



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 06:15 AM BST

PDB ID : 6MP1
Title : Crystal structures of the murine class I major histocompatibility complex H-2Db in complex with the mutant TRP1-K8 peptide
Authors : Clancy-Thompson, E.; Devlin, C.A.; Birnbaum, M.E.; Dougan, S.K.
Deposited on : 2018-10-05
Resolution : 2.21 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 following versions of software and data (see [references ⓘ](#)) 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	:	2.13.1
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)	:	2.13.1

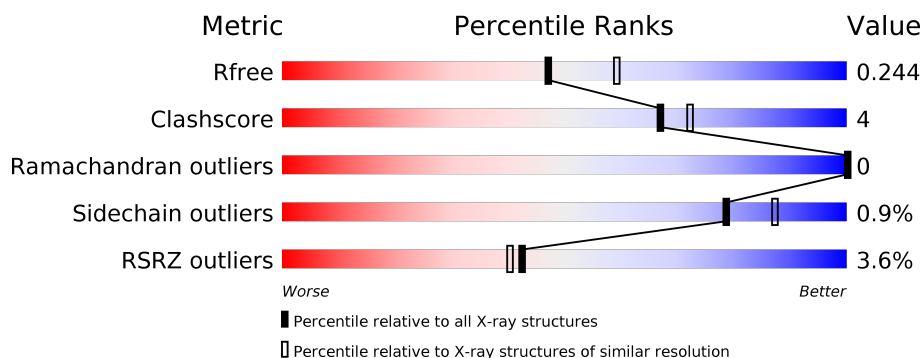
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 on 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	447	<div> <div>3%</div> <div>78%</div> <div>8%</div> <div>14%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3225 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 TRP1-K8 peptide, Beta-2-microglobulin,H-2 class I histocompatibility antigen, D-B alpha chain, chimeric construct.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	0	0
			3139	1985	550	588	16			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	LYS	TYR	engineered mutation	UNP P07147
A	9	MET	ALA	engineered mutation	UNP P07147
A	10	GLY	-	linker	UNP P07147
A	987	GLY	-	linker	UNP P07147
A	988	GLY	-	linker	UNP P07147
A	989	GLY	-	linker	UNP P07147
A	990	SER	-	linker	UNP P07147
A	991	GLY	-	linker	UNP P07147
A	992	GLY	-	linker	UNP P07147
A	993	GLY	-	linker	UNP P07147
A	994	GLY	-	linker	UNP P07147
A	995	SER	-	linker	UNP P07147
A	996	GLY	-	linker	UNP P07147
A	997	GLY	-	linker	UNP P07147
A	998	GLY	-	linker	UNP P07147
A	999	GLY	-	linker	UNP P07147
A	1000	SER	-	linker	UNP P07147
A	1981	GLY	-	linker	UNP P01887
A	1982	GLY	-	linker	UNP P01887
A	1983	GLY	-	linker	UNP P01887
A	1984	GLY	-	linker	UNP P01887
A	1985	SER	-	linker	UNP P01887
A	1986	GLY	-	linker	UNP P01887
A	1987	GLY	-	linker	UNP P01887
A	1988	GLY	-	linker	UNP P01887
A	1989	GLY	-	linker	UNP P01887

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1990	SER	-	linker	UNP P01887
A	1991	GLY	-	linker	UNP P01887
A	1992	GLY	-	linker	UNP P01887
A	1993	GLY	-	linker	UNP P01887
A	1994	GLY	-	linker	UNP P01887
A	1995	SER	-	linker	UNP P01887
A	1996	GLY	-	linker	UNP P01887
A	1997	GLY	-	linker	UNP P01887
A	1998	GLY	-	linker	UNP P01887
A	1999	GLY	-	linker	UNP P01887
A	2000	SER	-	linker	UNP P01887
A	2084	ALA	TYR	engineered mutation	UNP P01899
A	2277	ALA	-	expression tag	UNP P01899
A	2278	ALA	-	expression tag	UNP P01899
A	2279	ALA	-	expression tag	UNP P01899
A	2280	GLY	-	expression tag	UNP P01899
A	2281	GLY	-	expression tag	UNP P01899
A	2282	GLY	-	expression tag	UNP P01899
A	2283	LEU	-	expression tag	UNP P01899
A	2284	ASN	-	expression tag	UNP P01899
A	2285	ASP	-	expression tag	UNP P01899
A	2286	ILE	-	expression tag	UNP P01899
A	2287	PHE	-	expression tag	UNP P01899
A	2288	GLU	-	expression tag	UNP P01899
A	2289	ALA	-	expression tag	UNP P01899
A	2290	GLN	-	expression tag	UNP P01899
A	2291	LYS	-	expression tag	UNP P01899
A	2292	ILE	-	expression tag	UNP P01899
A	2293	GLU	-	expression tag	UNP P01899
A	2294	TRP	-	expression tag	UNP P01899
A	2295	HIS	-	expression tag	UNP P01899
A	2296	GLU	-	expression tag	UNP P01899
A	2297	HIS	-	expression tag	UNP P01899
A	2298	HIS	-	expression tag	UNP P01899
A	2299	HIS	-	expression tag	UNP P01899
A	2300	HIS	-	expression tag	UNP P01899
A	2301	HIS	-	expression tag	UNP P01899
A	2302	HIS	-	expression tag	UNP P01899
A	2303	HIS	-	expression tag	UNP P01899
A	2304	HIS	-	expression tag	UNP P01899

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

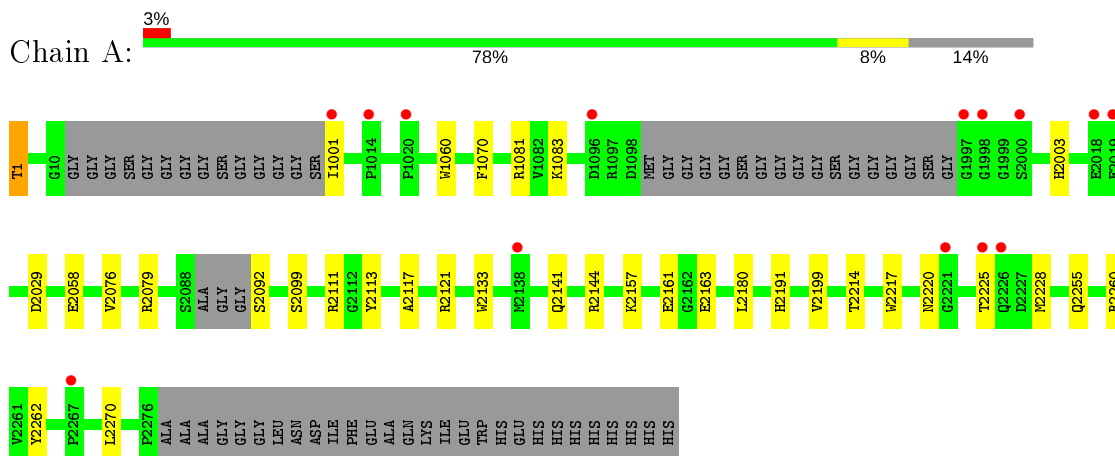
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	58	Total	O	0	0
			58	58		

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 ($\text{RSRZ} > 2$). 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: TRP1-K8 peptide, Beta-2-microglobulin, H-2 class I histocompatibility antigen, D-B alpha chain, chimeric construct



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.57Å 68.33Å 117.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.01 – 2.21 48.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.01-2.21) 99.0 (48.00-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.209 , 0.244 0.209 , 0.244	Depositor DCC
R_{free} test set	1136 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3225	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.26	0/3230	0.46	0/4382

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	3139	0	2984	24	0
2	A	28	0	26	2	0
3	A	58	0	0	1	0
All	All	3225	0	3010	24	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 4.

The worst 5 of 24 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:1:THR:HG21	1:A:2163:GLU:HG2	1.73	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:THR:OG1	1:A:2163:GLU:OE2	2.13	0.66
1:A:2003:HIS:ND1	1:A:2029:ASP:OD2	2.26	0.66
1:A:2225:THR:HA	1:A:2228:MET:HE3	1.80	0.64
1:A:2111:ARG:HD3	1:A:2113:TYR:CZ	2.39	0.58

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	377/447 (84%)	368 (98%)	9 (2%)	0	100	100

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	Percentiles	
1	A	333/361 (92%)	330 (99%)	3 (1%)	78	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	THR
1	A	1070	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2099	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

2 ligands are 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	A	2902	1	14,14,15	0.37	0	17,19,21	1.06	1 (5%)
2	NAG	A	2901	1	14,14,15	0.55	0	17,19,21	0.70	1 (5%)

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
2	NAG	A	2902	1	-	1/6/23/26	0/1/1/1
2	NAG	A	2901	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2902	NAG	C1-O5-C5	3.09	116.38	112.19
2	A	2901	NAG	C1-O5-C5	2.47	115.53	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2901	NAG	O5-C5-C6-O6
2	A	2901	NAG	C4-C5-C6-O6
2	A	2902	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2902	NAG	1	0
2	A	2901	NAG	1	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, 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	385/447 (86%)	0.18	14 (3%) 42 40	37, 55, 89, 113	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1001	ILE	4.1
1	A	2018	GLU	3.9
1	A	1014	PRO	3.1
1	A	2226	GLN	2.9
1	A	2138	MET	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](#)

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, 95th 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	B-factors(Å ²)	Q<0.9
2	NAG	A	2901	14/15	0.60	0.26	74,82,85,85	0
2	NAG	A	2902	14/15	0.71	0.28	78,92,97,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.