



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 16, 2017 – 02:34 PM EDT

PDB ID : 3EGH  
Title : Crystal structure of a complex between Protein Phosphatase 1 alpha (PP1), the PP1 binding and PDZ domains of Spinophilin and the small natural molecular toxin Nodularin-R  
Authors : Ragusa, M.J.; Page, R.; Peti, W.  
Deposited on : unknown  
Resolution : 2.00 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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

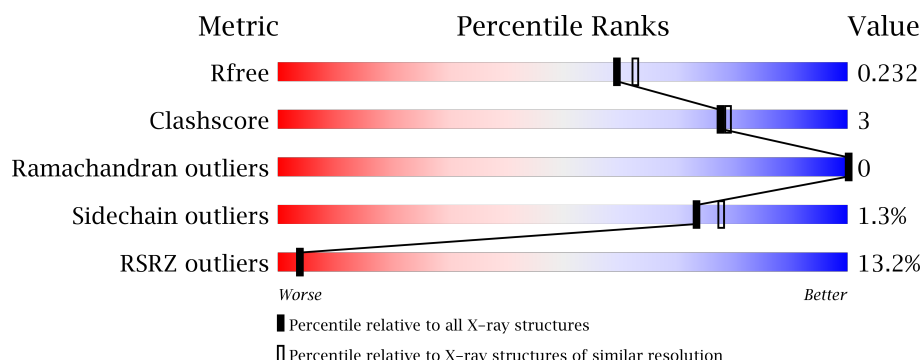
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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.

Mol	Chain	Length	Quality of chain
1	A	329	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>7%</div> <div>11%</div> </div> </div>
1	B	329	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>5%</div> <div>11%</div> </div> </div>
2	C	170	<div> <div>35%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>6%</div> </div> </div>
2	D	170	<div> <div>10%</div> <div> <div></div> <div>36%</div> <div>61%</div> </div> </div>
3	E	5	<div> <div></div> <div> <div>80%</div> <div>20%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	5	<div><div></div><div>80%</div><div>20%</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	402	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6990 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 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	5	0
			2358	1520	390	429	19			
1	B	294	Total	C	N	O	S	0	2	0
			2346	1509	387	431	19			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	EXPRESSION TAG	UNP P62136
A	3	HIS	-	EXPRESSION TAG	UNP P62136
A	4	MET	-	EXPRESSION TAG	UNP P62136
A	5	GLY	-	EXPRESSION TAG	UNP P62136
A	6	SER	-	EXPRESSION TAG	UNP P62136
B	2	GLY	-	EXPRESSION TAG	UNP P62136
B	3	HIS	-	EXPRESSION TAG	UNP P62136
B	4	MET	-	EXPRESSION TAG	UNP P62136
B	5	GLY	-	EXPRESSION TAG	UNP P62136
B	6	SER	-	EXPRESSION TAG	UNP P62136

- Molecule 2 is a protein called Spinophilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	160	Total	C	N	O	S	0	1	0
			1172	736	201	231	4			
2	D	66	Total	C	N	O	S	0	2	0
			496	312	79	104	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	414	GLY	-	EXPRESSION TAG	UNP O35274

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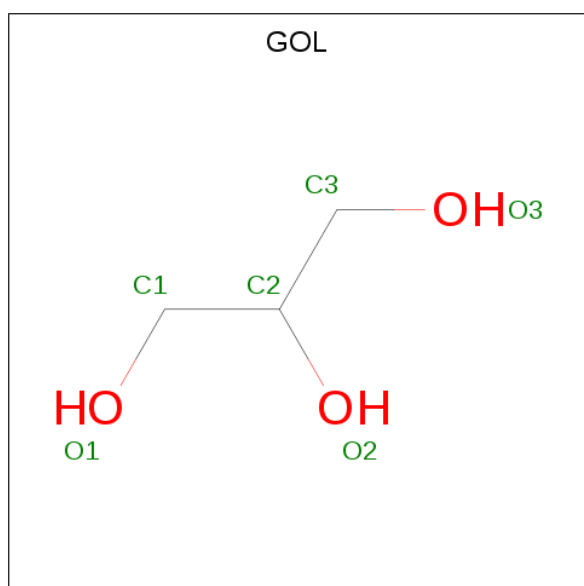
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Chain	Residue	Modelled	Actual	Comment	Reference
C	415	SER	-	EXPRESSION TAG	UNP O35274
C	416	MET	-	EXPRESSION TAG	UNP O35274
D	414	GLY	-	EXPRESSION TAG	UNP O35274
D	415	SER	-	EXPRESSION TAG	UNP O35274
D	416	MET	-	EXPRESSION TAG	UNP O35274

- Molecule 3 is a protein called nodularin R.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	5	Total	C	N	O	0	0	0
			55	40	5	10			
3	F	5	Total	C	N	O	0	0	0
			54	39	5	10			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Mn	0	0
			2	2		
5	A	2	Total	Mn	0	0
			2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	179	Total	O	0	0
			179	179		
6	B	198	Total	O	0	0
			198	198		
6	C	61	Total	O	0	0
			61	61		
6	D	38	Total	O	0	0
			38	38		
6	E	3	Total	O	0	0
			3	3		
6	F	2	Total	O	0	0
			2	2		



GLY  
MET  
GLY  
ALA  
GLY  
ALA  
ASP  
MET  
GLY  
LEU  
GLU  
LYS  
LEU  
GLY  
ILE  
PHE  
VAL  
LYS  
THR  
VAL  
THR  
GLU  
GLY  
GLY  
ALA  
ALA  
HIS  
ARG  
ASP  
GLY  
ARG  
ILE  
GLN  
VAL  
ASN  
ASP  
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SER  
VAL  
LEU  
ARG  
ASN

THR  
LYS  
GLY  
ARG  
VAL  
PHE  
MET  
ILE  
GLY  
ARG  
GLU

● Molecule 3: nodularin R

Chain E: 

80%

20%

D1

X5

● Molecule 3: nodularin R

Chain F: 

80%

20%

D1

X5



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.41Å 84.43Å 109.31Å 90.00° 93.58° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 39.37 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.3 (40.00-2.00) 96.3 (39.37-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.04 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.192 , 0.235 0.191 , 0.232	Depositor DCC
$R_{free}$ test set	3528 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.0	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 52.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6990	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.52 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5088e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: ACB, MDH, GOL, MN, 1ZN, FGA

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	1/2428 (0.0%)	0.75	1/3285 (0.0%)
1	B	0.79	1/2406 (0.0%)	0.77	1/3256 (0.0%)
2	C	0.61	0/1195	0.67	0/1619
2	D	0.70	0/516	0.66	0/705
3	E	0.39	0/6	0.67	0/6
3	F	0.41	0/5	1.02	0/5
All	All	0.73	2/6556 (0.0%)	0.74	2/8876 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	CYS	CB-SG	-5.83	1.72	1.81
1	B	300	ASP	CA-CB	5.25	1.65	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	300	ASP	N-CA-C	6.11	127.49	111.00
1	A	223	VAL	CB-CA-C	-5.65	100.66	111.40

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	2358	0	2304	20	0
1	B	2346	0	2282	12	0
2	C	1172	0	1126	15	0
2	D	496	0	440	6	0
3	E	55	0	48	1	0
3	F	54	0	46	1	0
4	A	18	0	24	4	0
4	C	6	0	8	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	179	0	0	2	0
6	B	198	0	0	0	0
6	C	61	0	0	0	0
6	D	38	0	0	0	0
6	E	3	0	0	0	0
6	F	2	0	0	0	0
All	All	6990	0	6278	44	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 3.

The worst 5 of 44 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:B:290[B]:MET:HE3	2:D:450:HIS:ND1	1.96	0.81
1:A:85:SER:HB3	4:A:402:GOL:H31	1.71	0.73
2:C:509:SER:OG	2:C:530:THR:HB	1.89	0.73
1:B:290[B]:MET:CE	2:D:450:HIS:ND1	2.58	0.67
1:A:290[B]:MET:HE3	2:C:450:HIS:ND1	2.09	0.66

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	297/329 (90%)	287 (97%)	10 (3%)	0	100	100
1	B	294/329 (89%)	281 (96%)	13 (4%)	0	100	100
2	C	159/170 (94%)	158 (99%)	1 (1%)	0	100	100
2	D	66/170 (39%)	65 (98%)	1 (2%)	0	100	100
All	All	816/998 (82%)	791 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	253/285 (89%)	249 (98%)	4 (2%)	68	72
1	B	252/285 (88%)	249 (99%)	3 (1%)	75	80
2	C	120/141 (85%)	117 (98%)	3 (2%)	53	54
2	D	52/141 (37%)	52 (100%)	0	100	100
All	All	677/852 (80%)	667 (98%)	10 (2%)	73	74

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	83	PRO
1	B	161	ILE
2	C	437	LEU
1	A	246	ARG
1	B	246	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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
3	ACB	E	1	3	4,8,9	0.88	0	3,10,12	0.87	0
3	1ZN	E	3	3	22,23,24	0.75	1 (4%)	24,29,31	1.31	3 (12%)
3	FGA	E	4	3	3,8,9	0.47	0	2,9,11	1.59	0
3	MDH	E	5	3	5,6,7	1.18	1 (20%)	1,6,8	6.64	1 (100%)
3	ACB	F	1	3	4,8,9	1.12	1 (25%)	3,10,12	2.21	1 (33%)
3	1ZN	F	3	3	22,23,24	0.89	0	24,29,31	1.16	2 (8%)
3	FGA	F	4	3	3,8,9	0.59	0	2,9,11	1.01	0
3	MDH	F	5	3	5,6,7	1.91	1 (20%)	1,6,8	3.99	1 (100%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ACB	E	1	3	-	0/5/10/12	0/0/0/0
3	1ZN	E	3	3	-	0/22/25/27	0/1/1/1
3	FGA	E	4	3	-	0/3/8/9	0/0/0/0
3	MDH	E	5	3	-	0/1/6/8	0/0/0/0
3	ACB	F	1	3	-	0/5/10/12	0/0/0/0
3	1ZN	F	3	3	-	0/22/25/27	0/1/1/1
3	FGA	F	4	3	-	0/3/8/9	0/0/0/0
3	MDH	F	5	3	-	0/1/6/8	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	3	1ZN	C18-C17	-2.10	1.53	1.55
3	F	1	ACB	CB-CA	-2.06	1.53	1.55
3	E	5	MDH	C-CA	2.48	1.46	1.43
3	F	5	MDH	C-CA	3.99	1.48	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	5	MDH	O-C-CA	-6.64	116.99	125.47
3	F	5	MDH	O-C-CA	-3.99	120.37	125.47
3	E	3	1ZN	C18-C17-C16	-3.67	107.64	113.01
3	E	3	1ZN	C17-C16-C15	-2.59	119.54	123.70
3	E	3	1ZN	O3-C20-C18	-2.45	117.57	124.78

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
3	E	5	MDH	1	0
3	F	5	MDH	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z  > 2$
4	GOL	A	401	-	5,5,5	0.37	0	5,5,5	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	A	402	-	5,5,5	0.37	0	5,5,5	0.34	0
4	GOL	A	403	-	5,5,5	0.16	0	5,5,5	0.75	0
4	GOL	C	601	-	5,5,5	0.18	0	5,5,5	0.27	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	401	-	-	0/4/4/4	0/0/0/0
4	GOL	A	402	-	-	0/4/4/4	0/0/0/0
4	GOL	A	403	-	-	0/4/4/4	0/0/0/0
4	GOL	C	601	-	-	0/4/4/4	0/0/0/0

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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	GOL	2	0
4	A	403	GOL	2	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 ⓘ

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	294/329 (89%)	0.37	14 (4%) 31 31	23, 29, 36, 40	5 (1%)
1	B	294/329 (89%)	0.37	17 (5%) 24 24	25, 28, 34, 39	7 (2%)
2	C	160/170 (94%)	1.79	60 (37%) 0 1	22, 31, 40, 45	6 (3%)
2	D	66/170 (38%)	1.20	17 (25%) 1 1	23, 30, 43, 47	1 (1%)
3	E	1/5 (20%)	1.83	0 100 100	30, 30, 30, 30	1 (100%)
3	F	1/5 (20%)	-0.33	0 100 100	30, 30, 30, 30	1 (100%)
All	All	816/1008 (80%)	0.72	108 (13%) 4 4	22, 29, 37, 47	21 (2%)

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	424	PRO	8.1
2	C	445	PRO	6.9
2	C	425	TYR	6.6
2	C	543	ILE	6.5
2	D	424	PRO	6.3

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

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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MDH	E	5	7/8	0.87	0.21	-	28,29,30,31	7
3	ACB	E	1	9/10	0.89	0.17	-	27,29,30,30	9

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	1ZN	F	3	23/24	0.86	0.16	-	22,28,30,31	23
3	ACB	F	1	9/10	0.84	0.20	-	30,32,34,36	9
3	MDH	F	5	7/8	0.86	0.17	-	30,31,32,33	7
3	FGA	F	4	9/10	0.85	0.16	-	28,30,31,31	9
3	FGA	E	4	9/10	0.76	0.20	-	29,31,33,36	9
3	1ZN	E	3	23/24	0.90	0.15	-	24,27,28,31	23

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	402	6/6	0.84	0.29	4.98	25,33,35,40	6
4	GOL	C	601	6/6	0.92	0.17	1.52	30,32,33,34	6
4	GOL	A	403	6/6	0.81	0.19	0.88	42,46,48,50	6
5	MN	A	405	1/1	0.99	0.08	-2.83	27,27,27,27	0
5	MN	A	404	1/1	0.99	0.09	-2.89	23,23,23,23	1
5	MN	B	401	1/1	0.99	0.04	-3.88	21,21,21,21	1
5	MN	B	402	1/1	1.00	0.05	-4.97	22,22,22,22	0
4	GOL	A	401	6/6	0.80	0.13	-	42,43,43,44	6

### 6.5 Other polymers [i](#)

There are no such residues in this entry.