



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2021 – 03:11 PM EDT

PDB ID : 2ONO  
Title : Arg475Gln Mutant of Mitochondrial Aldehyde Dehydrogenase, apo form,  
pseudo-merohedrally twinned  
Authors : Larson, H.N.; Hurley, T.D.  
Deposited on : 2007-01-24  
Resolution : 2.15 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](mailto: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.

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

MolProbity	:	4.02b-467
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



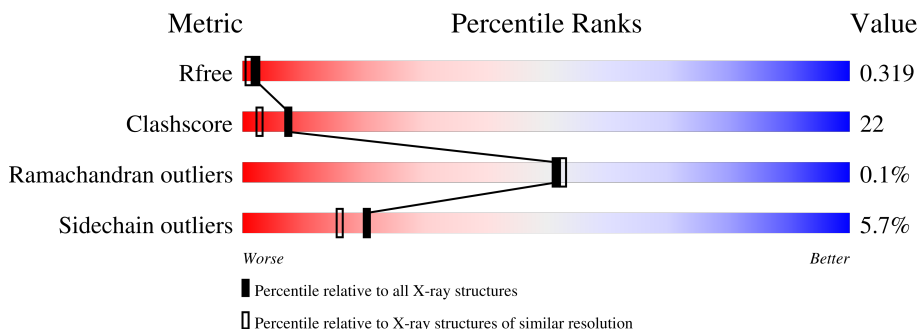
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)


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  $\geq 3$ , 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	500	
1	B	500	
1	C	500	
1	D	500	
1	E	500	
1	F	500	
1	G	500	

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Mol	Chain	Length	Quality of chain
1	H	500	 58% 39% ..



## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 31388 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 Aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	B	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	C	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	D	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	E	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	F	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	G	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			
1	H	494	Total	C	N	O	S	0	0	0
			3796	2414	646	718	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	475	GLN	ARG	engineered mutation	UNP P05091
B	475	GLN	ARG	engineered mutation	UNP P05091
C	475	GLN	ARG	engineered mutation	UNP P05091
D	475	GLN	ARG	engineered mutation	UNP P05091
E	475	GLN	ARG	engineered mutation	UNP P05091
F	475	GLN	ARG	engineered mutation	UNP P05091
G	475	GLN	ARG	engineered mutation	UNP P05091
H	475	GLN	ARG	engineered mutation	UNP P05091

- Molecule 2 is water.



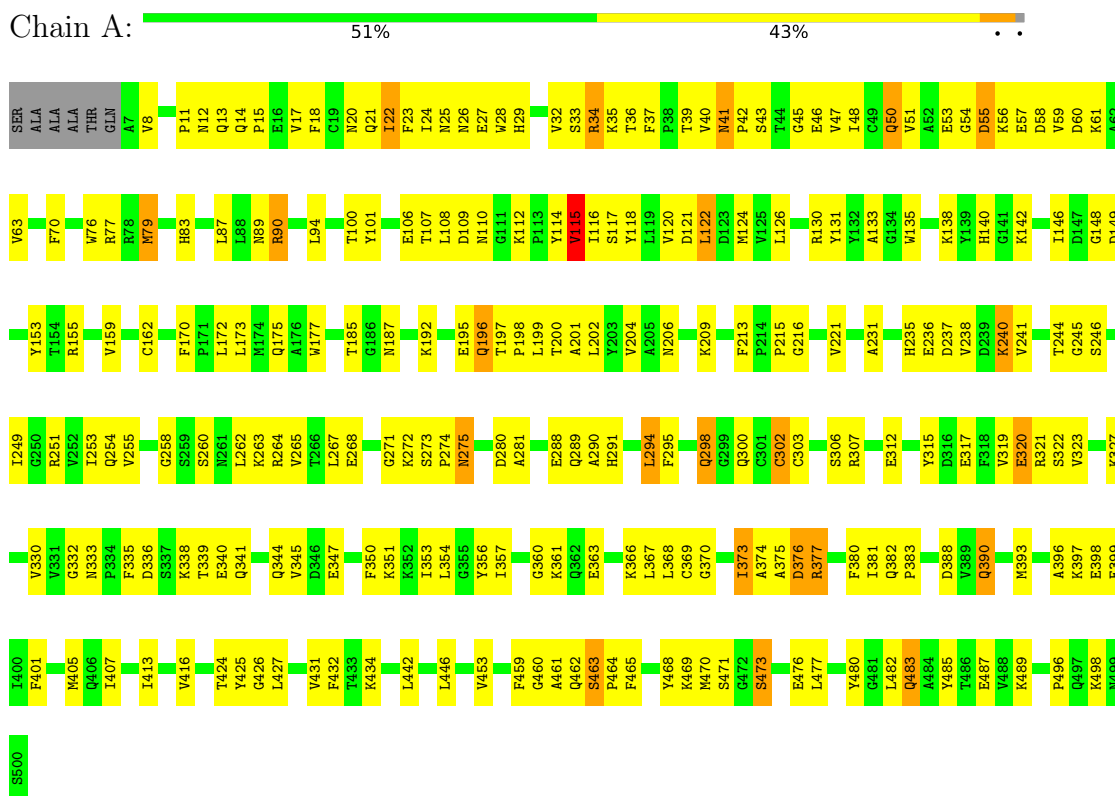
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	134	Total 134	O 134	0	0
2	B	131	Total 131	O 131	0	0
2	C	145	Total 145	O 145	0	0
2	D	133	Total 133	O 133	0	0
2	E	140	Total 140	O 140	0	0
2	F	114	Total 114	O 114	0	0
2	G	118	Total 118	O 118	0	0
2	H	105	Total 105	O 105	0	0



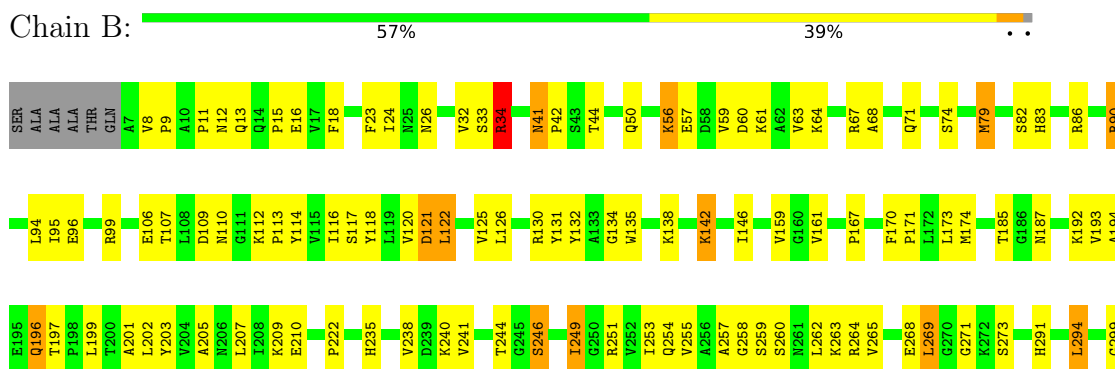
### 3 Residue-property plots

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.

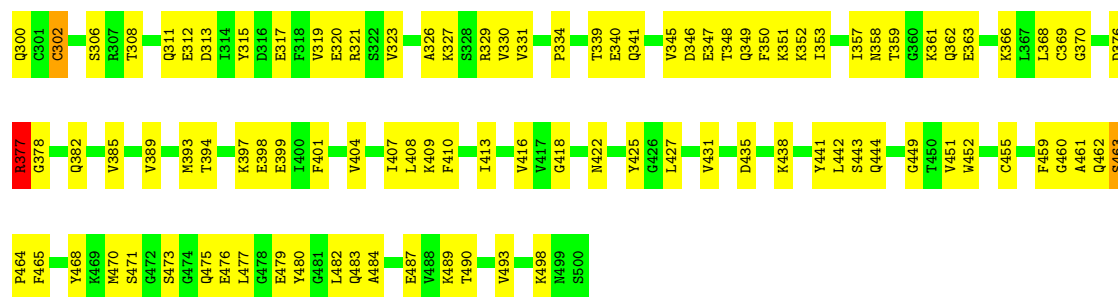
#### • Molecule 1: Aldehyde dehydrogenase



#### • Molecule 1: Aldehyde dehydrogenase

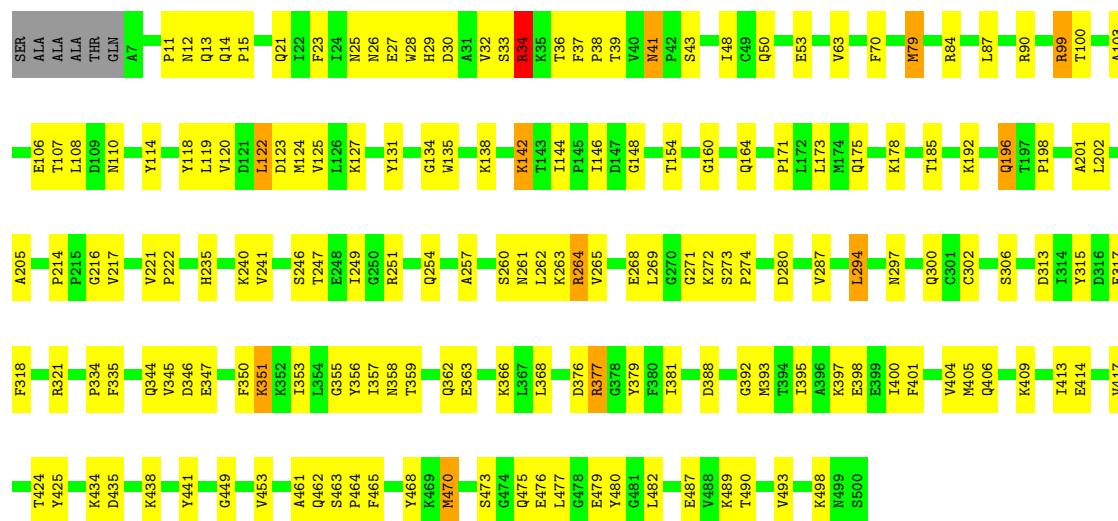






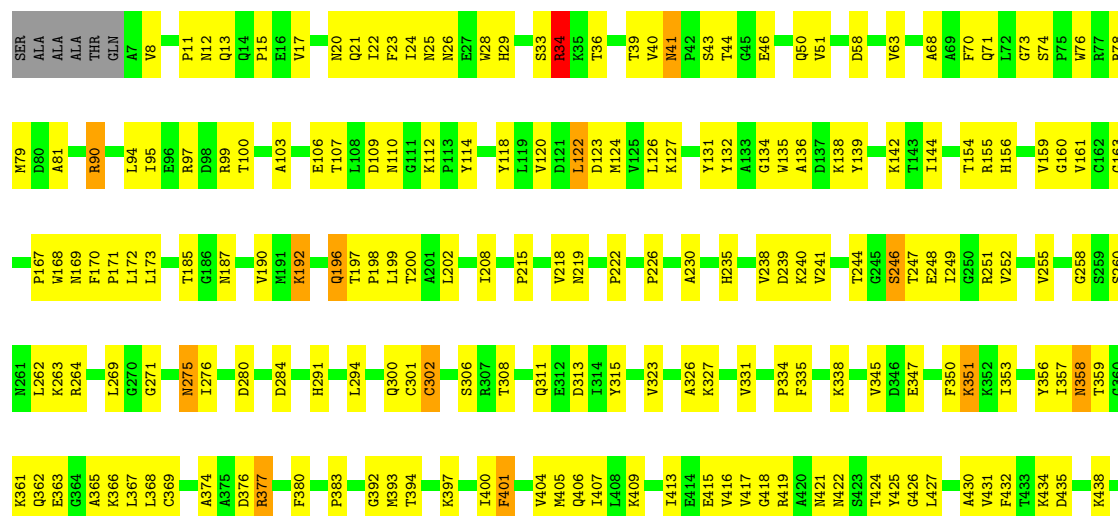
• Molecule 1: Aldehyde dehydrogenase

Chain C: 65% 32% ..



• Molecule 1: Aldehyde dehydrogenase

Chain D: 55% 41% ..

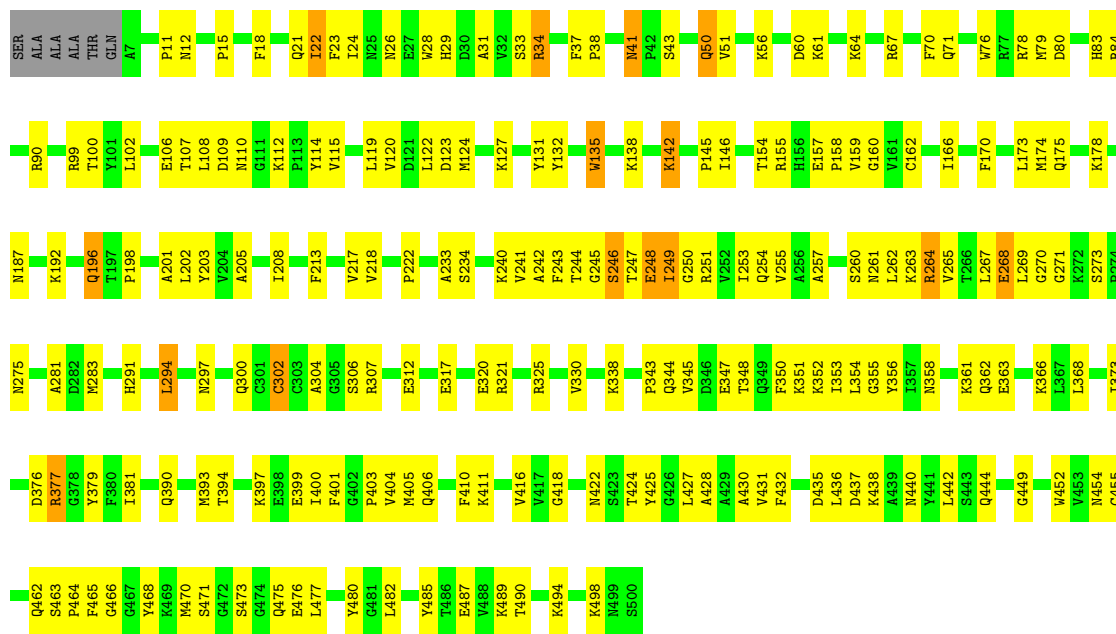






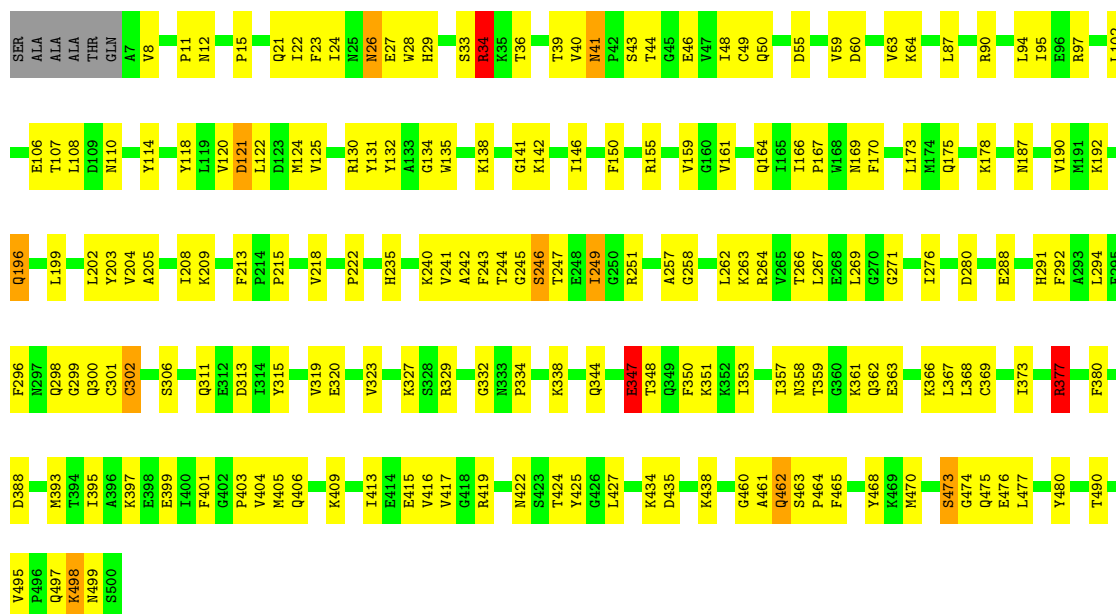
• Molecule 1: Aldehyde dehydrogenase

Chain E: 57% 39%



• Molecule 1: Aldehyde dehydrogenase

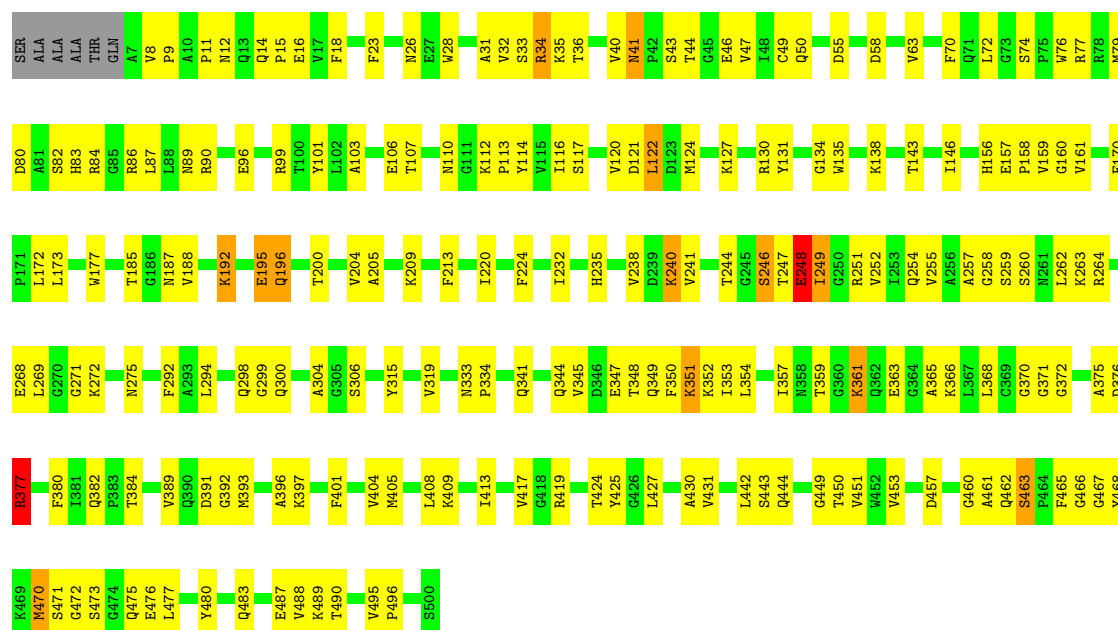
Chain F: 61% 35%



• Molecule 1: Aldehyde dehydrogenase

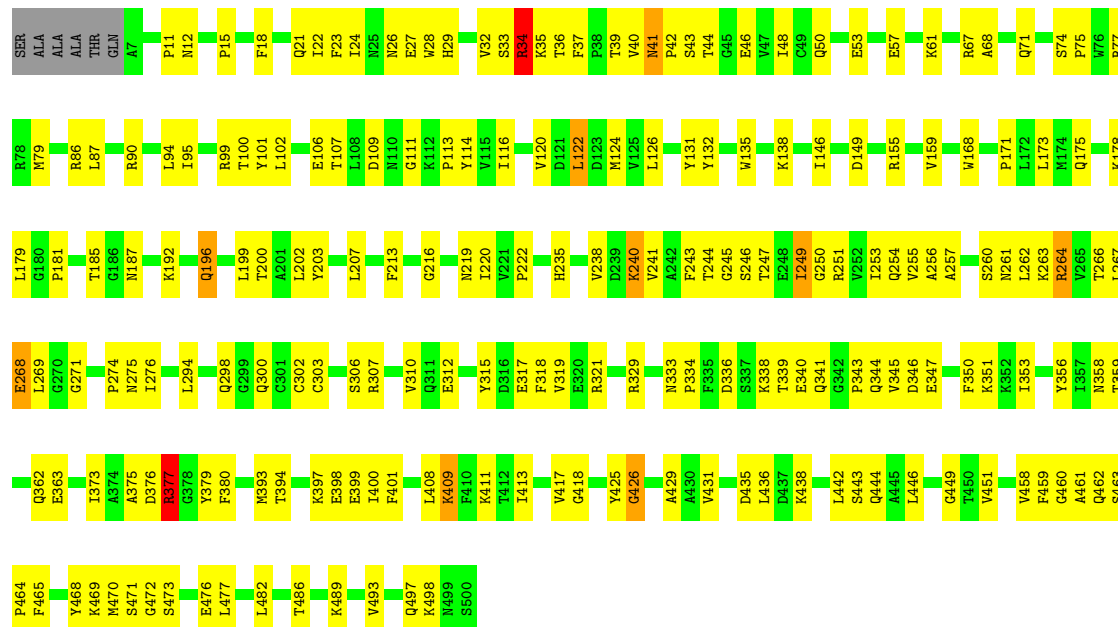


Chain G:  58% 38% ..



• Molecule 1: Aldehyde dehydrogenase

Chain H:  58% 39% ..





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.47Å 175.85Å 101.46Å 90.00° 94.79° 90.00°	Depositor
Resolution (Å)	10.00 – 2.15 24.89 – 2.15	Depositor EDS
% Data completeness (in resolution range)	92.5 (10.00-2.15) 96.5 (24.89-2.15)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.93 (at 2.15Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.251 , 0.314 0.264 , 0.319	Depositor DCC
$R_{free}$ test set	9468 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.8	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 24.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.467 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	31388	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	0.38	3/3880 (0.1%)	0.87	10/5265 (0.2%)
1	B	0.28	0/3880	0.67	7/5265 (0.1%)
1	C	0.36	2/3880 (0.1%)	0.95	10/5265 (0.2%)
1	D	0.29	0/3880	0.67	6/5265 (0.1%)
1	E	0.36	2/3880 (0.1%)	1.01	11/5265 (0.2%)
1	F	0.30	0/3880	0.68	8/5265 (0.2%)
1	G	0.33	2/3880 (0.1%)	0.81	8/5265 (0.2%)
1	H	0.31	1/3880 (0.0%)	0.68	7/5265 (0.1%)
All	All	0.33	10/31040 (0.0%)	0.80	67/42120 (0.2%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	248	GLU	CD-OE1	10.60	1.37	1.25
1	G	361	LYS	CD-CE	9.20	1.74	1.51
1	A	115	VAL	CB-CG1	9.17	1.72	1.52
1	C	268	GLU	CG-CD	8.86	1.65	1.51
1	C	268	GLU	CD-OE2	8.37	1.34	1.25

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	90	ARG	CD-NE-CZ	37.79	176.51	123.60
1	E	99	ARG	NE-CZ-NH1	27.66	134.13	120.30
1	C	34	ARG	NE-CZ-NH1	27.45	134.03	120.30
1	A	90	ARG	CD-NE-CZ	26.80	161.12	123.60
1	E	99	ARG	NE-CZ-NH2	-25.64	107.48	120.30

There are no chirality outliers.

There are no planarity outliers.



## 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	3796	0	3740	221	0
1	B	3796	0	3740	171	0
1	C	3796	0	3740	140	0
1	D	3796	0	3740	182	0
1	E	3796	0	3740	191	0
1	F	3796	0	3740	171	0
1	G	3796	0	3740	182	0
1	H	3796	0	3740	173	0
2	A	134	0	0	27	0
2	B	131	0	0	9	0
2	C	145	0	0	10	0
2	D	133	0	0	11	0
2	E	140	0	0	13	0
2	F	114	0	0	11	0
2	G	118	0	0	18	0
2	H	105	0	0	18	0
All	All	31388	0	29920	1330	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 22.

The worst 5 of 1330 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:249:ILE:CD1	1:D:249:ILE:CG1	1.83	1.52
1:E:424:THR:HG22	1:E:470:MET:HB2	1.20	1.11
1:A:262:LEU:HD21	1:B:251:ARG:HG2	1.41	1.02
1:E:424:THR:HG21	1:E:470:MET:SD	2.02	0.99
1:H:247:THR:HA	1:H:269:LEU:HD22	1.45	0.99

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	492/500 (98%)	475 (96%)	16 (3%)	1 (0%)	47	46
1	B	492/500 (98%)	476 (97%)	16 (3%)	0	100	100
1	C	492/500 (98%)	471 (96%)	21 (4%)	0	100	100
1	D	492/500 (98%)	473 (96%)	18 (4%)	1 (0%)	47	46
1	E	492/500 (98%)	472 (96%)	19 (4%)	1 (0%)	47	46
1	F	492/500 (98%)	476 (97%)	16 (3%)	0	100	100
1	G	492/500 (98%)	472 (96%)	20 (4%)	0	100	100
1	H	492/500 (98%)	477 (97%)	14 (3%)	1 (0%)	47	46
All	All	3936/4000 (98%)	3792 (96%)	140 (4%)	4 (0%)	51	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	270	GLY
1	H	426	GLY
1	A	426	GLY
1	D	426	GLY

### 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	399/402 (99%)	371 (93%)	28 (7%)	15	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	399/402 (99%)	373 (94%)	26 (6%)	17	12
1	C	399/402 (99%)	378 (95%)	21 (5%)	22	19
1	D	399/402 (99%)	381 (96%)	18 (4%)	27	24
1	E	399/402 (99%)	377 (94%)	22 (6%)	21	17
1	F	399/402 (99%)	376 (94%)	23 (6%)	20	15
1	G	399/402 (99%)	378 (95%)	21 (5%)	22	19
1	H	399/402 (99%)	377 (94%)	22 (6%)	21	17
All	All	3192/3216 (99%)	3011 (94%)	181 (6%)	20	16

5 of 181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	26	ASN
1	G	195	GLU
1	F	121	ASP
1	F	347	GLU
1	G	259	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	300	GLN
1	H	83	HIS
1	G	26	ASN
1	G	300	GLN
1	H	462	GLN

### 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 [i](#)

There are no monosaccharides 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

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.