



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:20 PM UTC

PDB ID : 2DU6 / pdb\_00002du6  
Title : Crystal structure of Archaeoglobus fulgidus O-phosphoseryl-tRNA synthetase E418N/E420N mutant complexed with tRNA<sup>Amber</sup> and O-phosphoserine ("amber complex")  
Authors : Fukunaga, R.  
Deposited on : 2006-07-20  
Resolution : 3.30 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

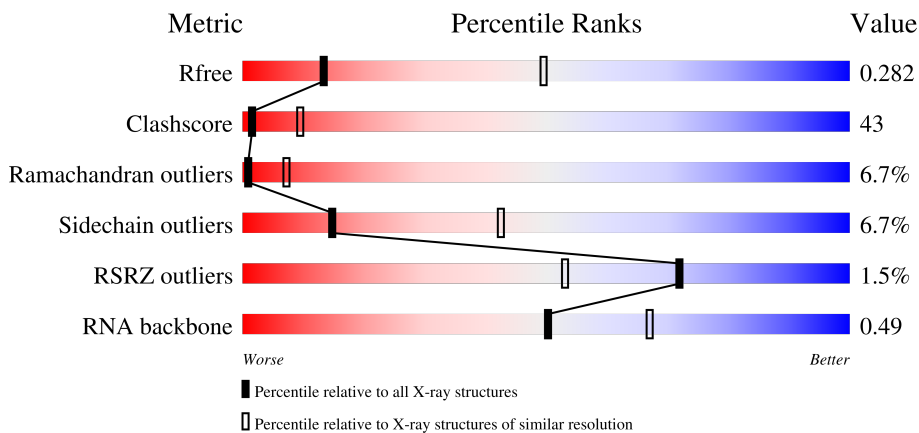
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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))
$R_{free}$	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)
RNA backbone	3983	1048 (3.60-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	D	71	 42% 37% 20% .
2	A	534	 34% 55% 11% .
2	B	534	 29% 50% 7% . 13%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9619 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	D	71	1517	674	269	503	71	0	0	0

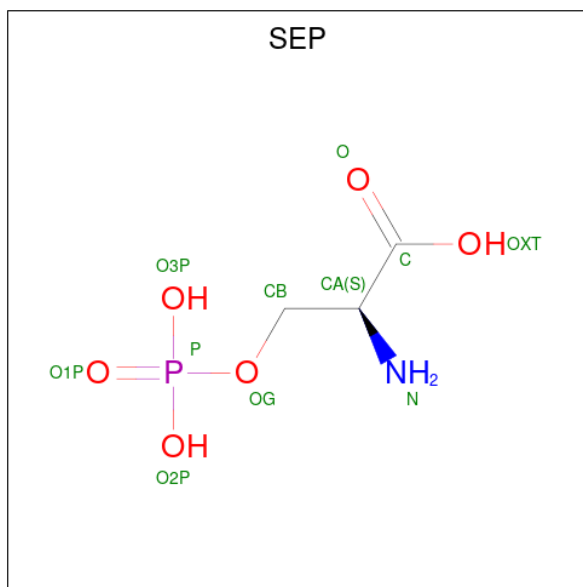
- Molecule 2 is a protein called O-phosphoseryl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	534	4319	2784	721	801	13	0	0	0
2	B	465	3761	2427	632	689	13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	418	ASN	GLU	engineered mutation	UNP O30126
A	420	ASN	GLU	engineered mutation	UNP O30126
B	418	ASN	GLU	engineered mutation	UNP O30126
B	420	ASN	GLU	engineered mutation	UNP O30126

- Molecule 3 is PHOSPHOSERINE (CCD ID: SEP) (formula: C<sub>3</sub>H<sub>8</sub>NO<sub>6</sub>P).



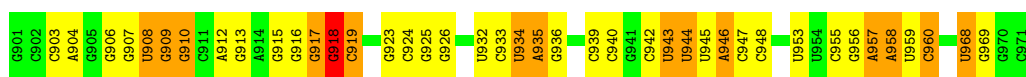
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	11	3	1	6	1	0	0
3	A	1	11	3	1	6	1	0	0

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

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

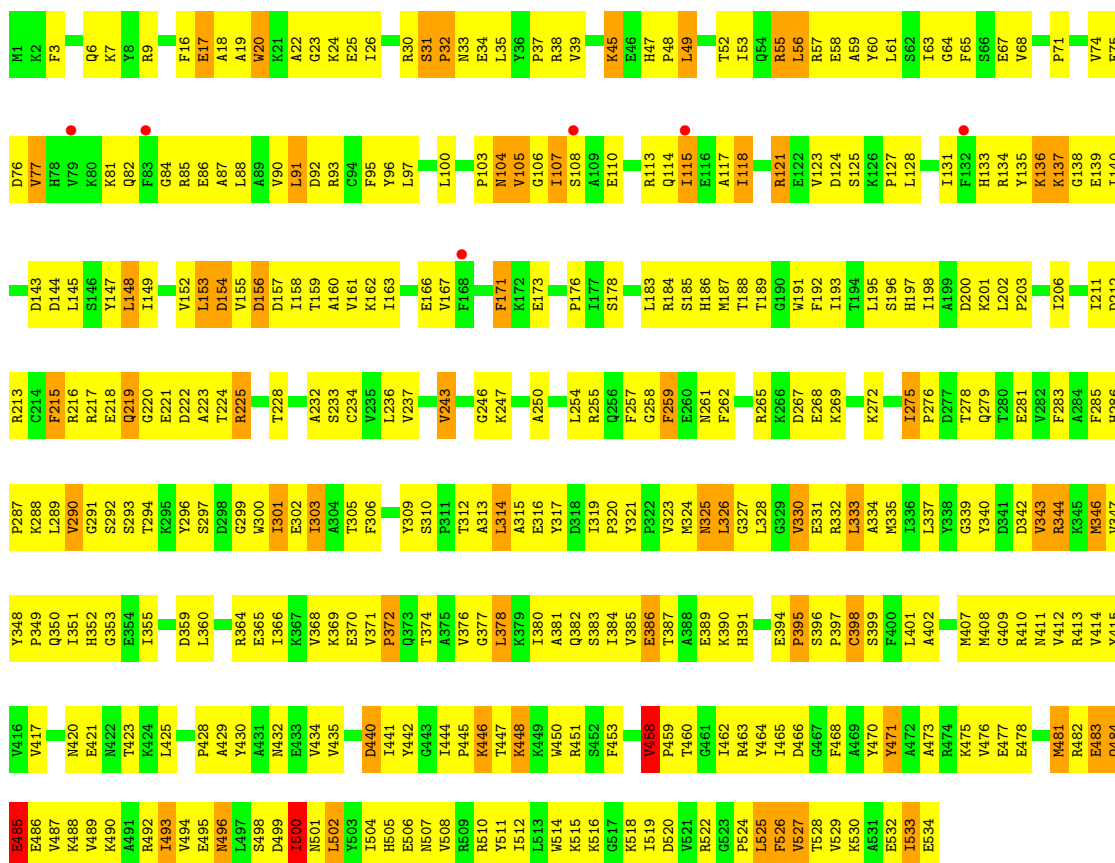
- Molecule 1: tRNA

Chain D: 



- Molecule 2: O-phosphoseryl-tRNA synthetase

Chain A: 



- Molecule 2: O-phosphoseryl-tRNA synthetase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.32Å 148.32Å 152.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.14 – 3.30 49.14 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.14-3.30) 99.7 (49.14-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.15 (at 3.33Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.265 , 0.329 0.228 , 0.282	Depositor DCC
$R_{free}$ test set	1458 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	95.8	Xtrriage
Anisotropy	0.076	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 119.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9619	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	104.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	D	0.31	0/1693	0.59	0/2637
2	A	0.37	0/4416	0.89	14/5966 (0.2%)
2	B	0.40	0/3849	0.91	8/5200 (0.2%)
All	All	0.37	0/9958	0.85	22/13803 (0.2%)

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	D	0	1

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	330	VAL	N-CA-C	9.34	119.36	110.30
2	B	243	VAL	N-CA-C	-8.86	99.96	113.16
2	B	444	ILE	N-CA-C	7.65	115.46	109.19
2	A	448	LYS	N-CA-C	-7.01	104.46	113.16
2	B	278	THR	N-CA-C	-6.70	104.27	113.18

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	918	G	Sidechain

## 5.2 Too-close contacts [i](#)

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	D	1517	0	768	41	0
2	A	4319	0	4339	433	0
2	B	3761	0	3774	342	0
3	A	22	0	10	3	0
All	All	9619	0	8891	787	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 43.

The worst 5 of 787 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)
2:B:216:ARG:HG2	2:B:218:GLU:HG2	1.37	1.06
2:A:148:LEU:HG	2:A:160:ALA:HB2	1.34	1.06
2:B:448:LYS:H	2:B:448:LYS:HD3	1.15	1.05
1:D:957:A:H1'	1:D:959:U:H5	1.23	1.03
2:B:232:ALA:HB3	2:B:328:LEU:HB3	1.41	1.02

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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
2	A	532/534 (100%)	387 (73%)	100 (19%)	45 (8%)	<b>0</b> <b>4</b>
2	B	461/534 (86%)	372 (81%)	67 (14%)	22 (5%)	<b>2</b> <b>12</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	993/1068 (93%)	759 (76%)	167 (17%)	67 (7%)	<b>1</b> <b>7</b>

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	31	SER
2	A	156	ASP
2	A	220	GLY
2	A	225	ARG
2	A	372	PRO

### 5.3.2 Protein sidechains [i](#)

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
2	A	464/464 (100%)	433 (93%)	31 (7%)	<b>15</b> 42
2	B	402/464 (87%)	375 (93%)	27 (7%)	<b>15</b> 42
All	All	866/928 (93%)	808 (93%)	58 (7%)	<b>15</b> 42

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	502	LEU
2	B	504	ILE
2	B	49	LEU
2	B	502	LEU
2	B	435	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	420	ASN
2	B	496	ASN
2	A	496	ASN

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Mol	Chain	Res	Type
2	B	47	HIS
2	B	219	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	70/71 (98%)	17 (24%)	3 (4%)

5 of 17 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	906	G
1	D	908	U
1	D	909	G
1	D	910	G
1	D	917	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D	917	G
1	D	934	U
1	D	957	A

## 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 oligosaccharides 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
3	SEP	A	1002	-	9,10,10	1.61	1 (11%)	9,14,14	2.04	2 (22%)
3	SEP	A	1001	-	9,10,10	1.62	1 (11%)	9,14,14	1.84	2 (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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SEP	A	1002	-	-	4/10/10/10	-
3	SEP	A	1001	-	-	4/10/10/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1002	SEP	P-O1P	3.54	1.61	1.50
3	A	1001	SEP	P-O1P	3.52	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1002	SEP	OG-CB-CA	5.29	112.67	108.06
3	A	1001	SEP	OG-CB-CA	4.52	112.00	108.06
3	A	1001	SEP	O3P-P-OG	2.56	113.34	106.67
3	A	1002	SEP	O3P-P-OG	2.52	113.25	106.67

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	SEP	CA-CB-OG-P
3	A	1001	SEP	CB-OG-P-O2P
3	A	1001	SEP	CB-OG-P-O3P
3	A	1002	SEP	CB-OG-P-O1P
3	A	1002	SEP	CB-OG-P-O2P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	SEP	1	0
3	A	1001	SEP	2	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	D	71/71 (100%)	-0.06	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	112, 199, 201, 201	0
2	A	534/534 (100%)	-0.26	6 (1%) <span style="border: 1px solid blue; padding: 2px;">78</span> <span style="border: 1px solid blue; padding: 2px;">60</span>	15, 79, 197, 201	0
2	B	465/534 (87%)	-0.33	10 (2%) <span style="border: 1px solid blue; padding: 2px;">62</span> <span style="border: 1px solid red; padding: 2px;">43</span>	9, 66, 175, 200	0
All	All	1070/1139 (93%)	-0.28	16 (1%) <span style="border: 1px solid blue; padding: 2px;">72</span> <span style="border: 1px solid blue; padding: 2px;">53</span>	9, 77, 199, 201	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	468	PHE	3.6
2	B	416	VAL	3.5
2	B	529	VAL	2.8
2	B	388	ALA	2.7
2	B	331	GLU	2.6

### 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 oligosaccharides 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
3	SEP	A	1002	11/11	0.88	0.14	35,68,109,116	0
3	SEP	A	1001	11/11	0.90	0.12	55,90,119,121	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.