



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 09:17 pm GMT

PDB ID : 1MAL  
Title : STRUCTURAL BASIS FOR SUGAR TRANSLOCATION THROUGH MAL-  
TOPORIN CHANNELS AT 3.1 ANGSTROMS RESOLUTION  
Authors : Schirmer, T.  
Deposited on : 1994-11-24  
Resolution : 3.10 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](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

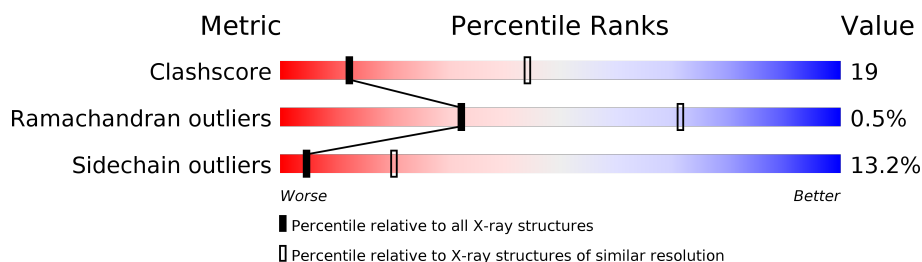
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)

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	421	
1	B	421	
1	C	421	

## 2 Entry composition

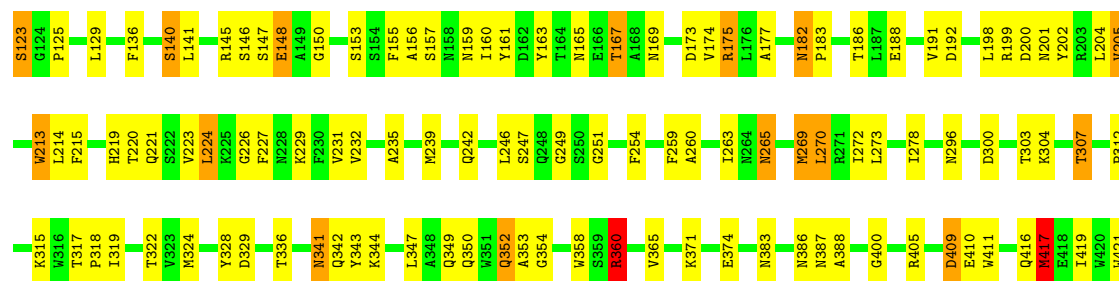
There is only 1 type of molecule in this entry. The entry contains 10050 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MALTOPORIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	73	0	0
			3350	2110	571	655	14			
1	B	421	Total	C	N	O	S	73	0	0
			3350	2110	571	655	14			
1	C	421	Total	C	N	O	S	73	0	0
			3350	2110	571	655	14			





## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.89Å 214.79Å 220.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 3.10	Depositor
% Data completeness (in resolution range)	95.5 (8.00-3.10)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.217 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10050	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	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	0.92	7/3443 (0.2%)	1.05	8/4668 (0.2%)
1	B	0.92	6/3443 (0.2%)	1.05	8/4668 (0.2%)
1	C	0.92	7/3443 (0.2%)	1.05	8/4668 (0.2%)
All	All	0.92	20/10329 (0.2%)	1.05	24/14004 (0.2%)

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	3
1	B	0	3
1	C	0	3
All	All	0	9

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	78	ASP	CB-CG	7.06	1.66	1.51
1	A	78	ASP	CB-CG	7.05	1.66	1.51
1	B	78	ASP	CB-CG	7.04	1.66	1.51
1	B	239	MET	SD-CE	-5.79	1.45	1.77
1	A	239	MET	SD-CE	-5.78	1.45	1.77

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	ASP	CB-CG-OD1	11.22	128.40	118.30
1	A	78	ASP	CB-CG-OD1	11.21	128.39	118.30
1	C	78	ASP	CB-CG-OD1	11.20	128.38	118.30
1	A	239	MET	CG-SD-CE	7.22	111.76	100.20
1	C	239	MET	CG-SD-CE	7.22	111.76	100.20

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	TYR	Sidechain
1	A	33	ARG	Sidechain
1	A	360	ARG	Mainchain
1	B	107	TYR	Sidechain
1	B	33	ARG	Sidechain

## 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	3350	0	3070	122	0
1	B	3350	0	3070	122	0
1	C	3350	0	3070	122	0
All	All	10050	0	9210	354	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 19.

The worst 5 of 354 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:417:MET:SD	1:A:417:MET:CE	2.03	1.47
1:B:417:MET:SD	1:B:417:MET:CE	2.03	1.45
1:C:417:MET:SD	1:C:417:MET:CE	2.03	1.44
1:B:317:THR:HG22	1:B:319:ILE:H	1.22	1.05
1:C:317:THR:HG22	1:C:319:ILE:H	1.22	1.03

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	419/421 (100%)	383 (91%)	34 (8%)	2 (0%)	32	71
1	B	419/421 (100%)	383 (91%)	34 (8%)	2 (0%)	32	71
1	C	419/421 (100%)	383 (91%)	34 (8%)	2 (0%)	32	71
All	All	1257/1263 (100%)	1149 (91%)	102 (8%)	6 (0%)	32	71

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	LEU
1	B	224	LEU
1	C	224	LEU
1	A	400	GLY
1	B	400	GLY

### 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	340/340 (100%)	295 (87%)	45 (13%)	5	20
1	B	340/340 (100%)	295 (87%)	45 (13%)	5	20
1	C	340/340 (100%)	295 (87%)	45 (13%)	5	20
All	All	1020/1020 (100%)	885 (87%)	135 (13%)	5	20

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	159	ASN
1	B	273	LEU
1	C	307	THR
1	B	160	ILE
1	B	205	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	219	HIS
1	B	268	HIS
1	C	275	HIS
1	B	221	GLN
1	B	265	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.