



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:19 AM GMT

PDB ID : 2G0A
Title : X-ray structure of mouse pyrimidine 5'-nucleotidase type 1 with lead(II) bound in active site
Authors : Bitto, E.; Bingman, C.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2006-02-11
Resolution : 2.35 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

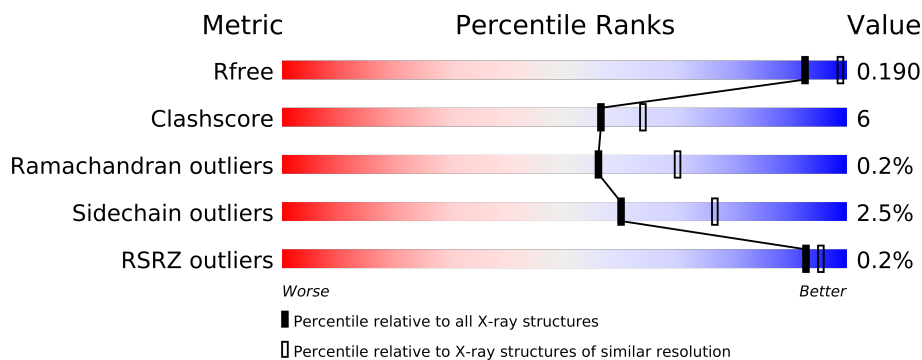
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.35 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	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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 ≥ 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	297	
1	B	297	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5546 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 Cytosolic 5'-nucleotidase III.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	Se	0	1	0
			2326	1487	387	439	5	8			
1	B	291	Total	C	N	O	S	Se	0	1	0
			2326	1487	387	439	5	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	CLONING ARTIFACT	UNP Q9D020
A	12	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	13	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	52	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	110	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	141	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	192	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	245	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
A	273	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	1	SER	-	CLONING ARTIFACT	UNP Q9D020
B	12	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	13	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	52	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	110	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	141	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	192	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	245	MSE	MET	MODIFIED RESIDUE	UNP Q9D020
B	273	MSE	MET	MODIFIED RESIDUE	UNP Q9D020

- Molecule 2 is LEAD (II) ION (three-letter code: PB) (formula: Pb).

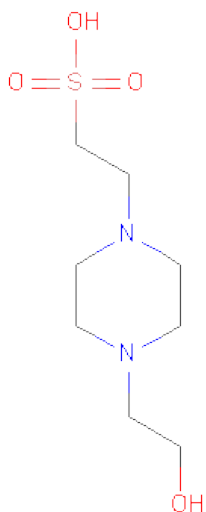
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Pb	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Pb	0	0
			1	1		

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINEETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 4 is water.

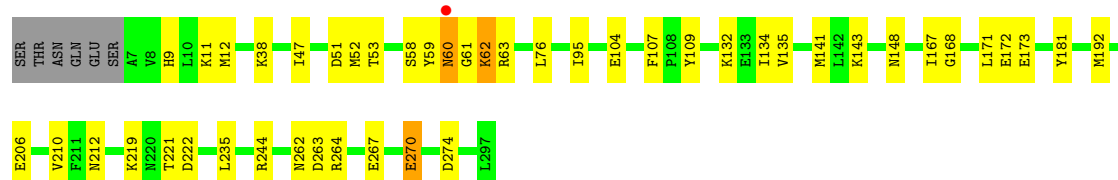
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	430	Total	O	0	0
			430	430		
4	B	432	Total	O	0	0
			432	432		

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.

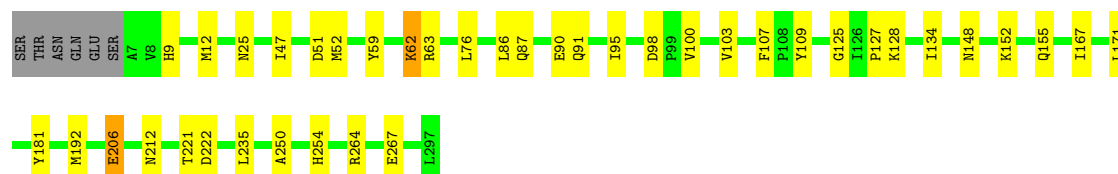
- Molecule 1: Cytosolic 5'-nucleotidase III

Chain A: 



- Molecule 1: Cytosolic 5'-nucleotidase III

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	134.55Å 134.55Å 39.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	67.27 – 2.35 38.84 – 2.35	Depositor EDS
% Data completeness (in resolution range)	100.0 (67.27-2.35) 100.0 (38.84-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.149 , 0.229 0.145 , 0.190	Depositor DCC
R_{free} test set	1668 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 81.4	EDS
Estimated twinning fraction	0.488 for -h,-k,l 0.036 for h,-h-k,-l 0.036 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 33098 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5546	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: PB, EPE

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	0.77	0/2358	0.73	0/3161
1	B	0.79	1/2358 (0.0%)	0.74	0/3161
All	All	0.78	1/4716 (0.0%)	0.74	0/6322

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	206	GLU	CB-CG	5.11	1.61	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	262	ASN	Peptide

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	2326	0	2346	32	0
1	B	2326	0	2346	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	15	0	17	0	0
3	B	15	0	17	1	0
4	A	430	0	0	10	0
4	B	432	0	0	11	1
All	All	5546	0	4726	61	1

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

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:62:LYS:HD2	1:A:63:ARG:H	1.52	0.74
1:B:59:TYR:O	4:B:1024:HOH:O	2.06	0.72
1:A:76:LEU:HD12	1:A:134:ILE:HD11	1.79	0.64
1:B:76:LEU:HD12	1:B:134:ILE:HD11	1.79	0.64
1:B:62:LYS:HG2	1:B:63:ARG:H	1.63	0.63
1:A:62:LYS:HG2	4:A:1211:HOH:O	2.00	0.61
1:B:152:LYS:HD3	1:B:155:GLN:HE21	1.65	0.61
1:B:167:ILE:HG21	1:B:192:MSE:HE3	1.85	0.58
1:A:270:GLU:HG2	4:A:1269:HOH:O	2.01	0.58
1:B:87:GLN:O	1:B:91:GLN:HG3	2.06	0.56
1:A:168:GLY:O	1:A:172:GLU:HG3	2.06	0.56
1:B:206:GLU:CG	4:B:1091:HOH:O	2.53	0.56
1:B:206:GLU:HG3	4:B:1091:HOH:O	2.06	0.56
1:B:98:ASP:OD1	1:B:100:VAL:HG22	2.09	0.53
1:A:264:ARG:HD2	1:A:267:GLU:OE1	2.11	0.51
1:A:59:TYR:CD2	1:A:60:ASN:ND2	2.77	0.51
1:B:86:LEU:O	1:B:90:GLU:HG3	2.11	0.50
1:A:141:MSE:HE3	4:A:1213:HOH:O	2.12	0.50
1:B:264:ARG:HD2	1:B:267:GLU:OE1	2.11	0.50
1:A:210:VAL:HG23	4:A:970:HOH:O	2.10	0.49
1:A:206:GLU:HG3	4:A:1236:HOH:O	2.11	0.49
1:B:221:THR:HG22	4:B:955:HOH:O	2.13	0.49
1:A:132:LYS:HE3	4:A:948:HOH:O	2.13	0.47
1:A:38:LYS:NZ	4:A:1234:HOH:O	2.43	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:107:PHE:CE2	1:B:212:ASN:HB3	2.50	0.47
1:A:58:SER:HB2	1:A:62:LYS:O	2.13	0.46
1:A:104:GLU:HB3	4:A:1156:HOH:O	2.15	0.46
1:B:51:ASP:C	1:B:52:MSE:HG2	2.36	0.46
1:A:9:HIS:CD2	1:A:12:MSE:HE2	2.51	0.46
1:A:167:ILE:HG21	1:A:192:MSE:HE3	1.98	0.45
1:A:132:LYS:HE2	4:A:1160:HOH:O	2.17	0.45
1:B:59:TYR:N	1:B:62:LYS:O	2.40	0.45
1:A:60:ASN:HA	1:A:61:GLY:HA2	1.54	0.45
1:B:254:HIS:HD2	4:B:1002:HOH:O	2.00	0.45
1:A:206:GLU:OE2	1:A:219:LYS:HE3	2.17	0.44
1:B:25:ASN:HB2	4:B:1042:HOH:O	2.18	0.44
1:A:132:LYS:NZ	1:B:155:GLN:OE1	2.51	0.44
1:A:59:TYR:N	1:A:62:LYS:O	2.43	0.44
1:A:210:VAL:O	1:A:210:VAL:HG22	2.18	0.44
1:B:221:THR:CG2	4:B:955:HOH:O	2.66	0.43
1:B:171:LEU:O	1:B:171:LEU:HD23	2.18	0.43
1:B:95:ILE:HG21	1:B:109:TYR:CG	2.53	0.43
1:B:9:HIS:HD2	1:B:12:MSE:HE2	1.83	0.43
1:B:206:GLU:HG2	4:B:1091:HOH:O	2.16	0.43
1:B:128:LYS:HE2	4:B:1034:HOH:O	2.17	0.43
1:A:51:ASP:C	1:A:52:MSE:HG2	2.39	0.43
1:A:95:ILE:HG21	1:A:109:TYR:CG	2.54	0.43
1:B:9:HIS:CD2	1:B:12:MSE:HE2	2.53	0.43
1:A:53:THR:O	1:A:143:LYS:CE	2.67	0.42
1:B:103:VAL:HG23	4:B:948:HOH:O	2.19	0.42
1:A:47:ILE:O	1:A:235:LEU:HA	2.19	0.42
1:A:107:PHE:CE2	1:A:212:ASN:HB3	2.54	0.42
1:B:47:ILE:O	1:B:235:LEU:HA	2.20	0.42
1:B:125:GLY:O	1:B:127:PRO:HD3	2.20	0.41
1:A:60:ASN:HB3	4:A:933:HOH:O	2.20	0.41
1:A:135:VAL:HG21	1:A:173:GLU:HB3	2.02	0.41
3:B:902:EPE:H82	4:B:1288:HOH:O	2.20	0.41
1:A:171:LEU:HD23	1:A:171:LEU:O	2.21	0.41
1:A:263:ASP:O	1:A:264:ARG:C	2.59	0.40
1:A:244:ARG:HA	1:A:244:ARG:HD2	1.97	0.40
1:B:171:LEU:C	1:B:171:LEU:HD23	2.42	0.40

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.

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
--------	--------	-------------	----------

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:B:946:HOH:O	4:B:1320:HOH:O[1_554]	1.95	0.25

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	289/297 (97%)	279 (96%)	10 (4%)	0	100	100
1	B	289/297 (97%)	279 (96%)	9 (3%)	1 (0%)	50	62
All	All	578/594 (97%)	558 (96%)	19 (3%)	1 (0%)	56	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	250	ALA

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	260/258 (101%)	251 (96%)	9 (4%)	48	63
1	B	260/258 (101%)	256 (98%)	4 (2%)	76	88
All	All	520/516 (101%)	507 (98%)	13 (2%)	60	76

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	60	ASN
1	A	62	LYS
1	A	148	ASN
1	A	181	TYR
1	A	221	THR
1	A	222	ASP
1	A	270	GLU
1	A	274	ASP
1	B	62	LYS
1	B	148	ASN
1	B	181	TYR
1	B	222	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	B	9	HIS
1	B	60	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, 2 are monoatomic - leaving 2 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
3	EPE	A	901	-	15,15,15	0.89	1 (6%)	20,20,20	2.19	8 (40%)
3	EPE	B	902	-	15,15,15	0.82	1 (6%)	20,20,20	2.02	8 (40%)

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	EPE	A	901	-	-	0/9/19/19	0/1/1/1
3	EPE	B	902	-	-	0/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	EPE	C10-S	3.09	1.82	1.77
3	B	902	EPE	C10-S	2.82	1.81	1.77

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	902	EPE	C5-N4-C3	5.29	122.00	108.86
3	A	901	EPE	C5-N4-C3	5.21	121.79	108.86
3	A	901	EPE	O2S-S-C10	3.83	110.09	106.81
3	A	901	EPE	O1S-S-C10	3.31	109.64	106.81
3	B	902	EPE	C7-N4-C3	3.04	119.17	111.32
3	A	901	EPE	C6-C5-N4	3.02	116.56	110.61
3	B	902	EPE	O2S-S-C10	2.89	109.28	106.81
3	A	901	EPE	C7-N4-C3	2.76	118.44	111.32
3	A	901	EPE	C7-N4-C5	2.70	118.28	111.32
3	B	902	EPE	O3S-S-C10	2.59	109.21	105.93
3	B	902	EPE	O1S-S-C10	2.54	108.98	106.81
3	B	902	EPE	C7-N4-C5	2.51	117.80	111.32
3	A	901	EPE	C2-C3-N4	2.25	115.05	110.61
3	A	901	EPE	O3S-S-C10	2.21	108.73	105.93
3	B	902	EPE	C6-C5-N4	2.11	114.77	110.61
3	B	902	EPE	C2-C3-N4	2.11	114.76	110.61

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, 95th 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 ²)	Q<0.9
1	A	291/297 (97%)	-0.40	1 (0%) 91 94	26, 35, 43, 54	1 (0%)
1	B	291/297 (97%)	-0.38	0 100 100	27, 35, 43, 54	1 (0%)
All	All	582/594 (97%)	-0.39	1 (0%) 93 95	26, 35, 43, 54	2 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	ASN	3.3

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, 95th 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 ²)	Q<0.9
3	EPE	B	902	15/15	0.15	1.12	76,78,85,86	0
3	EPE	A	901	15/15	0.14	0.30	83,84,90,90	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	PB	B	904	1/1	0.07	-3.09	39,39,39,39	1
2	PB	A	903	1/1	0.08	-3.71	40,40,40,40	1

6.5 Other polymers ⓘ

There are no such residues in this entry.