



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 14, 2019 – 06:43 AM EST

PDB ID : 6N0X  
Title : Crystal structure of Anaerolinea thermophila mevalonate 5-phosphate decarboxylase complexed with (R)-MVAP  
Authors : Noel, J.P.; Thomas, S.T.; Louie, G.V.  
Deposited on : 2018-11-07  
Resolution : 1.44 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

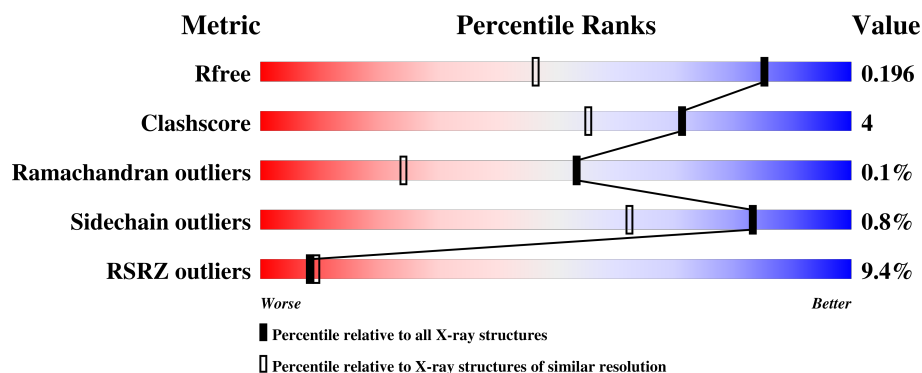
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.44 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))
$R_{free}$	111664	1592 (1.46-1.42)
Clashscore	122126	1643 (1.46-1.42)
Ramachandran outliers	120053	1618 (1.46-1.42)
Sidechain outliers	120020	1618 (1.46-1.42)
RSRZ outliers	108989	1566 (1.46-1.42)

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	330	<div> <div>8%</div> <div>90%</div> <div>7%</div> </div>
1	B	330	<div> <div>6%</div> <div>89%</div> <div>8%</div> </div>
1	C	330	<div> <div>5%</div> <div>91%</div> <div>7%</div> </div>
1	D	330	<div> <div>7%</div> <div>91%</div> <div>7%</div> </div>
1	E	330	<div> <div>12%</div> <div>91%</div> <div>5%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	330	<div><div></div><div>17%</div><div></div><div>84%</div><div></div><div>12%</div><div></div><div>• •</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 31274 atoms, of which 14514 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 Diphosphomevalonate decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	321	Total	C	H	N	O	S	0	0	0
			4852	1544	2411	427	459	11			
1	B	320	Total	C	H	N	O	S	0	0	0
			4839	1539	2405	426	458	11			
1	C	324	Total	C	H	N	O	S	0	0	0
			4888	1558	2424	431	464	11			
1	D	323	Total	C	H	N	O	S	0	0	0
			4880	1555	2419	431	464	11			
1	E	320	Total	C	H	N	O	S	0	0	0
			4856	1542	2419	427	457	11			
1	F	317	Total	C	H	N	O	S	0	0	0
			4786	1526	2376	419	454	11			

There are 24 discrepancies between the modelled and reference sequences:

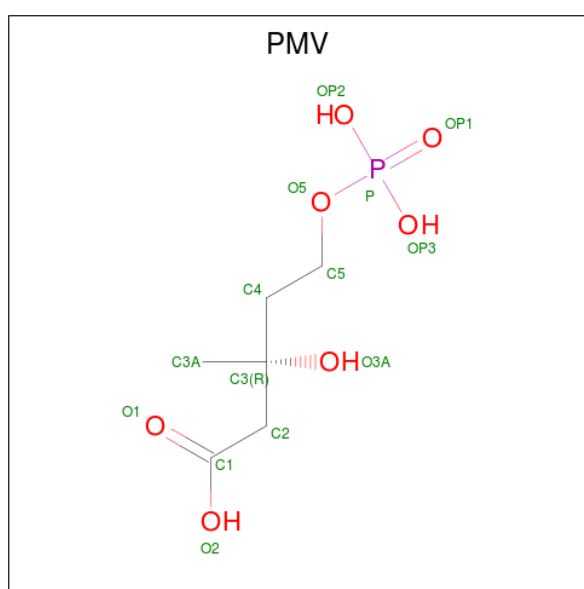
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP E8N6F3
A	-2	SER	-	expression tag	UNP E8N6F3
A	-1	HIS	-	expression tag	UNP E8N6F3
A	0	GLY	-	expression tag	UNP E8N6F3
B	-3	GLY	-	expression tag	UNP E8N6F3
B	-2	SER	-	expression tag	UNP E8N6F3
B	-1	HIS	-	expression tag	UNP E8N6F3
B	0	GLY	-	expression tag	UNP E8N6F3
C	-3	GLY	-	expression tag	UNP E8N6F3
C	-2	SER	-	expression tag	UNP E8N6F3
C	-1	HIS	-	expression tag	UNP E8N6F3
C	0	GLY	-	expression tag	UNP E8N6F3
D	-3	GLY	-	expression tag	UNP E8N6F3
D	-2	SER	-	expression tag	UNP E8N6F3
D	-1	HIS	-	expression tag	UNP E8N6F3
D	0	GLY	-	expression tag	UNP E8N6F3
E	-3	GLY	-	expression tag	UNP E8N6F3

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	SER	-	expression tag	UNP E8N6F3
E	-1	HIS	-	expression tag	UNP E8N6F3
E	0	GLY	-	expression tag	UNP E8N6F3
F	-3	GLY	-	expression tag	UNP E8N6F3
F	-2	SER	-	expression tag	UNP E8N6F3
F	-1	HIS	-	expression tag	UNP E8N6F3
F	0	GLY	-	expression tag	UNP E8N6F3

- Molecule 2 is (3R)-3-HYDROXY-3-METHYL-5-(PHOSPHONOOXY)PENTANOIC ACID (three-letter code: PMV) (formula: C<sub>6</sub>H<sub>13</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			24	6	10	7	1		
2	B	1	Total	C	H	O	P	0	0
			24	6	10	7	1		
2	C	1	Total	C	H	O	P	0	0
			24	6	10	7	1		
2	D	1	Total	C	H	O	P	0	0
			24	6	10	7	1		
2	E	1	Total	C	H	O	P	0	0
			24	6	10	7	1		
2	F	1	Total	C	H	O	P	0	0
			24	6	10	7	1		

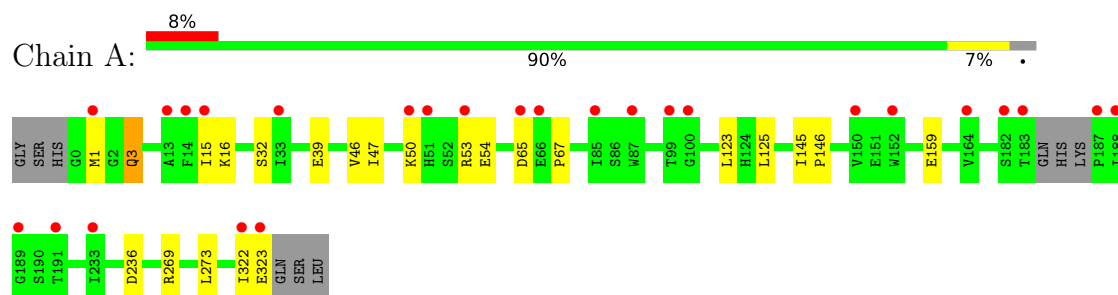
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	362	Total 362	O 362	0	0
3	B	357	Total 357	O 357	0	0
3	C	352	Total 352	O 352	0	0
3	D	371	Total 371	O 371	0	0
3	E	289	Total 289	O 289	0	0
3	F	298	Total 298	O 298	0	0

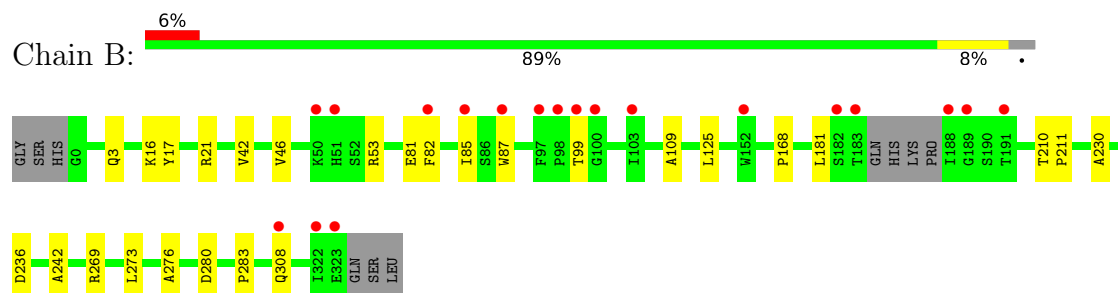
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

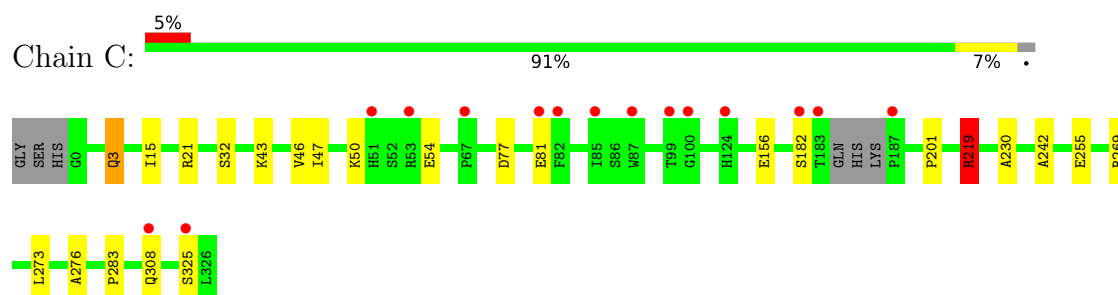
#### • Molecule 1: Diphosphomevalonate decarboxylase



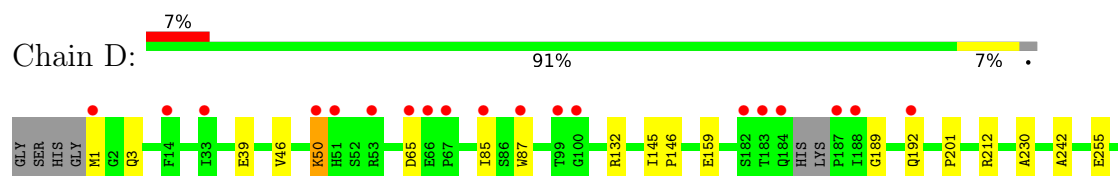
#### • Molecule 1: Diphosphomevalonate decarboxylase

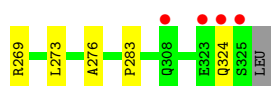


#### • Molecule 1: Diphosphomevalonate decarboxylase

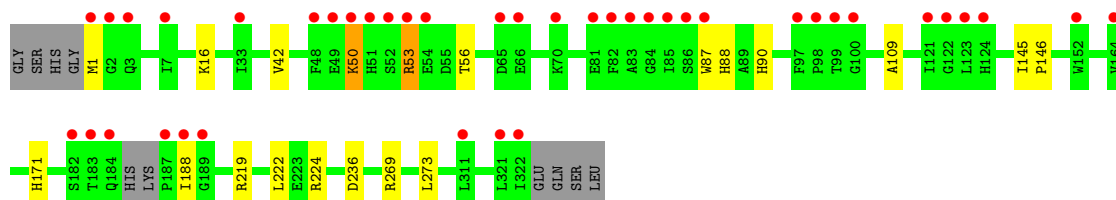
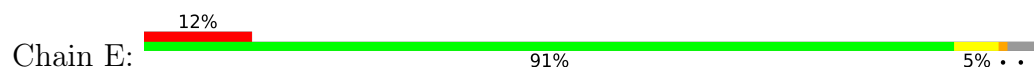


#### • Molecule 1: Diphosphomevalonate decarboxylase

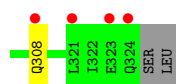
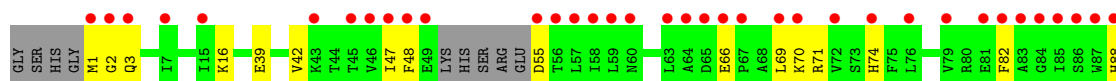
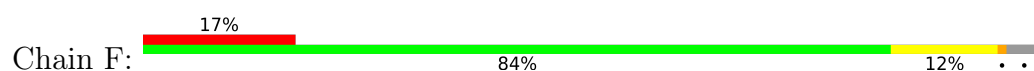




• Molecule 1: Diphosphomevalonate decarboxylase



• Molecule 1: Diphosphomevalonate decarboxylase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.60Å 135.63Å 105.70Å 90.00° 97.72° 90.00°	Depositor
Resolution (Å)	37.57 – 1.44 37.57 – 1.44	Depositor EDS
% Data completeness (in resolution range)	89.8 (37.57-1.44) 89.9 (37.57-1.44)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 1.44Å)	Xtriage
Refinement program	PHENIX (1.14_3260)	Depositor
R, $R_{free}$	0.172 , 0.196 0.172 , 0.196	Depositor DCC
$R_{free}$ test set	18015 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.3	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 42.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	31274	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PMV

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	0.56	0/2496	0.71	0/3398
1	B	0.56	0/2488	0.70	0/3387
1	C	0.62	0/2519	0.73	0/3429
1	D	0.60	0/2516	0.71	0/3425
1	E	0.54	0/2492	0.69	0/3393
1	F	0.52	0/2463	0.69	0/3354
All	All	0.57	0/14974	0.71	0/20386

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	C	0	1
1	F	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	219	ARG	Sidechain
1	F	132	ARG	Sidechain

## 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	2441	2411	2434	14	0
1	B	2434	2405	2426	19	0
1	C	2464	2424	2458	15	0
1	D	2461	2419	2452	20	0
1	E	2437	2419	2433	17	0
1	F	2410	2376	2402	31	0
2	A	14	10	10	0	0
2	B	14	10	10	0	0
2	C	14	10	10	0	0
2	D	14	10	10	0	0
2	E	14	10	10	0	0
2	F	14	10	10	0	0
3	A	362	0	0	0	0
3	B	357	0	0	7	0
3	C	352	0	0	3	0
3	D	371	0	0	6	0
3	E	289	0	0	2	0
3	F	298	0	0	0	0
All	All	16760	14514	14665	112	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 4.

The worst 5 of 112 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:F:129:ASP:OD1	1:F:132:ARG:NH2	1.96	0.98
1:F:3:GLN:HG3	1:F:47:ILE:HG12	1.66	0.76
1:E:219:ARG:NH1	3:E:501:HOH:O	2.23	0.71
1:E:53:ARG:NE	1:E:53:ARG:HA	2.05	0.71
1:B:53:ARG:NH2	3:B:503:HOH:O	2.23	0.71

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	317/330 (96%)	313 (99%)	4 (1%)	0	100	100
1	B	316/330 (96%)	313 (99%)	3 (1%)	0	100	100
1	C	320/330 (97%)	317 (99%)	3 (1%)	0	100	100
1	D	319/330 (97%)	316 (99%)	3 (1%)	0	100	100
1	E	316/330 (96%)	311 (98%)	4 (1%)	1 (0%)	43	19
1	F	311/330 (94%)	304 (98%)	6 (2%)	1 (0%)	43	19
All	All	1899/1980 (96%)	1874 (99%)	23 (1%)	2 (0%)	53	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	50	LYS
1	F	183	THR

### 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	260/268 (97%)	258 (99%)	2 (1%)	83	62
1	B	259/268 (97%)	258 (100%)	1 (0%)	92	81
1	C	263/268 (98%)	260 (99%)	3 (1%)	76	48
1	D	263/268 (98%)	261 (99%)	2 (1%)	83	62
1	E	260/268 (97%)	259 (100%)	1 (0%)	92	81

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	257/268 (96%)	254 (99%)	3 (1%)	74	44
All	All	1562/1608 (97%)	1550 (99%)	12 (1%)	83	62

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	219	ARG
1	D	50	LYS
1	F	66	GLU
1	C	50	LYS
1	E	53	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	88	HIS
1	D	192	GLN
1	E	88	HIS
1	F	74	HIS

### 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](#)

6 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	PMV	A	1001	-	9,13,13	1.00	0	10,19,19	1.50	3 (30%)
2	PMV	B	401	-	9,13,13	0.90	0	10,19,19	1.07	1 (10%)
2	PMV	C	401	-	9,13,13	1.02	0	10,19,19	1.28	1 (10%)
2	PMV	D	401	-	9,13,13	0.87	0	10,19,19	1.16	1 (10%)
2	PMV	E	401	-	9,13,13	1.00	1 (11%)	10,19,19	1.00	0
2	PMV	F	401	-	9,13,13	0.85	0	10,19,19	1.29	2 (20%)

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	PMV	A	1001	-	-	4/11/13/13	-
2	PMV	B	401	-	-	3/11/13/13	-
2	PMV	C	401	-	-	5/11/13/13	-
2	PMV	D	401	-	-	4/11/13/13	-
2	PMV	E	401	-	-	3/11/13/13	-
2	PMV	F	401	-	-	3/11/13/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	401	PMV	P-OP3	-2.02	1.46	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	PMV	P-O5-C5	2.99	126.53	118.30
2	A	1001	PMV	P-O5-C5	2.71	125.77	118.30
2	A	1001	PMV	OP2-P-O5	2.36	113.02	106.73
2	F	401	PMV	OP3-P-OP2	2.30	116.52	107.57
2	B	401	PMV	P-O5-C5	2.30	124.63	118.30

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	PMV	C5-O5-P-OP2
2	A	1001	PMV	C5-O5-P-OP3
2	A	1001	PMV	C5-O5-P-OP1
2	C	401	PMV	C5-O5-P-OP2
2	C	401	PMV	C5-O5-P-OP3

There are no ring outliers.

No monomer is involved in short contacts.

## 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	321/330 (97%)	0.26	26 (8%) 12 13	12, 20, 37, 52	0
1	B	320/330 (96%)	0.21	19 (5%) 22 23	13, 20, 38, 52	0
1	C	324/330 (98%)	0.15	15 (4%) 32 34	12, 18, 39, 60	0
1	D	323/330 (97%)	0.28	23 (7%) 16 17	12, 20, 41, 57	0
1	E	320/330 (96%)	0.62	41 (12%) 3 4	13, 23, 55, 88	0
1	F	317/330 (96%)	0.84	57 (17%) 1 1	14, 25, 61, 83	0
All	All	1925/1980 (97%)	0.39	181 (9%) 8 9	12, 21, 46, 88	0

The worst 5 of 181 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	182	SER	10.7
1	F	82	PHE	10.4
1	F	87	TRP	10.0
1	F	184	GLN	9.2
1	E	1	MET	8.9

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PMV	A	1001	14/14	0.97	0.09	14,18,27,30	0
2	PMV	F	401	14/14	0.97	0.08	18,24,30,31	0
2	PMV	E	401	14/14	0.98	0.08	16,22,27,29	0
2	PMV	C	401	14/14	0.98	0.07	14,18,23,26	0
2	PMV	D	401	14/14	0.99	0.08	14,20,23,27	0
2	PMV	B	401	14/14	0.99	0.08	14,19,26,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.