



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 05:34 AM GMT

PDB ID : 2GM9  
Title : Structure of rabbit muscle glycogen phosphorylase in complex with thienopyrrole  
Authors : Otterbein, L.R.; Pannifer, A.D.; Tucker, J.; Breed, J.; Oikonomakos, N.G.; Minshull, C.; Rowsell, S.; Pauptit, R.A.  
Deposited on : 2006-04-06  
Resolution : 2.30 Å(reported)

This is a full wwPDB validation 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>

---

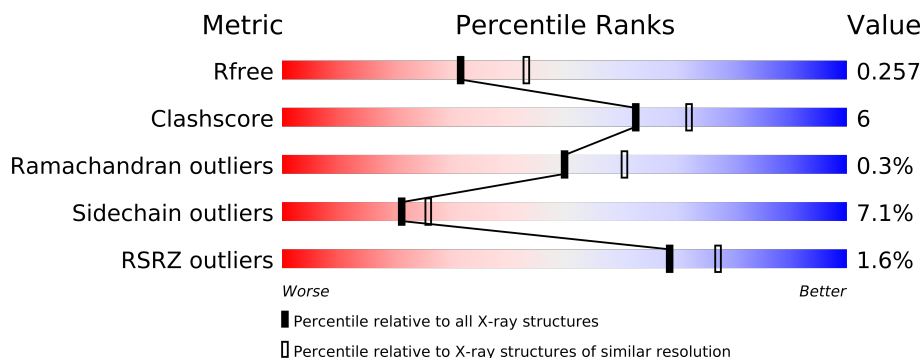
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.30 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	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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	825	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	3TH	A	1	-	X

## 2 Entry composition i

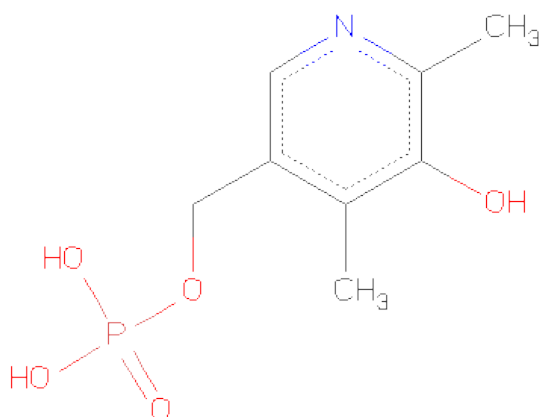
There are 4 unique types of molecules in this entry. The entry contains 7052 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Glycogen phosphorylase, muscle form.

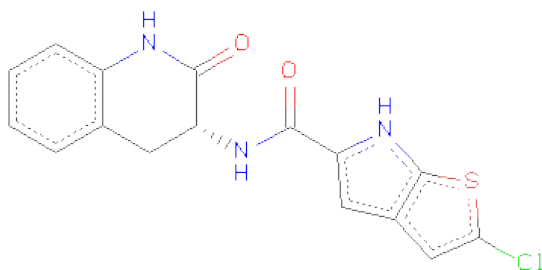
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	805	6559	4180	1157	1193	29	0	4	0

- Molecule 2 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYLDIHYDROGEN PHOSPHATE (three-letter code: PLR) (formula: C<sub>8</sub>H<sub>12</sub>NO<sub>5</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0

- Molecule 3 is 2-CHLORO-N-[(3R)-2-OXO-1,2,3,4-TETRAHYDROQUINOLIN-3-YL]-6H-THIENO[2,3-B]PYRROLE-5-CARBOXAMIDE (three-letter code: 3TH) (formula: C<sub>16</sub>H<sub>12</sub>ClN<sub>3</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	S		
3	A	1	23	16	1	3	2	1	0	0

- Molecule 4 is water.

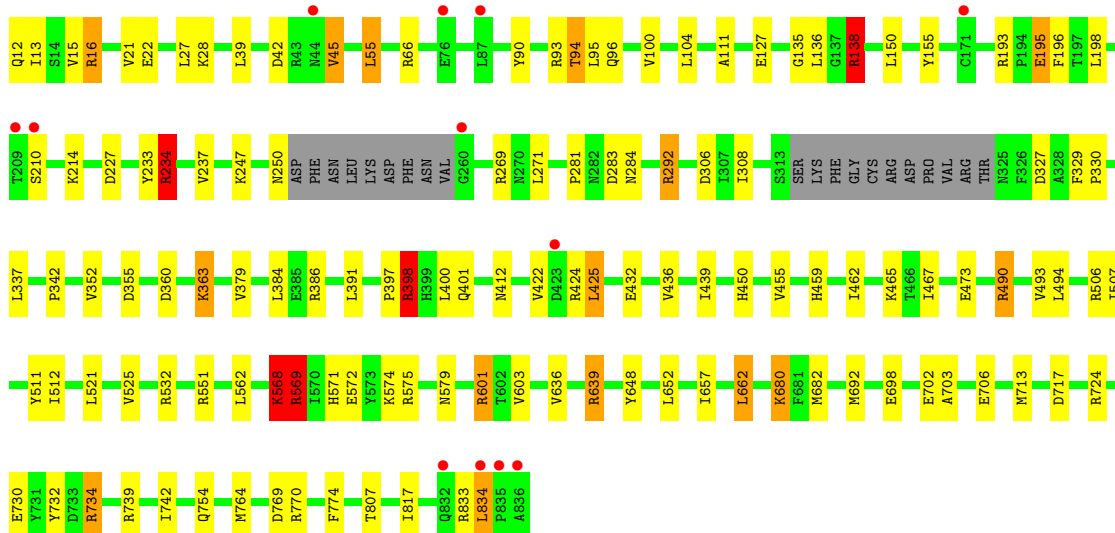
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	455	Total	O	0	0
			455	455		

### 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: Glycogen phosphorylase, muscle form

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.78Å 126.78Å 115.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.29 – 2.30 37.86 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.3 (91.29-2.30) 98.4 (37.86-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.08 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.182 , 0.245 0.196 , 0.257	Depositor DCC
$R_{free}$ test set	2093 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.3	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 36.9	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	0 of 41540 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7052	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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: 3TH, PLR

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	0.78	0/6725	0.88	19/9101 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	490	ARG	NE-CZ-NH2	-12.40	114.10	120.30
1	A	292	ARG	NE-CZ-NH1	10.21	125.41	120.30
1	A	138	ARG	NE-CZ-NH2	-10.11	115.25	120.30
1	A	292	ARG	NE-CZ-NH2	-8.90	115.85	120.30
1	A	490	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	A	575	ARG	NE-CZ-NH2	-7.75	116.43	120.30
1	A	506	ARG	NE-CZ-NH2	-6.97	116.81	120.30
1	A	601	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	16	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	A	575	ARG	NE-CZ-NH1	6.09	123.35	120.30
1	A	138	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	A	569	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	A	398	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	A	490	ARG	CG-CD-NE	-5.57	100.10	111.80
1	A	234	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	601	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	136	LEU	CA-CB-CG	5.26	127.41	115.30
1	A	532	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	93	ARG	CG-CD-NE	5.17	122.67	111.80

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	6559	0	6510	73	0
2	A	15	0	10	8	0
3	A	23	0	12	0	0
4	A	455	0	0	9	0
All	All	7052	0	6532	73	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 6.

All (73) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:572:GLU:OE2	1:A:764:MET:HE3	1.64	0.95
1:A:680:LYS:NZ	2:A:900:PLR:H4A3	1.84	0.93
1:A:680:LYS:HZ1	2:A:900:PLR:H4A3	1.34	0.92
1:A:680:LYS:NZ	2:A:900:PLR:C4A	2.35	0.89
1:A:569:ARG:NE	4:A:1353:HOH:O	1.96	0.89
1:A:680:LYS:HE2	2:A:900:PLR:H4A2	1.65	0.78
1:A:680:LYS:CE	2:A:900:PLR:H4A2	2.14	0.78
1:A:572:GLU:OE2	1:A:764:MET:CE	2.36	0.73
1:A:680:LYS:CE	2:A:900:PLR:C4A	2.67	0.71
1:A:355:ASP:OD2	1:A:398:ARG:HD3	1.91	0.71
1:A:703:ALA:HA	1:A:807:THR:HG21	1.74	0.70
1:A:450:HIS:HE1	4:A:1062:HOH:O	1.76	0.68
1:A:138:ARG:O	1:A:138:ARG:HD3	1.94	0.68
1:A:680:LYS:HZ3	2:A:900:PLR:C4A	2.09	0.66
1:A:507:ILE:O	1:A:507:ILE:HG22	1.98	0.64
1:A:42[A]:ASP:OD1	1:A:45:VAL:HG22	1.98	0.63
1:A:636:VAL:O	1:A:639:ARG:HG2	2.00	0.62
1:A:193[A]:ARG:NH1	1:A:227:ASP:OD2	2.32	0.62
1:A:730:GLU:O	1:A:734:ARG:HG3	2.00	0.61
1:A:648:TYR:HA	1:A:652:LEU:HD23	1.81	0.61
1:A:424:ARG:NH2	1:A:473:GLU:OE1	2.34	0.61
1:A:601:ARG:HD2	4:A:1026:HOH:O	2.01	0.60
1:A:703:ALA:CA	1:A:807:THR:HG21	2.32	0.59

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:569:ARG:NH2	4:A:1353:HOH:O	2.36	0.58
1:A:511:TYR:CE1	1:A:512:ILE:HD13	2.38	0.58
1:A:507:ILE:CD1	1:A:521:LEU:HD23	2.33	0.57
1:A:94:THR:CG2	4:A:931:HOH:O	2.53	0.57
1:A:493:VAL:CG2	1:A:512:ILE:HD12	2.34	0.57
1:A:150:LEU:HD12	1:A:817:ILE:HG22	1.88	0.55
1:A:100:VAL:HG21	1:A:494:LEU:HD23	1.89	0.55
1:A:195:GLU:HG2	4:A:1008:HOH:O	2.06	0.55
1:A:13:ILE:HG22	1:A:16:ARG:HG3	1.89	0.54
1:A:657:ILE:HD13	1:A:680:LYS:HB3	1.91	0.53
1:A:250:ASN:OD1	1:A:269:ARG:NH1	2.40	0.53
1:A:568:LYS:HG3	1:A:574:LYS:HD3	1.92	0.52
1:A:569:ARG:CZ	4:A:1353:HOH:O	2.45	0.51
1:A:507:ILE:CG2	1:A:507:ILE:O	2.58	0.51
1:A:379:VAL:HG22	4:A:1195:HOH:O	2.10	0.51
1:A:308:ILE:HD12	1:A:352:VAL:HG11	1.93	0.50
1:A:742:ILE:HD11	1:A:774:PHE:CZ	2.46	0.50
1:A:233:TYR:CE1	1:A:234:ARG:HD3	2.46	0.50
1:A:386:ARG:HD3	1:A:432:GLU:OE1	2.11	0.50
1:A:193[A]:ARG:HE	1:A:196:PHE:HE2	1.59	0.49
1:A:680:LYS:HE2	2:A:900:PLR:C4A	2.35	0.49
1:A:703:ALA:CB	1:A:807:THR:HG21	2.43	0.49
1:A:562:LEU:HD21	1:A:662:LEU:HB2	1.96	0.48
1:A:636:VAL:O	1:A:639:ARG:CG	2.61	0.48
1:A:732:TYR:CZ	1:A:739:ARG:HG3	2.49	0.47
1:A:455:VAL:H	1:A:459:HIS:HD2	1.63	0.47
1:A:462:ILE:HD12	1:A:465:LYS:HE2	1.96	0.47
1:A:327:ASP:OD1	1:A:363:LYS:NZ	2.40	0.47
1:A:96:GLN:CD	1:A:494:LEU:HD22	2.34	0.47
1:A:682:MET:CE	1:A:807:THR:HG23	2.46	0.46
1:A:55:LEU:HD13	1:A:95:LEU:HD21	1.97	0.46
1:A:764:MET:HE1	1:A:769:ASP:HA	1.97	0.46
1:A:283:ASP:OD1	1:A:571:HIS:NE2	2.46	0.46
1:A:713:MET:HB3	1:A:717:ASP:HB2	1.98	0.46
1:A:422:VAL:O	1:A:425:LEU:HB2	2.17	0.45
1:A:13:ILE:CG2	1:A:16:ARG:HG3	2.47	0.44
1:A:281:PRO:O	1:A:569:ARG:NH2	2.51	0.44
1:A:237:VAL:HG22	1:A:834:LEU:HD22	2.00	0.43
1:A:698:GLU:O	1:A:702:GLU:HG2	2.19	0.42
1:A:386:ARG:HA	1:A:439:ILE:O	2.19	0.42
1:A:412:ASN:HA	1:A:412:ASN:HD22	1.69	0.41
1:A:308:ILE:CD1	1:A:352:VAL:HG11	2.50	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:21:VAL:HG13	1:A:22:GLU:N	2.35	0.41
1:A:397:PRO:O	1:A:401:GLN:HG3	2.20	0.41
1:A:135:GLY:HA3	4:A:1325:HOH:O	2.19	0.41
1:A:329:PHE:HB3	1:A:330:PRO:HD3	2.02	0.41
1:A:155:TYR:CD1	1:A:155:TYR:N	2.88	0.41
1:A:13:ILE:CG2	1:A:15:VAL:HG12	2.50	0.41
1:A:28:LYS:HG3	1:A:111:ALA:HB1	2.03	0.41
1:A:657:ILE:HG21	1:A:680:LYS:HB3	2.03	0.41

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	803/825 (97%)	778 (97%)	23 (3%)	2 (0%)	56	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	568	LYS
1	A	342	PRO

### 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	699/714 (98%)	649 (93%)	50 (7%)	21	25

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	27	LEU
1	A	39	LEU
1	A	45	VAL
1	A	55	LEU
1	A	66	ARG
1	A	90	TYR
1	A	94	THR
1	A	104	LEU
1	A	127	GLU
1	A	138	ARG
1	A	195	GLU
1	A	198	LEU
1	A	210	SER
1	A	214	LYS
1	A	234	ARG
1	A	247	LYS
1	A	271	LEU
1	A	284	ASN
1	A	292	ARG
1	A	306	ASP
1	A	337	LEU
1	A	360[A]	ASP
1	A	360[B]	ASP
1	A	363	LYS
1	A	384	LEU
1	A	391	LEU
1	A	398	ARG
1	A	400	LEU
1	A	425	LEU
1	A	436	VAL
1	A	467	ILE
1	A	490	ARG
1	A	525	VAL
1	A	551	ARG
1	A	568	LYS
1	A	569	ARG
1	A	579	ASN
1	A	603	VAL
1	A	639	ARG
1	A	662	LEU
1	A	680	LYS
1	A	692	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	706	GLU
1	A	724	ARG
1	A	734	ARG
1	A	754	GLN
1	A	770	ARG
1	A	833	ARG
1	A	834	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	HIS
1	A	284	ASN
1	A	325	ASN
1	A	412	ASN
1	A	450	HIS
1	A	566	GLN
1	A	579	ASN
1	A	763	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 ⓘ

2 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
3	3TH	A	1	-	26,26,26	3.34	7 (26%)	34,38,38	1.51	5 (14%)
2	PLR	A	900	-	15,15,15	1.26	2 (13%)	22,22,22	1.01	2 (9%)

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	3TH	A	1	-	-	0/6/20/20	0/0/4/4
2	PLR	A	900	-	-	0/6/6/6	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	3TH	C2-CL	13.88	1.73	1.69
3	A	1	3TH	C3-C2	5.25	1.41	1.36
3	A	1	3TH	C9-S10	-4.44	1.68	1.74
3	A	1	3TH	C6-N7	3.26	1.40	1.36
3	A	1	3TH	C23-N22	3.08	1.38	1.34
3	A	1	3TH	C11-N13	2.96	1.40	1.34
2	A	900	PLR	C3-C2	-2.62	1.38	1.40
3	A	1	3TH	C5-C6	2.52	1.41	1.38
2	A	900	PLR	C2-N1	2.50	1.38	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	3TH	C4-C9-S10	4.41	116.80	112.31
3	A	1	3TH	C3-C2-S10	3.67	114.98	111.87
3	A	1	3TH	C15-C14-N13	2.78	115.37	111.52
3	A	1	3TH	O24-C23-N22	-2.30	118.69	122.11
2	A	900	PLR	C5-C6-N1	-2.19	119.91	123.86
3	A	1	3TH	C6-N7-C9	2.07	111.75	107.73
2	A	900	PLR	C3-C4-C5	2.06	120.89	118.71

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	805/825 (97%)	-0.20	12 (1%) 70 78	24, 31, 43, 67	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	GLY	3.8
1	A	832	GLN	3.7
1	A	835	PRO	3.3
1	A	209	THR	3.2
1	A	44	ASN	2.7
1	A	834	LEU	2.5
1	A	210	SER	2.3
1	A	836	ALA	2.3
1	A	87	LEU	2.2
1	A	171	CYS	2.2
1	A	76	GLU	2.1
1	A	423	ASP	2.0

### 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
3	3TH	A	1	23/23	0.16	3.23	46,48,50,54	0
2	PLR	A	900	15/15	0.15	-0.10	23,24,28,31	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.