



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2024 – 06:29 PM EDT

PDB ID : 8VRS
Title : Mucin 16 peptide fused to MBP in complex with 4H11-scFv antibody
Authors : Lee, K.; Perry, K.; Yeku, O.O.; Spriggs, D.R.
Deposited on : 2024-01-22
Resolution : 2.47 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36.1
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

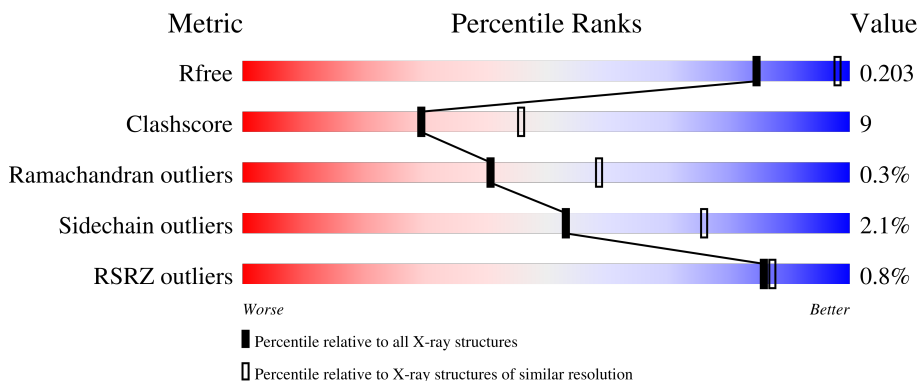
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


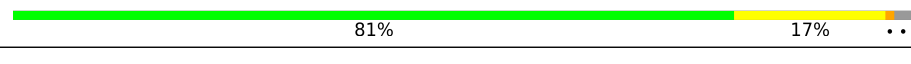
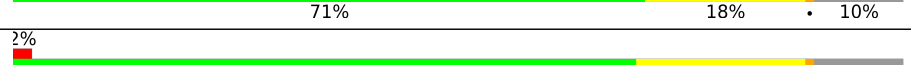

The reported resolution of this entry is 2.47 Å.

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}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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 $\leq 5\%$. 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	397	 79% 18% ..
1	B	397	 81% 17% ..
2	C	261	 71% 18% • 10%
2	D	261	 70% 19% • 10%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10040 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 Maltose/maltodextrin-binding periplasmic protein,Mucin-16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	390	3027	1944	492	584	7	0	0	0
1	B	390	3027	1944	492	584	7	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P0AEX9
A	312	VAL	ALA	conflict	UNP P0AEX9
A	367	ASN	-	linker	UNP P0AEX9
A	368	SER	-	linker	UNP P0AEX9
A	369	SER	-	linker	UNP P0AEX9
A	370	SER	-	linker	UNP P0AEX9
B	0	MET	-	initiating methionine	UNP P0AEX9
B	312	VAL	ALA	conflict	UNP P0AEX9
B	367	ASN	-	linker	UNP P0AEX9
B	368	SER	-	linker	UNP P0AEX9
B	369	SER	-	linker	UNP P0AEX9
B	370	SER	-	linker	UNP P0AEX9

- Molecule 2 is a protein called 4H11 scFv chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	236	1817	1137	312	358	10	0	0	0
2	D	236	1817	1137	312	358	10	0	0	0

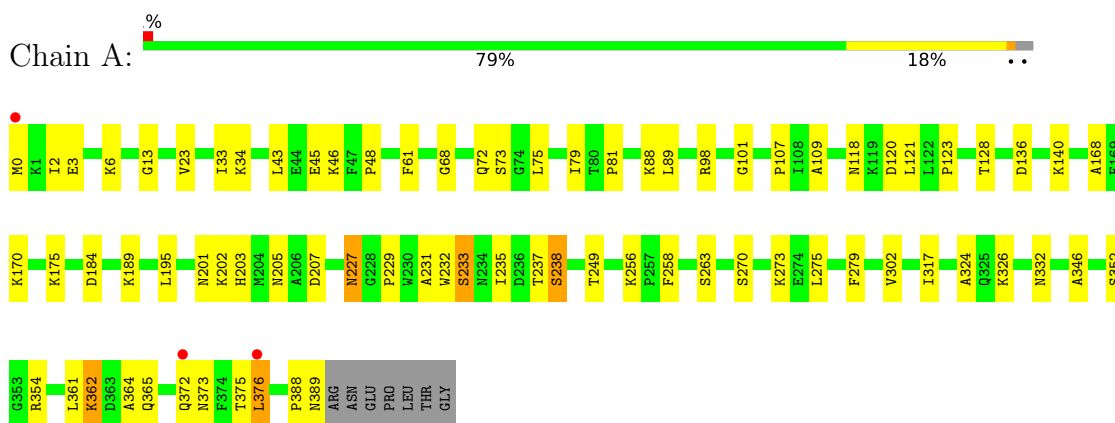
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	98	Total O 98 98	0	0
3	C	66	Total O 66 66	0	0
3	B	125	Total O 125 125	0	0
3	D	63	Total O 63 63	0	0

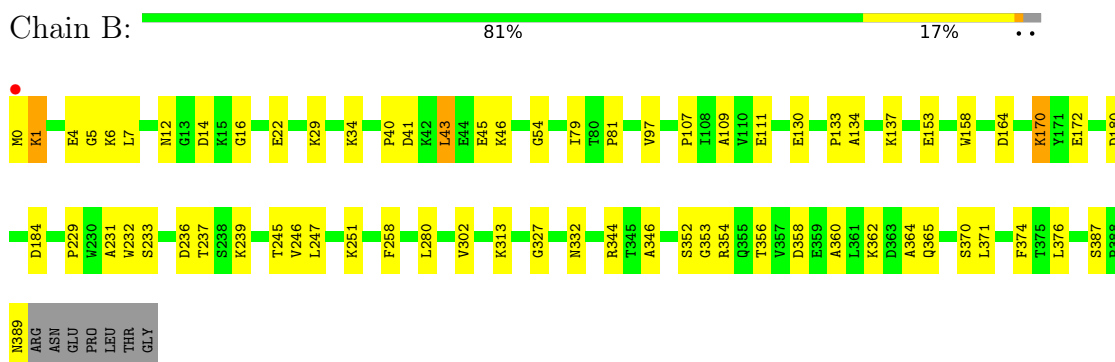
3 Residue-property plots

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.

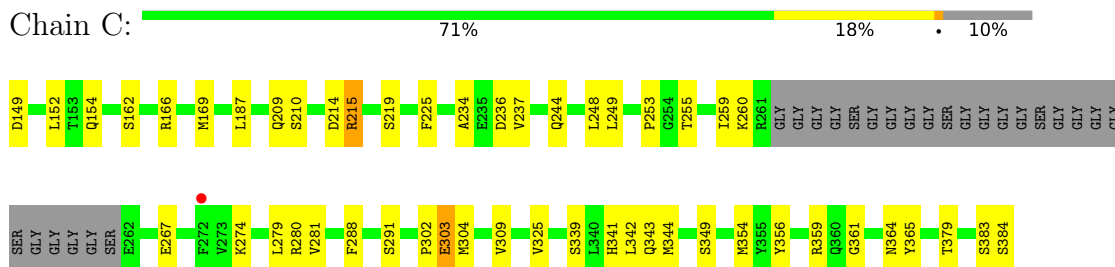
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Mucin-16



- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Mucin-16



- Molecule 2: 4H11 scFv chain



- Molecule 2: 4H11 scFv chain

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.81Å 112.63Å 110.81Å 90.00° 101.25° 90.00°	Depositor
Resolution (Å)	56.43 – 2.47 78.21 – 2.47	Depositor EDS
% Data completeness (in resolution range)	91.3 (56.43-2.47) 98.8 (78.21-2.47)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.45Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.192 , 0.237 0.203 , 0.203	Depositor DCC
R_{free} test set	2474 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtrriage
Anisotropy	0.497	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10040	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.45	0/3099	0.58	0/4208
1	B	0.47	0/3099	0.59	0/4208
2	C	0.51	1/1856 (0.1%)	0.74	4/2509 (0.2%)
2	D	0.47	0/1856	0.72	4/2509 (0.2%)
All	All	0.47	1/9910 (0.0%)	0.64	8/13434 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	303	GLU	CD-OE2	5.72	1.31	1.25

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	303	GLU	CA-CB-CG	11.23	138.11	113.40
2	D	279	LEU	CB-CG-CD2	-9.75	94.43	111.00
2	C	303	GLU	CB-CA-C	-8.98	92.44	110.40
2	C	303	GLU	N-CA-CB	7.21	123.58	110.60
2	D	215	ARG	NE-CZ-NH1	-6.25	117.17	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	A	3027	0	2991	50	0
1	B	3027	0	2991	56	0
2	C	1817	0	1741	38	0
2	D	1817	0	1741	39	0
3	A	98	0	0	17	0
3	B	125	0	0	16	1
3	C	66	0	0	13	0
3	D	63	0	0	16	0
All	All	10040	0	9464	181	1

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 9.

The worst 5 of 181 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:D:323:ASP:N	3:D:401:HOH:O	1.85	1.10
2:D:323:ASP:HA	3:D:401:HOH:O	1.52	1.06
2:D:323:ASP:CA	3:D:401:HOH:O	2.03	1.05
2:C:166:ARG:CD	3:C:401:HOH:O	2.03	1.05
2:C:166:ARG:NE	3:C:401:HOH:O	1.94	1.01

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:563:HOH:O	3:B:572:HOH:O[1_655]	2.11	0.09

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	388/397 (98%)	376 (97%)	10 (3%)	2 (0%)	29	46
1	B	388/397 (98%)	373 (96%)	14 (4%)	1 (0%)	41	59
2	C	232/261 (89%)	226 (97%)	5 (2%)	1 (0%)	34	52
2	D	232/261 (89%)	225 (97%)	7 (3%)	0	100	100
All	All	1240/1316 (94%)	1200 (97%)	36 (3%)	4 (0%)	41	59

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	376	LEU
1	B	376	LEU
1	A	168	ALA
2	C	302	PRO

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	317/323 (98%)	308 (97%)	9 (3%)	43	67
1	B	317/323 (98%)	311 (98%)	6 (2%)	57	78
2	C	196/201 (98%)	193 (98%)	3 (2%)	65	83
2	D	196/201 (98%)	192 (98%)	4 (2%)	55	77
All	All	1026/1048 (98%)	1004 (98%)	22 (2%)	53	76

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	43	LEU
1	B	387	SER
1	B	362	LYS
2	D	155	SER
1	A	238	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	39	HIS
1	B	253	GLN
2	D	360	GLN
2	D	343	GLN
2	C	364	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 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, 95th 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	A	390/397 (98%)	0.18	3 (0%) 86 87	35, 50, 66, 95	0
1	B	390/397 (98%)	0.15	1 (0%) 94 94	33, 44, 60, 83	0
2	C	236/261 (90%)	0.17	1 (0%) 92 93	33, 45, 65, 84	0
2	D	236/261 (90%)	0.28	5 (2%) 63 65	37, 51, 75, 87	0
All	All	1252/1316 (95%)	0.19	10 (0%) 86 87	33, 48, 68, 95	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	0	MET	9.9
1	A	0	MET	4.2
2	C	272	PHE	3.1
2	D	272	PHE	2.8
2	D	302	PRO	2.8

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.