



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1HW2  
Title : FADR-DNA COMPLEX: TRANSCRIPTIONAL CONTROL OF FATTY ACID METABOLISM IN ECHERICHIA COLI  
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Deposited on : 2001-01-09  
Resolution : 3.25 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  
<http://wwpdb.org/validation/2016/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  
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

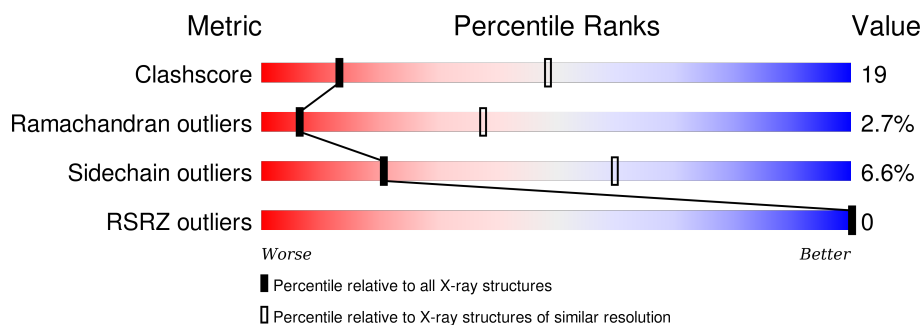
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 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	1806 (3.32-3.20)
Ramachandran outliers	100387	1773 (3.32-3.20)
Sidechain outliers	100360	1771 (3.32-3.20)
RSRZ outliers	91569	1632 (3.32-3.20)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	D	22	
2	E	22	
3	A	239	
3	B	239	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4294 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 DNA chain called 5'-D(\*CP\*GP\*AP\*TP\*CP\*TP\*GP\*GP\*TP\*CP\*CP\*GP\*AP\*CP\*CP\*AP\*GP\*AP\*TP\*GP\*CP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	20	Total	C	N	O	P	0	0	0
			407	194	76	118	19			

- Molecule 2 is a DNA chain called 5'-D(\*G\*CP\*AP\*TP\*CP\*TP\*GP\*GP\*TP\*CP\*GP\*GP\*AP\*CP\*CP\*AP\*GP\*AP\*TP\*CP\*GP\*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	18	Total	C	N	O	P	0	0	0
			366	175	68	106	17			

- Molecule 3 is a protein called FATTY ACID METABOLISM REGULATOR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	222	Total	C	N	O	S	0	0	0
			1760	1118	315	324	3			
3	B	222	Total	C	N	O	S	0	0	0
			1760	1118	315	324	3			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Mg	0	0
			1	1		



Y193		L196	S201	G203	A204	D205	Y209	E210	T211	V212	R214	G216	H217	E218	ASN	LEU	PBO	GLY	ASP	LEU	ALA	IIE	GLN	GLY	ARG
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.73Å 110.15Å 130.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.25 19.93 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.25) 94.9 (19.93-3.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.65 (at 3.22Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.235 , 0.278 0.228 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	80.2	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , 52.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20274 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4294	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG

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	D	0.78	1/456 (0.2%)	1.10	4/702 (0.6%)
2	E	1.04	3/410 (0.7%)	1.43	7/631 (1.1%)
3	A	0.40	0/1802	0.62	0/2449
3	B	0.42	0/1802	0.63	0/2449
All	All	0.54	4/4470 (0.1%)	0.81	11/6231 (0.2%)

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	D	0	2
2	E	1	2
All	All	1	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	12	DG	C2-N2	-8.97	1.25	1.34
1	D	7	DG	C5-C6	-5.89	1.36	1.42
2	E	12	DG	N9-C4	-5.47	1.33	1.38
2	E	12	DG	N1-C2	5.36	1.42	1.37

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	12	DG	N9-C1'-C2'	10.69	132.90	112.60
1	D	8	DG	O5'-P-OP2	-9.75	96.92	105.70
2	E	12	DG	O4'-C1'-C2'	9.29	113.33	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	8	DG	C5'-C4'-O4'	8.81	126.03	109.30
2	E	12	DG	O4'-C1'-N9	6.91	112.84	108.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	12	DG	C1'

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	5	DC	Sidechain
1	D	6	DT	Sidechain
2	E	4	DT	Sidechain
2	E	5	DC	Sidechain

## 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	D	407	0	226	23	0
2	E	366	0	202	7	0
3	A	1760	0	1709	68	0
3	B	1760	0	1709	69	0
4	E	1	0	0	0	0
All	All	4294	0	3846	154	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 19.

The worst 5 of 154 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:8:DG:OP2	3:B:49:ARG:NH2	2.04	0.90
1:D:7:DG:H2"	1:D:8:DG:OP2	1.78	0.83
2:E:10:DC:OP2	3:B:44:THR:HG22	1.81	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:DC:H2''	1:D:16:DA:O5'	1.81	0.80
3:A:78:SER:HB3	3:A:82:ILE:HD13	1.64	0.80

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	
3	A	220/239 (92%)	184 (84%)	30 (14%)	6 (3%)	6	37
3	B	220/239 (92%)	179 (81%)	35 (16%)	6 (3%)	6	37
All	All	440/478 (92%)	363 (82%)	65 (15%)	12 (3%)	6	37

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	23	ASN
3	B	23	ASN
3	B	205	HIS
3	A	170	GLY
3	A	205	HIS

### 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	
3	A	181/199 (91%)	169 (93%)	12 (7%)	21	60
3	B	181/199 (91%)	169 (93%)	12 (7%)	21	60
All	All	362/398 (91%)	338 (93%)	24 (7%)	21	60

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	213	ARG
3	B	45	ARG
3	B	213	ARG
3	A	218	GLU
3	B	36	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	65	HIS
3	B	81	ASN
3	B	72	ASN
3	A	81	ASN
3	B	73	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	D	20/22 (90%)	-0.31	0 100 100	46, 62, 78, 91	0
2	E	18/22 (81%)	-0.22	0 100 100	41, 63, 92, 125	0
3	A	222/239 (92%)	-0.69	0 100 100	18, 65, 158, 194	0
3	B	222/239 (92%)	-0.77	0 100 100	18, 50, 119, 177	0
All	All	482/522 (92%)	-0.69	0 100 100	18, 59, 143, 194	0

There are no RSRZ outliers to report.

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	MG	E	23	1/1	0.97	0.23	-	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.