



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:24 am GMT

PDB ID : 2MS2  
Title : THE REFINED STRUCTURE OF BACTERIOPHAGE MS2 AT 2.8  
ANGSTROMS RESOLUTION  
Authors : Valegard, K.; Liljas, L.  
Deposited on : 1994-08-23  
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

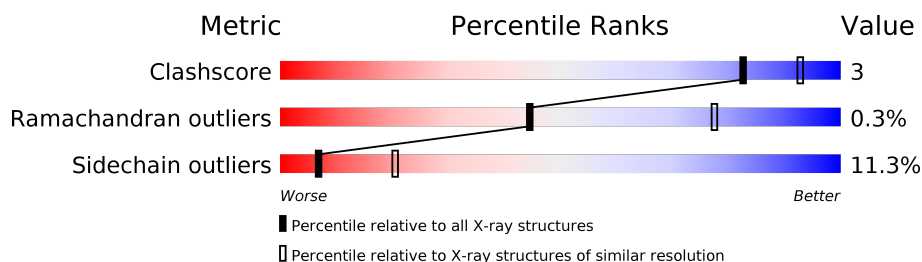
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	129	
1	B	129	
1	C	129	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3065 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 BACTERIOPHAGE MS2 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			965	606	165	190	4			
1	B	129	Total	C	N	O	S	0	0	0
			965	606	165	190	4			
1	C	129	Total	C	N	O	S	0	0	0
			965	606	165	190	4			

- Molecule 2 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	60	Total	O	0	0
			60	60		
2	B	63	Total	O	0	0
			63	63		
2	C	47	Total	O	0	0
			47	47		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.


Note EDS was not executed.

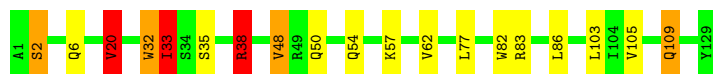
#### • Molecule 1: BACTERIOPHAGE MS2 COAT PROTEIN

Chain A: 




#### • Molecule 1: BACTERIOPHAGE MS2 COAT PROTEIN

Chain B: 



#### • Molecule 1: BACTERIOPHAGE MS2 COAT PROTEIN

Chain C: 



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	288.00Å 288.00Å 653.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.189 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3065	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

## 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	1.01	0/982	1.65	19/1337 (1.4%)
1	B	1.02	0/982	1.52	18/1337 (1.3%)
1	C	0.94	0/982	1.67	21/1337 (1.6%)
All	All	0.99	0/2946	1.61	58/4011 (1.4%)

There are no bond length outliers.

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	ARG	NE-CZ-NH2	-20.50	110.05	120.30
1	C	11	ASP	CB-CA-C	-10.57	89.27	110.40
1	C	11	ASP	N-CA-CB	10.18	128.92	110.60
1	A	56	ARG	NE-CZ-NH1	9.10	124.85	120.30
1	C	32	TRP	CE2-CD2-CG	-8.68	100.36	107.30
1	C	56	ARG	NE-CZ-NH2	-8.57	116.01	120.30
1	B	32	TRP	CD1-CG-CD2	8.22	112.88	106.30
1	C	49	ARG	NE-CZ-NH2	-8.09	116.26	120.30
1	A	32	TRP	CD1-CG-CD2	8.05	112.74	106.30
1	B	83	ARG	NE-CZ-NH2	-7.91	116.35	120.30
1	C	32	TRP	CG-CD2-CE3	7.86	140.98	133.90
1	B	82	TRP	CD1-CG-CD2	7.80	112.54	106.30
1	A	82	TRP	CD1-CG-CD2	7.77	112.51	106.30
1	C	32	TRP	CD1-CG-CD2	7.75	112.50	106.30
1	C	82	TRP	CD1-CG-CD2	7.64	112.41	106.30
1	A	32	TRP	CE2-CD2-CG	-7.60	101.22	107.30
1	B	32	TRP	CE2-CD2-CG	-7.43	101.36	107.30
1	C	32	TRP	CB-CG-CD1	-7.40	117.39	127.00
1	C	108	MET	CG-SD-CE	-7.32	88.50	100.20
1	A	2	SER	N-CA-C	-7.25	91.43	111.00
1	A	82	TRP	CE2-CD2-CG	-7.11	101.61	107.30
1	C	82	TRP	CE2-CD2-CG	-7.10	101.62	107.30
1	B	48	VAL	CB-CA-C	-7.09	97.93	111.40
1	C	58	TYR	CB-CG-CD2	-6.88	116.87	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	20	VAL	N-CA-CB	-6.63	96.92	111.50
1	B	82	TRP	CE2-CD2-CG	-6.62	102.01	107.30
1	B	20	VAL	N-CA-CB	-6.47	97.27	111.50
1	B	2	SER	N-CA-C	-6.33	93.92	111.00
1	A	49	ARG	NE-CZ-NH1	6.31	123.46	120.30
1	B	33	ILE	CA-CB-CG1	-6.27	99.09	111.00
1	A	20	VAL	N-CA-CB	-6.17	97.92	111.50
1	C	10	VAL	CA-C-N	6.03	130.47	117.20
1	A	79	VAL	N-CA-CB	-5.99	98.31	111.50
1	A	32	TRP	CB-CG-CD1	-5.96	119.25	127.00
1	B	32	TRP	CG-CD1-NE1	-5.87	104.23	110.10
1	B	50	GLN	CA-CB-CG	-5.84	100.55	113.40
1	B	82	TRP	CG-CD1-NE1	-5.67	104.43	110.10
1	B	20	VAL	CB-CA-C	5.64	122.13	111.40
1	C	11	ASP	CA-CB-CG	5.63	125.78	113.40
1	A	32	TRP	CG-CD1-NE1	-5.62	104.48	110.10
1	A	55	ASN	CB-CA-C	-5.62	99.17	110.40
1	C	20	VAL	CB-CA-C	5.57	121.98	111.40
1	B	38	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	B	32	TRP	CG-CD2-CE3	5.53	138.88	133.90
1	C	56	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	A	35	SER	N-CA-CB	-5.44	102.34	110.50
1	B	32	TRP	CB-CG-CD1	-5.43	119.93	127.00
1	A	38	ARG	CG-CD-NE	-5.42	100.41	111.80
1	C	101	CYS	CA-CB-SG	-5.41	104.27	114.00
1	B	57	LYS	CB-CA-C	-5.40	99.61	110.40
1	A	32	TRP	CG-CD2-CE3	5.37	138.74	133.90
1	C	49	ARG	N-CA-CB	-5.33	101.01	110.60
1	B	6	GLN	N-CA-CB	-5.25	101.14	110.60
1	C	6	GLN	N-CA-CB	-5.25	101.15	110.60
1	A	56	ARG	NH1-CZ-NH2	5.18	125.10	119.40
1	C	84	SER	N-CA-CB	5.15	118.22	110.50
1	A	82	TRP	CB-CG-CD1	-5.13	120.34	127.00
1	A	48	VAL	CB-CA-C	-5.09	101.73	111.40

There are no chirality outliers.

There are no planarity outliers.

## 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	965	0	964	6	0
1	B	965	0	964	4	0
1	C	965	0	964	7	0
2	A	60	0	0	1	0
2	B	63	0	0	0	0
2	C	47	0	0	2	0
All	All	3065	0	2892	17	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 3.

All (17) 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:C:10:VAL:HG12	1:C:12:ASN:HB2	1.79	0.64
1:A:97:THR:HG22	1:A:99:SER:H	1.63	0.64
1:B:20:VAL:HG13	1:B:32:TRP:HB3	1.83	0.59
1:A:20:VAL:HG13	1:A:32:TRP:HB3	1.88	0.56
1:C:20:VAL:HG13	1:C:32:TRP:HB3	1.89	0.55
1:B:105:VAL:O	1:B:109:GLN:HG2	2.08	0.54
1:A:97:THR:HG22	1:A:99:SER:N	2.25	0.51
1:C:125:ASN:HA	2:C:176:HOH:O	2.10	0.51
1:A:60:ILE:HB	1:A:88:MET:HG3	1.93	0.51
1:A:105:VAL:O	1:A:109:GLN:HG2	2.15	0.46
1:C:60:ILE:HB	1:C:88:MET:HG3	1.98	0.46
1:A:56:ARG:HD3	2:A:174:HOH:O	2.15	0.46
1:C:20:VAL:HG13	1:C:32:TRP:CB	2.46	0.45
1:B:62:VAL:HB	1:B:86:LEU:HB3	2.02	0.42
1:B:33:ILE:HD12	1:B:38:ARG:CZ	2.51	0.41
1:C:104:ILE:HG22	1:C:108:MET:CE	2.51	0.40
1:C:56:ARG:HD2	2:C:164:HOH:O	2.22	0.40

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	B	127/129 (98%)	123 (97%)	3 (2%)	1 (1%)	22	55
1	C	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
All	All	381/387 (98%)	369 (97%)	11 (3%)	1 (0%)	44	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2	SER

### 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	106/106 (100%)	91 (86%)	15 (14%)	4	12
1	B	106/106 (100%)	97 (92%)	9 (8%)	12	35
1	C	106/106 (100%)	94 (89%)	12 (11%)	7	20
All	All	318/318 (100%)	282 (89%)	36 (11%)	7	20

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	4	PHE

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Mol	Chain	Res	Type
1	A	6	GLN
1	A	8	VAL
1	A	19	THR
1	A	20	VAL
1	A	25	PHE
1	A	33	ILE
1	A	48	VAL
1	A	50	GLN
1	A	52	SER
1	A	79	VAL
1	A	109	GLN
1	A	126	SER
1	A	128	ILE
1	B	20	VAL
1	B	33	ILE
1	B	35	SER
1	B	38	ARG
1	B	48	VAL
1	B	54	GLN
1	B	77	LEU
1	B	103	LEU
1	B	109	GLN
1	C	11	ASP
1	C	20	VAL
1	C	23	SER
1	C	37	SER
1	C	38	ARG
1	C	49	ARG
1	C	66	LYS
1	C	76	GLU
1	C	84	SER
1	C	87	ASN
1	C	109	GLN
1	C	114	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	36	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 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.