



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 03:24 pm BST

PDB ID : 3SZR
Title : Crystal structure of modified nucleotide-free human MxA
Authors : Gao, S.; Daumke, O.
Deposited on : 2011-07-19
Resolution : 3.50 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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

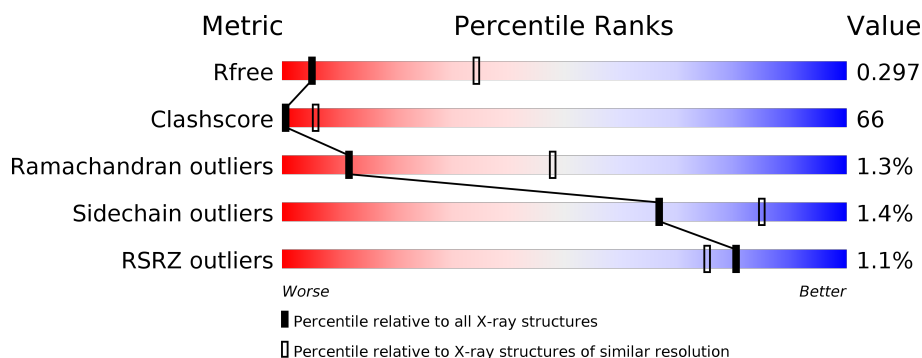
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	608	<div> <div></div> <div>29%</div> <div>60%</div> <div>8%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4507 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 Interferon-induced GTP-binding protein Mx1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4507	2855	774	861	17			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	GLY	-	EXPRESSION TAG	UNP P20591
A	27	PRO	-	EXPRESSION TAG	UNP P20591
A	28	HIS	-	EXPRESSION TAG	UNP P20591
A	29	MET	-	EXPRESSION TAG	UNP P20591
A	30	GLY	-	EXPRESSION TAG	UNP P20591
A	31	GLY	-	EXPRESSION TAG	UNP P20591
A	32	SER	-	EXPRESSION TAG	UNP P20591
A	440	ALA	TYR	ENGINEERED MUTATION	UNP P20591
A	441	ALA	ARG	ENGINEERED MUTATION	UNP P20591
A	442	ALA	GLY	ENGINEERED MUTATION	UNP P20591
A	443	ALA	ARG	ENGINEERED MUTATION	UNP P20591
A	?	-	CYS	DELETION	UNP P20591
A	?	-	GLN	DELETION	UNP P20591
A	?	-	ASP	DELETION	UNP P20591
A	?	-	GLN	DELETION	UNP P20591
A	?	-	VAL	DELETION	UNP P20591
A	?	-	TYR	DELETION	UNP P20591
A	?	-	ARG	DELETION	UNP P20591
A	?	-	GLY	DELETION	UNP P20591
A	?	-	ALA	DELETION	UNP P20591
A	?	-	LEU	DELETION	UNP P20591
A	?	-	GLN	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591
A	?	-	VAL	DELETION	UNP P20591
A	?	-	ARG	DELETION	UNP P20591
A	?	-	GLU	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591

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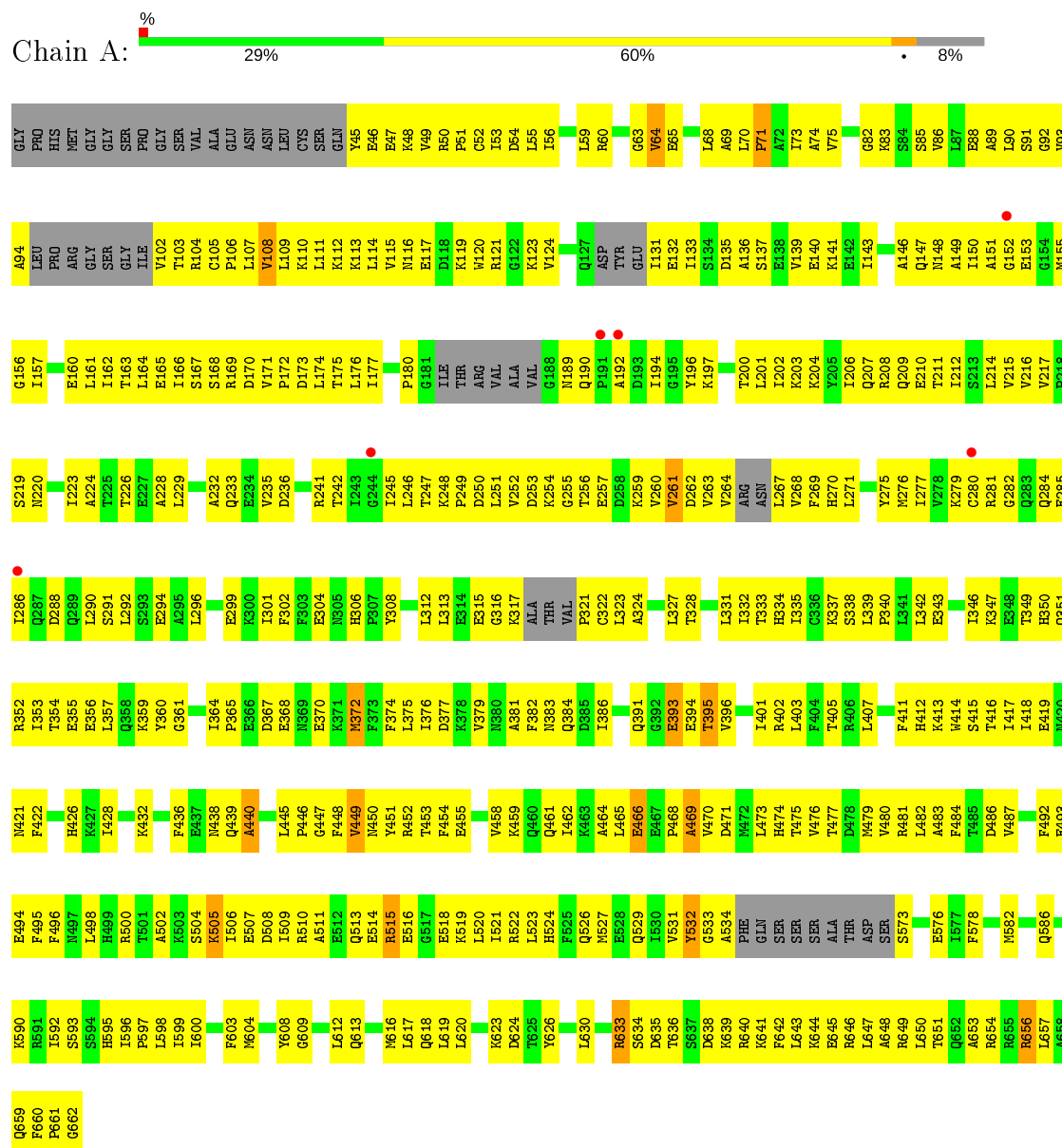
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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	DELETION	UNP P20591
A	?	-	LEU	DELETION	UNP P20591
A	?	-	GLU	DELETION	UNP P20591
A	?	-	GLU	DELETION	UNP P20591
A	?	-	GLU	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591
A	?	-	LYS	DELETION	UNP P20591
A	?	-	SER	DELETION	UNP P20591
A	?	-	TRP	DELETION	UNP P20591
A	?	-	ASP	DELETION	UNP P20591
A	?	-	PHE	DELETION	UNP P20591

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 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: Interferon-induced GTP-binding protein Mx1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	156.82Å 134.08Å 58.10Å 90.00° 106.34° 90.00°	Depositor
Resolution (Å)	34.98 – 3.50 32.81 – 3.50	Depositor EDS
% Data completeness (in resolution range)	71.0 (34.98-3.50) 71.0 (32.81-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.47Å)	Xtriage
Refinement program	REFMAC 5.6.0086, CNS 1.3	Depositor
R, R_{free}	0.262 , 0.295 0.260 , 0.297	Depositor DCC
R_{free} test set	520 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	76.4	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 88.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4507	wwPDB-VP
Average B, all atoms (Å ²)	140.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% 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	0.74	2/4572 (0.0%)	0.84	3/6146 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	466	GLU	CG-CD	6.14	1.61	1.51
1	A	393	GLU	CG-CD	5.70	1.60	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	515	ARG	NE-CZ-NH1	-6.52	117.04	120.30
1	A	372	MET	CG-SD-CE	5.72	109.35	100.20
1	A	656	ARG	NE-CZ-NH2	5.08	122.84	120.30

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	4507	0	4567	603	3
All	All	4507	0	4567	603	3

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 66.

The worst 5 of 603 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:63:GLY:CA	1:A:64:VAL:HG12	1.32	1.56
1:A:394:GLU:O	1:A:402:ARG:NH1	1.58	1.35
1:A:447:GLY:HA3	1:A:448:PHE:CD1	1.61	1.32
1:A:111:LEU:CD2	1:A:166:ILE:HB	1.71	1.19
1:A:119:LYS:HB2	1:A:167:SER:O	1.05	1.19

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:MET:SD	1:A:618:GLN:NE2[2_554]	1.82	0.38
1:A:376:ILE:CD1	1:A:618:GLN:OE1[2_554]	1.96	0.24
1:A:595:HIS:CE1	1:A:595:HIS:CE1[2_553]	2.09	0.11

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	545/608 (90%)	469 (86%)	69 (13%)	7 (1%)	12	48

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	VAL
1	A	71	PRO
1	A	261	VAL
1	A	449	VAL
1	A	440	ALA

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	499/538 (93%)	492 (99%)	7 (1%)	67 85

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	532	TYR
1	A	633	ARG
1	A	598	LEU
1	A	486	ASP
1	A	624	ASP

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 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 [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	559/608 (91%)	-0.34	6 (1%) 80 75	27, 138, 253, 291	1 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	ALA	3.8
1	A	244	GLY	3.5
1	A	191	PRO	2.6
1	A	286	ILE	2.3
1	A	152	GLY	2.3

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 carbohydrates 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.