



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 12, 2021 – 02:40 PM EDT

PDB ID : 2B7X
Title : Sequential reorganization of beta-sheet topology by insertion of a single strand
Authors : Sagermann, M.; Matthews, B.W.
Deposited on : 2005-10-05
Resolution : 3.00 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

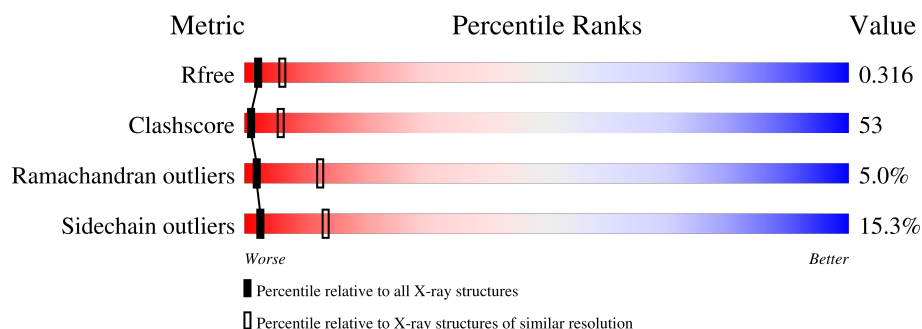
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	170	<div> <div>27%</div> <div>47%</div> <div>14%</div> <div>•</div> <div>8%</div> </div>
1	B	170	<div> <div>32%</div> <div>46%</div> <div>10%</div> <div>5%</div> <div>8%</div> </div>
1	C	170	<div> <div>26%</div> <div>49%</div> <div>16%</div> <div>•</div> <div>8%</div> </div>
1	D	170	<div> <div>36%</div> <div>42%</div> <div>12%</div> <div>•</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
2	SO4	A	807	-	-	X	-
2	SO4	D	802	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5085 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 Lysozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	B	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	C	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	D	160	Total	C	N	O	S	0	0	0
			1277	805	230	237	5			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	TYR	-	insertion	UNP P00720
A	32	THR	-	insertion	UNP P00720
A	33	ILE	-	insertion	UNP P00720
A	34	GLY	-	insertion	UNP P00720
A	35	ILE	-	insertion	UNP P00720
A	36	GLY	-	insertion	UNP P00720
A	60	THR	CYS	engineered mutation	UNP P00720
A	103	ALA	CYS	engineered mutation	UNP P00720
B	25	TYR	-	insertion	UNP P00720
B	26	THR	-	insertion	UNP P00720
B	27	ILE	-	insertion	UNP P00720
B	28	GLY	-	insertion	UNP P00720
B	29	ILE	-	insertion	UNP P00720
B	30	GLY	-	insertion	UNP P00720
B	60	THR	CYS	engineered mutation	UNP P00720
B	103	ALA	CYS	engineered mutation	UNP P00720
C	31	TYR	-	insertion	UNP P00720
C	32	THR	-	insertion	UNP P00720
C	33	ILE	-	insertion	UNP P00720
C	34	GLY	-	insertion	UNP P00720
C	35	ILE	-	insertion	UNP P00720

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Chain	Residue	Modelled	Actual	Comment	Reference
C	36	GLY	-	insertion	UNP P00720
C	60	THR	CYS	engineered mutation	UNP P00720
C	103	ALA	CYS	engineered mutation	UNP P00720
D	31	TYR	-	insertion	UNP P00720
D	32	THR	-	insertion	UNP P00720
D	33	ILE	-	insertion	UNP P00720
D	34	GLY	-	insertion	UNP P00720
D	35	ILE	-	insertion	UNP P00720
D	36	GLY	-	insertion	UNP P00720
D	60	THR	CYS	engineered mutation	UNP P00720
D	103	ALA	CYS	engineered mutation	UNP P00720

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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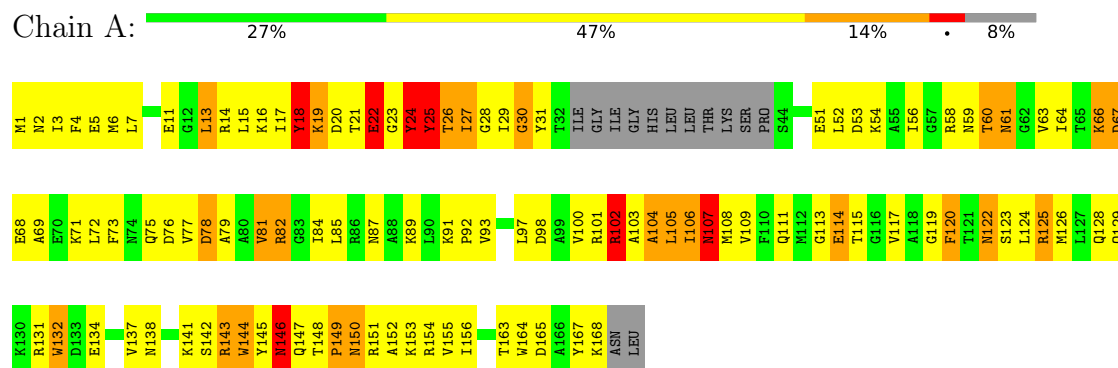
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

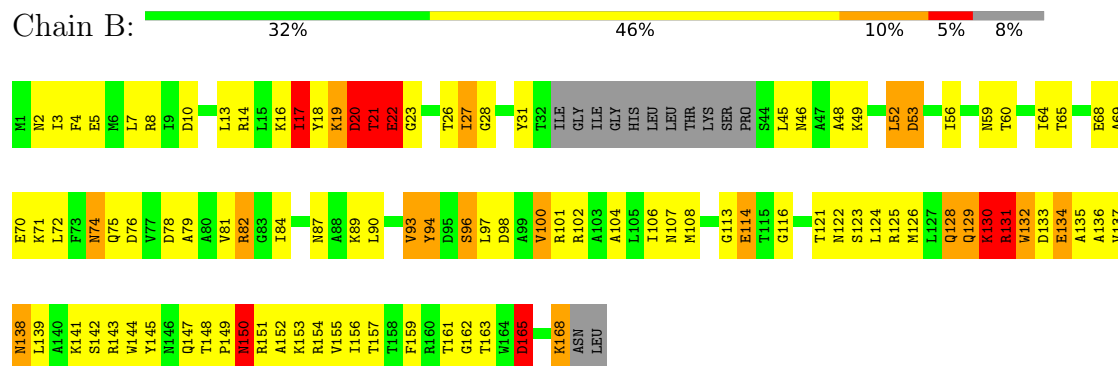
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

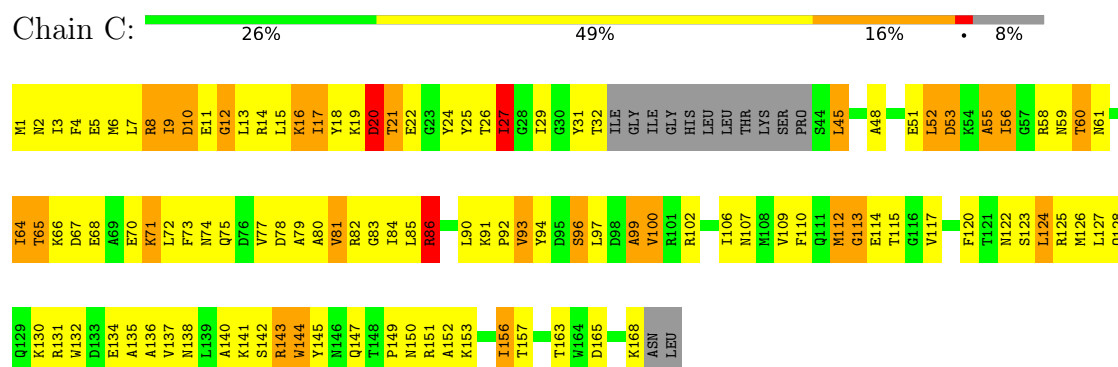
• Molecule 1: Lysozyme



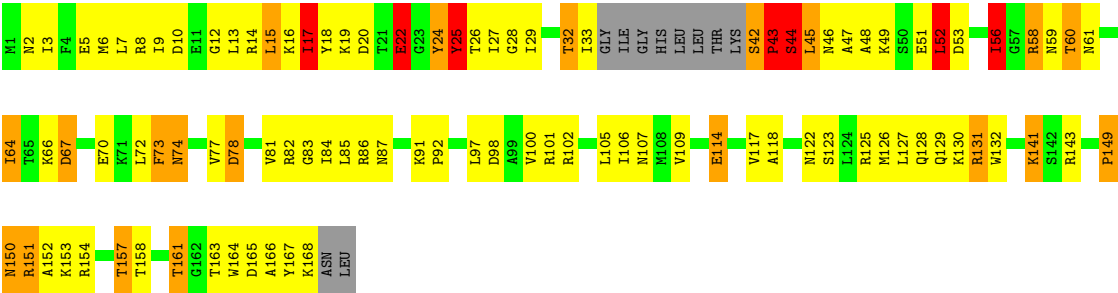
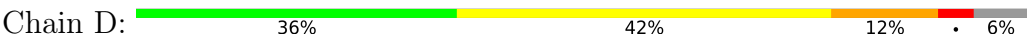
• Molecule 1: Lysozyme



• Molecule 1: Lysozyme



● Molecule 1: Lysozyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.38Å 78.08Å 143.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.01 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.00) 70.1 (20.01-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.41Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.239 , 0.319 0.237 , 0.316	Depositor DCC
R_{free} test set	673 reflections (3.47%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	5085	wwPDB-VP
Average B, all atoms (Å ²)	8.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.8790e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.87	22/1274 (1.7%)	2.60	42/1714 (2.5%)
1	B	2.51	18/1274 (1.4%)	2.61	32/1714 (1.9%)
1	C	1.26	5/1274 (0.4%)	1.20	7/1714 (0.4%)
1	D	1.95	10/1296 (0.8%)	1.43	14/1745 (0.8%)
All	All	1.95	55/5118 (1.1%)	2.06	95/6887 (1.4%)

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	1	2
1	B	0	6
1	D	1	1
All	All	2	9

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	21	THR	CB-OG1	64.69	2.72	1.43
1	D	43	PRO	N-CD	31.03	1.91	1.47
1	D	43	PRO	CB-CG	27.65	2.88	1.50
1	D	44	SER	CB-OG	-25.73	1.08	1.42
1	A	60	THR	CB-OG1	-23.03	0.97	1.43

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	TYR	CB-CG-CD1	47.27	149.36	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	TYR	CB-CG-CD2	-46.86	92.88	121.00
1	B	20	ASP	CB-CG-OD1	32.83	147.85	118.30
1	A	24	TYR	CB-CG-CD2	-32.43	101.54	121.00
1	B	20	ASP	CB-CG-OD2	-30.70	90.67	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	60	THR	CB
1	D	56	ILE	CB

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	24	TYR	Sidechain
1	A	25	TYR	Mainchain
1	B	20	ASP	Mainchain
1	B	21	THR	Mainchain,Peptide
1	B	22	GLU	Mainchain

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	1256	0	1271	125	0
1	B	1256	0	1266	124	0
1	C	1256	0	1271	139	0
1	D	1277	0	1294	152	0
2	A	10	0	0	3	0
2	C	15	0	0	3	0
2	D	15	0	0	4	0
All	All	5085	0	5102	540	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 53.

The worst 5 of 540 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:D:17:ILE:CG2	1:D:17:ILE:CB	1.79	1.57
1:A:60:THR:CB	1:A:60:THR:CG2	1.82	1.53
1:C:100:VAL:CB	1:C:100:VAL:CG1	1.84	1.52
1:B:22:GLU:CG	1:B:22:GLU:CB	1.85	1.50
1:D:24:TYR:CB	1:D:24:TYR:CA	1.89	1.49

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	153/170 (90%)	124 (81%)	22 (14%)	7 (5%)	2	14
1	B	153/170 (90%)	119 (78%)	27 (18%)	7 (5%)	2	14
1	C	153/170 (90%)	112 (73%)	31 (20%)	10 (6%)	1	7
1	D	156/170 (92%)	119 (76%)	30 (19%)	7 (4%)	2	14
All	All	615/680 (90%)	474 (77%)	110 (18%)	31 (5%)	2	12

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	17	ILE
1	C	113	GLY
1	D	43	PRO
1	D	118	ALA
1	A	30	GLY

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	130/141 (92%)	107 (82%)	23 (18%)	2	9
1	B	130/141 (92%)	112 (86%)	18 (14%)	3	17
1	C	130/141 (92%)	111 (85%)	19 (15%)	3	15
1	D	133/141 (94%)	113 (85%)	20 (15%)	3	14
All	All	523/564 (93%)	443 (85%)	80 (15%)	2	13

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	124	LEU
1	D	73	PHE
1	C	156	ILE
1	D	52	LEU
1	D	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	146	ASN
1	B	150	ASN
1	D	147	GLN
1	C	75	GLN
1	D	74	ASN

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	SO4	D	802	-	4,4,4	0.24	0	6,6,6	0.17	0
2	SO4	D	803	-	4,4,4	0.38	0	6,6,6	0.83	0
2	SO4	A	807	-	4,4,4	0.18	0	6,6,6	1.14	0
2	SO4	C	805	-	4,4,4	0.24	0	6,6,6	0.63	0
2	SO4	C	806	-	4,4,4	0.46	0	6,6,6	0.73	0
2	SO4	D	801	-	4,4,4	0.31	0	6,6,6	0.84	0
2	SO4	C	804	-	4,4,4	0.14	0	6,6,6	0.86	0
2	SO4	A	808	-	4,4,4	0.32	0	6,6,6	0.49	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	802	SO4	3	0
2	A	807	SO4	3	0
2	C	805	SO4	1	0
2	C	806	SO4	1	0
2	D	801	SO4	1	0
2	C	804	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	7
1	A	2
1	D	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	15:LEU	C	16:LYS	N	1.19
1	A	146:ASN	C	147:GLN	N	1.18
1	B	21:THR	C	22:GLU	N	1.17
1	A	25:TYR	C	26:THR	N	1.15
1	B	128:GLN	C	129:GLN	N	1.15

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.