

# wwPDB X-ray Structure Validation Summary Report (i)

#### Oct 18, 2023 – 12:21 AM EDT

:	1FY9
:	CRYSTAL STRUCTURE OF THE HEXA-SUBSTITUTED MUTANT OF
	THE MOLECULAR CHAPERONIN GROEL APICAL DOMAIN
:	Wang, Q.; Buckle, A.M.; Fersht, A.R.
	2000-09-28
:	2.20  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:

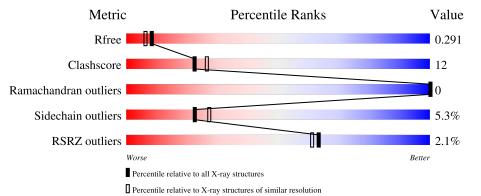
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.20 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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% 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		
			2%		
1	А	193	72%	24%	••



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1441 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 60 KD CHAPERONIN.

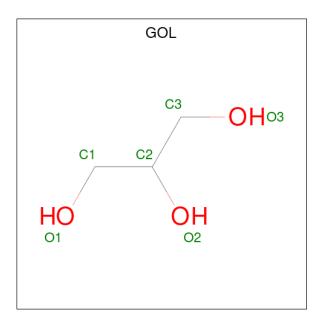
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	193	Total 1380	C 873	N 232	O 272	${ m S} { m 3}$	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	184	GLY	GLN	cloning artifact	UNP P0A6F5
А	185	LEU	ASP	cloning artifact	UNP P0A6F5
A	186	VAL	GLU	cloning artifact	UNP P0A6F5
A	187	PRO	LEU	cloning artifact	UNP P0A6F5
A	188	ARG	ASP	cloning artifact	UNP P0A6F5
А	189	GLY	VAL	cloning artifact	UNP P0A6F5
А	190	SER	VAL	cloning artifact	UNP P0A6F5
A	212	GLU	ALA	engineered mutation	UNP P0A6F5
А	223	VAL	ALA	engineered mutation	UNP P0A6F5
А	233	LEU	MET	engineered mutation	UNP P0A6F5
А	305	LEU	ILE	engineered mutation	UNP P0A6F5
А	308	LYS	GLU	engineered mutation	UNP P0A6F5
А	326	THR	ASN	engineered mutation	UNP P0A6F5

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





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

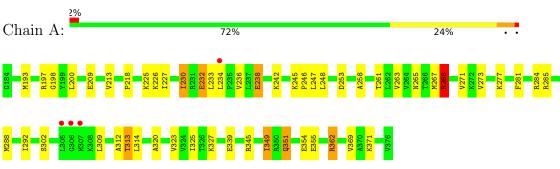
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	55	$\begin{array}{cc} {\rm Total} & {\rm O} \\ 55 & 55 \end{array}$	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 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: 60 KD CHAPERONIN



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	75.91Å 84.52Å 35.28Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	38.00 - 2.20	Depositor
Resolution (A)	37.95 - 2.21	EDS
% Data completeness	98.0 (38.00-2.20)	Depositor
(in resolution range)	97.7 (37.95-2.21)	EDS
R <sub>merge</sub>	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.30 (at 2.22 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
B B.	0.257 , $0.292$	Depositor
$R, R_{free}$	0.245 , $0.291$	DCC
$R_{free}$ test set	600 reflections $(5.18%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	27.5	Xtriage
Anisotropy	1.075	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, $51.5$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.47, \langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	1441	wwPDB-VP
Average B, all atoms $(Å^2)$	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.52% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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		
NIOI	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.37	0/1393	1.11	9/1894~(0.5%)	

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	351	GLN	CA-CB-CG	10.21	135.86	113.40
1	А	351	GLN	CB-CG-CD	9.29	135.75	111.60
1	А	354	GLU	OE1-CD-OE2	-8.61	112.97	123.30
1	А	268	ARG	CD-NE-CZ	8.13	134.98	123.60
1	А	268	ARG	NE-CZ-NH1	8.12	124.36	120.30

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	А	1380	0	1357	32	0
2	А	6	0	8	0	0
3	А	55	0	0	4	0
All	All	1441	0	1365	32	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 12.

The worst 5 of 32 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:193:MET:SD	1:A:292:ILE:HD13	2.28	0.74
1:A:349:ILE:HG21	1:A:369:VAL:HG23	1.75	0.68
1:A:362:ARG:HD3	3:A:1:HOH:O	1.96	0.64
1:A:247:LEU:HB3	1:A:273:VAL:HG22	1.80	0.63
1:A:230:ILE:HD13	1:A:258:ALA:HA	1.81	0.63

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	А	191/193~(99%)	186 (97%)	5(3%)	0	100 100	

There are no Ramachandran outliers to report.

#### 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	А	132/155~(85%)	125~(95%)	7~(5%)	22 27	

5 of 7 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	302	SER
1	А	313	THR
1	А	349	ILE
1	А	339	GLU
1	А	268	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:

Mol	Chain	Res	Type
1	А	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)

1 ligand is 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	l Type Chain Res Link			Link	B	ond leng	$\operatorname{gths}$	Bond angles			
	туре	Chain	ani nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
2	GOL	А	111	-	$5,\!5,\!5$	0.21	0	$5,\!5,\!5$	0.62	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.

Ν	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	2	GOL	А	111	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	111	GOL	C1-C2-C3-O3
2	А	111	GOL	O2-C2-C3-O3
2	А	111	GOL	O1-C1-C2-C3
2	А	111	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

#### 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,  $95^{th}$  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		$OWAB(Å^2)$	Q<0.9	
1	А	193/193~(100%)	-0.07	4 (2%)	63	61	19, 30, 49, 55	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	234	LEU	3.1
1	А	307	MET	2.9
1	А	306	GLY	2.6
1	А	305	LEU	2.6

### 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 monosaccharides 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,  $95^{th}$  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	$B-factors(Å^2)$	Q < 0.9
2	GOL	A	111	6/6	0.73	0.20	$34,\!35,\!38,\!38$	0



### 6.5 Other polymers (i)

There are no such residues in this entry.

