



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 07:15 AM GMT

PDB ID : 2B39
Title : Structure of mammalian C3 with an intact thioester at 3Å resolution
Authors : Fredslund, F.; Jenner, L.; Husted, L.B.; Nyborg, J.; Andersen, G.R.; Sottrup-Jensen, L.
Deposited on : 2005-09-20
Resolution : 3.00 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>

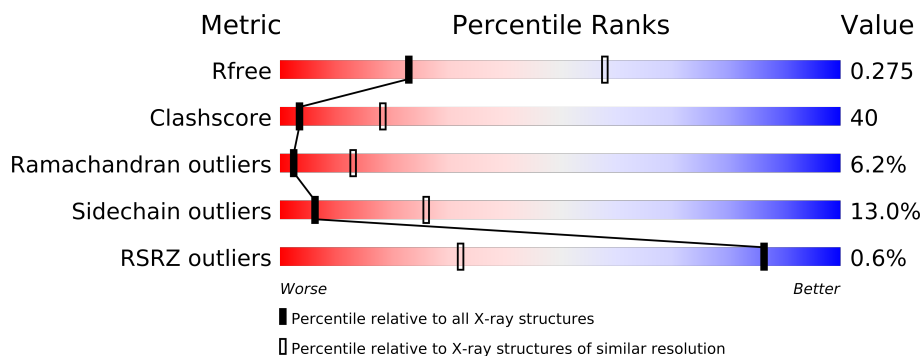
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.00 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}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (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 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	1661	
1	B	1661	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25624 atoms, of which 0 are hydrogen and 0 are deuterium.

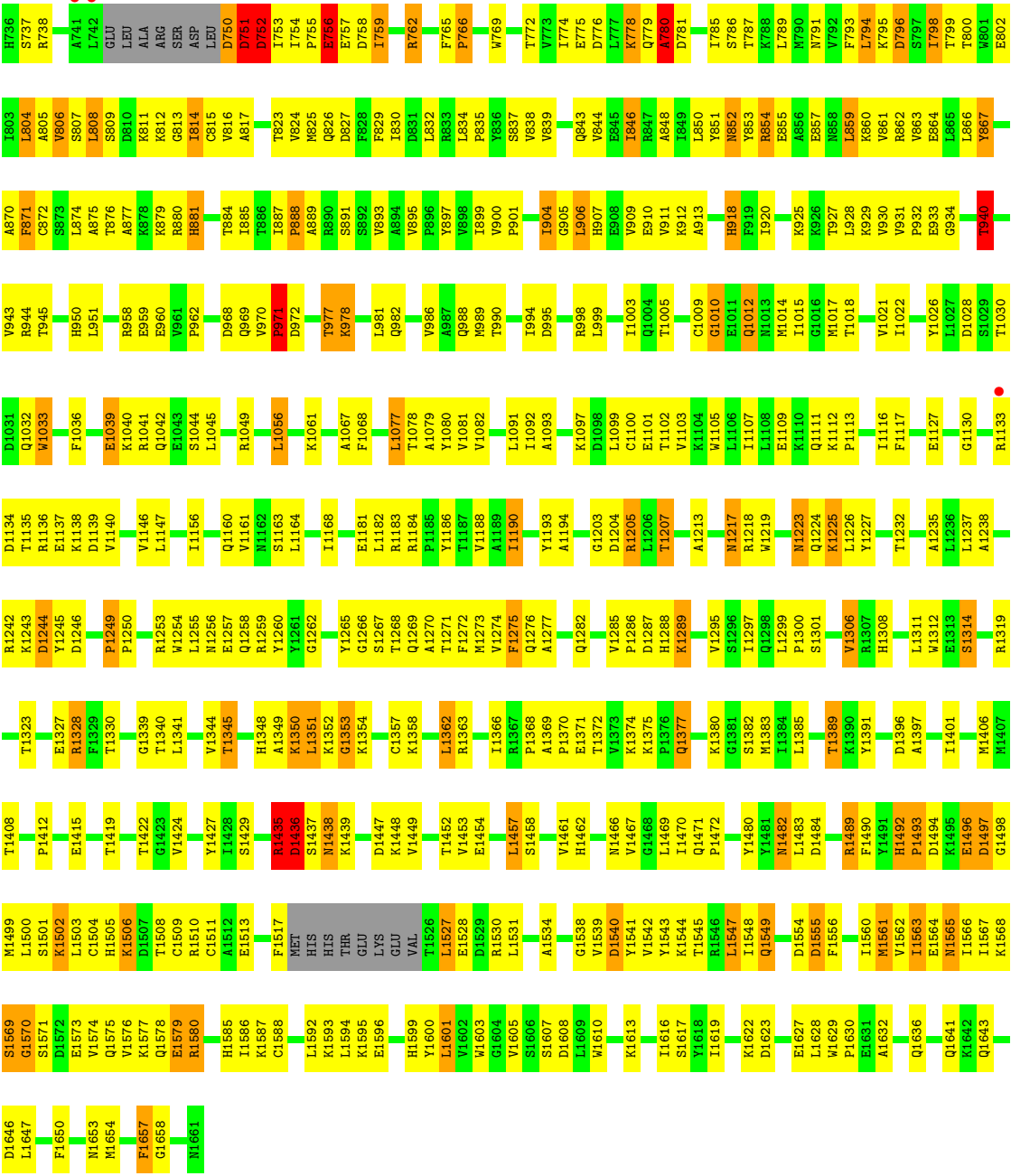
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1610	Total	C	N	O	S	0	0	0
			12773	8093	2187	2439	54			
1	B	1610	Total	C	N	O	S	0	0	0
			12773	8093	2187	2439	54			

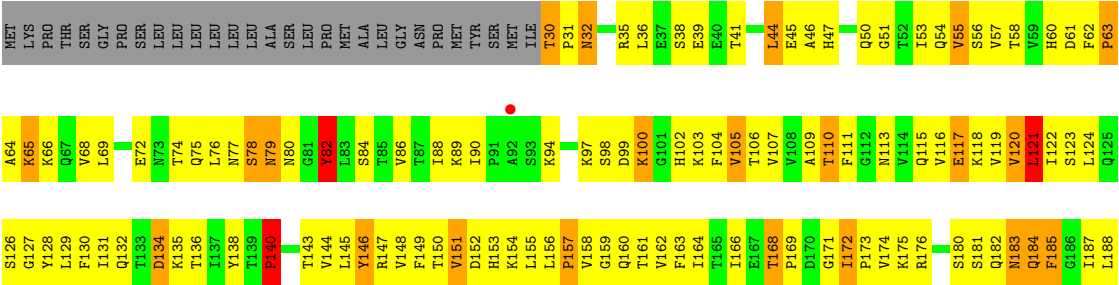
- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			39	22	2	15		
2	B	3	Total	C	N	O	0	0
			39	22	2	15		



• Molecule 1: C3

Chain B:







4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	254.25Å 246.86Å 113.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.00 37.85 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.00) 97.2 (37.85-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.278 , 0.286 0.267 , 0.275	Depositor DCC
R_{free} test set	1392 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	69.3	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 46.0	EDS
Estimated twinning fraction	0.008 for k,h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	2 of 138964 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	25624	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, 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	0.58	1/13020 (0.0%)	0.82	15/17632 (0.1%)
1	B	0.57	0/13020	0.81	11/17632 (0.1%)
All	All	0.57	1/26040 (0.0%)	0.82	26/35264 (0.1%)

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	1
1	B	0	1
2	A	1	0
2	B	1	0
All	All	2	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	102	HIS	CB-CG	6.64	1.61	1.50

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	121	LEU	CA-CB-CG	-9.75	92.87	115.30
1	A	91	PRO	N-CA-C	7.91	132.66	112.10
1	B	1362	LEU	CA-CB-CG	6.57	130.40	115.30
1	A	1362	LEU	CA-CB-CG	6.54	130.34	115.30
1	A	1130	GLY	N-CA-C	-6.49	96.87	113.10

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2001	NAG	C1
2	B	2001	NAG	C1

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	TYR	Sidechain
1	B	820	TYR	Sidechain

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	12773	0	12782	1027	0
1	B	12773	0	12782	1002	0
2	A	39	0	34	3	0
2	B	39	0	34	3	0
All	All	25624	0	25632	2029	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 40.

The worst 5 of 2029 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:117:GLU:O	1:B:118:LYS:HG2	1.47	1.14
1:B:369:PHE:HB3	1:B:409:ILE:HD12	1.32	1.10
1:A:44:LEU:HD13	1:A:55:VAL:HG11	1.34	1.09
1:B:244:ILE:HD11	1:B:319:VAL:CG2	1.84	1.08
1:B:116:VAL:HG13	1:B:645:LYS:HG2	1.28	1.06

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	1602/1661 (96%)	1285 (80%)	213 (13%)	104 (6%)	2	11
1	B	1602/1661 (96%)	1268 (79%)	239 (15%)	95 (6%)	2	14
All	All	3204/3322 (96%)	2553 (80%)	452 (14%)	199 (6%)	2	13

5 of 199 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	PRO
1	A	91	PRO
1	A	187	ILE
1	A	212	SER
1	A	244	ILE

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	1420/1465 (97%)	1238 (87%)	182 (13%)	6	27
1	B	1420/1465 (97%)	1234 (87%)	186 (13%)	6	25
All	All	2840/2930 (97%)	2472 (87%)	368 (13%)	6	26

5 of 368 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1447	ASP
1	B	151	VAL
1	B	1351	LEU
1	A	1492	HIS

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Mol	Chain	Res	Type
1	B	54	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	71	ASN
1	B	296	ASN
1	B	1298	GLN
1	B	79	ASN
1	B	184	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 ⓘ

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	$\# Z > 2$
2	NAG	A	2001	1,2	12,14,15	0.59	0	15,19,21	1.12	1 (6%)
2	NAG	A	2002	2	12,14,15	0.64	0	15,19,21	1.02	2 (13%)
2	BMA	A	2003	2	10,11,12	0.43	0	11,15,17	0.79	1 (9%)
2	NAG	B	2001	1,2	12,14,15	0.60	0	15,19,21	1.35	2 (13%)
2	NAG	B	2002	2	12,14,15	0.61	0	15,19,21	1.36	2 (13%)
2	BMA	B	2003	2	10,11,12	0.43	0	11,15,17	0.84	1 (9%)

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	2001	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	2002	2	-	0/6/23/26	0/1/1/1
2	BMA	A	2003	2	-	0/2/19/22	0/1/1/1
2	NAG	B	2001	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	B	2002	2	-	0/6/23/26	0/1/1/1
2	BMA	B	2003	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2002	NAG	O5-C5-C6	3.28	110.42	106.98
2	A	2001	NAG	O5-C5-C6	3.17	110.31	106.98
2	B	2001	NAG	O5-C5-C6	3.15	110.28	106.98
2	B	2001	NAG	O5-C5-C4	2.74	114.13	110.65
2	B	2002	NAG	C3-C2-N2	-2.57	107.85	111.76

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2001	NAG	C1
2	B	2001	NAG	C1

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

There are no ligands in this entry.

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	1610/1661 (96%)	-0.11	11 (0%) 84 28	15, 101, 169, 200	0
1	B	1610/1661 (96%)	-0.13	7 (0%) 90 41	17, 96, 169, 200	0
All	All	3220/3322 (96%)	-0.12	18 (0%) 86 32	15, 99, 169, 200	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	742	LEU	3.4
1	A	348	VAL	3.1
1	B	1654	MET	3.0
1	A	741	ALA	3.0
1	A	349	THR	2.6

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	A	2002	14/15	0.32	2.71	80,81,82,82	0
2	NAG	A	2001	14/15	0.24	1.15	74,80,81,82	0
2	NAG	B	2002	14/15	0.26	0.74	80,80,81,82	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	BMA	B	2003	11/12	0.23	0.69	80,81,81,82	0
2	NAG	B	2001	14/15	0.14	-1.10	73,80,81,82	0
2	BMA	A	2003	11/12	0.40	-	81,81,82,82	0

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.