

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

#### May 30, 2023 – 01:14 pm BST

PDB ID	:	8AS2
Title	:	Structure of arrestin2 in complex with 4P CCR5 phosphopeptide and Fab30
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Deposited on		
Resolution	:	3.20 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:

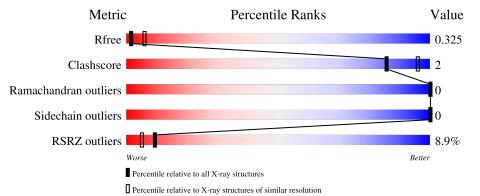
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.33
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

# 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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	
1	А	359	3% 94%	• •
2	В	22	9% 9% 82%	
3	Н	233	87%	7% 6%
4	L	220	90%	7% •



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6096 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 Beta-arrestin-1.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	352	Total 2787	C 1783	N 481	0 517	S 6	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	150	LEU	CYS	engineered mutation	UNP P49407
А	242	VAL	CYS	engineered mutation	UNP P49407
А	251	VAL	CYS	engineered mutation	UNP P49407
А	269	SER	CYS	engineered mutation	UNP P49407

• Molecule 2 is a protein called C-C chemokine receptor type 5.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
2	В	4	Total 32	C 14	N 4	0 12	Р 2	0	0	0

• Molecule 3 is a protein called Fab30 heavy chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	Н	220	Total 1650	C 1046	N 275	0 324	${ m S}{ m 5}$	0	0	0

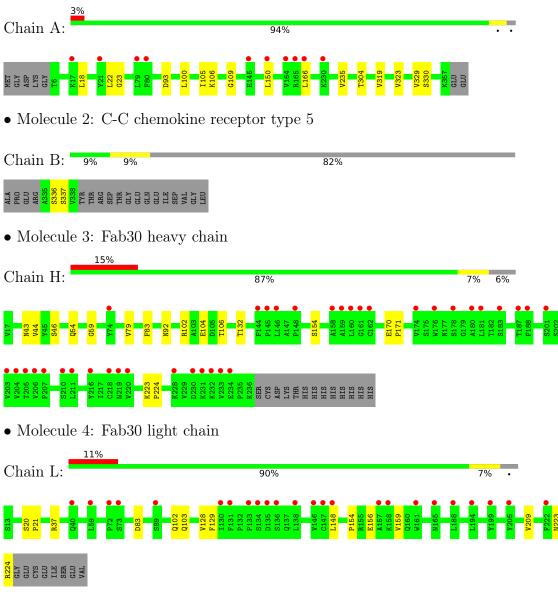
• Molecule 4 is a protein called Fab30 light chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
4	L	212	Total 1627	C 1020	N 273	O 329	${S \atop 5}$	0	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: Beta-arrestin-1



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants	116.64Å 122.18Å 145.56Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	-
Resolution (Å)	49.49 - 3.20	Depositor
	49.49 - 3.20	EDS
% Data completeness	99.5(49.49-3.20)	Depositor
(in resolution range)	99.5~(49.49-3.20)	EDS
$R_{merge}$	0.31	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.08 (at 3.19 Å)	Xtriage
Refinement program	BUSTER	Depositor
D D	0.280 , $0.316$	Depositor
$R, R_{free}$	0.295 , $0.325$	DCC
$R_{free}$ test set	827 reflections $(4.74%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	118.5	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.23, $87.1$	EDS
L-test for $twinning^2$	$<  L  > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6096	wwPDB-VP
Average B, all atoms $(Å^2)$	197.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.82% 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: SEP

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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.26	0/2846	0.48	0/3861	
2	В	0.10	0/10	0.25	0/11	
3	Н	0.26	0/1693	0.48	0/2309	
4	L	0.26	0/1662	0.51	0/2257	
All	All	0.26	0/6211	0.49	0/8438	

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	А	2787	0	2860	9	0
2	В	32	0	19	0	0
3	Н	1650	0	1604	11	0
4	L	1627	0	1593	8	0
All	All	6096	0	6076	27	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.

The worst 5 of 27 close contacts within the same asymmetric unit are listed below, sorted by their



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:44:VAL:CG2	3:H:92:ASN:OD1	2.15	0.94
3:H:44:VAL:HG23	3:H:92:ASN:OD1	1.79	0.81
4:L:37:ARG:HB3	4:L:83:ASP:OD1	1.99	0.61
3:H:102:ARG:HB3	3:H:104:GLU:OE1	2.06	0.56
3:H:44:VAL:HG21	3:H:92:ASN:OD1	2.03	0.54

clash magnitude.

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	350/359~(98%)	332~(95%)	18 (5%)	0	100	100
3	Н	218/233~(94%)	205 (94%)	13 (6%)	0	100	100
4	L	210/220 (96%)	194 (92%)	16 (8%)	0	100	100
All	All	778/812~(96%)	731 (94%)	47 (6%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	5		Percentiles		
1	А	312/317~(98%)	312~(100%)	0	100 100		

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
2	В	1/14~(7%)	1 (100%)	0	100	100
3	Н	183/196~(93%)	183 (100%)	0	100	100
4	L	188/195~(96%)	188 (100%)	0	100	100
All	All	684/722~(95%)	684 (100%)	0	100	100

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There are no protein residues with a non-rotameric sidechain to report.

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)

2 non-standard protein/DNA/RNA residues 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).

Mal	Mol Type Chain Re	Chain	Dec	Link	Bond lengths			Bond angles		
IVIOI		nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
2	SEP	В	336	2	8,9,10	1.56	1 (12%)	8,12,14	1.53	2 (25%)
2	SEP	В	337	2	8,9,10	1.56	1 (12%)	8,12,14	1.71	2 (25%)

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	SEP	В	336	2	-	5/5/8/10	-
2	SEP	В	337	2	-	1/5/8/10	-



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	В	337	SEP	P-O1P	3.39	1.61	1.50
2	В	336	SEP	P-O1P	3.38	1.61	1.50

All (2) bond length outliers are listed below:

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^{o})$	$Ideal(^{o})$
2	В	337	SEP	OG-CB-CA	3.38	111.44	108.14
2	В	336	SEP	OG-CB-CA	3.03	111.10	108.14
2	В	337	SEP	P-OG-CB	-2.82	110.54	118.30
2	В	336	SEP	P-OG-CB	-2.23	112.14	118.30

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	336	SEP	N-CA-CB-OG
2	В	336	SEP	CA-CB-OG-P
2	В	336	SEP	CB-OG-P-O1P
2	В	336	SEP	CB-OG-P-O2P
2	В	336	SEP	CB-OG-P-O3P

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)

There are no ligands in this entry.

#### 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	$OWAB(A^2)$	Q<0.9
1	А	352/359~(98%)	0.15	10 (2%) 53 37	109, 163, 259, 349	0
2	В	2/22~(9%)	0.95	0 100 100	209, 209, 209, 225	0
3	Н	220/233~(94%)	0.67	36 (16%) 1 1	133, 182, 365, 515	0
4	L	212/220~(96%)	0.58	24 (11%) 5 3	148, 221, 299, 459	0
All	All	786/834~(94%)	0.42	70 (8%) 9 5	109, 184, 317, 515	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	L	134	SER	8.7
3	Н	160	LEU	5.8
3	Н	180	ALA	5.6
4	L	40	GLN	5.3
3	Н	232	LYS	5.3

### 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.

M	ol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
2		SEP	В	337	10/11	0.77	0.21	230,236,256,266	0
2		SEP	В	336	10/11	0.89	0.26	193,205,215,217	0

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



### 6.4 Ligands (i)

There are no ligands in this entry.

### 6.5 Other polymers (i)

There are no such residues in this entry.

