



# wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 01:02 AM GMT

PDB ID : 2O1W  
Title : Structure of N-terminal plus middle domains (N+M) of GRP94  
Authors : Dollins, D.E.; Warren, J.J.; Immormino, R.M.; Gewirth, D.T.  
Deposited on : 2006-11-29  
Resolution : 3.40 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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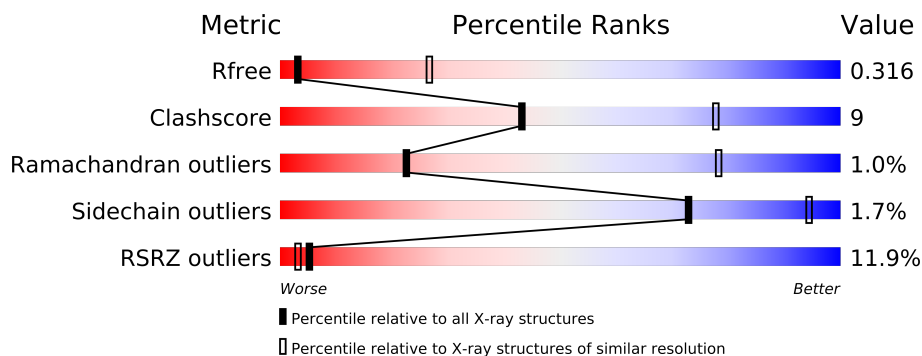
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.40 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))
$R_{free}$	66092	1017 (3.52-3.28)
Clashscore	79885	1214 (3.50-3.30)
Ramachandran outliers	78287	1177 (3.50-3.30)
Sidechain outliers	78261	1177 (3.50-3.30)
RSRZ outliers	66119	1017 (3.52-3.28)

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	506	
1	B	506	
1	C	506	
1	D	506	
1	E	506	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17042 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 Endoplasmin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	1	0
			3333	2133	552	638	10			
1	B	469	Total	C	N	O	S	0	0	0
			3710	2373	615	709	13			
1	C	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			
1	D	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			
1	E	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	MET	-	EXPRESSION TAG	UNP P41148
A	53	GLY	-	EXPRESSION TAG	UNP P41148
A	54	SER	-	EXPRESSION TAG	UNP P41148
A	55	SER	-	EXPRESSION TAG	UNP P41148
A	56	HIS	-	EXPRESSION TAG	UNP P41148
A	57	HIS	-	EXPRESSION TAG	UNP P41148
A	58	HIS	-	EXPRESSION TAG	UNP P41148
A	59	HIS	-	EXPRESSION TAG	UNP P41148
A	60	HIS	-	EXPRESSION TAG	UNP P41148
A	61	HIS	-	EXPRESSION TAG	UNP P41148
A	62	SER	-	EXPRESSION TAG	UNP P41148
A	63	SER	-	EXPRESSION TAG	UNP P41148
A	64	GLY	-	EXPRESSION TAG	UNP P41148
A	65	LEU	-	EXPRESSION TAG	UNP P41148
A	66	VAL	-	EXPRESSION TAG	UNP P41148
A	67	PRO	-	EXPRESSION TAG	UNP P41148
A	68	ARG	-	EXPRESSION TAG	UNP P41148
A	69	GLY	-	EXPRESSION TAG	UNP P41148
A	70	SER	-	EXPRESSION TAG	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
A	71	HIS	-	EXPRESSION TAG	UNP P41148
A	72	MET	-	EXPRESSION TAG	UNP P41148
A	287	GLY	-	see remark 999	UNP P41148
A	288	GLY	-	see remark 999	UNP P41148
A	289	GLY	-	see remark 999	UNP P41148
A	290	GLY	-	see remark 999	UNP P41148
B	52	MET	-	EXPRESSION TAG	UNP P41148
B	53	GLY	-	EXPRESSION TAG	UNP P41148
B	54	SER	-	EXPRESSION TAG	UNP P41148
B	55	SER	-	EXPRESSION TAG	UNP P41148
B	56	HIS	-	EXPRESSION TAG	UNP P41148
B	57	HIS	-	EXPRESSION TAG	UNP P41148
B	58	HIS	-	EXPRESSION TAG	UNP P41148
B	59	HIS	-	EXPRESSION TAG	UNP P41148
B	60	HIS	-	EXPRESSION TAG	UNP P41148
B	61	HIS	-	EXPRESSION TAG	UNP P41148
B	62	SER	-	EXPRESSION TAG	UNP P41148
B	63	SER	-	EXPRESSION TAG	UNP P41148
B	64	GLY	-	EXPRESSION TAG	UNP P41148
B	65	LEU	-	EXPRESSION TAG	UNP P41148
B	66	VAL	-	EXPRESSION TAG	UNP P41148
B	67	PRO	-	EXPRESSION TAG	UNP P41148
B	68	ARG	-	EXPRESSION TAG	UNP P41148
B	69	GLY	-	EXPRESSION TAG	UNP P41148
B	70	SER	-	EXPRESSION TAG	UNP P41148
B	71	HIS	-	EXPRESSION TAG	UNP P41148
B	72	MET	-	EXPRESSION TAG	UNP P41148
B	287	GLY	-	see remark 999	UNP P41148
B	288	GLY	-	see remark 999	UNP P41148
B	289	GLY	-	see remark 999	UNP P41148
B	290	GLY	-	see remark 999	UNP P41148
C	52	MET	-	EXPRESSION TAG	UNP P41148
C	53	GLY	-	EXPRESSION TAG	UNP P41148
C	54	SER	-	EXPRESSION TAG	UNP P41148
C	55	SER	-	EXPRESSION TAG	UNP P41148
C	56	HIS	-	EXPRESSION TAG	UNP P41148
C	57	HIS	-	EXPRESSION TAG	UNP P41148
C	58	HIS	-	EXPRESSION TAG	UNP P41148
C	59	HIS	-	EXPRESSION TAG	UNP P41148
C	60	HIS	-	EXPRESSION TAG	UNP P41148
C	61	HIS	-	EXPRESSION TAG	UNP P41148
C	62	SER	-	EXPRESSION TAG	UNP P41148

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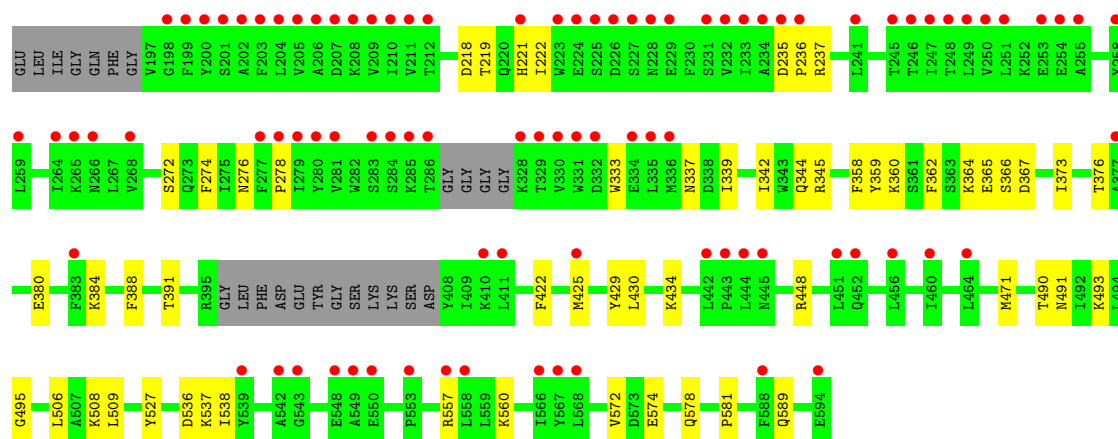
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Chain	Residue	Modelled	Actual	Comment	Reference
C	63	SER	-	EXPRESSION TAG	UNP P41148
C	64	GLY	-	EXPRESSION TAG	UNP P41148
C	65	LEU	-	EXPRESSION TAG	UNP P41148
C	66	VAL	-	EXPRESSION TAG	UNP P41148
C	67	PRO	-	EXPRESSION TAG	UNP P41148
C	68	ARG	-	EXPRESSION TAG	UNP P41148
C	69	GLY	-	EXPRESSION TAG	UNP P41148
C	70	SER	-	EXPRESSION TAG	UNP P41148
C	71	HIS	-	EXPRESSION TAG	UNP P41148
C	72	MET	-	EXPRESSION TAG	UNP P41148
C	287	GLY	-	see remark 999	UNP P41148
C	288	GLY	-	see remark 999	UNP P41148
C	289	GLY	-	see remark 999	UNP P41148
C	290	GLY	-	see remark 999	UNP P41148
D	52	MET	-	EXPRESSION TAG	UNP P41148
D	53	GLY	-	EXPRESSION TAG	UNP P41148
D	54	SER	-	EXPRESSION TAG	UNP P41148
D	55	SER	-	EXPRESSION TAG	UNP P41148
D	56	HIS	-	EXPRESSION TAG	UNP P41148
D	57	HIS	-	EXPRESSION TAG	UNP P41148
D	58	HIS	-	EXPRESSION TAG	UNP P41148
D	59	HIS	-	EXPRESSION TAG	UNP P41148
D	60	HIS	-	EXPRESSION TAG	UNP P41148
D	61	HIS	-	EXPRESSION TAG	UNP P41148
D	62	SER	-	EXPRESSION TAG	UNP P41148
D	63	SER	-	EXPRESSION TAG	UNP P41148
D	64	GLY	-	EXPRESSION TAG	UNP P41148
D	65	LEU	-	EXPRESSION TAG	UNP P41148
D	66	VAL	-	EXPRESSION TAG	UNP P41148
D	67	PRO	-	EXPRESSION TAG	UNP P41148
D	68	ARG	-	EXPRESSION TAG	UNP P41148
D	69	GLY	-	EXPRESSION TAG	UNP P41148
D	70	SER	-	EXPRESSION TAG	UNP P41148
D	71	HIS	-	EXPRESSION TAG	UNP P41148
D	72	MET	-	EXPRESSION TAG	UNP P41148
D	287	GLY	-	see remark 999	UNP P41148
D	288	GLY	-	see remark 999	UNP P41148
D	289	GLY	-	see remark 999	UNP P41148
D	290	GLY	-	see remark 999	UNP P41148



Chain C:







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	210.33Å 137.50Å 133.15Å 90.00° 124.10° 90.00°	Depositor
Resolution (Å)	47.30 – 3.40 47.73 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.30-3.40) 98.1 (47.73-3.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.68 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.314 , 0.332 0.298 , 0.316	Depositor DCC
$R_{free}$ test set	2122 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	148.6	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 248.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	3 of 42416 reflections (0.007%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	17042	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	195.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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 ⓘ

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	0.49	0/3400	0.56	0/4599
1	B	0.83	9/3783 (0.2%)	0.71	3/5117 (0.1%)
1	C	0.57	3/3400 (0.1%)	0.56	0/4599
1	D	0.53	1/3400 (0.0%)	0.58	1/4599 (0.0%)
1	E	0.37	0/3400	0.52	0/4599
All	All	0.58	13/17383 (0.1%)	0.59	4/23513 (0.0%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	87	LYS	CE-NZ	18.68	1.95	1.49
1	C	164	GLY	C-N	12.88	1.63	1.34
1	B	87	LYS	CD-CE	10.94	1.78	1.51
1	B	87	LYS	CG-CD	10.16	1.86	1.52
1	C	165	THR	CB-OG1	8.56	1.60	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	87	LYS	CD-CE-NZ	-10.41	87.76	111.70
1	B	76	PHE	CB-CG-CD2	-6.54	116.22	120.80
1	B	87	LYS	CG-CD-CE	-5.73	94.70	111.90
1	D	557	ARG	NE-CZ-NH2	-5.34	117.63	120.30

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	3333	0	3257	52	1
1	B	3710	0	3611	111	5
1	C	3333	0	3258	82	1
1	D	3333	0	3258	48	0
1	E	3333	0	3258	47	3
All	All	17042	0	16642	297	5

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 9.

The worst 5 of 297 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:87:LYS:CE	1:B:87:LYS:CD	1.78	1.61
1:B:87:LYS:CG	1:B:87:LYS:CD	1.87	1.49
1:B:455:LYS:CB	1:C:594:GLU:HB2	1.45	1.44
1:B:414:ARG:NH2	1:C:578:GLN:HG2	1.38	1.36
1:B:414:ARG:NH2	1:C:578:GLN:CG	1.89	1.34

All (5) 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	Distance(Å)	Clash(Å)
1:B:349:GLU:O	1:E:560:LYS:NZ[4_555]	1.61	0.59
1:B:561:LYS:NZ	1:C:544:SER:OG[2_655]	2.04	0.16
1:A:445:ASN:OD1	1:B:284:SER:OG[4_545]	2.08	0.12
1:B:349:GLU:C	1:E:560:LYS:NZ[4_555]	2.12	0.08
1:B:352:ASP:N	1:E:557:ARG:NH2[4_555]	2.13	0.07

## 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	408/506 (81%)	381 (93%)	23 (6%)	4 (1%)	22	78
1	B	463/506 (92%)	409 (88%)	47 (10%)	7 (2%)	15	68
1	C	408/506 (81%)	379 (93%)	27 (7%)	2 (0%)	38	87
1	D	408/506 (81%)	379 (93%)	24 (6%)	5 (1%)	19	74
1	E	408/506 (81%)	379 (93%)	27 (7%)	2 (0%)	38	87
All	All	2095/2530 (83%)	1927 (92%)	148 (7%)	20 (1%)	22	78

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	PHE
1	B	168	LYS
1	B	365	GLU
1	A	200	TYR
1	A	365	GLU

### 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	365/456 (80%)	361 (99%)	4 (1%)	84	96
1	B	400/456 (88%)	386 (96%)	14 (4%)	48	87
1	C	365/456 (80%)	360 (99%)	5 (1%)	78	95
1	D	365/456 (80%)	361 (99%)	4 (1%)	84	96
1	E	365/456 (80%)	361 (99%)	4 (1%)	84	96
All	All	1860/2280 (82%)	1829 (98%)	31 (2%)	73	94

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	376	THR
1	B	448	ARG
1	E	376	THR
1	B	412	TYR
1	C	117	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	182	GLN
1	C	578	GLN

### 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 ⓘ

There are no ligands in this entry.

## 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	416/506 (82%)	0.71	31 (7%) 14 6	179, 194, 209, 226	0
1	B	469/506 (92%)	0.58	20 (4%) 34 13	179, 195, 223, 253	0
1	C	416/506 (82%)	0.68	33 (7%) 13 6	179, 194, 209, 226	0
1	D	416/506 (82%)	0.85	51 (12%) 5 3	179, 194, 209, 226	0
1	E	416/506 (82%)	1.64	119 (28%) 1 1	179, 194, 209, 226	0
All	All	2133/2530 (84%)	0.88	254 (11%) 5 3	179, 194, 211, 253	0

The worst 5 of 254 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	285	LYS	39.0
1	E	286	THR	20.0
1	E	258	TYR	9.8
1	E	202	ALA	9.2
1	E	205	VAL	9.1

### 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 ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.