



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:31 AM GMT

PDB ID : 2V0N  
Title : ACTIVATED RESPONSE REGULATOR PLED IN COMPLEX WITH C-DIGMP AND GTP-ALPHA-S  
Authors : Wassmann, P.; Schirmer, T.  
Deposited on : 2007-05-15  
Resolution : 2.71 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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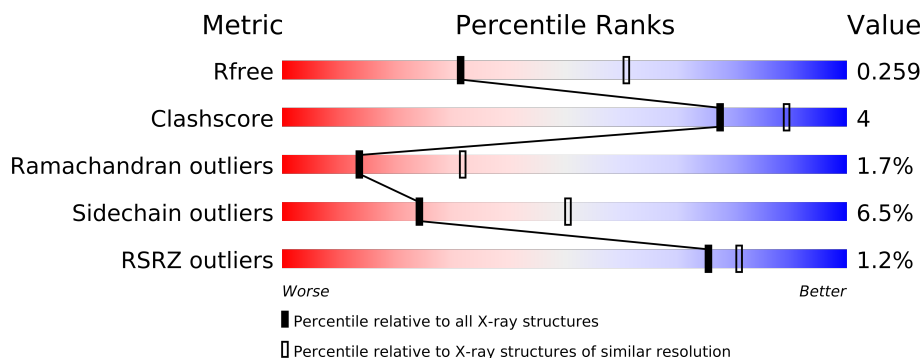
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.71 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	1770 (2.74-2.70)
Clashscore	79885	2183 (2.74-2.70)
Ramachandran outliers	78287	2147 (2.74-2.70)
Sidechain outliers	78261	2148 (2.74-2.70)
RSRZ outliers	66119	1772 (2.74-2.70)

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	459	
1	B	459	

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	MG	B	502	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7298 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.

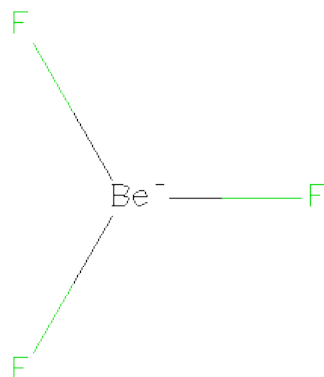
- Molecule 1 is a protein called RESPONSE REGULATOR PLED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	96	0	0
			3531	2196	654	666	15			
1	B	454	Total	C	N	O	S	97	0	0
			3481	2166	639	661	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	455	HIS	-	EXPRESSION TAG	UNP Q9A5I5
A	456	HIS	-	EXPRESSION TAG	UNP Q9A5I5
A	457	HIS	-	EXPRESSION TAG	UNP Q9A5I5
A	458	HIS	-	EXPRESSION TAG	UNP Q9A5I5
A	459	HIS	-	EXPRESSION TAG	UNP Q9A5I5
A	460	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	455	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	456	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	457	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	458	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	459	HIS	-	EXPRESSION TAG	UNP Q9A5I5
B	460	HIS	-	EXPRESSION TAG	UNP Q9A5I5

- Molecule 2 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF<sub>3</sub>).

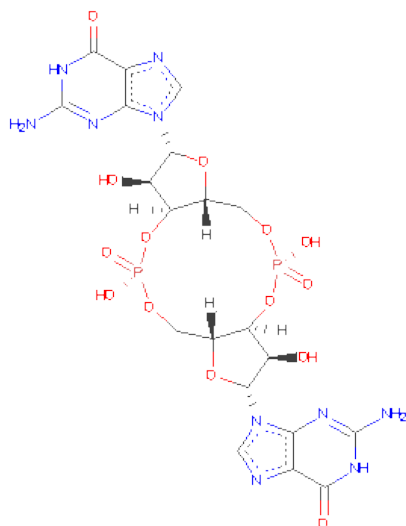


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Be	F	0	0
			4	1	3		
2	B	1	Total	Be	F	0	0
			4	1	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

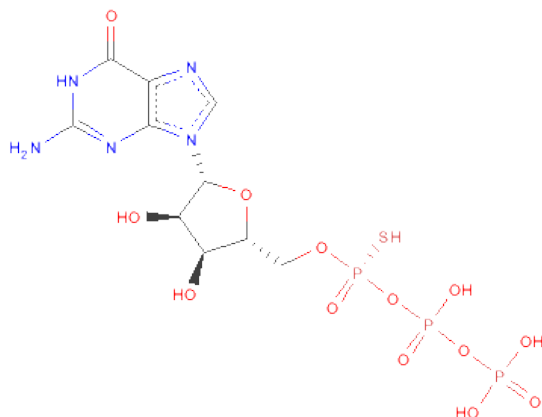
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		
3	A	3	Total	Mg	0	0
			3	3		

- Molecule 4 is 9,9'-[(2R,3R,3AS,5S,7AR,9R,10R,10AS,12S,14AR)-3,5,10,12-TETRAHYDROXY-5,12-DIOXIDOOCTAHYDRO-2H,7H-DIFURO[3,2-D:3',2'-J][1,3,7,9,2,8]TETRAOXA DIPHOSPHACYCLODODECINE-2,9-DIYL]BIS(2-AMINO-1,9-DIHYDRO-6H-PURIN-6-ONE) (three-letter code: C2E) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>14</sub>P<sub>2</sub>).



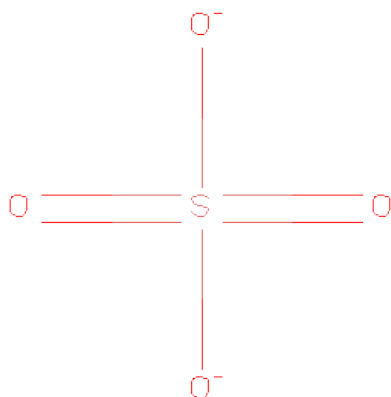
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
4	A	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
4	B	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
4	B	1	Total	C	N	O	P	0	0
			46	20	10	14	2		

- Molecule 5 is GUANOSINE-5'-RP-ALPHA-THIO-TRIPHOSPHATE (three-letter code: GAV) (formula:  $C_{10}H_{16}N_5O_{13}P_3S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		
5	B	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		

- Molecule 6 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		
8	B	6	Total	O	0	0
			6	6		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.97Å 132.56Å 88.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.71 73.56 – 2.71	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.71) 94.0 (73.56-2.71)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.15 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.215 , 0.252 0.220 , 0.259	Depositor DCC
$R_{free}$ test set	1971 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.1	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 18.7	EDS
Estimated twinning fraction	0.005 for k,h,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 39295 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	7298	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: MG, CL, GAV, BEF, SO4, C2E

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	2.47	24/3580 (0.7%)	3.00	48/4840 (1.0%)
1	B	1.04	12/3524 (0.3%)	0.97	18/4762 (0.4%)
All	All	1.90	36/7104 (0.5%)	2.24	66/9602 (0.7%)

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	9
1	B	0	1
All	All	0	10

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	GLU	CD-OE2	111.38	2.48	1.25
1	A	44	ARG	NE-CZ	-50.31	0.67	1.33
1	A	12	GLU	CG-CD	-33.96	1.01	1.51
1	A	406	ARG	NE-CZ	30.01	1.72	1.33
1	A	206	LYS	CG-CD	-28.49	0.55	1.52

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	ARG	NE-CZ-NH2	-110.75	64.93	120.30
1	A	44	ARG	NE-CZ-NH1	94.48	167.54	120.30
1	A	186	GLU	OE1-CD-OE2	-50.93	62.18	123.30
1	A	406	ARG	NE-CZ-NH1	-46.14	97.23	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	287	GLU	O-C-N	-45.42	50.03	122.70

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	ALA	Mainchain
1	A	148	ARG	Peptide
1	A	149	LEU	Mainchain,Peptide
1	A	287	GLU	Mainchain,Peptide
1	A	288	LEU	Mainchain

## 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	3531	0	3586	19	0
1	B	3481	0	3551	30	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
4	A	92	0	44	3	0
4	B	92	0	43	2	0
5	A	32	0	13	0	0
5	B	32	0	13	0	0
6	A	10	0	0	0	0
7	A	1	0	0	0	0
8	A	8	0	0	0	0
8	B	6	0	0	1	0
All	All	7298	0	7250	52	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 4.

The worst 5 of 52 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:324:LEU:HD13	1:A:376:MET:HE1	1.36	1.02
1:B:324:LEU:HD13	1:B:376:MET:HE1	1.50	0.92
1:B:324:LEU:HD13	1:B:376:MET:CE	2.00	0.92
1:A:324:LEU:HD13	1:A:376:MET:CE	1.99	0.91
1:B:229:LEU:HD13	1:B:250:ASP:HB3	1.68	0.73

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	457/459 (100%)	437 (96%)	13 (3%)	7 (2%)	15	36
1	B	450/459 (98%)	427 (95%)	15 (3%)	8 (2%)	13	30
All	All	907/918 (99%)	864 (95%)	28 (3%)	15 (2%)	14	32

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	ALA
1	A	149	LEU
1	A	289	ALA
1	B	143	ALA
1	B	149	LEU

### 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	374/374 (100%)	353 (94%)	21 (6%)	30	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	369/374 (99%)	342 (93%)	27 (7%)	20	44
All	All	743/748 (99%)	695 (94%)	48 (6%)	24	50

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	18	LEU
1	B	103	LEU
1	B	404	HIS
1	B	33	MET
1	B	73	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	207	ASN
1	B	335	ASN
1	B	280	ASN
1	A	280	ASN
1	B	293	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 ⓘ

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	$\# Z  > 2$
6	SO4	A	1470	-	4,4,4	0.07	0	6,6,6	0.26	0
6	SO4	A	1471	-	4,4,4	0.09	0	6,6,6	0.13	0
2	BEF	A	501	1,3	0,3,3	0.00	-	0,3,3	0.00	-
4	C2E	A	503	-	52,52,52	1.22	6 (11%)	76,82,82	2.98	23 (30%)
4	C2E	A	505	-	52,52,52	1.09	4 (7%)	76,82,82	2.46	26 (34%)
5	GAV	A	600	3	34,34,34	2.85	4 (11%)	48,54,54	2.29	11 (22%)
2	BEF	B	501	1,3	0,3,3	0.00	-	0,3,3	0.00	-
4	C2E	B	503	-	52,52,52	1.10	5 (9%)	76,82,82	2.96	25 (32%)
4	C2E	B	505	-	52,52,52	1.11	3 (5%)	76,82,82	2.66	22 (28%)
5	GAV	B	600	3	34,34,34	2.94	3 (8%)	48,54,54	2.38	11 (22%)

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
6	SO4	A	1470	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1471	-	-	0/0/0/0	0/0/0/0
2	BEF	A	501	1,3	-	0/0/0/0	0/0/0/0
4	C2E	A	503	-	1/1/10/10	0/30/62/62	0/0/7/7
4	C2E	A	505	-	2/2/10/10	0/30/62/62	0/0/7/7
5	GAV	A	600	3	-	0/20/38/38	0/1/3/3
2	BEF	B	501	1,3	-	0/0/0/0	0/0/0/0
4	C2E	B	503	-	2/2/10/10	0/30/62/62	0/0/7/7
4	C2E	B	505	-	2/2/10/10	0/30/62/62	0/0/7/7
5	GAV	B	600	3	-	0/20/38/38	0/1/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	600	GAV	PA-S1A	-15.48	1.71	2.06
5	A	600	GAV	PA-S1A	-15.11	1.71	2.06
5	B	600	GAV	C2-N3	4.65	1.39	1.33
5	A	600	GAV	C2-N3	4.00	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	C2E	C41-N91	-3.65	1.32	1.37

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	C2E	C6-C5-N7	-19.57	131.50	134.14
4	B	503	C2E	C6-C5-N7	-14.47	132.19	134.14
4	B	505	C2E	C6-C5-N7	-12.34	132.48	134.14
5	B	600	GAV	C6-C5-N7	-11.49	132.59	134.14
5	A	600	GAV	O4'-C1'-N9	9.99	117.74	108.44

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	505	C2E	C4'
4	B	505	C2E	C4A
4	A	505	C2E	C4'
4	A	505	C2E	C4A
4	A	503	C2E	C4'

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	456/459 (99%)	0.33	3 (0%) 84 89	23, 42, 51, 83	23 (5%)
1	B	444/459 (96%)	0.31	7 (1%) 68 74	25, 42, 53, 80	10 (2%)
All	All	900/918 (98%)	0.32	10 (1%) 75 82	23, 42, 52, 83	33 (3%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	138	ARG	4.7
1	B	137	ARG	3.6
1	B	136	GLY	3.2
1	B	134	ALA	2.5
1	A	150	ASP	2.4

### 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( $\text{\AA}^2$ )	Q<0.9
3	MG	B	502	1/1	0.20	2.03	36,36,36,36	0
4	C2E	A	505	46/46	0.21	-0.05	37,41,43,45	0
4	C2E	A	503	46/46	0.22	-0.14	37,42,44,45	0
6	SO4	A	1471	5/5	0.22	-0.18	85,86,88,89	0
3	MG	A	502	1/1	0.17	-0.43	37,37,37,37	0
4	C2E	B	505	46/46	0.16	-0.88	37,41,43,44	0
5	GAV	B	600	32/32	0.14	-0.92	33,41,64,70	0
5	GAV	A	600	32/32	0.15	-0.94	48,60,70,76	0
2	BEF	A	501	4/4	0.12	-1.26	35,35,39,39	0
4	C2E	B	503	46/46	0.15	-2.11	37,41,43,44	0
2	BEF	B	501	4/4	0.12	-2.29	35,35,39,39	0
3	MG	A	602	1/1	0.14	-2.73	52,52,52,52	0
6	SO4	A	1470	5/5	0.12	-3.14	71,76,79,80	0
7	CL	A	1472	1/1	0.14	-3.54	38,38,38,38	0
3	MG	B	601	1/1	0.05	-4.17	46,46,46,46	0
3	MG	A	601	1/1	0.08	-6.80	45,45,45,45	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.