



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 14, 2020 – 03:13 pm BST

PDB ID : 2OAQ  
Title : Crystal structure of the archaeal secretion ATPase GspE in complex with phosphate  
Authors : Yamagata, A.; Tainer, J.A.  
Deposited on : 2006-12-17  
Resolution : 3.15 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.

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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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

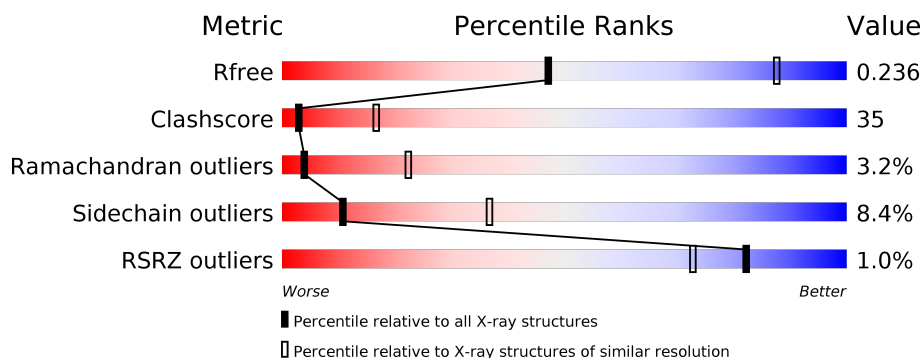
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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))
$R_{free}$	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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 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	1	511	<div> <div>2%</div> <div> <div></div> <div>44%</div> <div>46%</div> <div>7%</div> <div>••</div> </div> </div>
1	2	511	<div> <div>45%</div> <div>46%</div> <div>7%</div> <div>•</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	2	512	-	-	X	-
2	PO4	2	513	-	-	X	-
2	PO4	2	514	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7997 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 Type II secretion system protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1	498	Total	C	N	O	S	Se	0	0	0
			3916	2501	669	728	1	17			
1	2	503	Total	C	N	O	S	Se	0	0	0
			4061	2593	681	770	1	16			

There are 36 discrepancies between the modelled and reference sequences:

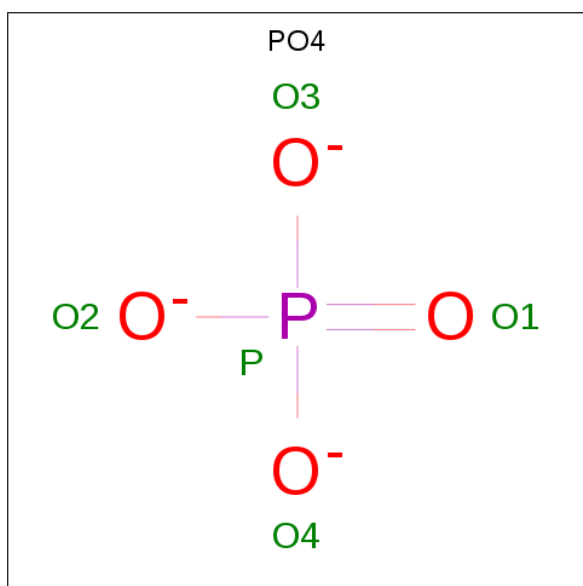
Chain	Residue	Modelled	Actual	Comment	Reference
1	1	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	121	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	139	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	180	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	281	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	282	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	315	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	322	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	354	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	372	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	387	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	399	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	446	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	453	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	468	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	478	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	504	MSE	MET	MODIFIED RESIDUE	UNP O29598
1	507	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	1	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	121	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	139	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	180	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	281	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	282	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	315	MSE	MET	MODIFIED RESIDUE	UNP O29598

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Chain	Residue	Modelled	Actual	Comment	Reference
2	322	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	354	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	372	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	387	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	399	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	446	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	453	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	468	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	478	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	504	MSE	MET	MODIFIED RESIDUE	UNP O29598
2	507	MSE	MET	MODIFIED RESIDUE	UNP O29598

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).

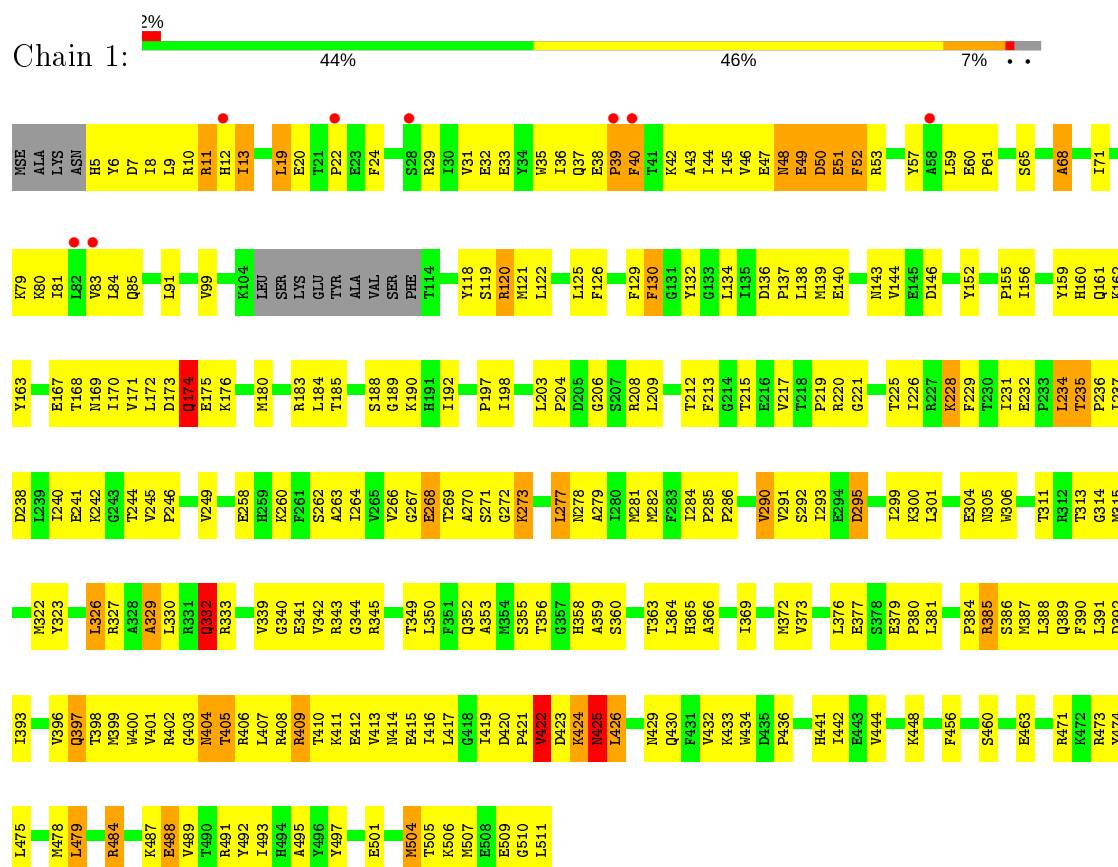


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1	1	Total O P 5 4 1	0	0
2	2	1	Total O P 5 4 1	0	0
2	2	1	Total O P 5 4 1	0	0
2	2	1	Total O P 5 4 1	0	0

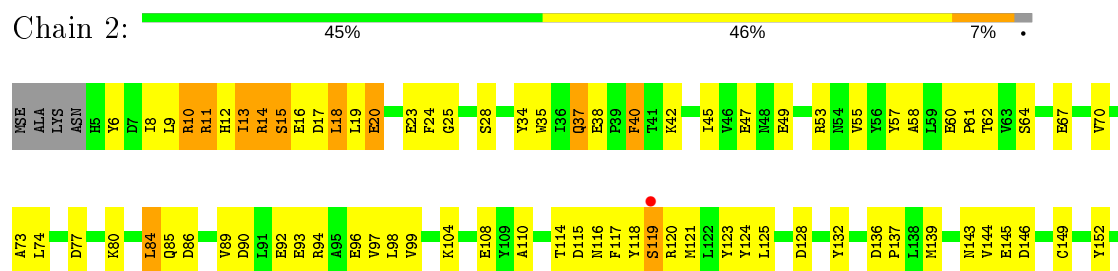
### 3 Residue-property plots [i](#)

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: Type II secretion system protein



#### • Molecule 1: Type II secretion system protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.61 Å   132.61 Å   445.28 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	20.00 – 3.15 50.09 – 3.16	Depositor EDS
% Data completeness (in resolution range)	93.2 (20.00-3.15) 93.8 (50.09-3.16)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.67 (at 3.19 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.221   ,   0.236 0.218   ,   0.236	Depositor DCC
$R_{free}$ test set	1248 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.6	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7997	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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: PO4

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	1	0.47	1/3977 (0.0%)	0.74	4/5365 (0.1%)
1	2	0.44	0/4125	0.70	1/5560 (0.0%)
All	All	0.46	1/8102 (0.0%)	0.72	5/10925 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	270	ALA	CA-CB	5.11	1.63	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	333	ARG	NE-CZ-NH1	-9.95	115.32	120.30
1	1	424	LYS	N-CA-C	-6.41	93.70	111.00
1	1	422	VAL	N-CA-C	-5.30	96.68	111.00
1	1	333	ARG	NE-CZ-NH2	5.22	122.91	120.30
1	2	408	ARG	N-CA-C	-5.19	96.99	111.00

There are no chirality outliers.

There are no planarity outliers.

### 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	1	3916	0	3816	278	0
1	2	4061	0	4040	281	0
2	1	5	0	0	1	0
2	2	15	0	0	9	0
All	All	7997	0	7856	548	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 35.

The worst 5 of 548 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)
1:1:180:MSE:HE2	1:1:184:LEU:HG	1.43	0.99
1:2:446:MSE:HG2	1:2:447:PRO:HD2	1.42	0.98
1:1:215:THR:HG22	1:1:221:GLY:HA2	1.47	0.95
1:2:180:MSE:HE2	1:2:184:LEU:HG	1.50	0.94
1:1:391:LEU:HD22	1:1:416:ILE:HD12	1.52	0.90

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	
1	1	494/511 (97%)	417 (84%)	54 (11%)	23 (5%)	2	15
1	2	499/511 (98%)	441 (88%)	49 (10%)	9 (2%)	8	37
All	All	993/1022 (97%)	858 (86%)	103 (10%)	32 (3%)	4	22

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	11	ARG

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Mol	Chain	Res	Type
1	1	52	PHE
1	1	68	ALA
1	2	13	ILE
1	1	120	ARG

### 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	1	406/439 (92%)	372 (92%)	34 (8%)	11	37
1	2	444/439 (101%)	407 (92%)	37 (8%)	11	37
All	All	850/878 (97%)	779 (92%)	71 (8%)	11	37

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	501	GLU
1	2	40	PHE
1	2	407	LEU
1	1	504	MSE
1	2	18	LEU

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	2	116	ASN
1	2	259	HIS
1	2	429	ASN
1	2	143	ASN
1	2	210	GLN

### 5.3.3 RNA ⓘ

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](#)

4 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	PO4	2	513	-	4,4,4	1.36	1 (25%)	6,6,6	1.26	1 (16%)
2	PO4	2	514	-	4,4,4	1.63	1 (25%)	6,6,6	0.99	0
2	PO4	1	512	-	4,4,4	1.57	1 (25%)	6,6,6	0.77	0
2	PO4	2	512	-	4,4,4	1.71	1 (25%)	6,6,6	0.97	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	512	PO4	P-O1	2.94	1.57	1.50
2	1	512	PO4	P-O1	2.64	1.57	1.50
2	2	514	PO4	P-O1	2.62	1.57	1.50
2	2	513	PO4	P-O1	2.12	1.55	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	513	PO4	O3-P-O2	2.08	114.65	107.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	513	PO4	4	0
2	2	514	PO4	4	0
2	1	512	PO4	1	0
2	2	512	PO4	3	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	1	481/511 (94%)	-0.14	8 (1%) 70 57	24, 58, 118, 127	0
1	2	487/511 (95%)	-0.18	2 (0%) 92 89	32, 56, 89, 104	0
All	All	968/1022 (94%)	-0.16	10 (1%) 82 73	24, 57, 110, 127	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1	83	VAL	4.0
1	2	423	ASP	3.0
1	1	82	LEU	2.9
1	1	39	PRO	2.7
1	1	40	PHE	2.7

### 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	PO4	2	512	5/5	0.83	0.47	55,57,57,57	5
2	PO4	2	513	5/5	0.85	0.46	53,53,55,57	5
2	PO4	2	514	5/5	0.89	0.27	61,61,62,62	0
2	PO4	1	512	5/5	0.90	0.57	51,52,53,54	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.