

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

#### Mar 28, 2024 - 03:12 pm GMT

PDB ID	:	8RMO
Title	:	Crystal structure of anti-FLAG M2 Fab fragment bound to FLAG-tag peptide
		epitope
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Deposited on		
Resolution	:	1.16 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* 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:

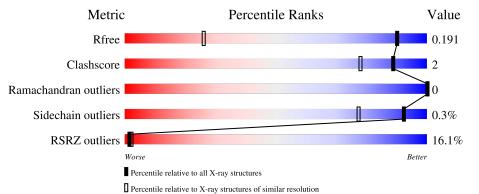
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 1.16 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	1758 (1.20-1.12)
Clashscore	141614	1832 (1.20-1.12)
Ramachandran outliers	138981	1768 (1.20-1.12)
Sidechain outliers	138945	1768 (1.20-1.12)
RSRZ outliers	127900	1724 (1.20-1.12)

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	
1	F	8	75%	25%
2	Н	228	88%	• 10%
3	L	219	92%	• •



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## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7394 atoms, of which 3374 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 FLAG-tag.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	F	6	Total 105	$\begin{array}{c} \mathrm{C} \\ 35 \end{array}$	Н 44	N 8	0 18	1	1	0

• Molecule 2 is a protein called anti-FLAG M2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	Н	206	Total 3335	C 1070	Н 1632	N 276	O 348	S 9	76	18	0

• Molecule 3 is a protein called anti-FLAG M2 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
3	L	211	Total 3434	C 1084	Н 1698	N 304	0 341	S 7	64	11	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Н	3	Total Cl 3 3	0	0

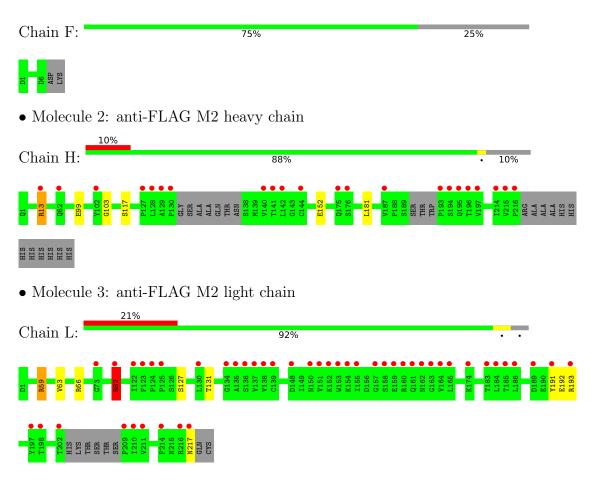
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	F	12	Total         O           12         12	0	0
5	Н	276	Total O 276 276	0	0
5	L	229	Total O 229 229	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: FLAG-tag



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	87.43Å 134.62Å 41.80Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	73.33 - 1.16	Depositor
Resolution (A)	73.32 - 1.16	EDS
% Data completeness	71.1 (73.33-1.16)	Depositor
(in resolution range)	71.1 (73.32-1.16)	EDS
R <sub>merge</sub>	0.15	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.28 (at 1.16 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
D D.	0.158 , $0.185$	Depositor
$R, R_{free}$	0.159 , $0.191$	DCC
$R_{free}$ test set	6057 reflections $(5.02%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	9.6	Xtriage
Anisotropy	1.318	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40, 50.2	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7394	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.17% 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: PCA, CL

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
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	F	0.57	0/60	0.95	0/78
2	Н	0.60	0/1738	0.87	0/2376
3	L	0.51	0/1773	0.78	0/2398
All	All	0.56	0/3571	0.83	0/4852

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
2	Η	0	1
3	L	0	3
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Н	13[A]	ARG	Sidechain
3	L	193	ARG	Sidechain
3	L	59[B]	ARG	Mainchain
3	L	82[A]	ARG	Sidechain



### 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	F	61	44	44	0	0
2	Н	1703	1632	1614	5	0
3	L	1736	1698	1685	7	0
4	Н	3	0	0	1	0
5	F	12	0	0	0	0
5	Н	276	0	0	1	0
5	L	229	0	0	0	0
All	All	4020	3374	3343	12	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 2.

All (12) 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)
2:H:152[A]:GLU:OE1	5:H:401:HOH:O	1.65	1.12
3:L:66[A]:ARG:HG2	3:L:82[A]:ARG:HH12	1.25	1.01
3:L:66[A]:ARG:CG	3:L:82[A]:ARG:HH12	2.05	0.68
3:L:66[A]:ARG:HG2	3:L:82[A]:ARG:NH1	2.08	0.65
3:L:192:GLU:HA	3:L:217:ASN:O	2.08	0.54
2:H:99[B]:GLU:C	2:H:99[B]:GLU:OE1	2.56	0.43
3:L:191:TYR:CD2	3:L:217:ASN:O	2.72	0.43
2:H:181:LEU:C	2:H:181:LEU:HD12	2.39	0.43
3:L:59[A]:ARG:HG2	3:L:63:VAL:HB	2.02	0.41
3:L:127:SER:O	3:L:131:THR:HG23	2.20	0.41
2:H:103:GLY:O	4:H:301:CL:CL	2.75	0.40
2:H:13[A]:ARG:NE	2:H:117:SER:HA	2.37	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	Percent	iles
1	F	4/8~(50%)	4 (100%)	0	0	100 1	100
2	Н	218/228~(96%)	213~(98%)	5(2%)	0	100 1	100
3	L	218/219~(100%)	212~(97%)	6 (3%)	0	100 1	100
All	All	440/455~(97%)	429 (98%)	11 (2%)	0	100 1	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	Perce	ntiles
1	F	7/8~(88%)	7~(100%)	0	100	100
2	Н	193/191~(101%)	193 (100%)	0	100	100
3	L	199/196~(102%)	197~(99%)	2(1%)	76	45
All	All	399/395~(101%)	397 (100%)	2(0%)	92	66

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	82[A]	ARG
3	L	82[B]	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains identified.



#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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).

ſ	Mol	Type	Chain	Res	Link	В	ond leng	$\operatorname{gths}$	В	ond ang	gles
	WIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
	2	PCA	Н	1	2	$7,\!8,\!9$	0.64	0	$9,\!10,\!12$	0.76	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	PCA	Н	1	2	-	0/0/11/13	0/1/1/1

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.

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 are 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 (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	< <b>RSRZ</b> >	#RSRZ>2		$\mathbf{OWAB}(\mathbf{A}^2)$	$\mathbf{Q}{<}0.9$
1	F	6/8~(75%)	0.16	0 100 100		16, 21, 26, 31	0
2	Н	205/228~(89%)	0.77	22 (10%) 6	7	9, 17, 51, 84	0
3	L	211/219 (96%)	0.97	46 (21%) 0	1	9, 23, 58, 73	0
All	All	422/455~(92%)	0.86	68 (16%) 1	2	9, 20, 58, 84	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Н	195	GLN	8.7
3	L	210	ILE	8.2
2	Н	194	SER	7.1
3	L	155	ILE	6.6
2	Н	215	VAL	6.3
2	Н	216	PRO	6.0
3	L	165	LEU	5.6
3	L	185	THR	5.5
3	L	186	LEU	5.4
3	L	124	PRO	5.3
3	L	73	GLY	5.2
2	Н	197	VAL	4.9
3	L	164	VAL	4.8
2	Н	193	PRO	4.8
2	Н	196	THR	4.7
3	L	159	GLU	4.5
3	L	125	PRO	4.2
3	L	189	ASP	4.2
3	L	123	PHE	4.1
2	Н	129	ALA	4.1
3	L	137	VAL	4.0
3	L	162	ASN	4.0
3	L	153	TRP	3.9

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Mol	nued fron Chain	Res	Type	RSRZ
3	L	202	THR	3.8
3	L	184	LEU	3.7
3	L	134	GLY	3.6
2	Н	187	VAL	3.3
3	L	214	PHE	3.3
2	Н	128	LEU	3.2
2	Н	175	GLN	3.2
3	L	138	VAL	3.2
3	L	151	VAL	3.2
2	Н	214	ILE	3.1
3	L	161	GLN	3.1
3	L	130	LEU	3.0
3	L	148	ASP	3.0
2	Н	142	LEU	3.0
2	Н	140	VAL	2.9
3	L	122	ILE	2.9
3	L	193	ARG	2.8
2	Н	130	PRO	2.8
3	L	216	ARG	2.8
3	L	158	SER	2.8
3	L	217	ASN	2.6
2	Н	144[A]	CYS	2.6
2	Н	13[A]	ARG	2.6
3	L	82[A]	ARG	2.6
3	L	135	ALA	2.5
3	L	211	VAL	2.5
2	Н	141	THR	2.5
2	Н	62[A]	GLN	2.5
3	L	198	THR	2.5
3	L	139	CYS	2.5
3	L	152	LYS	2.4
2	Н	102	TYR	2.4
3	L	183	THR	2.3
3	L	174	LYS	2.3
3	L	150	ASN	2.3
2	Н	176	SER	2.3
3	L	197	TYR	2.3
3	L	163	GLY	2.3
3	L	209	PRO	2.2
3	L	160	ARG	2.2
3	L	136	SER	2.2
3	L	154	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
3	L	157	GLY	2.1
3	L	191	TYR	2.1
2	Н	127	PRO	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	PCA	Н	1	8/9	0.98	0.07	$15,\!21,\!24,\!27$	0

## 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	CL	Н	303	1/1	0.97	0.07	$25,\!25,\!25,\!25$	1
4	CL	Н	301	1/1	0.99	0.12	14,14,14,14	1
4	CL	Н	302	1/1	1.00	0.11	12,12,12,12	1

## 6.5 Other polymers (i)

There are no such residues in this entry.

