



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:01 AM GMT

PDB ID : 2F74
Title : Murine MHC class I H-2Db in complex with human b2-microglobulin and LCMV-derived immunodominant peptide gp33
Authors : Achour, A.; Michaelsson, J.; Harris, R.A.; Ljunggren, H.G.; Karre, K.; Schneider, G.; Sandalova, T.
Deposited on : 2005-11-30
Resolution : 2.70 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

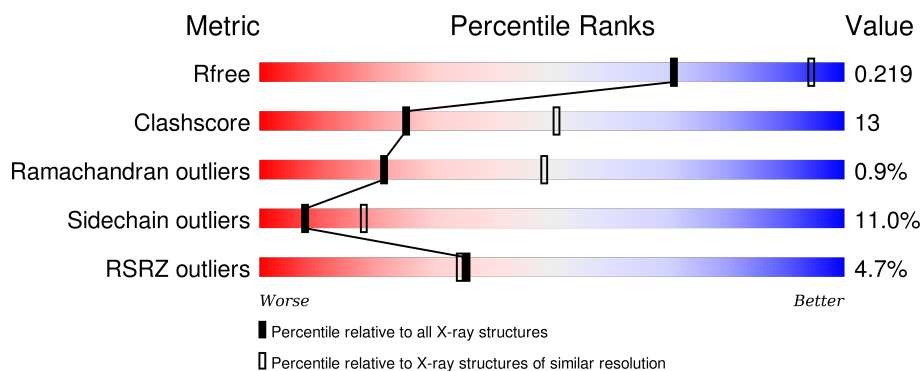
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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. 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	276	<div> <div>3%</div> <div>65%</div> <div>29%</div> <div>5%</div> </div>
1	D	276	<div> <div>8%</div> <div>65%</div> <div>29%</div> <div>6%</div> </div>
2	B	100	<div> <div>63%</div> <div>27%</div> <div>9%</div> <div>.</div> </div>
2	E	100	<div> <div>2%</div> <div>73%</div> <div>22%</div> <div>.</div> <div>.</div> </div>
3	C	9	<div> <div>89%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	9	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment on the left labeled '44%', a green segment in the middle labeled '89%', and a yellow segment on the right labeled '11%'. The segments are stacked horizontally, with the red segment starting from the left, followed by the green segment, and the yellow segment at the end.

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6419 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, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2261	1428	399	425	9			
1	D	276	Total	C	N	O	S	0	0	0
			2265	1430	400	426	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			
2	E	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	CLONING ARTIFACT	UNP P61769
E	0	MET	-	CLONING ARTIFACT	UNP P61769

- Molecule 3 is a protein called NONAMERIC PEPTIDE, GP33, DERIVED FROM LYMPHOCYTIC CHORIOMENINGITIS VIRUS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			73	48	11	13	1			
3	F	9	Total	C	N	O	S	0	0	0
			73	48	11	13	1			

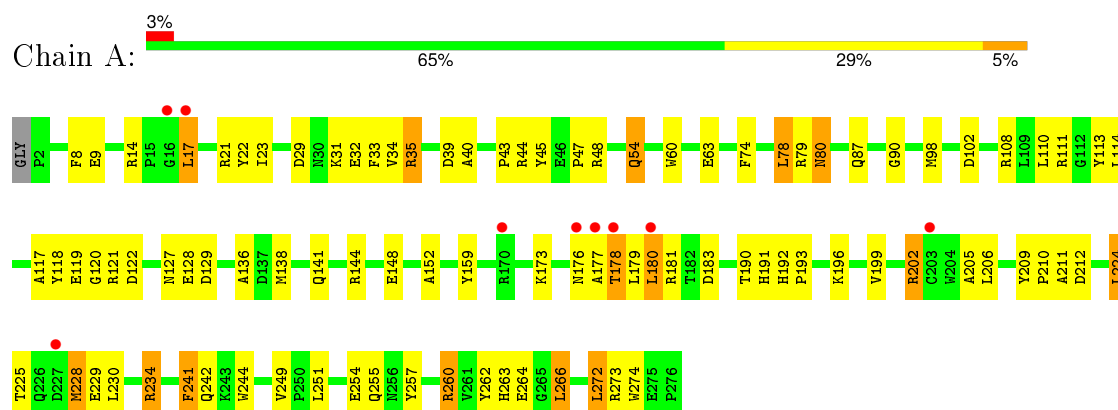
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	28	Total 28	O 28	0	0
4	B	17	Total 17	O 17	0	0
4	D	25	Total 25	O 25	0	0
4	E	11	Total 11	O 11	0	0

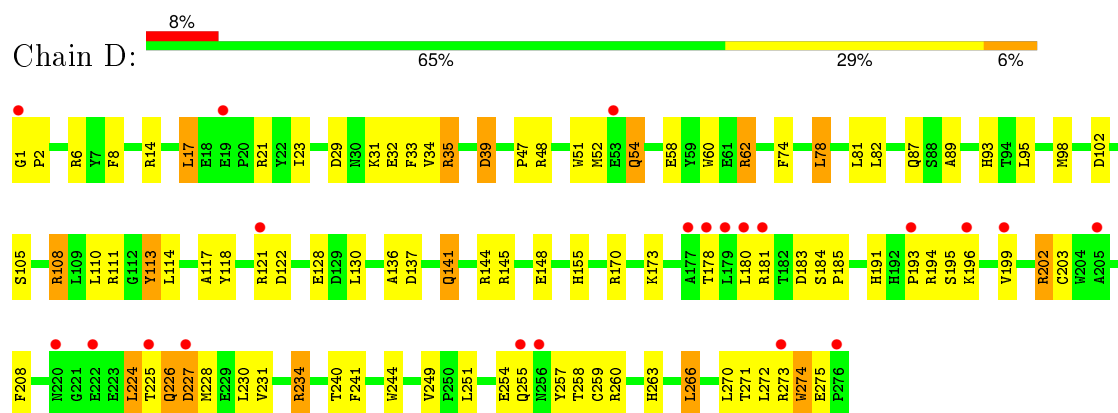
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

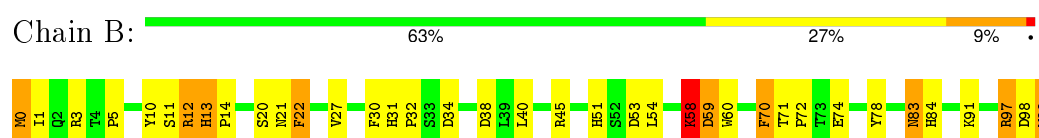
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



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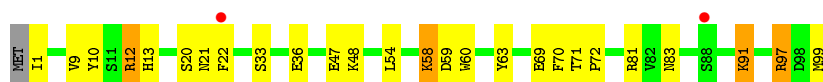


- Molecule 2: Beta-2-microglobulin

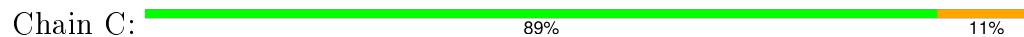


- Molecule 2: Beta-2-microglobulin

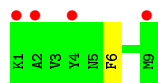
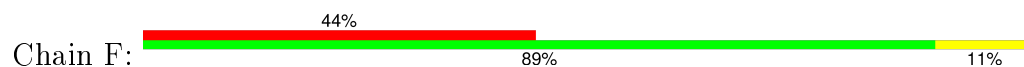




- Molecule 3: NONAMERIC PEPTIDE, GP33, DERIVED FROM LYMPHOCYTIC CHORIOMENINGITIS VIRUS



- Molecule 3: NONAMERIC PEPTIDE, GP33, DERIVED FROM LYMPHOCYTIC CHORIOMENINGITIS VIRUS



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.14Å 65.20Å 101.94Å 90.00° 102.43° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 19.97 – 2.69	Depositor EDS
% Data completeness (in resolution range)	92.5 (30.00-2.70) 92.0 (19.97-2.69)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.223 , 0.298 0.221 , 0.219	Depositor DCC
R_{free} test set	1135 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	62.9	Xtriage
Anisotropy	0.698	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 22473 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6419	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 27.75 % 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 2.0802e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	1.30	9/2328 (0.4%)	1.12	9/3160 (0.3%)
1	D	1.25	9/2332 (0.4%)	1.10	12/3166 (0.4%)
2	B	1.23	3/860 (0.3%)	1.22	7/1162 (0.6%)
2	E	1.16	2/852 (0.2%)	1.12	2/1152 (0.2%)
3	C	1.18	0/74	1.02	0/97
3	F	1.54	0/74	1.28	0/97
All	All	1.26	23/6520 (0.4%)	1.13	30/8834 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	D	0	1
All	All	0	3

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	113	TYR	CE1-CZ	-15.26	1.18	1.38
1	D	113	TYR	CG-CD2	-14.63	1.20	1.39
1	A	113	TYR	CE2-CZ	-14.27	1.20	1.38
1	A	241	PHE	CE1-CZ	-13.83	1.11	1.37
1	D	113	TYR	CE2-CZ	-13.48	1.21	1.38

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	137	ASP	CB-CG-OD2	10.53	127.78	118.30
2	B	12	ARG	NE-CZ-NH2	-8.37	116.11	120.30
2	E	12	ARG	NE-CZ-NH2	-7.98	116.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	29	ASP	CB-CG-OD2	7.71	125.24	118.30
1	A	122	ASP	CB-CG-OD2	7.27	124.85	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	177	ALA	Peptide
1	A	178	THR	Peptide
1	D	89	ALA	Peptide

5.2 Too-close contacts

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	2261	0	2131	54	0
1	D	2265	0	2136	58	0
2	B	837	0	803	34	0
2	E	829	0	794	21	0
3	C	73	0	74	1	0
3	F	73	0	74	3	0
4	A	28	0	0	2	0
4	B	17	0	0	5	0
4	D	25	0	0	2	0
4	E	11	0	0	1	0
All	All	6419	0	6012	157	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 13.

The worst 5 of 157 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:D:255:GLN:NE2	1:D:274:TRP:O	1.87	1.07
2:E:12:ARG:HG2	2:E:13:HIS:CE1	2.09	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:58:LYS:NZ	4:B:102:HOH:O	2.10	0.82
1:D:35:ARG:HB2	1:D:48:ARG:HD2	1.63	0.80
1:D:155:HIS:HB3	3:F:6:PHE:CE1	2.16	0.79

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	273/276 (99%)	253 (93%)	15 (6%)	5 (2%)	11	27
1	D	274/276 (99%)	246 (90%)	26 (10%)	2 (1%)	26	55
2	B	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
2	E	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	756/770 (98%)	697 (92%)	52 (7%)	7 (1%)	21	49

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	THR
1	A	17	LEU
1	D	17	LEU
1	A	136	ALA
1	A	80	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	234/234 (100%)	210 (90%)	24 (10%)	9	20
1	D	234/234 (100%)	207 (88%)	27 (12%)	7	16
2	B	95/95 (100%)	86 (90%)	9 (10%)	11	24
2	E	94/95 (99%)	81 (86%)	13 (14%)	4	10
3	C	7/7 (100%)	6 (86%)	1 (14%)	4	10
3	F	7/7 (100%)	7 (100%)	0	100	100
All	All	671/672 (100%)	597 (89%)	74 (11%)	8	18

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	6	PHE
1	D	114	LEU
2	E	58	LYS
1	D	14	ARG
1	D	54	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	5	ASN
1	D	87	GLN
2	E	13	HIS
2	B	89	GLN
2	E	83	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 carbohydrates 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	275/276 (99%)	-0.00	9 (3%)	50	50	8, 16, 26, 37	0
1	D	276/276 (100%)	0.37	21 (7%)	17	15	9, 16, 26, 39	0
2	B	100/100 (100%)	-0.21	0	100	100	11, 17, 24, 59	0
2	E	99/100 (99%)	0.08	2 (2%)	68	69	11, 17, 24, 47	0
3	C	9/9 (100%)	0.85	0	100	100	15, 16, 18, 24	0
3	F	9/9 (100%)	1.95	4 (44%)	0	0	15, 16, 18, 25	0
All	All	768/770 (99%)	0.15	36 (4%)	35	34	8, 16, 26, 59	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	178	THR	5.6
1	D	177	ALA	5.2
1	D	276	PRO	4.8
1	D	220	ASN	4.4
1	D	227	ASP	4.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.