



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 04:06 am BST

PDB ID : 4ZIU  
Title : Crystal structure of native alpha-2-macroglobulin from Escherichia coli spanning the residues from domain MG7 to the C-terminus.  
Authors : Garcia-Ferrer, I.; Arede, P.; Gomez-Blanco, J.; Luque, D.; Duquerroy, S.; Caston, J.R.; Goulas, T.; Gomis-Ruth, X.F.  
Deposited on : 2015-04-28  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

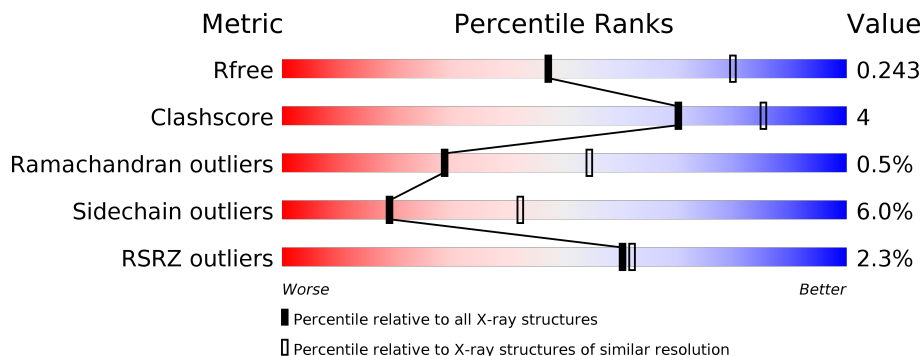
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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  $\leq 5\%$ . 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	639	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5048 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 Uncharacterized lipoprotein YfhM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	639	4920	3102	853	950	15	0	3	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1015	GLY	-	expression tag	UNP P76578
A	1016	HIS	-	expression tag	UNP P76578
A	1017	MET	-	expression tag	UNP P76578

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ni	0	0
			2	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

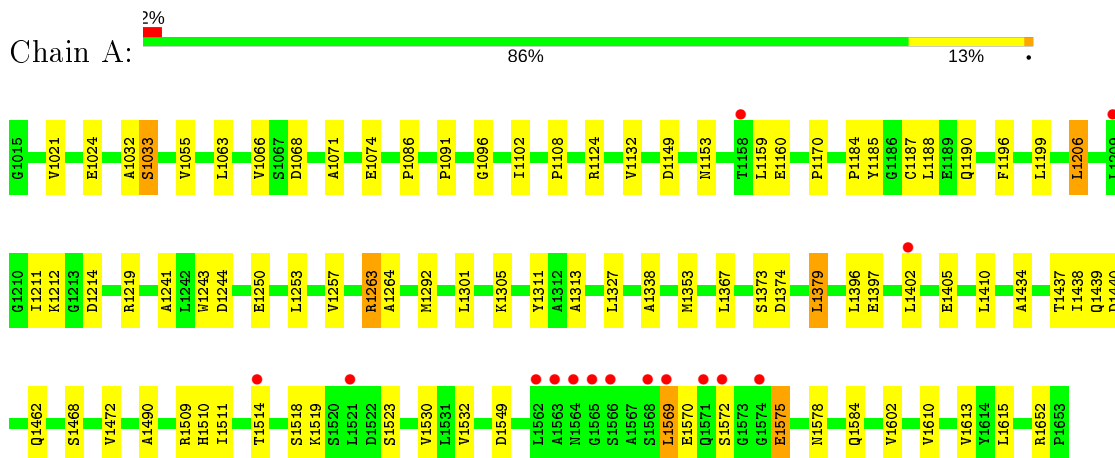
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	96	Total O 96 96	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 the various outlier classes 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: Uncharacterized lipoprotein YfhM



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.72Å 136.19Å 172.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.98 – 2.70 47.98 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.98-2.70) 99.4 (47.98-2.70)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 2.69Å)	Xtrriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.190 , 0.240 0.195 , 0.243	Depositor DCC
$R_{free}$ test set	747 reflections (2.63%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.1	Xtrriage
Anisotropy	0.402	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 56.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5048	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NI

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	0.49	0/5024	0.69	0/6836

There are no bond length outliers.

There are no bond angle outliers.

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	4920	0	4916	36	0
2	A	2	0	0	0	0
3	A	30	0	40	1	0
4	A	96	0	0	0	0
All	All	5048	0	4956	36	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.

All (36) 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:1196:PHE:HE2	1:A:1263:ARG:HH12	1.25	0.84
1:A:1033:SER:HB3	1:A:1091:PRO:HA	1.73	0.70
1:A:1196:PHE:HE2	1:A:1263:ARG:NH1	2.00	0.57
1:A:1066:VAL:HB	1:A:1086:PRO:HB2	1.86	0.56
1:A:1367:LEU:HD21	1:A:1396:LEU:HD11	1.90	0.54
1:A:1523:SER:HA	1:A:1652:ARG:HE	1.73	0.53
1:A:1602:VAL:HG21	1:A:1610:VAL:HG11	1.90	0.53
1:A:1367:LEU:HD12	1:A:1402:LEU:HD13	1.89	0.53
1:A:1338:ALA:HB3	1:A:1379:LEU:HD21	1.91	0.53
1:A:1402:LEU:HD22	1:A:1405:GLU:HG3	1.91	0.52
1:A:1063:LEU:HG	1:A:1096:GLY:HA3	1.91	0.51
1:A:1514:THR:HB	1:A:1569:LEU:HD21	1.91	0.51
1:A:1511:ILE:HD13	1:A:1532:VAL:HG22	1.92	0.51
1:A:1397:GLU:HG3	1:A:1437:THR:HG23	1.94	0.50
1:A:1434:ALA:O	1:A:1437:THR:HB	2.13	0.49
1:A:1032:ALA:HA	1:A:1124:ARG:O	2.13	0.49
1:A:1519:LYS:HD3	1:A:1530:VAL:HG12	1.94	0.49
1:A:1159:LEU:HB3	1:A:1468:SER:HB3	1.95	0.48
1:A:1055:VAL:HG22	1:A:1102:ILE:HG12	1.96	0.47
1:A:1468:SER:O	1:A:1472:VAL:HG23	2.15	0.47
1:A:1410:LEU:HD11	1:A:1438:ILE:HD13	1.98	0.46
1:A:1188:LEU:HD11	1:A:1257:VAL:HG21	1.97	0.45
1:A:1509:ARG:NH1	1:A:1549:ASP:OD1	2.49	0.45
1:A:1301:LEU:HG	1:A:1305:LYS:HE3	1.98	0.45
1:A:1132:VAL:HG22	1:A:1490:ALA:HB3	1.99	0.44
1:A:1575:GLU:HG2	1:A:1575:GLU:H	1.52	0.43
1:A:1199:LEU:HD11	1:A:1264:ALA:HA	2.01	0.43
1:A:1250:GLU:HG2	1:A:1253:LEU:HD12	2.01	0.42
1:A:1241:ALA:HB3	1:A:1244:ASP:O	2.20	0.42
1:A:1437:THR:HG22	1:A:1438:ILE:HG23	2.02	0.42
1:A:1206:LEU:HG	1:A:1211:ILE:HB	2.03	0.41
1:A:1184:PRO:HG2	1:A:1185:TYR:CE2	2.56	0.41
1:A:1313:ALA:HB1	1:A:1327:LEU:CD2	2.51	0.41
1:A:1187:CYS:HB3	1:A:1243:TRP:CH2	2.56	0.41
1:A:1569:LEU:HD13	1:A:1572:SER:HB3	2.03	0.40
1:A:1510:HIS:NE2	3:A:1705:GOL:H32	2.35	0.40

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	640/639 (100%)	622 (97%)	15 (2%)	3 (0%)	29 54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1033	SER
1	A	1071	ALA
1	A	1170	PRO

### 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	524/521 (101%)	493 (94%)	31 (6%)	19 43

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1021	VAL
1	A	1024	GLU
1	A	1068	ASP
1	A	1074	GLU
1	A	1108	PRO
1	A	1149	ASP
1	A	1153	ASN
1	A	1160	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1190	GLN
1	A	1206	LEU
1	A	1212	LYS
1	A	1214	ASP
1	A	1219	ARG
1	A	1263	ARG
1	A	1292	MET
1	A	1311	TYR
1	A	1353	MET
1	A	1373	SER
1	A	1374	ASP
1	A	1379	LEU
1	A	1439	GLN
1	A	1440	ASP
1	A	1462	GLN
1	A	1518	SER
1	A	1569	LEU
1	A	1570	GLU
1	A	1575	GLU
1	A	1578	ASN
1	A	1584	GLN
1	A	1613	VAL
1	A	1615	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1116	HIS
1	A	1578	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	A	1703	-	5,5,5	0.12	0	5,5,5	0.23	0
3	GOL	A	1705	-	5,5,5	0.06	0	5,5,5	0.24	0
3	GOL	A	1707	-	5,5,5	0.26	0	5,5,5	0.28	0
3	GOL	A	1704	2	5,5,5	0.21	0	5,5,5	0.39	0
3	GOL	A	1706	-	5,5,5	0.11	0	5,5,5	0.21	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
3	GOL	A	1703	-	-	0/4/4/4	-
3	GOL	A	1705	-	-	0/4/4/4	-
3	GOL	A	1707	-	-	4/4/4/4	-
3	GOL	A	1704	2	-	0/4/4/4	-
3	GOL	A	1706	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1707	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	1706	GOL	C1-C2-C3-O3
3	A	1707	GOL	O1-C1-C2-O2
3	A	1707	GOL	O2-C2-C3-O3
3	A	1706	GOL	O2-C2-C3-O3
3	A	1707	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1705	GOL	1	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](#)

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	A	639/639 (100%)	0.10	15 (2%) 60 62	51, 75, 116, 174	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1566	SER	6.5
1	A	1563	ALA	4.6
1	A	1564	ASN	3.4
1	A	1571	GLN	3.2
1	A	1402	LEU	3.2
1	A	1565	GLY	3.1
1	A	1209	LEU	2.7
1	A	1569	LEU	2.7
1	A	1574	GLY	2.6
1	A	1521	LEU	2.5
1	A	1514	THR	2.4
1	A	1568	SER	2.4
1	A	1158	THR	2.3
1	A	1572	SER	2.2
1	A	1562	LEU	2.1

### 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	A	1706	6/6	0.67	0.24	111,113,115,116	0
3	GOL	A	1705	6/6	0.80	0.13	114,117,118,118	0
3	GOL	A	1707	6/6	0.88	0.62	83,86,87,87	6
3	GOL	A	1703	6/6	0.92	0.24	85,90,92,92	0
3	GOL	A	1704	6/6	0.96	0.16	74,77,80,81	0
2	NI	A	1701	1/1	0.99	0.20	63,63,63,63	0
2	NI	A	1702	1/1	1.00	0.15	73,73,73,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.