



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 05:47 AM EDT

PDB ID : 1G8L
Title : CRYSTAL STRUCTURE OF ESCHERICHIA COLI MOEA
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Deposited on : 2000-11-17
Resolution : 1.95 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	2.36.2

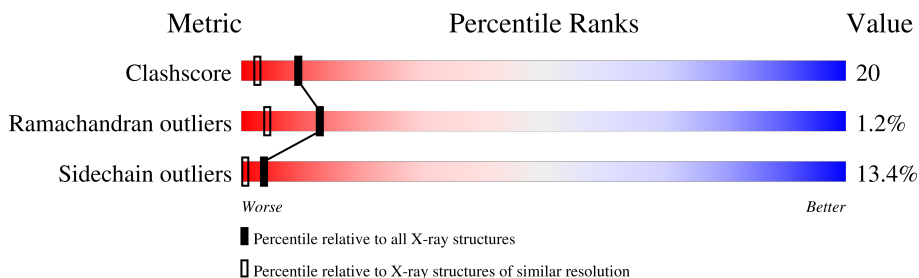
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	411	 61% 31% 6% •
1	B	411	 61% 29% 8% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6781 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 MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	0	0
			3040	1918	531	578	13			
1	B	403	Total	C	N	O	S	0	0	0
			3040	1918	531	578	13			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	312	Total O 312 312	0	0
3	B	281	Total O 281 281	0	0

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.32Å 97.41Å 98.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95	Depositor
% Data completeness (in resolution range)	91.5 (20.00-1.95)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.228 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6781	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: GOL

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	0.67	0/3099	0.73	3/4212 (0.1%)
1	B	0.67	0/3099	0.70	0/4212
All	All	0.67	0/6198	0.71	3/8424 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	38	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	347	ASP	CB-CG-OD2	5.39	123.15	118.30

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	3040	0	3037	119	0
1	B	3040	0	3037	128	0
2	A	42	0	56	9	0
2	B	66	0	88	9	0
3	A	312	0	0	13	0
3	B	281	0	0	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6781	0	6218	244	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 20.

The worst 5 of 244 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:356:ASN:HD21	1:A:360:GLU:HB2	1.09	1.17
1:B:368:HIS:HD2	1:B:370:GLY:H	1.00	0.95
1:B:374:PHE:H	2:B:703:GOL:H31	1.30	0.94
1:A:177:LYS:HA	2:A:706:GOL:H11	1.52	0.92
1:A:356:ASN:ND2	1:A:360:GLU:HB2	1.83	0.92

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	401/411 (98%)	383 (96%)	13 (3%)	5 (1%)	13	4
1	B	401/411 (98%)	378 (94%)	18 (4%)	5 (1%)	13	4
All	All	802/822 (98%)	761 (95%)	31 (4%)	10 (1%)	13	4

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	ASP
1	A	282	LYS
1	B	282	LYS
1	A	82	ALA

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Mol	Chain	Res	Type
1	A	228	ASP

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	325/331 (98%)	283 (87%)	42 (13%)	4	0
1	B	325/331 (98%)	280 (86%)	45 (14%)	3	0
All	All	650/662 (98%)	563 (87%)	87 (13%)	4	0

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	118	GLU
1	B	223	LEU
1	B	121	ASP
1	B	182	LEU
1	B	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	55	ASN
1	B	194	GLN
1	B	134	GLN
1	B	210	HIS
1	A	194	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

18 ligands 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	GOL	A	709	-	5,5,5	0.38	0	5,5,5	0.35	0
2	GOL	B	702	-	5,5,5	0.49	0	5,5,5	0.78	0
2	GOL	A	714	-	5,5,5	0.40	0	5,5,5	0.26	0
2	GOL	A	701	-	5,5,5	0.60	0	5,5,5	0.79	0
2	GOL	A	715	-	5,5,5	0.43	0	5,5,5	0.44	0
2	GOL	B	703	-	5,5,5	0.36	0	5,5,5	0.47	0
2	GOL	A	706	-	5,5,5	0.57	0	5,5,5	0.99	0
2	GOL	A	704	-	5,5,5	0.44	0	5,5,5	0.52	0
2	GOL	B	707	-	5,5,5	0.32	0	5,5,5	0.32	0
2	GOL	B	708	-	5,5,5	0.38	0	5,5,5	0.49	0
2	GOL	B	712	-	5,5,5	0.33	0	5,5,5	0.55	0
2	GOL	A	717	-	5,5,5	0.39	0	5,5,5	0.33	0
2	GOL	B	713	-	5,5,5	0.35	0	5,5,5	0.46	0
2	GOL	B	705	-	5,5,5	0.38	0	5,5,5	0.24	0
2	GOL	B	718	-	5,5,5	0.39	0	5,5,5	0.40	0
2	GOL	B	710	-	5,5,5	0.35	0	5,5,5	0.48	0
2	GOL	B	716	-	5,5,5	0.41	0	5,5,5	0.24	0
2	GOL	B	711	-	5,5,5	0.29	0	5,5,5	0.41	0

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	GOL	A	709	-	-	2/4/4/4	-
2	GOL	B	702	-	-	0/4/4/4	-
2	GOL	A	714	-	-	2/4/4/4	-
2	GOL	A	701	-	-	4/4/4/4	-
2	GOL	A	715	-	-	0/4/4/4	-
2	GOL	B	703	-	-	0/4/4/4	-
2	GOL	A	706	-	-	4/4/4/4	-
2	GOL	A	704	-	-	2/4/4/4	-
2	GOL	B	707	-	-	2/4/4/4	-
2	GOL	B	708	-	-	2/4/4/4	-
2	GOL	B	712	-	-	2/4/4/4	-
2	GOL	A	717	-	-	2/4/4/4	-
2	GOL	B	713	-	-	4/4/4/4	-
2	GOL	B	705	-	-	2/4/4/4	-
2	GOL	B	718	-	-	0/4/4/4	-
2	GOL	B	710	-	-	2/4/4/4	-
2	GOL	B	716	-	-	2/4/4/4	-
2	GOL	B	711	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	706	GOL	O1-C1-C2-C3
2	A	709	GOL	O1-C1-C2-C3
2	A	714	GOL	O1-C1-C2-C3
2	B	707	GOL	O1-C1-C2-C3
2	B	708	GOL	C1-C2-C3-O3

There are no ring outliers.

10 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	709	GOL	1	0
2	B	702	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	GOL	3	0
2	A	715	GOL	1	0
2	B	703	GOL	2	0
2	A	706	GOL	3	0
2	A	704	GOL	1	0
2	B	707	GOL	2	0
2	B	708	GOL	1	0
2	B	711	GOL	2	0

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.