

wwPDB X-ray Structure Validation Summary Report (i)

Oct 15, 2023 – 01:51 PM EDT

PDB ID : 7UFQ

Title: Structure of PfCSP peptide 21 with antibody P3-43

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Deposited on : 2022-03-23

Resolution : 2.30 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 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

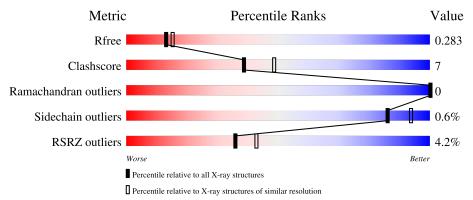
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	В	226	7% 77%	20%	6 •
1	Н	226	7%	23%	• •
2	A	15		13%	13%
2	С	15	7% 87%		13%
3	D	220	89%		11%

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Mol	Chain	Length	Quality of chain	
			<u>%</u>	
3	L	220	89%	10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	Н	301	-	-	X	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7045 atoms, of which 8 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 P3-43 Fab Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Н	221	Total 1661	C 1047	7.1	O 326	S 7	0	0	0
1	В	221	Total 1661	C 1047		O 326	S 7	0	0	0

• Molecule 2 is a protein called PfCSP peptide 21.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A 13		Total				0	0	0
	10	96	56	18	22				
2	C	13	Total	С	N	O	0	0	0
		10	96	56	18	22	0	U	0

• Molecule 3 is a protein called P3-43 Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Т	219	Total	С	N	О	S	0	1	0
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	219	1701	1068	283	344	6	U	1	U	
9) D	210	Total	С	N	О	S	0	1	0
3 D	219	1701	1068	283	344	6	0	1	U	

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
1	П	1	Total	С	Н	О	0	0
4	4 H	1	14	3	8	3	0	. 0

• Molecule 5 is water.

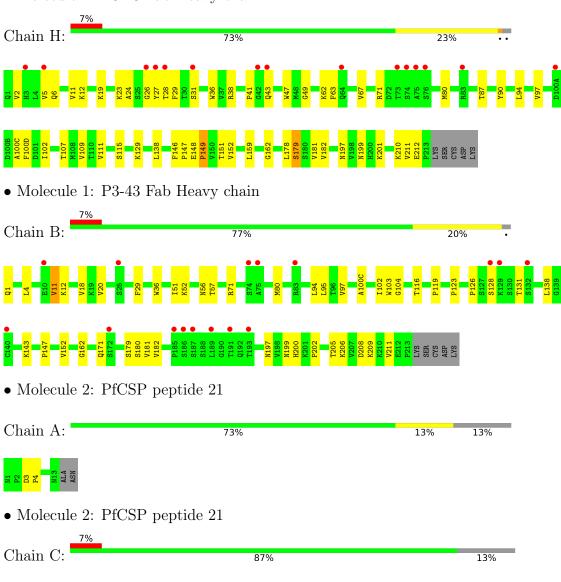
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	Н	23	Total O 23 23	0	0
5	A	2	Total O 2 2	0	0
5	L	35	Total O 35 35	0	0
5	В	19	Total O 19 19	0	0
5	С	7	Total O 7 7	0	0
5	D	29	Total O 29 29	0	0



3 Residue-property plots (i)

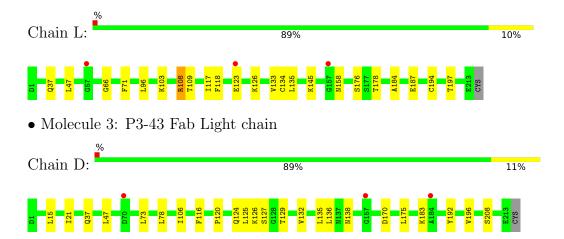
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: P3-43 Fab Heavy chain



• Molecule 3: P3-43 Fab Light chain







4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	74.48Å 61.70Å 89.60Å	Donogitor	
a, b, c, α , β , γ	90.00° 103.74° 90.00°	Depositor	
Resolution (Å)	43.52 - 2.30	Depositor	
resolution (A)	43.52 - 2.30	EDS	
% Data completeness	97.5 (43.52-2.30)	Depositor	
(in resolution range)	97.5 (43.52-2.30)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.76 (at 2.29Å)	Xtriage	
Refinement program	PHENIX 1.18.2_3874	Depositor	
R, R_{free}	0.215 , 0.285	Depositor	
it, it free	0.220 , 0.283	DCC	
R_{free} test set	1703 reflections (4.94%)	wwPDB-VP	
Wilson B-factor (Å ²)	32.1	Xtriage	
Anisotropy	0.199	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.41, 45.3	EDS	
L-test for twinning ²	$ < L > = 0.50, < L^2> = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.93	EDS	
Total number of atoms	7045	wwPDB-VP	
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 28.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6919e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities 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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	В	0.46	0/1700	0.71	0/2316	
1	Н	0.51	0/1700	0.73	1/2316 (0.0%)	
2	A	0.43	0/99	0.55	0/139	
2	С	0.45	0/99	0.62	0/139	
3	D	0.51	0/1743	0.68	0/2368	
3	L	0.49	0/1743	0.68	0/2368	
All	All	0.49	0/7084	0.70	1/9646 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	Н	149	PRO	N-CA-CB	-5.24	96.84	102.60

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	В	1661	0	1641	31	0
1	Н	1661	0	1641	46	0
2	A	96	0	82	1	0
2	С	96	0	82	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1701	0	1645	15	0
3	L	1701	0	1645	15	0
4	Н	6	8	8	5	0
5	A	2	0	0	0	0
5	В	19	0	0	0	0
5	С	7	0	0	0	0
5	D	29	0	0	0	0
5	Н	23	0	0	0	0
5	L	35	0	0	0	0
All	All	7037	8	6744	102	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 7.

The worst 5 of 102 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:H:138:LEU:HD13	1:H:211:VAL:HG21	1.69	0.73
1:H:28:THR:HG23	1:H:31:SER:HB2	1.71	0.71
1:H:28:THR:HG23	1:H:28:THR:O	1.90	0.70
3:L:123:GLU:HA	3:L:126:LYS:HD3	1.76	0.67
4:H:301:GOL:H12	3:L:178:THR:OG1	1.95	0.66

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	Perce	entiles
1	В	219/226 (97%)	210 (96%)	9 (4%)	0	100	100
1	Н	219/226 (97%)	205 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentil	les
2	A	11/15 (73%)	10 (91%)	1 (9%)	0	100 10	0
2	С	11/15 (73%)	11 (100%)	0	0	100 10	0
3	D	218/220 (99%)	210 (96%)	8 (4%)	0	100 10	0
3	L	218/220 (99%)	209 (96%)	9 (4%)	0	100 10	0
All	All	896/922 (97%)	855 (95%)	41 (5%)	0	100 10	0

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	В	187/192~(97%)	185 (99%)	2 (1%)	73	86
1	Н	187/192 (97%)	185 (99%)	2 (1%)	73	86
2	A	12/13 (92%)	12 (100%)	0	100	100
2	\mathbf{C}	$12/13 \; (92\%)$	12 (100%)	0	100	100
3	D	194/194 (100%)	194 (100%)	0	100	100
3	L	194/194 (100%)	193 (100%)	1 (0%)	88	95
All	All	786/798 (98%)	781 (99%)	5 (1%)	86	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Н	71	ARG
1	Н	179	SER
3	L	108	ARG
1	В	11	VAL
1	В	179	SER

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



Mol	Chain	Res	Type
1	В	171	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	Type	Chain	$\operatorname{in} \left \operatorname{Res} \right $	tes Link	Bond lengths			Bond angles		
WIOI	Type				Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	GOL	Н	301	-	5,5,5	0.07	0	5,5,5	0.25	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
4	GOL	Н	301	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.



There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Н	301	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Н	301	GOL	5	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^{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>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	В	221/226 (97%)	0.59	16 (7%) 15 20	24, 35, 55, 64	0
1	Н	221/226 (97%)	0.61	15 (6%) 17 22	23, 34, 54, 66	0
2	A	13/15 (86%)	0.34	0 100 100	26, 31, 44, 46	0
2	С	13/15 (86%)	0.23	1 (7%) 13 17	27, 31, 37, 38	0
3	D	219/220 (99%)	0.34	3 (1%) 75 80	21, 31, 44, 52	0
3	L	219/220 (99%)	0.35	3 (1%) 75 80	22, 30, 42, 62	0
All	All	906/922 (98%)	0.47	38 (4%) 36 43	21, 32, 49, 66	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Н	74	SER	7.4
1	Н	75	ALA	5.9
1	В	132	SER	5.0
1	В	74	SER	4.8
1	В	129	LYS	4.0

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	GOL	Н	301	6/6	0.77	0.27	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.

