



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:11 AM GMT

PDB ID : 3GDF  
Title : Crystal structure of the NADP-dependent mannitol dehydrogenase from *Cladosporium herbarum*.  
Authors : Nuess, D.; Goettig, P.; Magler, I.; Denk, U.; Breitenbach, M.; Schneider, P.B.; Brandstetter, H.; Simon-Nobbe, B.  
Deposited on : 2009-02-24  
Resolution : 2.50 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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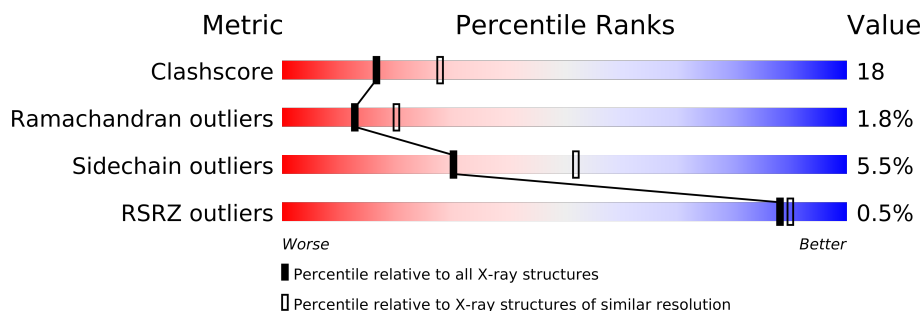
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.50 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))
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	267	
1	B	267	
1	C	267	
1	D	267	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8548 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Probable NADP-dependent mannitol dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total 1998	C 1248	N 346	O 392	S 12	30	0	0
1	B	267	Total 1998	C 1248	N 346	O 392	S 12	18	0	0
1	C	267	Total 1998	C 1248	N 346	O 392	S 12	35	0	0
1	D	267	Total 1998	C 1248	N 346	O 392	S 12	28	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Zn 2	0	0
2	A	2	Total 2	Zn 2	0	0

- Molecule 3 is water.

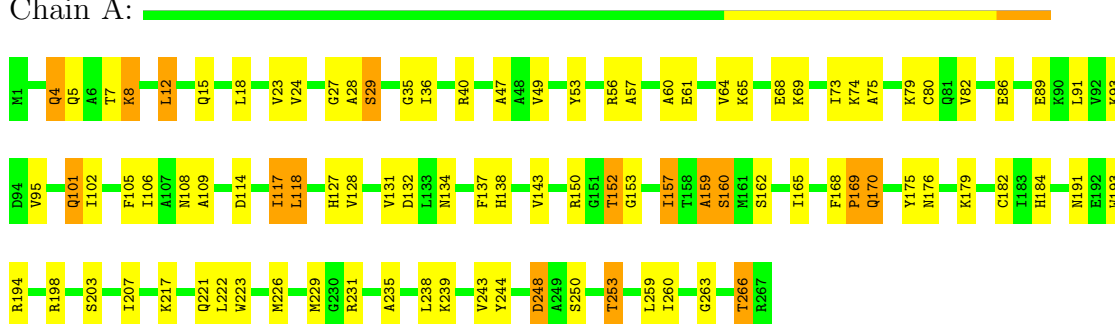
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	141	Total 141	O 141	0	0
3	B	133	Total 133	O 133	0	0
3	C	136	Total 136	O 136	0	0
3	D	142	Total 142	O 142	0	0

### 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.

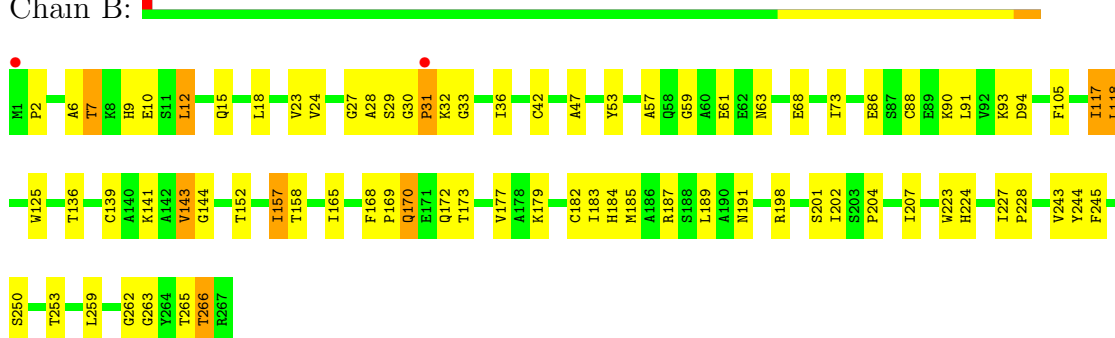
- Molecule 1: Probable NADP-dependent mannitol dehydrogenase

Chain A:



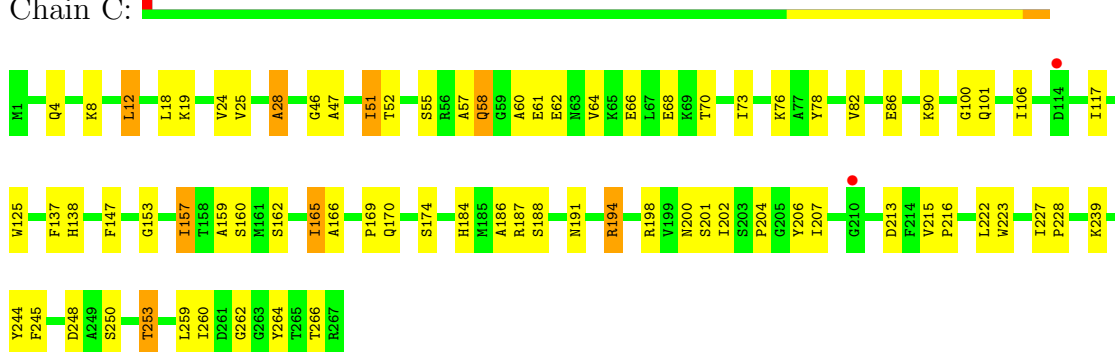
- Molecule 1: Probable NADP-dependent mannitol dehydrogenase

Chain B:



- Molecule 1: Probable NADP-dependent mannitol dehydrogenase

Chain C:



- Molecule 1: Probable NADP-dependent mannitol dehydrogenase

G230	L118	M1
K239	E123	P2
Y244	V129	L12
S250	Q130	G3
T253	V131	L16
G263	D132	S17
T266	L133	L18
R267	N134	K19
	G135	V24
	T136	A28
	F137	S29
	H138	G30
	C139	P31
	V143	I36
	R150	R40
	G151	G46
	T152	A47
	G153	A48
	I157	V49
	S160	A50
	M161	I51
	S162	T52
	T165	Y53
	F168	A57
	P169	Q58
	Q170	G59
	E171	A60
	Q172	E61
	K179	E62
	C182	N63
	T183	V64
	H184	K65
	M185	E66
	A186	L67
	R187	E68
	N191	K69
	R194	T70
	R198	I73
	T209	K74
	F214	A75
	Q221	K79
	L222	V82
	V223	A109
	W224	G110
		A111
		T112
		T117

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.01Å 106.54Å 132.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.50 19.89 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.5 (19.89-2.50) 97.6 (19.89-2.50)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.50Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.181 , 0.262 0.189 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	24.6	Xtriage
Anisotropy	0.823	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 33705 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8548	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.36	0/2035	0.56	0/2749
1	B	0.35	0/2035	0.55	0/2749
1	C	0.35	0/2035	0.57	0/2749
1	D	0.37	0/2035	0.56	0/2749
All	All	0.36	0/8140	0.56	0/10996

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1998	0	1951	85	0
1	B	1998	0	1951	76	0
1	C	1998	0	1951	69	0
1	D	1998	0	1951	76	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	141	0	0	10	0
3	B	133	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	136	0	0	5	0
3	D	142	0	0	10	0
All	All	8548	0	7804	278	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 18.

The worst 5 of 278 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:8:LYS:H	1:A:8:LYS:HE2	1.20	1.05
1:A:27:GLY:HA3	1:A:108:ASN:HD22	1.26	0.98
1:B:189:LEU:HD21	1:D:117:ILE:HD12	1.48	0.94
1:C:260:ILE:HG13	1:D:253:THR:HG22	1.53	0.88
1:C:250:SER:HB2	1:C:253:THR:HG23	1.57	0.85

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	265/267 (99%)	240 (91%)	20 (8%)	5 (2%)	12	19
1	B	265/267 (99%)	247 (93%)	14 (5%)	4 (2%)	15	25
1	C	265/267 (99%)	246 (93%)	15 (6%)	4 (2%)	15	25
1	D	265/267 (99%)	241 (91%)	18 (7%)	6 (2%)	10	14
All	All	1060/1068 (99%)	974 (92%)	67 (6%)	19 (2%)	13	20

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	C	28	ALA
1	C	55	SER

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Mol	Chain	Res	Type
1	B	27	GLY
1	D	29	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	205/205 (100%)	191 (93%)	14 (7%)	22	39
1	B	205/205 (100%)	194 (95%)	11 (5%)	31	53
1	C	205/205 (100%)	194 (95%)	11 (5%)	31	53
1	D	205/205 (100%)	196 (96%)	9 (4%)	39	64
All	All	820/820 (100%)	775 (94%)	45 (6%)	30	52

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	152	THR
1	C	12	LEU
1	D	143	VAL
1	B	170	GLN
1	C	24	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	172	GLN
1	C	4	GLN
1	D	170	GLN
1	B	184	HIS
1	C	63	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	265/267 (99%)	-0.51	0 <b>100</b> <b>100</b>	10, 22, 46, 59	4 (1%)
1	B	267/267 (100%)	-0.55	2 (0%) <b>84</b> <b>86</b>	9, 23, 42, 77	10 (3%)
1	C	265/267 (99%)	-0.51	2 (0%) <b>83</b> <b>84</b>	11, 23, 46, 62	5 (1%)
1	D	265/267 (99%)	-0.50	1 (0%) <b>90</b> <b>92</b>	9, 22, 45, 72	4 (1%)
All	All	1062/1068 (99%)	-0.52	5 (0%) <b>88</b> <b>90</b>	9, 23, 45, 77	23 (2%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	214	PHE	5.2
1	B	1	MET	3.8
1	C	210	GLY	2.7
1	B	31	PRO	2.6
1	C	114	ASP	2.3

### 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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	A	1004	1/1	0.05	-3.27	43,43,43,43	0
2	ZN	B	1002	1/1	0.03	-3.39	38,38,38,38	0
2	ZN	B	1001	1/1	0.04	-3.83	41,41,41,41	0
2	ZN	A	1003	1/1	0.03	-5.06	46,46,46,46	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.