



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:29 AM UTC

PDB ID : 8FBN / pdb\_00008fbn  
Title : Improving the secretion of designed protein assemblies through negative design of cryptic transmembrane domains  
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Deposited on : 2022-11-29  
Resolution : 3.04 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

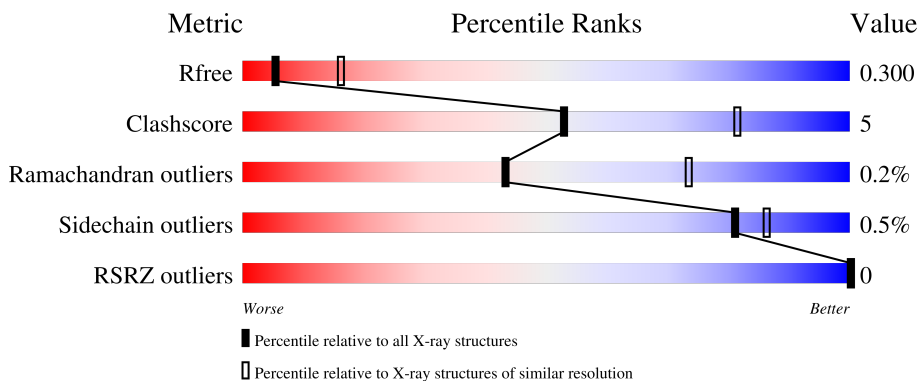
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.04 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))
$R_{free}$	180053	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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  $\geq 3$ , 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	226	 89% 11%
1	B	226	 88% 12%
1	C	226	 88% 12%
1	D	226	 84% 15%
1	E	226	 88% 12%

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Mol	Chain	Length	Quality of chain
1	F	226	 77% 20%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10153 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 KWOCA\_73.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	1703	1055	312	334	2	0	0	0
1	B	226	1703	1055	312	334	2	0	0	0
1	C	226	1703	1055	312	334	2	0	0	0
1	D	225	1688	1044	310	332	2	0	0	0
1	E	226	1703	1055	312	334	2	0	0	0
1	F	220	1653	1025	302	324	2	0	0	0

### 3 Residue-property plots


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: KWOCA\_73

Chain A:  89% 11%




- Molecule 1: KWOCA\_73

Chain B:  88% 12%




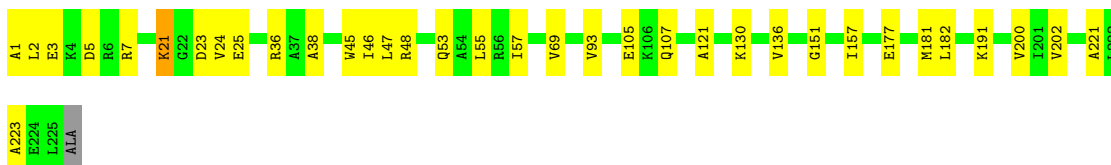
- Molecule 1: KWOCA\_73

Chain C:  88% 12%




- Molecule 1: KWOCA\_73

Chain D:  84% 15%


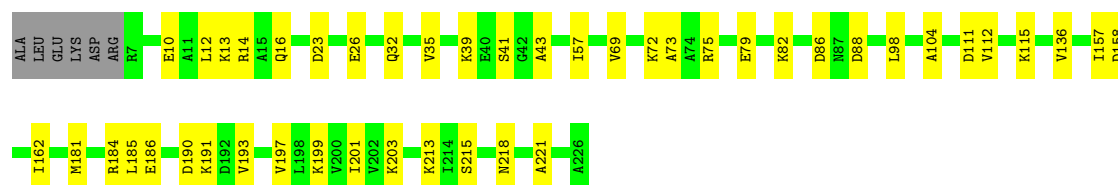


- Molecule 1: KWOCA\_73

Chain E:  88% 12%



## ● Molecule 1: KWOCA\_73

Chain F:  77% 20%

## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.00Å 170.81Å 72.15Å 90.00° 117.83° 90.00°	Depositor
Resolution (Å)	42.70 – 3.04 42.70 – 3.04	Depositor EDS
% Data completeness (in resolution range)	99.2 (42.70-3.04) 98.5 (42.70-3.04)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.23 (at 3.06Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122, PHENIX 1.19.1_4122	Depositor
R, $R_{free}$	0.255 , 0.300 0.256 , 0.300	Depositor DCC
$R_{free}$ test set	2034 reflections (6.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	98.9	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 107.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.078 for -h-l,k,h 0.078 for l,k,-h-l 0.094 for h,-k,-h-l 0.086 for -h-l,-k,l 0.218 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10153	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.75% 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](#)

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	0.09	0/1705	0.22	0/2280
1	B	0.09	0/1705	0.24	0/2280
1	C	0.09	0/1705	0.23	0/2280
1	D	0.10	0/1688	0.24	0/2257
1	E	0.10	0/1705	0.22	0/2280
1	F	0.12	0/1655	0.27	0/2214
All	All	0.10	0/10163	0.24	0/13591

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	1703	0	1818	17	0
1	B	1703	0	1818	19	0
1	C	1703	0	1818	17	0
1	D	1688	0	1805	21	0
1	E	1703	0	1818	15	0
1	F	1653	0	1763	28	0
All	All	10153	0	10840	105	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 5.

The worst 5 of 105 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:C:4:LYS:HD2	1:C:41:SER:HA	1.62	0.82
1:C:181:MET:HB3	1:C:197:VAL:HG12	1.72	0.72
1:C:79:GLU:O	1:C:83:GLN:NE2	2.26	0.69
1:E:55:LEU:HD21	1:E:93:VAL:HG22	1.76	0.68
1:D:23:ASP:O	1:D:25:GLU:N	2.26	0.67

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	224/226 (99%)	217 (97%)	7 (3%)	0	100	100
1	B	224/226 (99%)	216 (96%)	8 (4%)	0	100	100
1	C	224/226 (99%)	215 (96%)	9 (4%)	0	100	100
1	D	223/226 (99%)	213 (96%)	8 (4%)	2 (1%)	14	44
1	E	224/226 (99%)	220 (98%)	4 (2%)	0	100	100
1	F	218/226 (96%)	206 (94%)	11 (5%)	1 (0%)	24	57
All	All	1337/1356 (99%)	1287 (96%)	47 (4%)	3 (0%)	43	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	43	ALA
1	D	2	LEU
1	D	46	ILE

### 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	167/167 (100%)	167 (100%)	0	100	100
1	B	167/167 (100%)	167 (100%)	0	100	100
1	C	167/167 (100%)	166 (99%)	1 (1%)	78	85
1	D	166/167 (99%)	164 (99%)	2 (1%)	63	79
1	E	167/167 (100%)	167 (100%)	0	100	100
1	F	162/167 (97%)	160 (99%)	2 (1%)	63	79
All	All	996/1002 (99%)	991 (100%)	5 (0%)	81	86

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

Mol	Chain	Res	Type
1	C	107	GLN
1	D	21	LYS
1	D	36	ARG
1	F	39	LYS
1	F	41	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	107	GLN
1	F	211	ASN
1	F	219	GLN
1	F	212	GLN
1	D	211	ASN

### 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 oligosaccharides 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<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	226/226 (100%)	-1.46	0 100 100	62, 93, 128, 152	0
1	B	226/226 (100%)	-1.43	0 100 100	55, 102, 142, 154	0
1	C	226/226 (100%)	-1.40	0 100 100	60, 96, 141, 159	0
1	D	225/226 (99%)	-1.44	0 100 100	59, 93, 136, 165	0
1	E	226/226 (100%)	-1.32	0 100 100	58, 117, 172, 186	0
1	F	220/226 (97%)	-1.29	0 100 100	76, 130, 180, 198	0
All	All	1349/1356 (99%)	-1.39	0 100 100	55, 102, 164, 198	0

There are no RSRZ outliers to report.

### 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 oligosaccharides 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.