



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:15 AM GMT

PDB ID : 3A3E  
Title : Crystal structure of penicillin binding protein 4 (dacB) from Haemophilus influenzae, complexed with novel beta-lactam (CMV)  
Authors : Kawai, F.; Roper, D.I.; Park, S.-Y.; Tame, J.R.H.  
Deposited on : 2009-06-12  
Resolution : 2.40 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

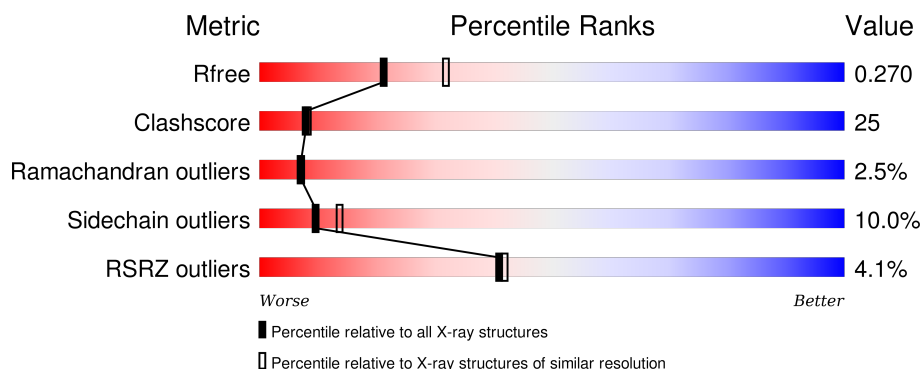
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	453	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 59%, yellow 30%, orange 5%, red 5%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>60%</span> <span>30%</span> <span>5% . .</span> </div> </div>
1	B	453	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 7%, green 53%, yellow 36%, orange 6%, red 2%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>7%</span> <span>53%</span> <span>36%</span> <span>6% . .</span> </div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6865 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.

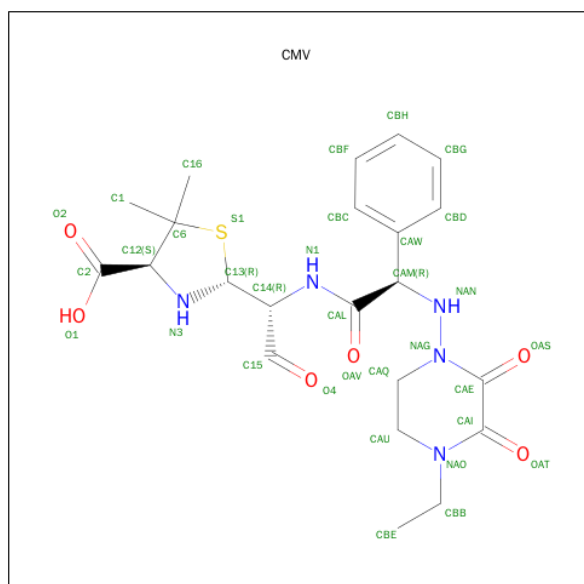
- Molecule 1 is a protein called Penicillin-binding protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3378	2154	582	630	12			
1	B	433	Total	C	N	O	S	0	0	0
			3333	2127	576	620	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	EXPRESSION TAG	UNP A8E0K8
B	27	MET	-	EXPRESSION TAG	UNP A8E0K8

- Molecule 2 is (2R,4S)-2-[(1R)-1-({(2R)-2-[(4-ETHYL-2,3-DIOXOPIPERAZIN-1-YL)AMINO]-2-PHENYLACETYL}AMINO)-2-OXOETHYL]-5,5-DIMETHYL-1,3-THIAZOLIDINE-4-CARBOXYLIC ACID (three-letter code: CMV) (formula: C<sub>22</sub>H<sub>29</sub>N<sub>5</sub>O<sub>6</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			34	22	5	6	1		
2	B	1	Total	C	N	O	S	0	0
			34	22	5	6	1		

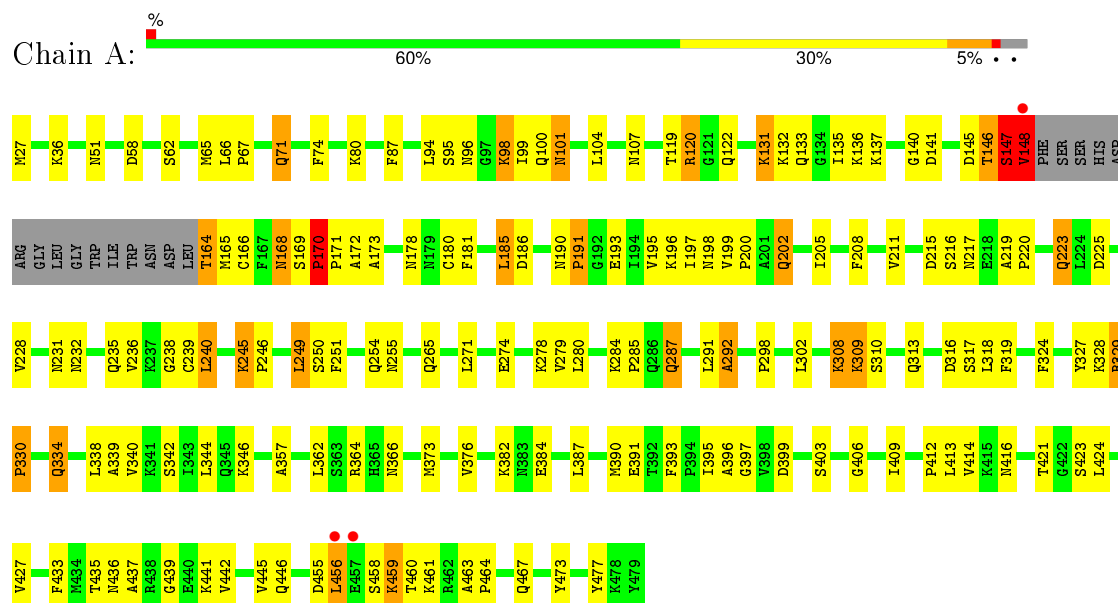
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	60	Total	O	0	0
			60	60		
3	B	26	Total	O	0	0
			26	26		

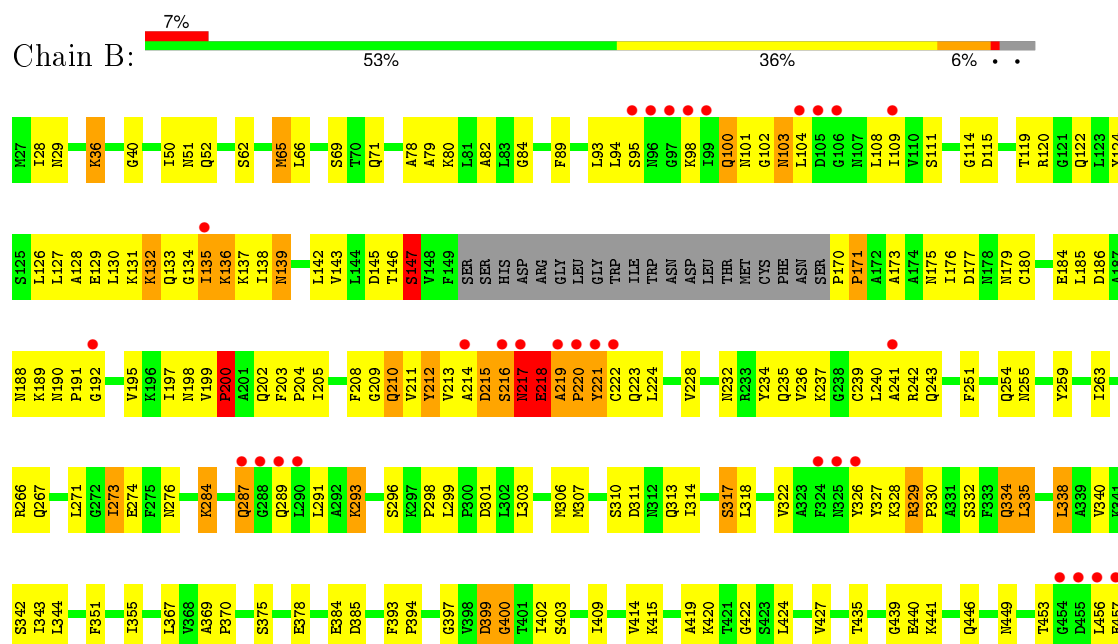
### 3 Residue-property plots

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: Penicillin-binding protein 4



#### • Molecule 1: Penicillin-binding protein 4



S458	K459	T460	K461	R462	A463	P464	E469	R470	N471	L472	Y473	L476	Y477	K478	Y479

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.90Å 92.82Å 104.17Å 90.00° 107.79° 90.00°	Depositor
Resolution (Å)	49.57 – 2.40 49.60 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.57-2.40) 93.0 (49.60-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.217 , 0.280 0.215 , 0.270	Depositor DCC
$R_{free}$ test set	2163 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 51.2	EDS
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 42895 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6865	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CMV

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	1.05	3/3437 (0.1%)	1.03	3/4644 (0.1%)
1	B	0.93	1/3391 (0.0%)	0.99	6/4582 (0.1%)
All	All	0.99	4/6828 (0.1%)	1.01	9/9226 (0.1%)

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
1	B	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	180	CYS	CB-SG	-7.14	1.70	1.82
1	B	378	GLU	CG-CD	5.59	1.60	1.51
1	A	148	VAL	CB-CG1	5.46	1.64	1.52
1	A	427	VAL	CB-CG1	5.09	1.63	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	PRO	C-N-CD	6.83	142.75	128.40
1	A	249	LEU	CA-CB-CG	-6.40	100.58	115.30
1	B	177	ASP	CB-CG-OD1	6.31	123.98	118.30
1	B	306	MET	CG-SD-CE	-5.75	91.01	100.20
1	B	456	LEU	CA-CB-CG	5.75	128.51	115.30



There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	146	THR	Peptide
1	B	147	SER	Peptide

## 5.2 Too-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 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	3378	0	3440	149	0
1	B	3333	0	3400	193	0
2	A	34	0	26	5	0
2	B	34	0	27	0	0
3	A	60	0	0	3	0
3	B	26	0	0	1	0
All	All	6865	0	6893	341	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 25.

The worst 5 of 341 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:212:TYR:CE2	1:B:239:CYS:HB3	1.66	1.29
1:B:218:GLU:C	1:B:220:PRO:HD2	1.53	1.29
1:B:218:GLU:C	1:B:220:PRO:CD	2.05	1.25
1:A:146:THR:HG22	1:A:147:SER:N	1.45	1.17
1:A:146:THR:CG2	1:A:147:SER:H	1.58	1.17

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	434/453 (96%)	406 (94%)	20 (5%)	8 (2%)	11	13
1	B	429/453 (95%)	384 (90%)	31 (7%)	14 (3%)	5	4
All	All	863/906 (95%)	790 (92%)	51 (6%)	22 (2%)	7	7

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	SER
1	B	171	PRO
1	B	215	ASP
1	B	216	SER
1	B	218	GLU

### 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	365/378 (97%)	329 (90%)	36 (10%)	10	14
1	B	358/378 (95%)	322 (90%)	36 (10%)	9	13
All	All	723/756 (96%)	651 (90%)	72 (10%)	9	14

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	458	SER

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Mol	Chain	Res	Type
1	B	100	GLN
1	B	375	SER
1	A	459	LYS
1	B	36	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	366	ASN
1	B	71	GLN
1	B	383	ASN
1	A	446	GLN
1	B	51	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](#)

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
2	CMV	A	1	1	27,36,36	2.63	5 (18%)	32,52,52	3.73	13 (40%)
2	CMV	B	1	1	27,36,36	2.75	4 (14%)	32,52,52	2.41	11 (34%)

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
2	CMV	A	1	1	-	1/16/60/60	0/3/3/3
2	CMV	B	1	1	-	0/16/60/60	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	CMV	CAE-CAI	-10.98	1.31	1.53
2	A	1	CMV	CAE-CAI	-8.69	1.36	1.53
2	B	1	CMV	C6-S1	-7.24	1.70	1.85
2	A	1	CMV	C6-S1	-6.76	1.71	1.85
2	A	1	CMV	CAE-NAG	-5.30	1.30	1.37

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	CMV	OAS-CAE-NAG	-8.23	112.50	120.66
2	A	1	CMV	C16-C6-C1	-4.28	104.04	110.88
2	B	1	CMV	CAL-CAM-NAN	-3.39	98.04	108.64
2	A	1	CMV	CBC-CAW-CAM	-2.97	115.87	120.80
2	B	1	CMV	C16-C6-C1	-2.83	106.36	110.88

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	CMV	CBE-CBB-NAO-CAI

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	CMV	5	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	438/453 (96%)	0.10	3 (0%) 89 88	16, 32, 54, 76	0
1	B	433/453 (95%)	0.39	33 (7%) 17 16	18, 40, 72, 86	0
All	All	871/906 (96%)	0.24	36 (4%) 41 42	16, 36, 67, 86	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	456	LEU	7.7
1	B	220	PRO	4.9
1	B	217	ASN	4.9
1	B	287	GLN	4.9
1	B	96	ASN	4.5

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 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
2	CMV	B	1	34/34	0.94	0.14	-0.71	25,33,54,57	0
2	CMV	A	1	34/34	0.96	0.15	-1.22	15,25,46,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.