



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 10:31 am BST

PDB ID : 2V3M  
Title : Structure of the Gar1 domain of Naf1  
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Deposited on : 2007-06-19  
Resolution : 2.74 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

<https://www.wwpdb.org/validation/2017/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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

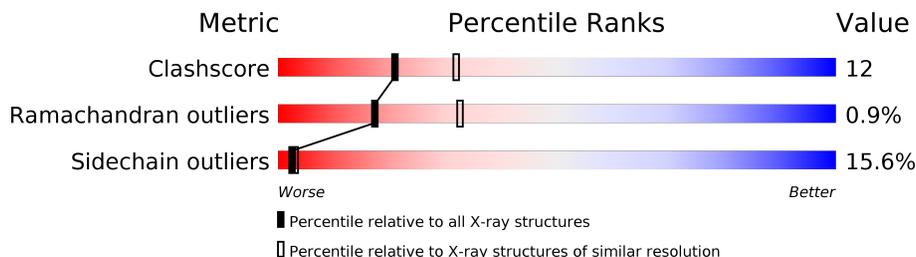
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)

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 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	131	
1	B	131	
1	C	131	
1	D	131	
1	E	131	
1	F	131	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4576 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 NAF1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	94	Total 754	C 492	N 121	O 139	S 1	Se 1	0	0	0
1	B	86	Total 694	C 455	N 109	O 128	S 1	Se 1	0	0	0
1	C	101	Total 806	C 522	N 129	O 152	S 1	Se 2	0	0	0
1	D	94	Total 752	C 491	N 118	O 141	S 1	Se 1	0	0	0
1	E	101	Total 806	C 522	N 129	O 152	S 1	Se 2	0	0	0
1	F	91	Total 729	C 476	N 115	O 136	S 1	Se 1	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

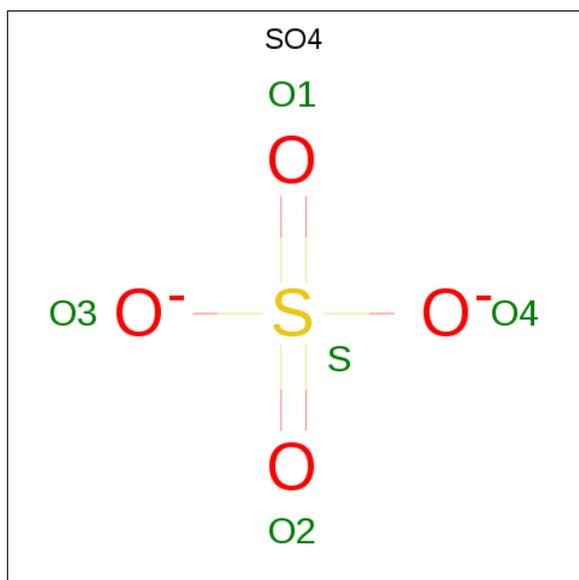
Chain	Residue	Modelled	Actual	Comment	Reference
A	108	MSE	-	expression tag	UNP P53919
A	233	HIS	-	expression tag	UNP P53919
A	234	HIS	-	expression tag	UNP P53919
A	235	HIS	-	expression tag	UNP P53919
A	236	HIS	-	expression tag	UNP P53919
A	237	HIS	-	expression tag	UNP P53919
A	238	HIS	-	expression tag	UNP P53919
B	108	MSE	-	expression tag	UNP P53919
B	233	HIS	-	expression tag	UNP P53919
B	234	HIS	-	expression tag	UNP P53919
B	235	HIS	-	expression tag	UNP P53919
B	236	HIS	-	expression tag	UNP P53919
B	237	HIS	-	expression tag	UNP P53919
B	238	HIS	-	expression tag	UNP P53919
C	108	MSE	-	expression tag	UNP P53919
C	233	HIS	-	expression tag	UNP P53919
C	234	HIS	-	expression tag	UNP P53919

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Chain	Residue	Modelled	Actual	Comment	Reference
C	235	HIS	-	expression tag	UNP P53919
C	236	HIS	-	expression tag	UNP P53919
C	237	HIS	-	expression tag	UNP P53919
C	238	HIS	-	expression tag	UNP P53919
D	108	MSE	-	expression tag	UNP P53919
D	233	HIS	-	expression tag	UNP P53919
D	234	HIS	-	expression tag	UNP P53919
D	235	HIS	-	expression tag	UNP P53919
D	236	HIS	-	expression tag	UNP P53919
D	237	HIS	-	expression tag	UNP P53919
D	238	HIS	-	expression tag	UNP P53919
E	108	MSE	-	expression tag	UNP P53919
E	233	HIS	-	expression tag	UNP P53919
E	234	HIS	-	expression tag	UNP P53919
E	235	HIS	-	expression tag	UNP P53919
E	236	HIS	-	expression tag	UNP P53919
E	237	HIS	-	expression tag	UNP P53919
E	238	HIS	-	expression tag	UNP P53919
F	108	MSE	-	expression tag	UNP P53919
F	233	HIS	-	expression tag	UNP P53919
F	234	HIS	-	expression tag	UNP P53919
F	235	HIS	-	expression tag	UNP P53919
F	236	HIS	-	expression tag	UNP P53919
F	237	HIS	-	expression tag	UNP P53919
F	238	HIS	-	expression tag	UNP P53919

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



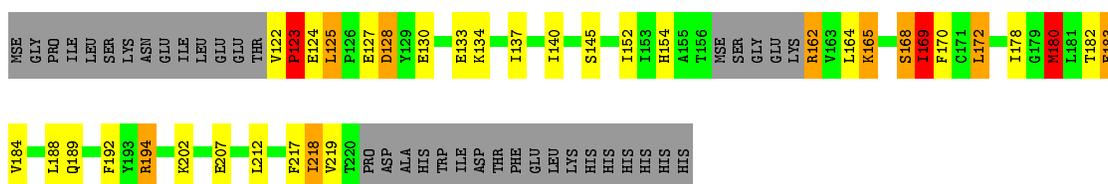
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

### 3 Residue-property plots [i](#)

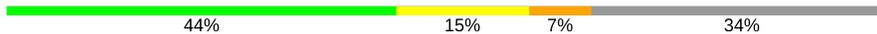
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

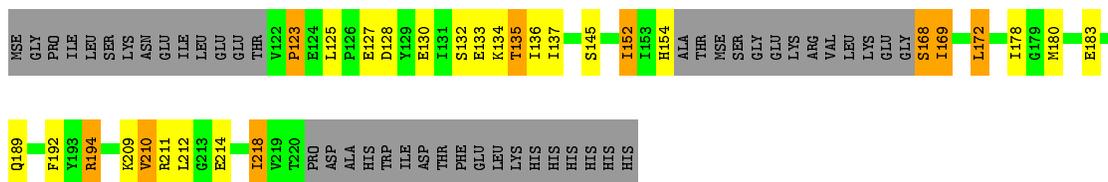
- Molecule 1: NAF1

Chain A: 



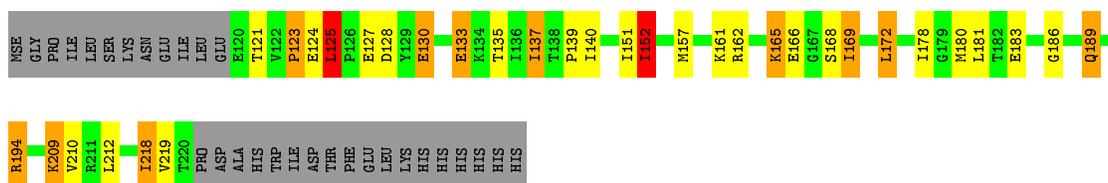
- Molecule 1: NAF1

Chain B: 



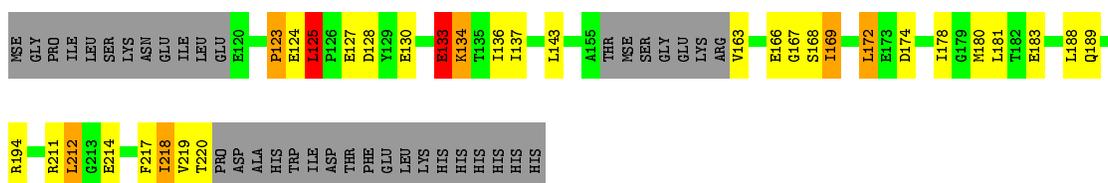
- Molecule 1: NAF1

Chain C: 



- Molecule 1: NAF1

Chain D: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.53Å 103.53Å 109.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.57 – 2.74 19.61 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.57-2.74) 99.3 (19.61-2.74)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.63 (at 2.75Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.257 , 0.287 0.307 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.4	Xtrriage
Anisotropy	0.023	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 13.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.030 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	4576	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.24% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.49	7/766 (0.9%)	1.34	8/1032 (0.8%)
1	B	1.31	7/706 (1.0%)	1.26	11/952 (1.2%)
1	C	1.43	9/818 (1.1%)	1.31	10/1100 (0.9%)
1	D	1.46	7/764 (0.9%)	1.25	7/1030 (0.7%)
1	E	1.26	7/818 (0.9%)	1.13	8/1100 (0.7%)
1	F	1.63	14/740 (1.9%)	1.40	10/996 (1.0%)
All	All	1.43	51/4612 (1.1%)	1.28	54/6210 (0.9%)

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	E	0	1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	124	GLU	CB-CG	-12.40	1.28	1.52
1	C	124	GLU	CB-CG	-11.18	1.30	1.52
1	D	124	GLU	CB-CG	-10.62	1.31	1.52
1	E	133	GLU	CD-OE1	-10.21	1.14	1.25
1	F	134	LYS	CB-CG	-9.72	1.26	1.52

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	209	LYS	CD-CE-NZ	12.31	140.01	111.70
1	B	128	ASP	CB-CG-OD1	-11.26	108.16	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	134	LYS	CD-CE-NZ	-11.25	85.82	111.70
1	A	180	MSE	CB-CG-SE	-9.38	84.55	112.70
1	F	128	ASP	CB-CA-C	-9.33	91.73	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	163	VAL	Peptide

## 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	754	0	785	22	0
1	B	694	0	718	20	0
1	C	806	0	835	18	0
1	D	752	0	778	30	0
1	E	806	0	835	31	1
1	F	729	0	756	15	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	10	0	0	0	0
2	E	5	0	0	1	0
2	F	5	0	0	0	0
All	All	4576	0	4707	113	1

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 12.

The worst 5 of 113 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:E:165:LYS:CD	1:E:165:LYS:H	1.63	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:LYS:N	1:E:165:LYS:HD2	1.70	1.04
1:E:165:LYS:H	1:E:165:LYS:HD2	0.86	0.99
1:B:209:LYS:HE2	1:D:133:GLU:HG3	1.46	0.96
1:C:165:LYS:HE2	1:C:165:LYS:H	1.31	0.92

All (1) 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:E:163:VAL:O	1:E:163:VAL:O[4_465]	1.43	0.77

## 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	90/131 (69%)	85 (94%)	4 (4%)	1 (1%)	14	26
1	B	82/131 (63%)	78 (95%)	4 (5%)	0	100	100
1	C	99/131 (76%)	94 (95%)	5 (5%)	0	100	100
1	D	90/131 (69%)	86 (96%)	4 (4%)	0	100	100
1	E	99/131 (76%)	90 (91%)	5 (5%)	4 (4%)	3	4
1	F	87/131 (66%)	80 (92%)	7 (8%)	0	100	100
All	All	547/786 (70%)	513 (94%)	29 (5%)	5 (1%)	17	32

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	156	THR
1	E	158	SER
1	A	123	PRO
1	E	124	GLU

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Mol	Chain	Res	Type
1	E	123	PRO

### 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	86/117 (74%)	73 (85%)	13 (15%)	3	3
1	B	80/117 (68%)	68 (85%)	12 (15%)	3	3
1	C	92/117 (79%)	77 (84%)	15 (16%)	2	3
1	D	86/117 (74%)	76 (88%)	10 (12%)	5	9
1	E	92/117 (79%)	75 (82%)	17 (18%)	1	2
1	F	83/117 (71%)	69 (83%)	14 (17%)	2	3
All	All	519/702 (74%)	438 (84%)	81 (16%)	2	3

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	209	LYS
1	D	169	ILE
1	F	166	GLU
1	C	210	VAL
1	D	127	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	203	ASN
1	F	203	ASN
1	D	203	ASN
1	B	203	ASN
1	E	203	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](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	D	1222	-	4,4,4	0.64	0	6,6,6	0.95	0
2	SO4	B	1221	-	4,4,4	0.28	0	6,6,6	0.33	0
2	SO4	E	1221	-	4,4,4	0.18	0	6,6,6	0.65	0
2	SO4	C	1221	-	4,4,4	0.51	0	6,6,6	1.82	3 (50%)
2	SO4	F	1221	-	4,4,4	0.27	0	6,6,6	0.96	0
2	SO4	D	1221	-	4,4,4	0.33	0	6,6,6	0.89	0
2	SO4	A	1221	-	4,4,4	0.24	0	6,6,6	0.51	0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1221	SO4	O4-S-O3	-2.63	97.84	109.06
2	C	1221	SO4	O4-S-O2	2.35	121.59	109.31
2	C	1221	SO4	O3-S-O1	2.26	121.12	109.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1221	SO4	1	0
2	E	1221	SO4	1	0

## 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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.