	SO4	C	298	-	4,4,4	0.44	0	6,6,6	0.64	0
4	SO4	C	301	-	4,4,4	0.24	0	6,6,6	0.19	0
4	SO4	D	293	-	4,4,4	1.40	1 (25%)	6,6,6	1.33	0
4	SO4	D	297	-	4,4,4	0.25	0	6,6,6	0.78	0
4	SO4	D	300	-	4,4,4	0.15	0	6,6,6	0.41	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
4	SO4	A	290	-	-	0/0/0/0	0/0/0/0
4	SO4	A	294	-	-	0/0/0/0	0/0/0/0
4	SO4	A	299	-	-	0/0/0/0	0/0/0/0
4	SO4	B	291	-	-	0/0/0/0	0/0/0/0
4	SO4	B	295	-	-	0/0/0/0	0/0/0/0
3	NAG	B	651	1	-	0/6/23/26	0/1/1/1
4	SO4	C	292	-	-	0/0/0/0	0/0/0/0
4	SO4	C	296	-	-	0/0/0/0	0/0/0/0
4	SO4	C	298	-	-	0/0/0/0	0/0/0/0
4	SO4	C	301	-	-	0/0/0/0	0/0/0/0
4	SO4	D	293	-	-	0/0/0/0	0/0/0/0
4	SO4	D	297	-	-	0/0/0/0	0/0/0/0
4	SO4	D	300	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	290	SO4	O4-S	-2.43	1.38	1.47
4	C	292	SO4	O2-S	-2.23	1.39	1.47
4	D	293	SO4	O4-S	-2.09	1.39	1.47
3	B	651	NAG	C1-C2	3.68	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	294	SO4	O2-S-O1	-2.46	101.71	109.50
3	B	651	NAG	O5-C5-C6	2.12	111.95	107.35
3	B	651	NAG	O3-C3-C2	2.16	113.40	109.11
4	B	295	SO4	O2-S-O1	2.18	116.41	109.50
3	B	651	NAG	C1-O5-C5	4.90	118.47	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	294	SO4	1	0
4	B	295	SO4	1	0
4	D	300	SO4	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	157/160 (98%)	-0.07	4 (2%) 61 54	29, 41, 60, 87	0
1	B	157/160 (98%)	0.95	27 (17%) 2 1	51, 79, 103, 110	0
1	C	155/160 (96%)	-0.19	0 100 100	34, 47, 77, 108	0
1	D	155/160 (96%)	-0.02	2 (1%) 79 75	30, 42, 66, 100	0
All	All	624/640 (97%)	0.17	33 (5%) 30 23	29, 47, 96, 110	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	83	GLN	6.2
1	B	155	HIS	6.1
1	B	157	ASP	5.4
1	B	160	ARG	5.3
1	B	51	VAL	5.0

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	NAG	D	651	14/15	0.86	0.21	0.54	60,69,74,80	0
2	NAG	A	651	14/15	0.86	0.17	0.21	56,60,71,73	0
2	NAG	C	652	14/15	0.76	0.28	-	82,90,99,103	0
2	FUC	C	653	10/11	0.94	0.20	-	59,66,69,69	0
2	FUC	A	653	10/11	0.95	0.22	-	60,68,71,74	0
2	NAG	A	652	14/15	0.82	0.24	-	67,76,85,88	0
2	NAG	C	651	14/15	0.90	0.17	-	57,67,75,81	0
2	FUC	D	653	10/11	0.95	0.20	-	63,69,72,72	0
2	NAG	D	652	14/15	0.81	0.32	-	69,87,92,93	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	SO4	D	297	5/5	0.95	0.16	-0.46	64,68,71,74	0
4	SO4	C	298	5/5	0.88	0.38	-	89,90,91,95	0
4	SO4	D	300	5/5	0.80	0.22	-	125,126,127,129	0
4	SO4	C	292	5/5	0.98	0.14	-	52,54,58,59	0
3	NAG	B	651	14/15	0.32	0.26	-	120,124,126,126	0
4	SO4	C	296	5/5	0.89	0.25	-	82,88,89,90	0
4	SO4	B	295	5/5	0.80	0.37	-	97,97,102,102	0
4	SO4	C	301	5/5	0.78	0.19	-	118,120,120,123	0
4	SO4	A	299	5/5	0.90	0.17	-	80,86,88,93	0
4	SO4	A	290	5/5	0.96	0.12	-	48,49,51,56	0
4	SO4	B	291	5/5	0.91	0.22	-	83,83,86,86	0
4	SO4	A	294	5/5	0.78	0.22	-	66,68,78,81	0
4	SO4	D	293	5/5	0.98	0.12	-	41,45,51,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.