



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:56 AM UTC

PDB ID : 2QRT / pdb_00002qrt
Title : Crystal Structure of a disulfide trapped single chain trimer composed of the MHC I heavy chain H-2Kb Y84C, beta-2microglobulin, and ovalbumin-derived peptide.
Authors : Mitaksov, V.E.; Fremont, D.H.
Deposited on : 2007-07-29
Resolution : 1.80 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	:	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

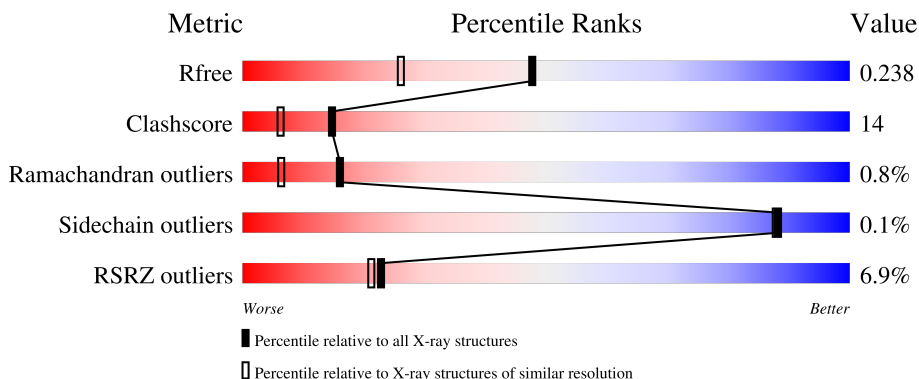
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	422	6% 73% 19% • 6%
1	B	422	7% 74% 19% • 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7143 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 H-2 class I histocompatibility antigen K-B alpha chain, Beta-2 microglobulin, ovalbumin-derived peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	0	0
			3194	2015	558	603	18			
1	B	398	Total	C	N	O	S	0	0	0
			3194	2015	558	603	18			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9P	GLY	-	linker	UNP P01901
A	10P	CYS	-	linker	UNP P01901
A	11P	GLY	-	linker	UNP P01901
A	12P	ALA	-	linker	UNP P01901
A	13P	SER	-	linker	UNP P01901
A	14P	GLY	-	linker	UNP P01901
A	15P	GLY	-	linker	UNP P01901
A	16P	GLY	-	linker	UNP P01901
A	17P	GLY	-	linker	UNP P01901
A	18P	SER	-	linker	UNP P01901
A	19P	GLY	-	linker	UNP P01901
A	20P	GLY	-	linker	UNP P01901
A	21P	GLY	-	linker	UNP P01901
A	22P	GLY	-	linker	UNP P01901
A	23P	SER	-	linker	UNP P01901
A	100B	GLY	-	linker	UNP P01901
A	101B	GLY	-	linker	UNP P01901
A	102B	GLY	-	linker	UNP P01901
A	103B	GLY	-	linker	UNP P01901
A	104B	SER	-	linker	UNP P01901
A	105B	GLY	-	linker	UNP P01901
A	106B	GLY	-	linker	UNP P01901
A	107B	GLY	-	linker	UNP P01901
A	108B	GLY	-	linker	UNP P01901

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Chain	Residue	Modelled	Actual	Comment	Reference
A	109B	SER	-	linker	UNP P01901
A	110B	GLY	-	linker	UNP P01901
A	111B	GLY	-	linker	UNP P01901
A	112B	GLY	-	linker	UNP P01901
A	113B	GLY	-	linker	UNP P01901
A	114B	SER	-	linker	UNP P01901
A	115B	GLY	-	linker	UNP P01901
A	116B	GLY	-	linker	UNP P01901
A	117B	GLY	-	linker	UNP P01901
A	118B	GLY	-	linker	UNP P01901
A	119B	SER	-	linker	UNP P01901
A	84H	CYS	TYR	engineered mutation	UNP P01901
B	9P	GLY	-	linker	UNP P01901
B	10P	CYS	-	linker	UNP P01901
B	11P	GLY	-	linker	UNP P01901
B	12P	ALA	-	linker	UNP P01901
B	13P	SER	-	linker	UNP P01901
B	14P	GLY	-	linker	UNP P01901
B	15P	GLY	-	linker	UNP P01901
B	16P	GLY	-	linker	UNP P01901
B	17P	GLY	-	linker	UNP P01901
B	18P	SER	-	linker	UNP P01901
B	19P	GLY	-	linker	UNP P01901
B	20P	GLY	-	linker	UNP P01901
B	21P	GLY	-	linker	UNP P01901
B	22P	GLY	-	linker	UNP P01901
B	23P	SER	-	linker	UNP P01901
B	100B	GLY	-	linker	UNP P01901
B	101B	GLY	-	linker	UNP P01901
B	102B	GLY	-	linker	UNP P01901
B	103B	GLY	-	linker	UNP P01901
B	104B	SER	-	linker	UNP P01901
B	105B	GLY	-	linker	UNP P01901
B	106B	GLY	-	linker	UNP P01901
B	107B	GLY	-	linker	UNP P01901
B	108B	GLY	-	linker	UNP P01901
B	109B	SER	-	linker	UNP P01901
B	110B	GLY	-	linker	UNP P01901
B	111B	GLY	-	linker	UNP P01901
B	112B	GLY	-	linker	UNP P01901
B	113B	GLY	-	linker	UNP P01901
B	114B	SER	-	linker	UNP P01901

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Chain	Residue	Modelled	Actual	Comment	Reference
B	115B	GLY	-	linker	UNP P01901
B	116B	GLY	-	linker	UNP P01901
B	117B	GLY	-	linker	UNP P01901
B	118B	GLY	-	linker	UNP P01901
B	119B	SER	-	linker	UNP P01901
B	84H	CYS	TYR	engineered mutation	UNP P01901

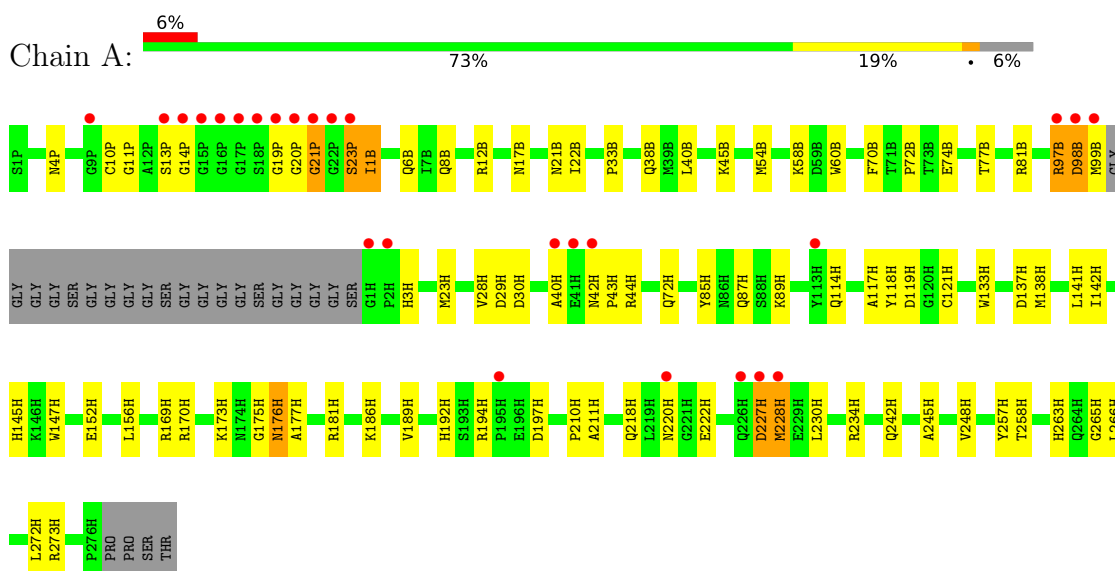
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	368	Total O 368 368	0	0
2	B	387	Total O 387 387	0	0

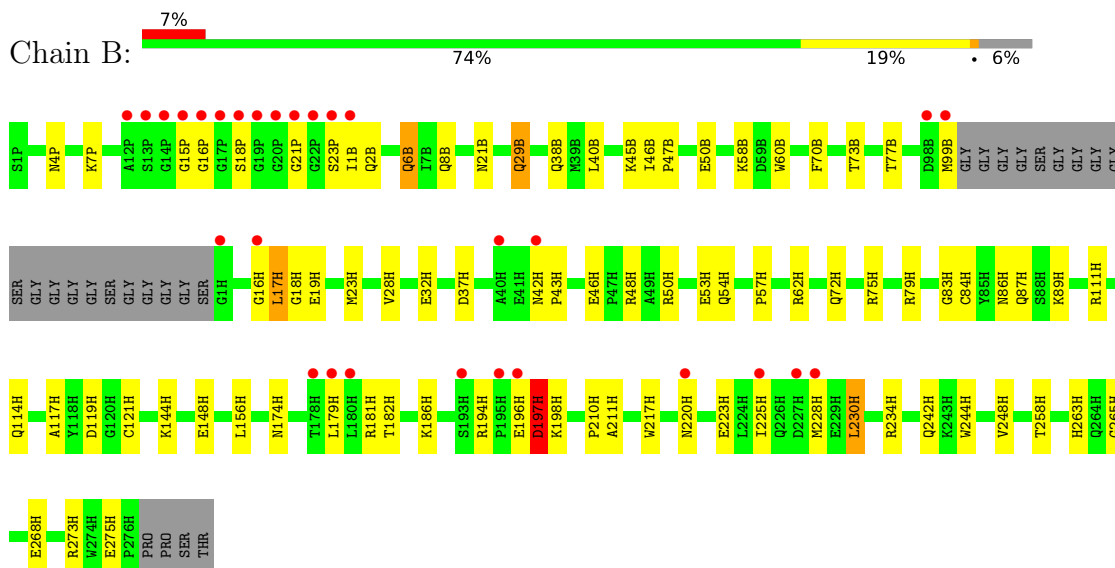
3 Residue-property plots [i](#)

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: H-2 class I histocompatibility antigen K-B alpha chain, Beta-2 microglobulin, ovalbumin-derived peptide



- Molecule 1: H-2 class I histocompatibility antigen K-B alpha chain, Beta-2 microglobulin, ovalbumin-derived peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.60Å 89.10Å 88.60Å 90.00° 110.90° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 20.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.80) 99.8 (20.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 1.76Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.208 , 0.239 0.207 , 0.238	Depositor DCC
R_{free} test set	4851 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7143	wwPDB-VP
Average B, all atoms (Å ²)	35.0	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 41.61 % 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 2.3021e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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	0.51	0/3282	1.01	13/4451 (0.3%)
1	B	0.48	0/3282	0.95	13/4451 (0.3%)
All	All	0.50	0/6564	0.98	26/8902 (0.3%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1(B)	ILE	N-CA-C	-8.06	96.97	108.58
1	A	19(P)	GLY	N-CA-C	-7.21	96.08	113.18
1	B	179(H)	LEU	N-CA-C	-6.94	101.87	110.41
1	A	228(H)	MET	N-CA-C	6.89	120.37	110.10
1	B	28(H)	VAL	N-CA-C	-6.52	98.34	107.80

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	3194	0	3054	95	0
1	B	3194	0	3054	80	0
2	A	368	0	0	20	0
2	B	387	0	0	32	0
All	All	7143	0	6108	174	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 14.

The worst 5 of 174 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:A:99(B):MET:HB2	1:A:192(H):HIS:HE1	1.14	1.09
1:A:23(P):SER:HB3	1:A:119(H):ASP:HB3	1.37	1.03
1:A:77(B):THR:HB	2:A:648:HOH:O	1.63	0.98
1:A:99(B):MET:HB2	1:A:192(H):HIS:CE1	1.99	0.97
1:B:15(P):GLY:O	1:B:84(H):CYS:HA	1.70	0.92

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	394/422 (93%)	377 (96%)	14 (4%)	3 (1%)	16	6
1	B	394/422 (93%)	371 (94%)	20 (5%)	3 (1%)	16	6
All	All	788/844 (93%)	748 (95%)	34 (4%)	6 (1%)	16	6

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176(H)	ASN
1	B	17(H)	LEU
1	A	98(B)	ASP
1	B	197(H)	ASP
1	A	21(P)	GLY

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	339/347 (98%)	339 (100%)	0	100	100
1	B	339/347 (98%)	338 (100%)	1 (0%)	86	86
All	All	678/694 (98%)	677 (100%)	1 (0%)	88	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	230(H)	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	42(H)	ASN
1	B	174(H)	ASN
1	B	115(H)	GLN
1	B	226(H)	GLN
1	A	242(H)	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 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	398/422 (94%)	0.28	26 (6%) 25 23	20, 31, 61, 94	0
1	B	398/422 (94%)	0.26	29 (7%) 21 19	19, 32, 62, 93	0
All	All	796/844 (94%)	0.27	55 (6%) 23 21	19, 32, 62, 94	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21(P)	GLY	12.2
1	A	20(P)	GLY	10.8
1	A	23(P)	SER	9.9
1	B	21(P)	GLY	7.4
1	B	16(P)	GLY	6.4

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.