

wwPDB X-ray Structure Validation Summary Report (i)

Jan 28, 2024 - 01:14 PM EST

PDB ID	:	1DYH
Title	:	ISOMORPHOUS CRYSTAL STRUCTURES OF ESCHERICHIA COLI
		DIHYDROFOLATE REDUCTASE COMPLEXED WITH FOLATE, 5-
		DEAZAFOLATE AND 5,10-DIDEAZATETRAHYDROFOLATE: MECHA-
		NISTIC IMPLICATIONS
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Deposited on		
Resolution	:	1.90 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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

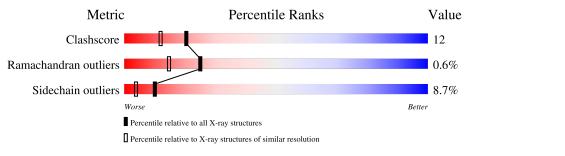
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.90 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 >=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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of cha	in	
1	А	159	58%	30%	9% •
1	В	159	62%	30%	6% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DZF	А	161	-	Х	-	-
3	DZF	В	161	-	Х	-	-



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$\mathbf{2}$ Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2997 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.

									-
Mol	Chain	Residues		At	oms			ZeroOcc	AltConf
1	Δ	159	Total	С	N	0	S	0	0

• Molecule 1 is a protein called DIHYDROFOLATE REDUCTASE.

Mol	Chain	Residues		At	\mathbf{oms}			ZeroOcc	AltConf	Trace
1	Δ	159	Total	С	Ν	0	S	0	0 0	
	A	159	1246	793	211	235	$\overline{7}$	0	0	0
1	Р	159	Total	С	Ν	0	S	0	0	0
	D	109	1262	803	216	236	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

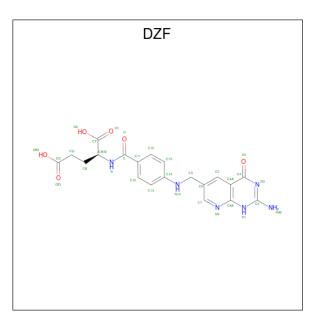
Chain	Residue	Modelled	Actual	Comment	Reference
A	37	ASP	ASN	conflict	UNP P0ABQ4
В	37	ASP	ASN	conflict	UNP P0ABQ4

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Cl 1 1	0	0
2	В	1	Total Cl 1 1	0	0

• Molecule 3 is 5-DEAZAFOLIC ACID (three-letter code: DZF) (formula: C₂₀H₂₀N₆O₆).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total C N O 32 20 6 6	0	0
3	В	1	Total C N O 32 20 6 6	0	0

• Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Ca 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	229	Total O 229 229	0	0
5	В	193	Total O 193 193	0	0

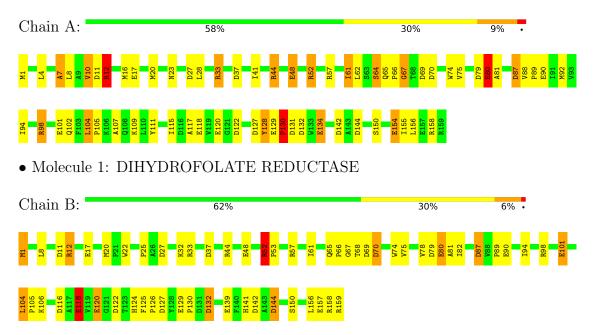


3 Residue-property plots (i)

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.

Note EDS was not executed.

• Molecule 1: DIHYDROFOLATE REDUCTASE





4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 61	Depositor
Cell constants	93.20Å 93.20Å 73.94Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) - 1.90	Depositor
% Data completeness	(Not available) ((Not available)-1.90)	Depositor
(in resolution range)		Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.149 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2997	wwPDB-VP
Average B, all atoms $(Å^2)$	30.0	wwPDB-VP



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: CL, CA, DZF

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	Bo	Bond lengths		ond angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	1.04	8/1279~(0.6%)	1.69	30/1740~(1.7%)
1	В	1.05	9/1296~(0.7%)	1.73	31/1762~(1.8%)
All	All	1.04	17/2575~(0.7%)	1.71	61/3502~(1.7%)

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	А	1	0

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	17	GLU	CD-OE2	7.52	1.33	1.25
1	А	90	GLU	CD-OE2	7.20	1.33	1.25
1	В	101	GLU	CD-OE2	6.97	1.33	1.25
1	В	80	GLU	CD-OE1	6.96	1.33	1.25
1	А	120	GLU	CD-OE2	6.66	1.32	1.25

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	В	144	ASP	CB-CG-OD1	9.77	127.09	118.30
1	В	33	ARG	NE-CZ-NH1	9.70	125.15	120.30
1	В	27	ASP	CB-CG-OD1	9.31	126.68	118.30
1	А	87	ASP	CB-CG-OD1	-9.21	110.01	118.30
1	В	87	ASP	CB-CG-OD2	-9.04	110.16	118.30



All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	А	65	GLN	CA

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	А	1246	0	1178	34	0
1	В	1262	0	1217	27	2
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	32	0	17	2	0
3	В	32	0	19	2	0
4	В	1	0	0	0	0
5	А	229	0	0	9	2
5	В	193	0	0	7	4
All	All	2997	0	2431	62	4

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 12.

The worst 5 of 62 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:20:MET:HG2	5:A:583:HOH:O	1.84	0.77
1:B:124:HIS:HB3	5:B:601:HOH:O	1.84	0.76
1:B:144:ASP:HB2	5:B:531:HOH:O	1.90	0.71
1:A:134:GLU:HG3	5:A:610:HOH:O	1.92	0.69
1:B:65:GLN:HB3	1:B:66:PRO:CD	2.22	0.69

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:467:HOH:O	5:B:528:HOH:O[3_564]	1.99	0.21
5:A:448:HOH:O	5:B:470:HOH:O[3_564]	2.12	0.08
1:B:159:ARG:NH1	5:B:561:HOH:O[2_665]	2.13	0.07
1:B:70:ASP:OD2	5:B:595:HOH:O[5_564]	2.19	0.01

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	Perce	ntiles
1	А	157/159~(99%)	150 (96%)	5(3%)	2(1%)	12	4
1	В	157/159~(99%)	153~(98%)	4 (2%)	0	100	100
All	All	314/318~(99%)	303~(96%)	9~(3%)	2(1%)	25	15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	130	PRO
1	А	67	GLY

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	Analysed Rotameric Outliers		Percentiles		
1	А	129/136~(95%)	115 (89%)	14 (11%)	6 2		
1	В	134/136~(98%)	125~(93%)	9~(7%)	16 7		
All	All	263/272 (97%)	240 (91%)	23~(9%)	10 4		



5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	1	MET
1	В	87	ASP
1	В	61	ILE
1	В	101	GLU
1	А	52	ARG

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

Mol	Chain	\mathbf{Res}	Type
1	В	18	ASN
1	В	65	GLN
1	В	124	HIS
1	А	23	ASN
1	А	18	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)

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)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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	Trune	Chain	Dec	Timle	В	ond leng	gths	B	Bond ang	gles
INIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	DZF	В	161	-	32,34,34	4.48	18 (56%)	42,47,47	4.37	22 (52%)
3	DZF	А	161	-	32,34,34	4.22	20 (62%)	42,47,47	<mark>3.68</mark>	21 (50%)

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.

Mo	l Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DZF	В	161	-	-	5/22/22/22	0/3/3/3
3	DZF	А	161	-	-	2/22/22/22	0/3/3/3

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	161	DZF	C16-C15	16.35	1.68	1.38
3	В	161	DZF	C4-N3	11.11	1.52	1.33
3	В	161	DZF	C16-C11	-10.11	1.22	1.39
3	В	161	DZF	C13-C14	8.08	1.52	1.39
3	В	161	DZF	OE1-CD	7.92	1.48	1.22

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	161	DZF	C4A-C4-N3	-13.64	114.89	124.40
3	А	161	DZF	C4A-C4-N3	-13.31	115.12	124.40
3	В	161	DZF	C6-C5-C4A	-9.86	107.90	122.65
3	В	161	DZF	N1-C2-N3	-8.82	115.46	127.22
3	А	161	DZF	N1-C2-N3	-8.40	116.01	127.22

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	161	DZF	N-CA-CB-CG
3	В	161	DZF	CT-CA-CB-CG
3	А	161	DZF	CT-CA-CB-CG
3	В	161	DZF	CA-CB-CG-CD
3	В	161	DZF	N-CA-CB-CG

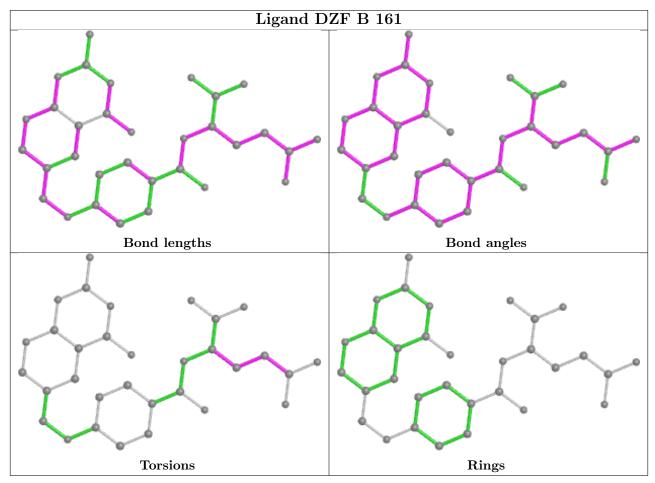
There are no ring outliers.



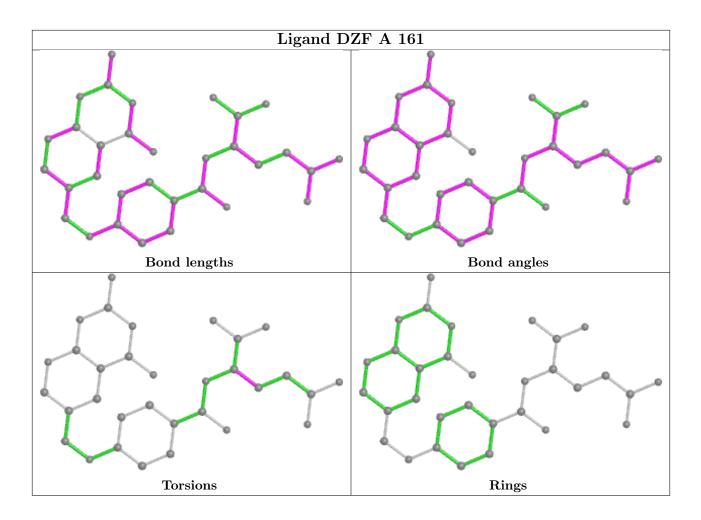
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	161	DZF	2	0
3	А	161	DZF	2	0

2 monomers are involved in 4 short contacts:

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and similar rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

