



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 04:58 AM GMT

PDB ID : 2FT3
Title : Crystal structure of the biglycan dimer core protein
Authors : Scott, P.G.; Dodd, C.M.; Bergmann, E.M.
Deposited on : 2006-01-23
Resolution : 3.40 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

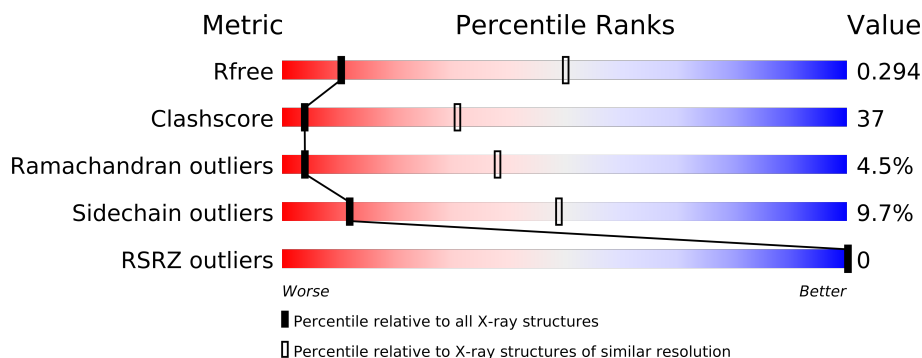
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

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}	66092	1017 (3.52-3.28)
Clashscore	79885	1214 (3.50-3.30)
Ramachandran outliers	78287	1177 (3.50-3.30)
Sidechain outliers	78261	1177 (3.50-3.30)
RSRZ outliers	66119	1017 (3.52-3.28)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	332	
1	B	332	
1	C	332	
1	D	332	
1	E	332	
1	F	332	

2 Entry composition i

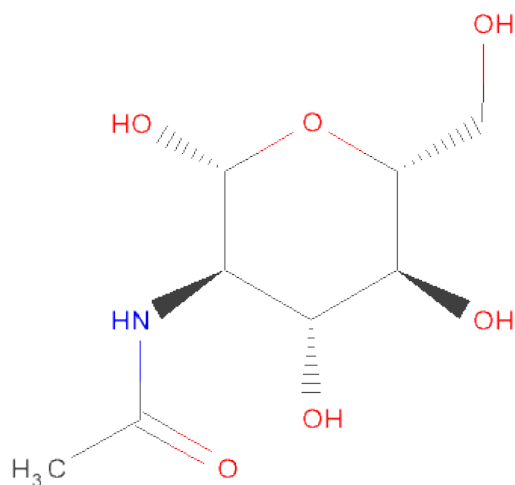
There are 3 unique types of molecules in this entry. The entry contains 14674 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Biglycan.

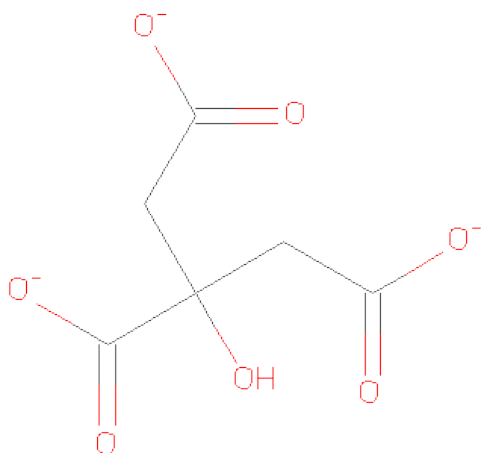
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2416	1545	428	432	11			
1	B	303	Total	C	N	O	S	0	0	0
			2416	1545	428	432	11			
1	C	303	Total	C	N	O	S	0	0	0
			2416	1545	428	432	11			
1	D	304	Total	C	N	O	S	0	0	0
			2420	1547	429	433	11			
1	E	303	Total	C	N	O	S	0	0	0
			2416	1545	428	432	11			
1	F	305	Total	C	N	O	S	0	0	0
			2428	1551	431	435	11			

- 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	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



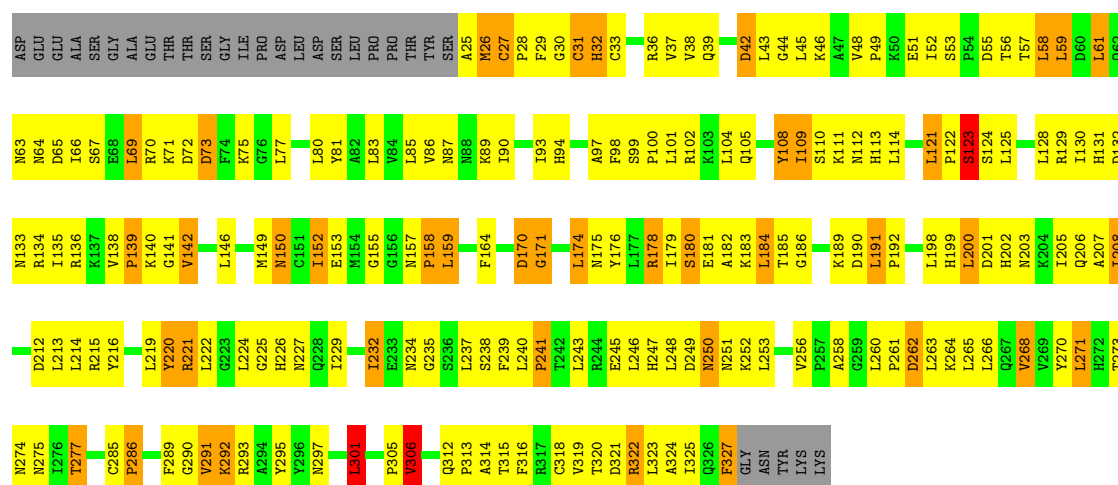
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		
3	F	1	Total	C	O	0	0
			13	6	7		

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.

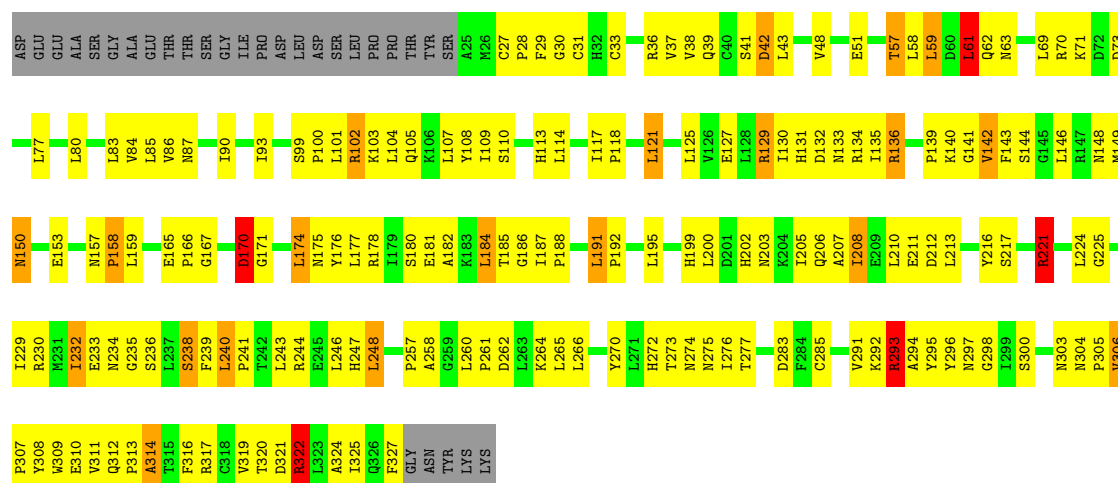
• Molecule 1: Biglycan

Chain A: 



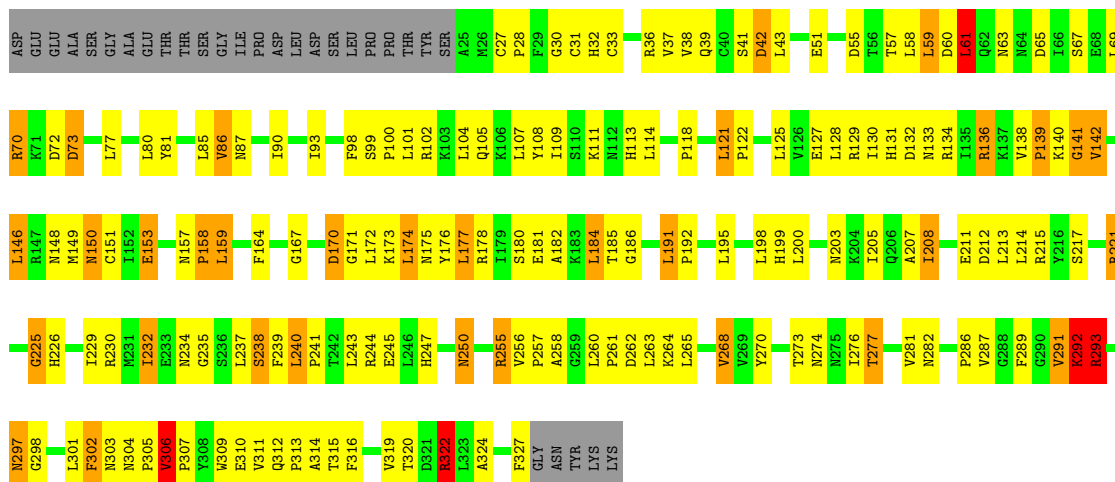
• Molecule 1: Biglycan

Chain B: 

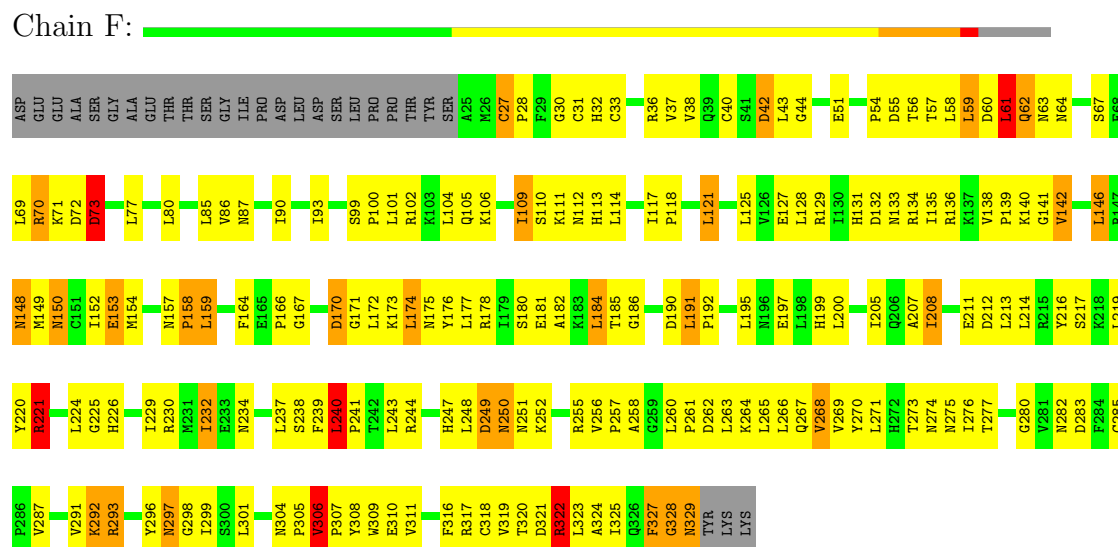


• Molecule 1: Biglycan

Chain C: 



Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	206.51Å 119.22Å 140.62Å 90.00° 116.61° 90.00°	Depositor
Resolution (Å)	23.00 – 3.40 22.86 – 3.40	Depositor EDS
% Data completeness (in resolution range)	96.5 (23.00-3.40) 96.5 (22.86-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.37Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.258 , 0.291 0.255 , 0.294	Depositor DCC
R_{free} test set	2040 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 30.0	EDS
Estimated twinning fraction	0.098 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h +1/2*k-l 0.090 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h- 1/2*k-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	1 of 40497 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	14674	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: FLC, 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	1.07	3/2468 (0.1%)	1.23	17/3342 (0.5%)
1	B	1.05	1/2468 (0.0%)	1.23	23/3342 (0.7%)
1	C	1.01	1/2468 (0.0%)	1.28	24/3342 (0.7%)
1	D	1.05	2/2472 (0.1%)	1.29	24/3347 (0.7%)
1	E	1.06	1/2468 (0.0%)	1.36	26/3342 (0.8%)
1	F	1.05	2/2480 (0.1%)	1.25	30/3358 (0.9%)
All	All	1.05	10/14824 (0.1%)	1.27	144/20073 (0.7%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	62	GLN	CD-NE2	-7.44	1.14	1.32
1	E	151	CYS	CB-SG	-6.55	1.71	1.82
1	F	62	GLN	CD-OE1	-6.31	1.10	1.24
1	A	108	TYR	CE1-CZ	-5.78	1.31	1.38
1	B	291	VAL	CA-CB	5.62	1.66	1.54

The worst 5 of 144 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	221	ARG	NE-CZ-NH2	-20.38	110.11	120.30
1	E	244	ARG	NE-CZ-NH2	18.19	129.40	120.30
1	D	317	ARG	NE-CZ-NH2	17.19	128.90	120.30
1	E	244	ARG	NE-CZ-NH1	-15.47	112.56	120.30
1	E	136	ARG	NE-CZ-NH2	-15.26	112.67	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2416	0	2466	222	0
1	B	2416	0	2466	163	0
1	C	2416	0	2466	188	0
1	D	2420	0	2469	167	0
1	E	2416	0	2466	173	0
1	F	2428	0	2475	191	0
2	A	14	0	13	5	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
2	D	14	0	13	1	0
2	E	14	0	13	0	0
2	F	14	0	13	0	0
3	A	13	0	5	0	0
3	B	13	0	5	3	0
3	C	13	0	5	3	0
3	D	13	0	5	6	0
3	E	13	0	5	2	0
3	F	13	0	5	2	0
All	All	14674	0	14916	1104	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 37.

The worst 5 of 1104 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:153:GLU:OE1	1:B:178:ARG:HD3	1.39	1.21
1:D:225:GLY:HA3	3:D:2193:FLC:OB2	1.00	1.15
1:E:27:CYS:HB2	1:E:28:PRO:HD2	1.33	1.10
1:C:121:LEU:HD12	1:C:121:LEU:H	1.15	1.09
1:A:93:ILE:HD11	1:A:114:LEU:HD21	1.32	1.09

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	301/332 (91%)	216 (72%)	70 (23%)	15 (5%)	3	34
1	B	301/332 (91%)	225 (75%)	68 (23%)	8 (3%)	8	55
1	C	301/332 (91%)	219 (73%)	68 (23%)	14 (5%)	4	36
1	D	302/332 (91%)	230 (76%)	59 (20%)	13 (4%)	4	40
1	E	301/332 (91%)	229 (76%)	53 (18%)	19 (6%)	2	27
1	F	303/332 (91%)	223 (74%)	67 (22%)	13 (4%)	4	40
All	All	1809/1992 (91%)	1342 (74%)	385 (21%)	82 (4%)	4	38

5 of 82 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	MET
1	A	291	VAL
1	B	150	ASN
1	C	150	ASN
1	C	291	VAL

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	273/297 (92%)	244 (89%)	29 (11%)	10	43
1	B	273/297 (92%)	253 (93%)	20 (7%)	20	65
1	C	273/297 (92%)	249 (91%)	24 (9%)	14	55
1	D	273/297 (92%)	243 (89%)	30 (11%)	9	41
1	E	273/297 (92%)	245 (90%)	28 (10%)	10	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	274/297 (92%)	246 (90%)	28 (10%)	11	46
All	All	1639/1782 (92%)	1480 (90%)	159 (10%)	12	49

5 of 159 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	306	VAL
1	D	191	LEU
1	F	191	LEU
1	D	61	LEU
1	D	142	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	62	GLN
1	D	175	ASN
1	F	175	ASN
1	D	105	GLN
1	D	206	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

12 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	FLC	A	2190	-	5,12,12	2.67	2 (40%)	7,17,17	2.63	1 (14%)
2	NAG	A	801	1	12,14,15	1.13	1 (8%)	15,19,21	1.53	3 (20%)
3	FLC	B	2191	-	5,12,12	3.25	2 (40%)	7,17,17	1.32	1 (14%)
2	NAG	B	803	1	12,14,15	1.06	0	15,19,21	2.01	5 (33%)
3	FLC	C	2192	-	5,12,12	1.42	0	7,17,17	4.23	4 (57%)
2	NAG	C	805	1	12,14,15	1.37	2 (16%)	15,19,21	2.35	5 (33%)
3	FLC	D	2193	1	5,12,12	3.49	1 (20%)	7,17,17	3.41	6 (85%)
2	NAG	D	807	1	12,14,15	1.01	0	15,19,21	2.34	4 (26%)
3	FLC	E	2194	-	5,12,12	2.17	1 (20%)	7,17,17	3.60	4 (57%)
2	NAG	E	809	1	12,14,15	1.23	2 (16%)	15,19,21	1.58	2 (13%)
3	FLC	F	2195	-	5,12,12	7.09	3 (60%)	7,17,17	4.56	5 (71%)
2	NAG	F	811	1	12,14,15	1.00	0	15,19,21	2.18	4 (26%)

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	FLC	A	2190	-	-	0/6/16/16	0/0/0/0
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	FLC	B	2191	-	-	0/6/16/16	0/0/0/0
2	NAG	B	803	1	-	0/6/23/26	0/1/1/1
3	FLC	C	2192	-	-	0/6/16/16	0/0/0/0
2	NAG	C	805	1	-	0/6/23/26	0/1/1/1
3	FLC	D	2193	1	-	0/6/16/16	0/0/0/0
2	NAG	D	807	1	-	0/6/23/26	0/1/1/1
3	FLC	E	2194	-	-	0/6/16/16	0/0/0/0
2	NAG	E	809	1	-	2/6/23/26	0/1/1/1
3	FLC	F	2195	-	-	0/6/16/16	0/0/0/0
2	NAG	F	811	1	-	0/6/23/26	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)
3	F	2195	FLC	CG-CGC	14.71	1.58	1.49
3	D	2193	FLC	CG-CGC	7.52	1.54	1.49
3	B	2191	FLC	CG-CGC	6.41	1.53	1.49
3	F	2195	FLC	CA-CAC	4.80	1.52	1.49
3	A	2190	FLC	CA-CAC	4.62	1.52	1.49

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2195	FLC	CB-CG-CGC	10.46	130.64	115.01
3	C	2192	FLC	CB-CA-CAC	-7.75	103.42	115.01
3	E	2194	FLC	CB-CG-CGC	-6.64	105.09	115.01
3	A	2190	FLC	CB-CG-CGC	-6.51	105.28	115.01
2	D	807	NAG	O5-C5-C6	6.42	113.71	106.98

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	809	NAG	C8-C7-N2-C2
2	E	809	NAG	O7-C7-N2-C2

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	303/332 (91%)	0.10	0 100 100	8, 38, 52, 57	0
1	B	303/332 (91%)	0.16	0 100 100	8, 38, 53, 70	0
1	C	303/332 (91%)	0.12	0 100 100	8, 38, 53, 67	0
1	D	304/332 (91%)	0.10	0 100 100	8, 38, 52, 57	0
1	E	303/332 (91%)	0.11	0 100 100	8, 37, 53, 64	0
1	F	305/332 (91%)	0.12	0 100 100	6, 38, 52, 58	0
All	All	1821/1992 (91%)	0.12	0 100 100	6, 38, 53, 70	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	E	809	14/15	0.40	1.86	59,61,62,62	0
3	FLC	B	2191	13/13	0.30	1.16	49,53,56,57	0
2	NAG	C	805	14/15	0.31	1.10	53,56,57,58	0
2	NAG	A	801	14/15	0.25	0.39	51,53,55,55	0
3	FLC	E	2194	13/13	0.21	-0.51	36,44,47,48	0
2	NAG	D	807	14/15	0.25	-0.56	58,59,61,62	0
3	FLC	A	2190	13/13	0.20	-0.77	47,50,53,53	0
3	FLC	F	2195	13/13	0.20	-0.91	38,42,42,43	0
3	FLC	D	2193	13/13	0.17	-1.23	38,40,44,45	0
2	NAG	B	803	14/15	0.26	-1.33	46,50,51,51	0
3	FLC	C	2192	13/13	0.18	-1.41	38,43,46,46	0
2	NAG	F	811	14/15	0.17	-	49,50,51,51	0

6.5 Other polymers ⓘ

There are no such residues in this entry.