



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:56 PM GMT

PDB ID : 1HXH
Title : COMAMONAS TESTOSTERONI 3BETA/17BETA HYDROXYSTEROID
DEHYDROGENASE
Authors : Benach, J.; Filling, C.; Oppermann, U.C.T.; Roversi, P.; Bricogne, G.; Berndt,
K.D.; Jornvall, H.; Ladenstein, R.
Deposited on : 2001-01-15
Resolution : 1.22 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

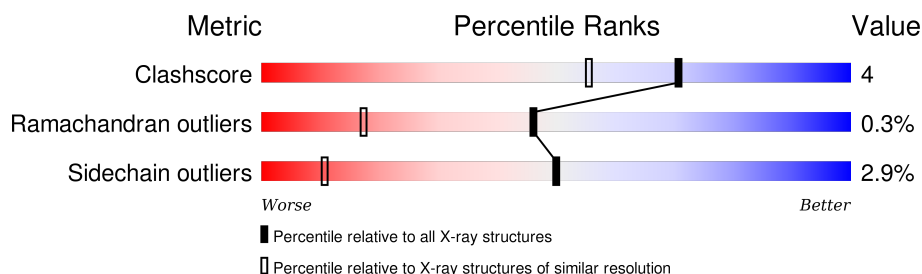
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.22 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	1295 (1.26-1.18)
Ramachandran outliers	100387	1239 (1.26-1.18)
Sidechain outliers	100360	1237 (1.26-1.18)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	253	
1	B	253	
1	C	253	
1	D	253	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9110 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 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	17	0
			1959	1220	350	375	14			
1	B	253	Total	C	N	O	S	0	18	0
			1971	1229	355	372	15			
1	C	253	Total	C	N	O	S	0	17	0
			1961	1221	347	378	15			
1	D	253	Total	C	N	O	S	0	17	0
			1963	1225	346	378	14			

- Molecule 2 is water.

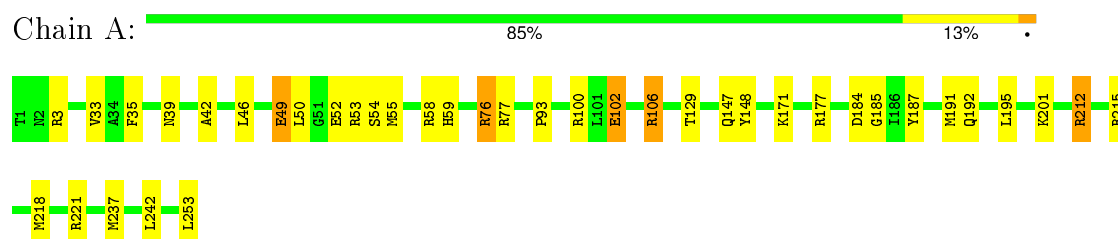
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	284	Total	O	0	0
			284	284		
2	B	323	Total	O	0	0
			323	323		
2	C	350	Total	O	0	0
			350	350		
2	D	299	Total	O	0	0
			299	299		

3 Residue-property plots [i](#)

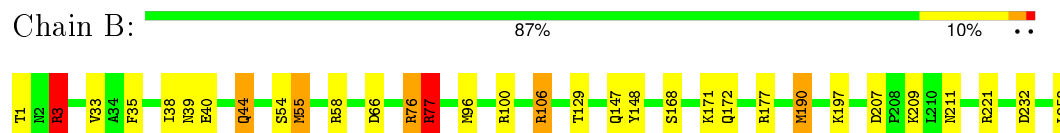
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($RSRZ > 2$). 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.

Note EDS was not executed.

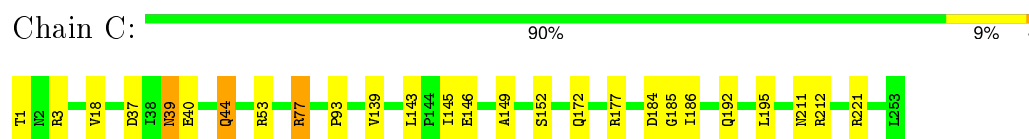
• Molecule 1: 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE



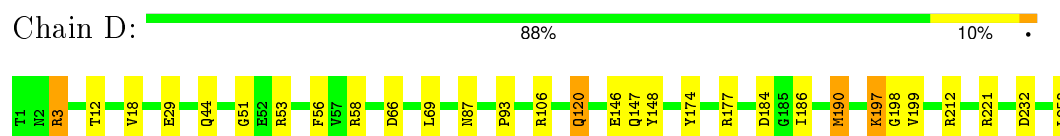
• Molecule 1: 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE



• Molecule 1: 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE



• Molecule 1: 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.02Å 110.59Å 115.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.22	Depositor
% Data completeness (in resolution range)	96.6 (20.00-1.22)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC, CNS, SHELXL-97	Depositor
R, R_{free}	0.146 , 0.180	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9110	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.70	1/2034 (0.0%)	1.35	22/2741 (0.8%)
1	B	0.68	1/2055 (0.0%)	1.28	18/2765 (0.7%)
1	C	0.69	0/2035	1.16	9/2742 (0.3%)
1	D	0.72	2/2032 (0.1%)	1.32	16/2739 (0.6%)
All	All	0.70	4/8156 (0.0%)	1.28	65/10987 (0.6%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	253	LEU	C-O	9.82	1.42	1.23
1	A	253	LEU	C-OXT	5.66	1.34	1.23
1	B	253	LEU	C-OXT	5.42	1.33	1.23
1	D	253	LEU	C-OXT	-5.23	1.13	1.23

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	76	ARG	CD-NE-CZ	16.25	146.36	123.60
1	A	76	ARG	NE-CZ-NH2	-12.40	114.10	120.30
1	A	3	ARG	NE-CZ-NH2	-10.98	114.81	120.30
1	A	106[A]	ARG	NE-CZ-NH1	10.91	125.76	120.30
1	A	106[B]	ARG	NE-CZ-NH1	10.91	125.76	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1959	0	2006	25	0
1	B	1971	0	2038	17	0
1	C	1961	0	2005	15	0
1	D	1963	0	2013	18	0
2	A	284	0	0	10	0
2	B	323	0	0	6	0
2	C	350	0	0	13	0
2	D	299	0	0	12	0
All	All	9110	0	8062	71	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 4.

The worst 5 of 71 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:C:192:GLN:HG3	2:C:599:HOH:O	1.84	0.78
1:B:76:ARG:HG3	2:B:550:HOH:O	1.86	0.75
1:B:96:MET:O	1:D:120[B]:GLN:HG2	1.88	0.73
1:A:76:ARG:HG3	2:A:495:HOH:O	1.92	0.67
1:B:40:GLU:OE2	1:B:58:ARG:HG3	1.97	0.65

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	268/253 (106%)	263 (98%)	4 (2%)	1 (0%)	39	12
1	B	269/253 (106%)	263 (98%)	6 (2%)	0	100	100
1	C	268/253 (106%)	262 (98%)	5 (2%)	1 (0%)	39	12
1	D	268/253 (106%)	263 (98%)	4 (2%)	1 (0%)	39	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1073/1012 (106%)	1051 (98%)	19 (2%)	3 (0%)	46	17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	184	ASP
1	A	184	ASP
1	C	184	ASP

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	214/198 (108%)	211 (99%)	3 (1%)	74	38
1	B	216/198 (109%)	202 (94%)	14 (6%)	21	1
1	C	215/198 (109%)	208 (97%)	7 (3%)	45	8
1	D	215/198 (109%)	212 (99%)	3 (1%)	74	38
All	All	860/792 (109%)	833 (97%)	27 (3%)	50	9

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	106[B]	ARG
1	B	197	LYS
1	D	44	GLN
1	B	177	ARG
1	B	39	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	121	GLN
1	C	192	GLN

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Mol	Chain	Res	Type
1	D	172	GLN
1	B	224	GLN
1	D	45	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.