



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 25, 2025 – 02:05 PM EDT

PDB ID : 9PIX / pdb_00009pix
Title : Mur14 Fab with HBV c18V pMHC
Authors : Mortenson, D.E.
Deposited on : 2025-07-11
Resolution : 2.35 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

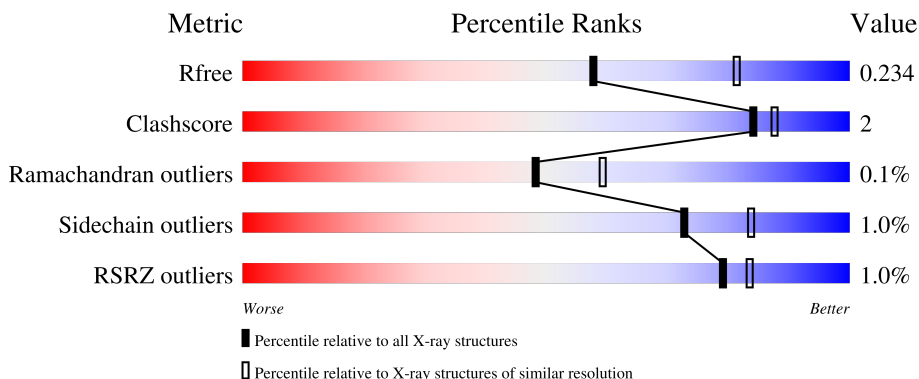
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	164625	1460 (2.36-2.36)
Clashscore	180529	1571 (2.36-2.36)
Ramachandran outliers	177936	1559 (2.36-2.36)
Sidechain outliers	177891	1559 (2.36-2.36)
RSRZ outliers	164620	1460 (2.36-2.36)

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	301	<div> <div>86%</div> <div>5%</div> <div>9%</div> </div>
2	H	240	<div> <div>81%</div> <div>8%</div> <div>10%</div> </div>
3	L	215	<div> <div>93%</div> <div>6%</div> </div>
4	P	10	<div> <div>100%</div> </div>
5	B	100	<div> <div>4%</div> <div>91%</div> <div>8%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6753 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	4	0
			2244	1404	409	422	9			

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q8WLS4
A	277	GLY	-	expression tag	UNP Q8WLS4
A	278	SER	-	expression tag	UNP Q8WLS4
A	279	GLY	-	expression tag	UNP Q8WLS4
A	280	GLY	-	expression tag	UNP Q8WLS4
A	281	SER	-	expression tag	UNP Q8WLS4
A	282	GLY	-	expression tag	UNP Q8WLS4
A	283	GLY	-	expression tag	UNP Q8WLS4
A	284	SER	-	expression tag	UNP Q8WLS4
A	285	ALA	-	expression tag	UNP Q8WLS4
A	286	GLY	-	expression tag	UNP Q8WLS4
A	287	GLY	-	expression tag	UNP Q8WLS4
A	288	GLY	-	expression tag	UNP Q8WLS4
A	289	LEU	-	expression tag	UNP Q8WLS4
A	290	ASN	-	expression tag	UNP Q8WLS4
A	291	ASP	-	expression tag	UNP Q8WLS4
A	292	ILE	-	expression tag	UNP Q8WLS4
A	293	PHE	-	expression tag	UNP Q8WLS4
A	294	GLU	-	expression tag	UNP Q8WLS4
A	295	ALA	-	expression tag	UNP Q8WLS4
A	296	GLN	-	expression tag	UNP Q8WLS4
A	297	LYS	-	expression tag	UNP Q8WLS4
A	298	ILE	-	expression tag	UNP Q8WLS4
A	299	GLU	-	expression tag	UNP Q8WLS4
A	300	TRP	-	expression tag	UNP Q8WLS4

- Molecule 2 is a protein called MUR14 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	215	Total	C	N	O	S	0	4	0
			1619	1031	260	322	6			

- Molecule 3 is a protein called MUR14 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	1	0
			1613	1013	270	325	5			

- Molecule 4 is a protein called c18V peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	P	10	Total	C	N	O	0	0	0
			83	58	10	15			

- Molecule 5 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	99	Total	C	N	O	S	0	1	0
			820	523	139	155	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

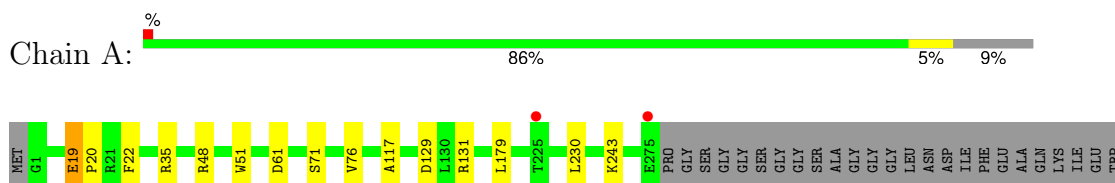
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	144	Total	O	0	0
			144	144		
6	H	113	Total	O	0	0
			113	113		
6	L	62	Total	O	0	0
			62	62		
6	P	8	Total	O	0	0
			8	8		
6	B	47	Total	O	0	0
			47	47		

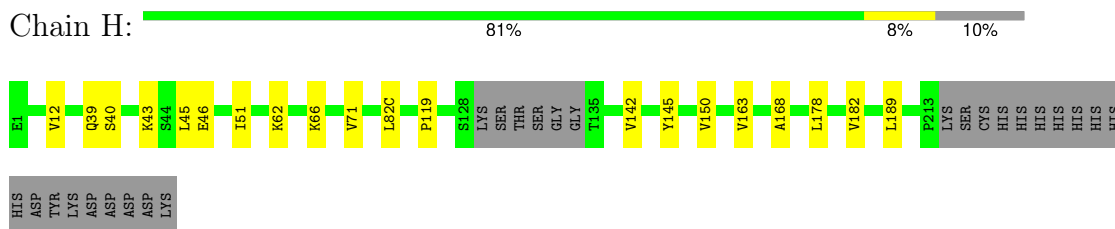
3 Residue-property plots [i](#)

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.

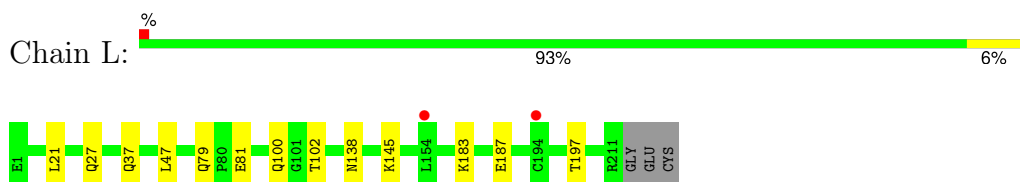
- Molecule 1: MHC class I antigen



- Molecule 2: MUR14 Heavy Chain



- Molecule 3: MUR14 Light Chain

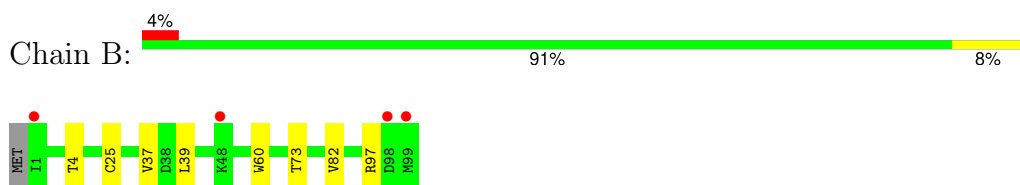


- Molecule 4: c18V peptide



There are no outlier residues recorded for this chain.

- Molecule 5: Beta-2-microglobulin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.60Å 73.36Å 93.89Å 90.00° 111.03° 90.00°	Depositor
Resolution (Å)	45.80 – 2.35 45.80 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.80-2.35) 99.7 (45.80-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.185 , 0.235 0.185 , 0.234	Depositor DCC
R_{free} test set	1900 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6753	wwPDB-VP
Average B, all atoms (Å ²)	43.0	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.*

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	0.10	0/2318	0.26	0/3150
2	H	0.10	0/1672	0.29	0/2282
3	L	0.09	0/1654	0.30	0/2254
4	P	0.13	0/87	0.34	0/117
5	B	0.09	0/846	0.28	0/1146
All	All	0.10	0/6577	0.28	0/8949

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	2244	0	2088	9	0
2	H	1619	0	1568	10	0
3	L	1613	0	1547	7	0
4	P	83	0	77	0	0
5	B	820	0	780	4	0
6	A	144	0	0	0	0
6	B	47	0	0	0	0
6	H	113	0	0	0	0
6	L	62	0	0	0	0
6	P	8	0	0	0	0
All	All	6753	0	6060	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 clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:73:THR:O	5:B:97:ARG:NH2	2.31	0.63
3:L:21:LEU:HD22	3:L:102:THR:HG21	1.83	0.60
3:L:145:LYS:HB2	3:L:197:THR:HB	1.85	0.58
1:A:19:GLU:HG3	1:A:20:PRO:HD2	1.87	0.56
1:A:35:ARG:HG2	1:A:48:ARG:HD3	1.88	0.56

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	277/301 (92%)	271 (98%)	6 (2%)	0	100	100
2	H	215/240 (90%)	208 (97%)	7 (3%)	0	100	100
3	L	211/215 (98%)	202 (96%)	8 (4%)	1 (0%)	25	28
4	P	8/10 (80%)	8 (100%)	0	0	100	100
5	B	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
All	All	809/866 (93%)	786 (97%)	22 (3%)	1 (0%)	48	59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	138	ASN

5.3.2 Protein sidechains

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	229/247 (93%)	227 (99%)	2 (1%)	75	85
2	H	182/205 (89%)	180 (99%)	2 (1%)	70	81
3	L	180/187 (96%)	178 (99%)	2 (1%)	70	81
4	P	10/10 (100%)	10 (100%)	0	100	100
5	B	92/95 (97%)	91 (99%)	1 (1%)	70	81
All	All	693/744 (93%)	686 (99%)	7 (1%)	73	84

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	189	LEU
3	L	79	GLN
5	B	4	THR
3	L	100	GLN
2	H	66	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
2	H	192	GLN
3	L	27	GLN
3	L	93	ASN
3	L	210	ASN

5.3.3 RNA

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, 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	275/301 (91%)	-0.28	2 (0%) 84 86	15, 33, 67, 133	4 (1%)
2	H	215/240 (89%)	-0.27	0 100 100	24, 39, 72, 89	4 (1%)
3	L	212/215 (98%)	0.10	2 (0%) 81 84	26, 56, 89, 104	1 (0%)
4	P	10/10 (100%)	-0.32	0 100 100	24, 31, 36, 37	0
5	B	99/100 (99%)	-0.26	4 (4%) 43 50	20, 37, 67, 96	1 (1%)
All	All	811/866 (93%)	-0.18	8 (0%) 79 83	15, 39, 80, 133	10 (1%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	GLU	3.5
5	B	1	ILE	3.0
5	B	99	MET	2.6
3	L	194	CYS	2.2
5	B	98	ASP	2.2

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.