



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:30 PM UTC

PDB ID : 2QYF / pdb_00002qyf
Title : Crystal structure of the Mad2/p31(comet)/Mad2-binding peptide ternary complex
Authors : Tomchick, D.R.; Luo, X.
Deposited on : 2007-08-14
Resolution : 2.30 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
Mogul : 2022.3.0, CSD as543be (2022)
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

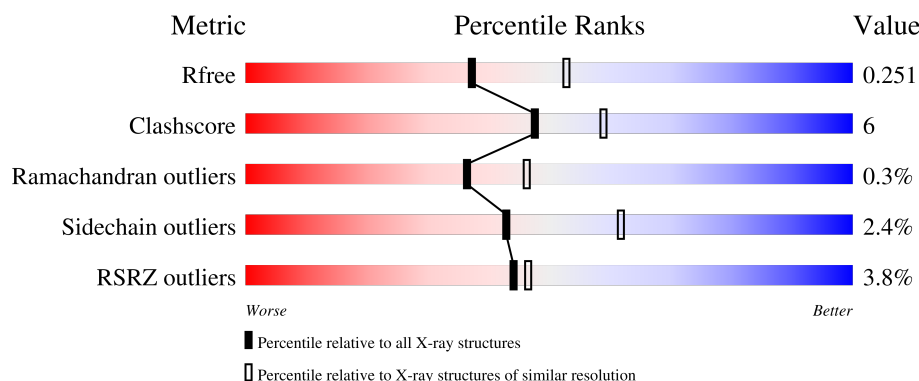
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

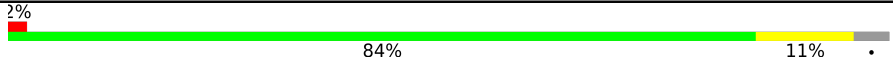
The reported resolution of this entry is 2.30 Å.

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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	206	
1	C	206	
2	B	240	
2	D	240	
3	E	12	

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Mol	Chain	Length	Quality of chain
3	F	12	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a green segment representing 67%, a yellow segment representing 17%, and a grey segment representing 17%. The percentages are labeled below each segment.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6944 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 Mitotic spindle assembly checkpoint protein MAD2A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	Se	0	0	0
			1589	1017	259	309	3	1			
1	C	183	Total	C	N	O	S	Se	0	0	0
			1484	955	239	286	3	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q13257
A	13	ALA	LEU	engineered mutation	UNP Q13257
C	0	GLY	-	expression tag	UNP Q13257
C	13	ALA	LEU	engineered mutation	UNP Q13257

- Molecule 2 is a protein called MAD2L1-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	188	Total	C	N	O	S	Se	0	0	0
			1500	968	258	261	8	5			
2	D	191	Total	C	N	O	S	Se	0	0	0
			1526	983	267	263	8	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	35	MSE	-	expression tag	UNP Q15013
D	35	MSE	-	expression tag	UNP Q15013

- Molecule 3 is a protein called peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	11	Total	C	N	O	0	0	0
			96	64	16	16			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	10	Total	C	N	O	0	0	0
			91	61	15	15			

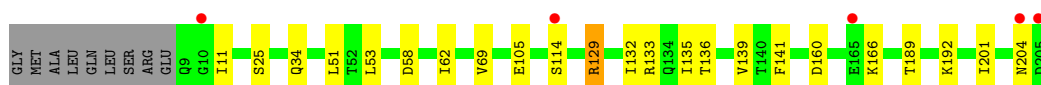
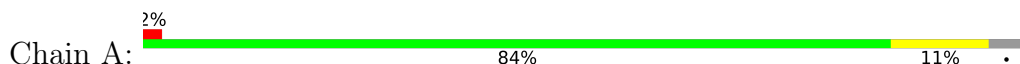
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	175	Total	O	0	0
			175	175		
4	B	163	Total	O	0	0
			163	163		
4	C	176	Total	O	0	0
			176	176		
4	D	132	Total	O	0	0
			132	132		
4	E	3	Total	O	0	0
			3	3		
4	F	9	Total	O	0	0
			9	9		

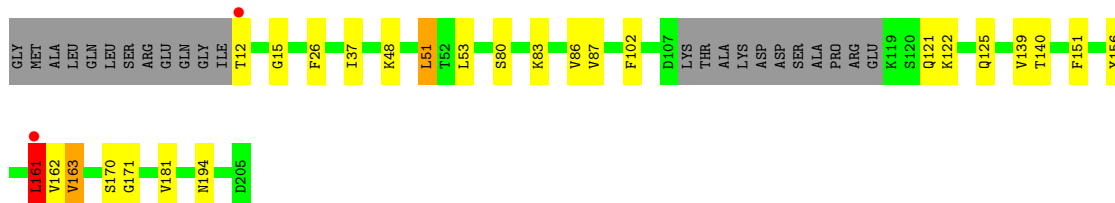
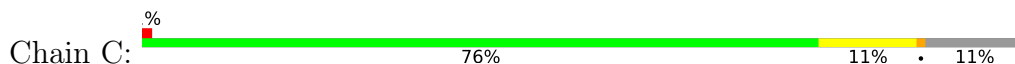
3 Residue-property plots [i](#)

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.

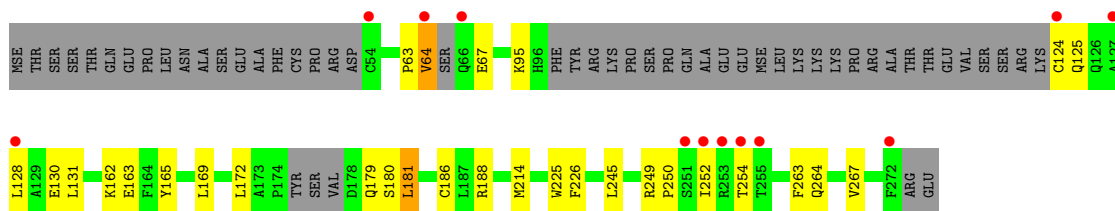
- Molecule 1: Mitotic spindle assembly checkpoint protein MAD2A



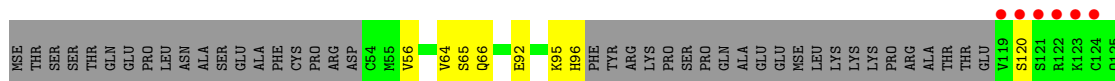
- Molecule 1: Mitotic spindle assembly checkpoint protein MAD2A



- Molecule 2: MAD2L1-binding protein

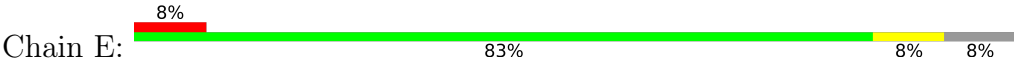


- Molecule 2: MAD2L1-binding protein





● Molecule 3: peptide



● Molecule 3: peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.67Å 104.52Å 138.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 30.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.4 (30.00-2.30) 97.3 (30.00-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.187 , 0.257 0.186 , 0.251	Depositor DCC
R_{free} test set	1771 reflections (3.92%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.3	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	0.94	EDS
Total number of atoms	6944	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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	0.97	2/1616 (0.1%)	1.01	1/2189 (0.0%)
1	C	0.98	1/1509 (0.1%)	1.06	4/2044 (0.2%)
2	B	0.91	0/1533	1.09	2/2069 (0.1%)
2	D	0.88	0/1559	1.03	2/2102 (0.1%)
3	E	0.80	0/102	1.40	2/141 (1.4%)
3	F	0.81	0/97	0.79	0/134
All	All	0.93	3/6416 (0.0%)	1.05	11/8679 (0.1%)

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
2	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	86	VAL	CA-CB	5.37	1.60	1.53
1	A	189	THR	CA-CB	5.25	1.62	1.53
1	A	11	ILE	CA-CB	5.09	1.60	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	67	GLU	N-CA-C	-9.23	100.60	112.23
1	C	163	VAL	N-CA-C	8.58	116.01	108.63
2	B	125	GLN	N-CA-C	-8.03	104.37	114.56
3	E	6	PRO	CA-C-N	7.54	128.15	120.38
3	E	6	PRO	C-N-CA	7.54	128.15	120.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	181	LEU	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	1589	0	1600	16	0
1	C	1484	0	1497	15	0
2	B	1500	0	1497	17	0
2	D	1526	0	1537	27	0
3	E	96	0	87	0	0
3	F	91	0	82	2	0
4	A	175	0	0	4	0
4	B	163	0	0	3	0
4	C	176	0	0	2	0
4	D	132	0	0	11	0
4	E	3	0	0	0	0
4	F	9	0	0	0	0
All	All	6944	0	6300	70	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 6.

The worst 5 of 70 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)
2:D:64:VAL:HB	4:D:347:HOH:O	1.65	0.94
2:B:130:GLU:HG2	4:B:328:HOH:O	1.89	0.72
2:D:169:LEU:HD23	2:D:245:LEU:HD12	1.71	0.72
2:B:95:LYS:HD3	2:B:128:LEU:HD21	1.77	0.66
2:D:255:THR:O	2:D:258:GLU:HB2	1.98	0.63

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	195/206 (95%)	191 (98%)	4 (2%)	0	100	100
1	C	179/206 (87%)	174 (97%)	4 (2%)	1 (1%)	21	27
2	B	180/240 (75%)	177 (98%)	2 (1%)	1 (1%)	21	27
2	D	185/240 (77%)	177 (96%)	8 (4%)	0	100	100
3	E	9/12 (75%)	9 (100%)	0	0	100	100
3	F	8/12 (67%)	8 (100%)	0	0	100	100
All	All	756/916 (82%)	736 (97%)	18 (2%)	2 (0%)	36	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	161	LEU
2	B	250	PRO

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	182/188 (97%)	180 (99%)	2 (1%)	65	81
1	C	171/188 (91%)	166 (97%)	5 (3%)	37	55
2	B	164/205 (80%)	159 (97%)	5 (3%)	36	53
2	D	167/205 (82%)	162 (97%)	5 (3%)	36	53
3	E	10/11 (91%)	10 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	10/11 (91%)	10 (100%)	0	100	100
All	All	704/808 (87%)	687 (98%)	17 (2%)	43	62

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	190	LEU
2	D	268	THR
1	C	51	LEU
1	C	53	LEU
1	C	139	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	9	GLN
2	D	264	GLN
2	B	137	HIS
2	B	96	HIS
2	B	179	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	196/206 (95%)	-0.25	5 (2%) 57 59	10, 25, 50, 64	0
1	C	182/206 (88%)	-0.35	2 (1%) 78 79	10, 24, 54, 65	0
2	B	183/240 (76%)	-0.01	12 (6%) 24 26	13, 26, 65, 90	0
2	D	186/240 (77%)	0.17	9 (4%) 35 37	12, 33, 67, 76	0
3	E	11/12 (91%)	0.45	1 (9%) 15 16	19, 32, 62, 66	0
3	F	10/12 (83%)	-0.12	0 100 100	23, 27, 51, 53	0
All	All	768/916 (83%)	-0.10	29 (3%) 44 46	10, 27, 59, 90	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	119	VAL	5.2
2	B	254	THR	4.1
2	B	124	CYS	4.0
1	A	114	SER	3.8
2	D	121	SER	3.8

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 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.