wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 02:49 AM GMT

PDB ID	:	2IUV
Title	:	CRYSTAL STRUCTURE OF N-QUINOL FORM OF AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS, FORM B
Authors	:	Roujeinikova, A.; Scrutton, N.; Leys, D.
Deposited on	:	2006-06-07
Resolution	:	1.55 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

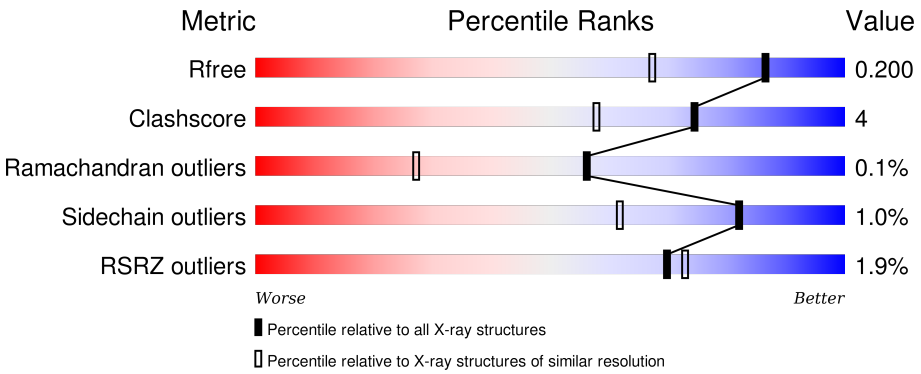
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

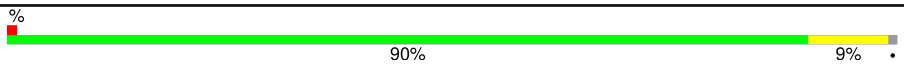
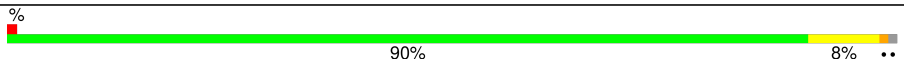
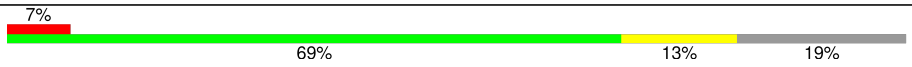
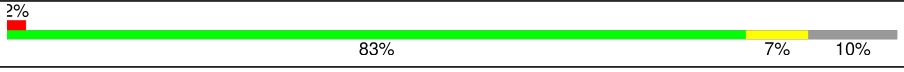
The reported resolution of this entry is 1.55 Å.

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}	91344	1665 (1.58-1.54)
Clashscore	102246	1014 (1.56-1.56)
Ramachandran outliers	100387	1704 (1.58-1.54)
Sidechain outliers	100360	1702 (1.58-1.54)
RSRZ outliers	91569	1668 (1.58-1.54)

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 <=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	361	
1	B	361	
2	D	135	
2	H	135	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8696 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 AROMATIC AMINE DEHYDROGENASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	359	2806	1770	489	533	14	0	1	0
1	B	358	2791	1761	486	530	14	0	1	0

- Molecule 2 is a protein called AROMATIC AMINE DEHYDROGENASE BETA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	110	833	508	149	161	15	0	0	1
2	H	122	925	564	163	183	15	0	0	0

- Molecule 3 is water.

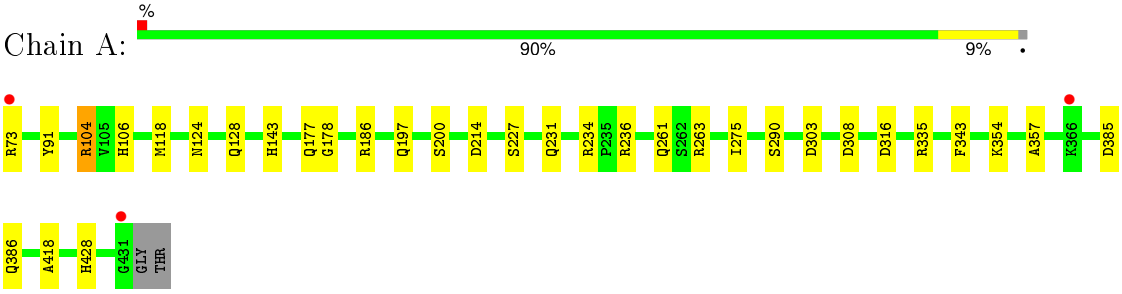
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	509	509	509	0	0
3	B	560	560	560	0	0
3	D	115	115	115	0	0
3	H	157	157	157	0	0

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.

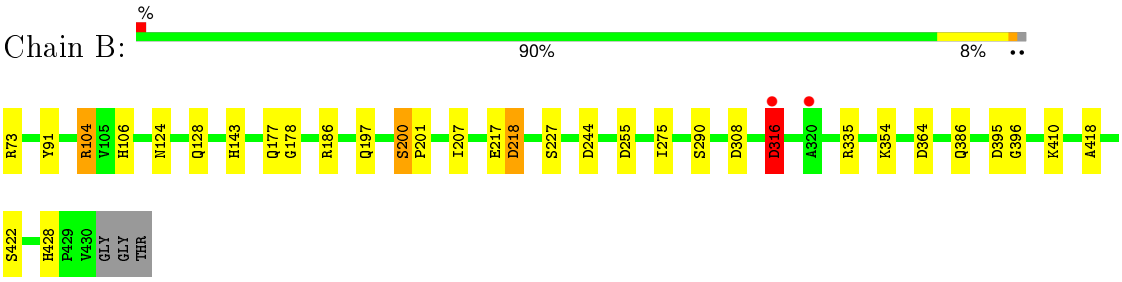
- Molecule 1: AROMATIC AMINE DEHYDROGENASE ALPHA SUBUNIT

Chain A:



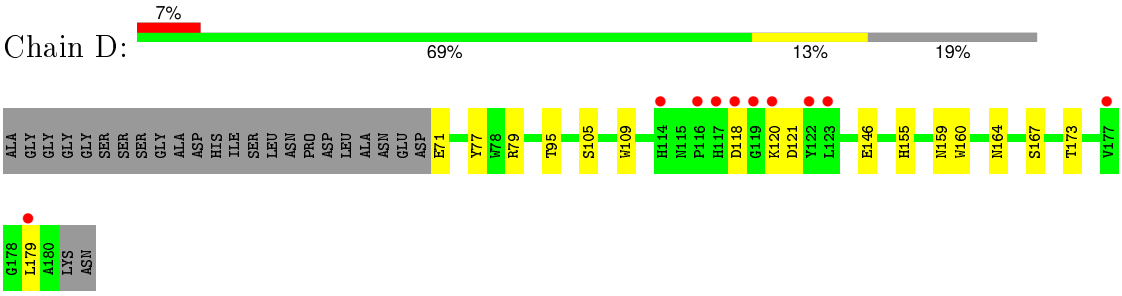
- Molecule 1: AROMATIC AMINE DEHYDROGENASE ALPHA SUBUNIT

Chain B:



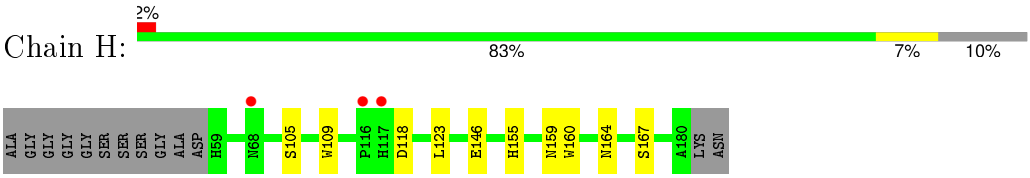
- Molecule 2: AROMATIC AMINE DEHYDROGENASE BETA SUBUNIT

Chain D:



- Molecule 2: AROMATIC AMINE DEHYDROGENASE BETA SUBUNIT

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	89.84Å 96.30Å 118.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.55 29.30 – 1.55	Depositor EDS
% Data completeness (in resolution range)	89.4 (15.00-1.55) 89.4 (29.30-1.55)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.56 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.1.9999	Depositor
R, R_{free}	0.155 , 0.190 0.167 , 0.200	Depositor DCC
R_{free} test set	6702 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	11.6	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 60.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 133720 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8696	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: TQQ

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	0.52	0/2874	0.74	5/3894 (0.1%)
1	B	0.54	0/2859	0.75	7/3877 (0.2%)
2	D	0.50	0/839	0.75	2/1143 (0.2%)
2	H	0.52	0/932	0.73	1/1271 (0.1%)
All	All	0.52	0/7504	0.74	15/10185 (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

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	218	ASP	CB-CG-OD2	7.88	125.40	118.30
1	B	316	ASP	CB-CG-OD2	6.23	123.91	118.30
1	B	244	ASP	CB-CG-OD2	6.12	123.80	118.30
2	D	121	ASP	CB-CG-OD2	6.11	123.80	118.30
1	A	303	ASP	CB-CG-OD2	5.90	123.61	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	200	SER	Peptide

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	2806	0	2749	21	0
1	B	2791	0	2722	23	0
2	D	833	0	729	13	0
2	H	925	0	812	8	0
3	A	509	0	0	3	0
3	B	560	0	0	4	0
3	D	115	0	0	5	0
3	H	157	0	0	1	0
All	All	8696	0	7012	58	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 58 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:118[A]:MET:SD	3:D:2069:HOH:O	2.40	0.80
1:A:104:ARG:HH11	1:A:106:HIS:HE1	1.36	0.73
1:B:91:TYR:OH	1:B:428:HIS:HD2	1.72	0.72
1:B:104:ARG:HH11	1:B:106:HIS:HE1	1.39	0.71
1:A:124:ASN:HD21	1:A:178:GLY:H	1.40	0.69

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	358/361 (99%)	344 (96%)	14 (4%)	0	100	100
1	B	357/361 (99%)	344 (96%)	12 (3%)	1 (0%)	46	20
2	D	107/135 (79%)	105 (98%)	2 (2%)	0	100	100
2	H	119/135 (88%)	115 (97%)	4 (3%)	0	100	100
All	All	941/992 (95%)	908 (96%)	32 (3%)	1 (0%)	56	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	200	SER

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	305/305 (100%)	301 (99%)	4 (1%)	76	51
1	B	302/305 (99%)	299 (99%)	3 (1%)	82	62
2	D	94/112 (84%)	94 (100%)	0	100	100
2	H	104/112 (93%)	103 (99%)	1 (1%)	82	62
All	All	805/834 (96%)	797 (99%)	8 (1%)	82	62

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	263	ARG
2	H	123	LEU
1	B	218	ASP
1	A	261	GLN
1	B	104	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	106	HIS
1	B	177	GLN
2	H	143	GLN
1	B	128	GLN
1	B	180	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	TQQ	D	109	2	14,17,18	4.32	6 (42%)	8,24,26	2.39	3 (37%)
2	TQQ	H	109	2	14,17,18	4.42	6 (42%)	8,24,26	1.76	3 (37%)

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	TQQ	D	109	2	-	0/3/19/21	0/2/2/2
2	TQQ	H	109	2	-	0/3/19/21	0/2/2/2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	109	TQQ	CE2-CZ2	-9.20	1.38	1.49
2	D	109	TQQ	CE2-CZ2	-8.89	1.39	1.49
2	H	109	TQQ	CH2-CZ2	-5.72	1.35	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	109	TQQ	CH2-CZ2	-5.31	1.36	1.50
2	D	109	TQQ	CZ3-CH2	-3.27	1.39	1.44

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	109	TQQ	O2-CZ2-CE2	-4.48	117.12	122.10
2	D	109	TQQ	CD2-CE3-CZ3	-2.67	118.17	121.16
2	H	109	TQQ	O2-CZ2-CE2	-2.43	119.40	122.10
2	H	109	TQQ	CD2-CE3-CZ3	-2.31	118.57	121.16
2	H	109	TQQ	CD1-NE1-CE2	2.03	109.58	104.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	109	TQQ	2	0
2	H	109	TQQ	2	0

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 (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, 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	359/361 (99%)	-0.04	3 (0%)	87	89	7, 13, 27, 50	0
1	B	358/361 (99%)	-0.30	2 (0%)	90	92	6, 11, 22, 34	0
2	D	109/135 (80%)	0.29	10 (9%)	11	11	9, 16, 40, 54	0
2	H	121/135 (89%)	-0.13	3 (2%)	61	64	7, 11, 26, 33	0
All	All	947/992 (95%)	-0.11	18 (1%)	70	73	6, 13, 27, 54	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	431	GLY	5.9
2	D	117	HIS	5.1
2	D	179	LEU	4.6
2	D	116	PRO	4.5
2	D	120	LYS	3.7

6.2 Non-standard residues in protein, DNA, RNA chains (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, 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	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	TQQ	D	109	16/17	0.94	0.08	-	9,13,19,25	0
2	TQQ	H	109	16/17	0.96	0.08	-	7,10,14,15	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.