



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2023 – 10:32 PM EDT

PDB ID : 4ZDP  
Title : The crystal structure of Y334C mutant of human SepSecS in complex with selenocysteine tRNA (tRNA<sup>Sec</sup>)  
Authors : French, R.L.; Simonovic, M.  
Deposited on : 2015-04-17  
Resolution : 2.70 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

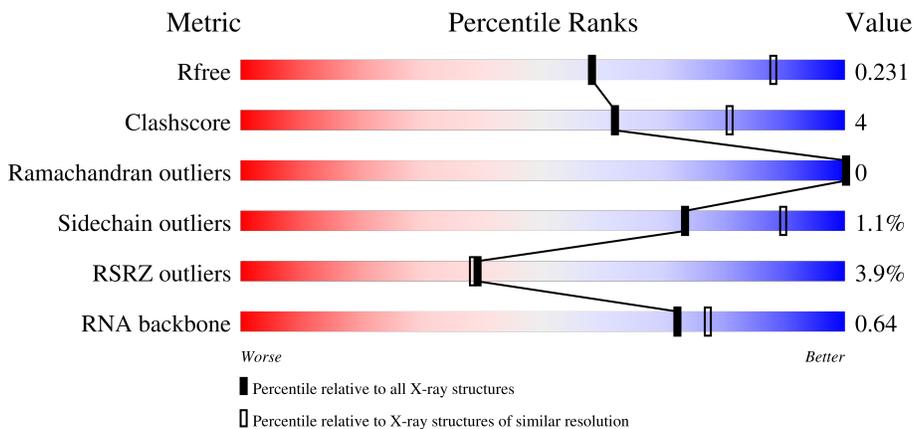
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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 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	A	501	 80% 8% 11%
1	B	501	 79% 9% 12%
1	C	501	 80% 8% 12%
1	D	501	 80% 8% 12%

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Mol	Chain	Length	Quality of chain
2	E	87	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left (56%), a red segment in the middle (29%), and a yellow segment on the right (15%). Above the green segment, the text '71%' is displayed. Below the green segment, the text '56%' is displayed. Below the red segment, the text '29%' is displayed. Below the yellow segment, the text '15%' is displayed.</p>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17306 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 O-phosphoseryl-tRNA(Sec) selenium transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	444	3399	2158	593	621	27	3	4	0
1	B	443	3387	2148	593	618	28	0	3	0
1	C	443	3374	2142	587	618	27	0	3	0
1	D	443	3370	2138	587	617	28	0	4	0

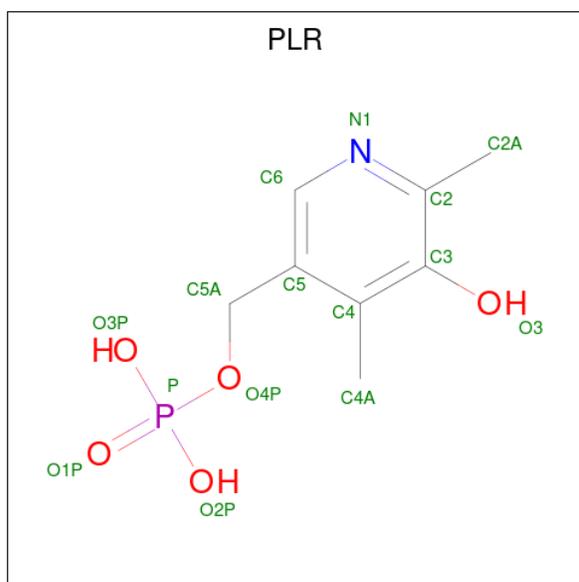
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	334	CYS	TYR	engineered mutation	UNP Q9HD40
B	334	CYS	TYR	engineered mutation	UNP Q9HD40
C	334	CYS	TYR	engineered mutation	UNP Q9HD40
D	334	CYS	TYR	engineered mutation	UNP Q9HD40

- Molecule 2 is a RNA chain called selenocysteine tRNA.

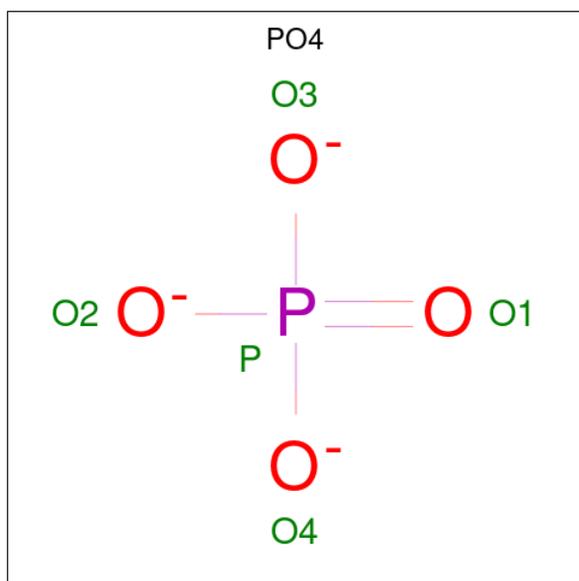
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	74	3160	1406	554	1052	148	0	74	0

- Molecule 3 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (three-letter code: PLR) (formula: C<sub>8</sub>H<sub>12</sub>NO<sub>5</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total 15	C 8	N 1	O 5	P 1	0	0
3	B	1	Total 15	C 8	N 1	O 5	P 1	0	0
3	C	1	Total 15	C 8	N 1	O 5	P 1	0	0
3	D	1	Total 15	C 8	N 1	O 5	P 1	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	C	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		

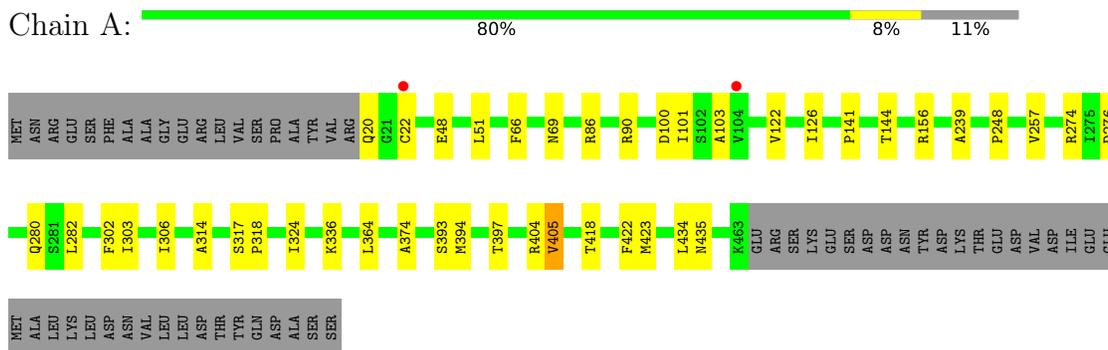
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	122	Total	O	0	0
			122	122		
5	B	136	Total	O	0	0
			136	136		
5	C	132	Total	O	0	0
			132	132		
5	D	142	Total	O	0	0
			142	142		
5	E	4	Total	O	0	0
			4	4		

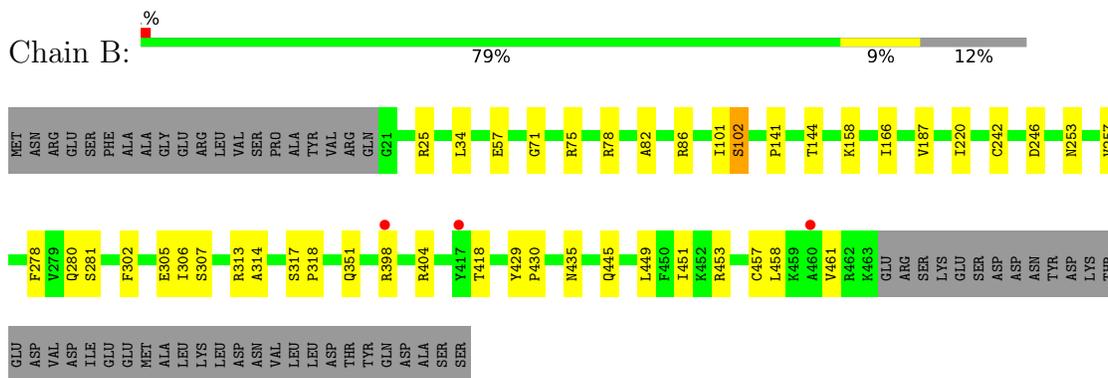
### 3 Residue-property plots [i](#)

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.

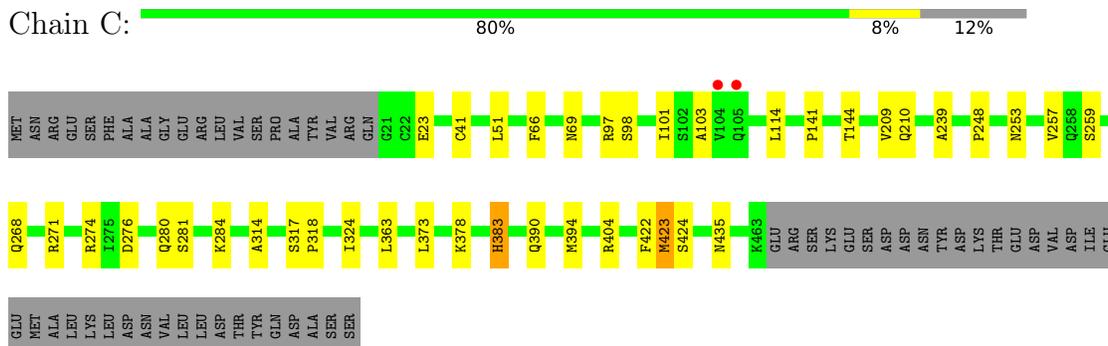
- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



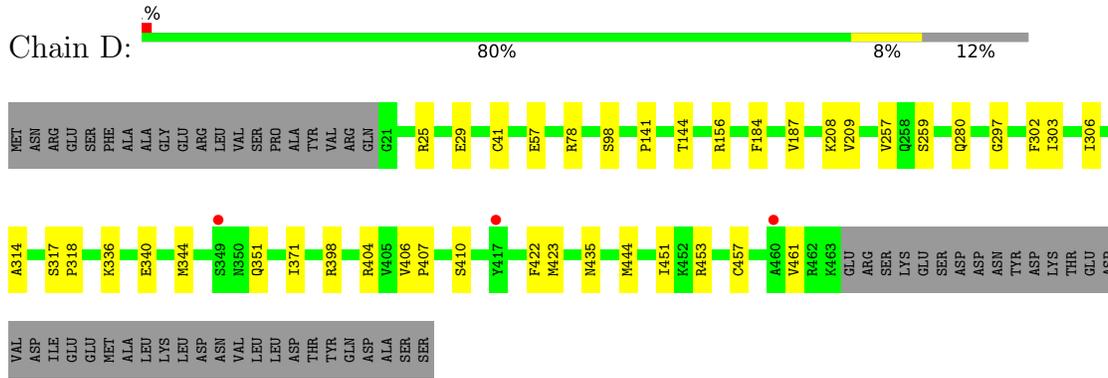
- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



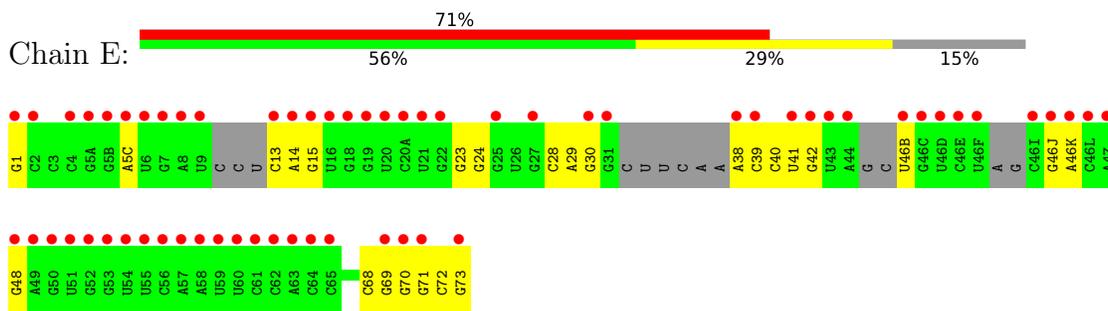
- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



● Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



● Molecule 2: selenocysteine tRNA



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	167.26Å 167.26Å 240.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.65 – 2.70 49.82 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.5 (41.65-2.70) 86.9 (49.82-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.36 (at 2.69Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.200 , 0.232 0.203 , 0.231	Depositor DCC
$R_{free}$ test set	5019 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.9	Xtrriage
Anisotropy	0.465	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 26.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.478 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	17306	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.94% 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: PLR, 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	A	0.63	0/3470	0.56	0/4695
1	B	0.60	0/3458	0.56	0/4679
1	C	0.65	1/3445 (0.0%)	0.57	2/4663 (0.0%)
1	D	0.61	1/3444 (0.0%)	0.55	0/4661
2	E	0.31	2/3520 (0.1%)	0.67	0/5462
All	All	0.57	4/17337 (0.0%)	0.59	2/24160 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1[A]	G	OP3-P	-10.96	1.48	1.61
2	E	1[B]	G	OP3-P	-10.96	1.48	1.61
1	D	41	CYS	CB-SG	-5.48	1.72	1.81
1	C	41	CYS	CB-SG	-5.45	1.73	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	423	MET	CB-CA-C	-6.63	97.15	110.40
1	C	424	SER	N-CA-CB	5.95	119.42	110.50

There are no chirality outliers.

There are no planarity outliers.

### 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	A	3399	0	3384	26	1
1	B	3387	0	3382	31	1
1	C	3374	0	3356	24	0
1	D	3370	0	3353	27	0
2	E	3160	0	1560	36	0
3	A	15	0	7	1	0
3	B	15	0	7	1	0
3	C	15	0	7	2	0
3	D	15	0	7	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
5	A	122	0	0	4	0
5	B	136	0	0	1	0
5	C	132	0	0	4	0
5	D	142	0	0	1	0
5	E	4	0	0	0	0
All	All	17306	0	15063	137	1

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 137 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:D:453:ARG:O	1:D:457:CYS:SG	2.29	0.91
1:D:398:ARG:HH22	2:E:38[A]:A:H4'	1.38	0.85
1:A:144:THR:HB	3:A:1001:PLR:H5A2	1.58	0.84
1:B:453:ARG:O	1:B:457:CYS:SG	2.35	0.83
1:C:144:THR:HB	3:C:1001:PLR:H5A2	1.61	0.81

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:GLU:OE1	1:B:86[B]:ARG:NH1[5_755]	2.19	0.01

## 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	A	446/501 (89%)	428 (96%)	18 (4%)	0	100	100
1	B	444/501 (89%)	425 (96%)	19 (4%)	0	100	100
1	C	444/501 (89%)	429 (97%)	15 (3%)	0	100	100
1	D	445/501 (89%)	434 (98%)	11 (2%)	0	100	100
All	All	1779/2004 (89%)	1716 (96%)	63 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
1	A	358/430 (83%)	355 (99%)	3 (1%)	81	93
1	B	360/430 (84%)	355 (99%)	5 (1%)	67	86
1	C	357/430 (83%)	351 (98%)	6 (2%)	60	84
1	D	357/430 (83%)	355 (99%)	2 (1%)	86	95
All	All	1432/1720 (83%)	1416 (99%)	16 (1%)	73	90

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	98	SER
1	C	383	HIS
1	C	98	SER

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Mol	Chain	Res	Type
1	C	259	SER
1	B	418	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	268	GLN
1	B	253	ASN
1	B	360	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	0/87	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

8 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	PLR	A	1001	1	15,15,15	3.06	3 (20%)	20,22,22	1.20	1 (5%)
3	PLR	B	1001	1	15,15,15	3.06	3 (20%)	20,22,22	1.20	1 (5%)
3	PLR	D	1001	1	15,15,15	3.06	3 (20%)	20,22,22	1.20	1 (5%)
3	PLR	C	1001	1	15,15,15	3.04	3 (20%)	20,22,22	1.19	1 (5%)
4	PO4	A	1002	-	4,4,4	0.97	0	6,6,6	0.38	0
4	PO4	B	1002	-	4,4,4	0.93	0	6,6,6	0.53	0
4	PO4	D	1002	-	4,4,4	1.04	0	6,6,6	0.33	0
4	PO4	C	1002	-	4,4,4	0.95	0	6,6,6	0.39	0

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
3	PLR	C	1001	1	-	0/6/6/6	0/1/1/1
3	PLR	A	1001	1	-	0/6/6/6	0/1/1/1
3	PLR	B	1001	1	-	4/6/6/6	0/1/1/1
3	PLR	D	1001	1	-	0/6/6/6	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1001	PLR	C3-C2	8.04	1.48	1.40
3	A	1001	PLR	C3-C2	8.02	1.48	1.40
3	D	1001	PLR	C3-C2	8.00	1.48	1.40
3	C	1001	PLR	C3-C2	7.98	1.48	1.40
3	D	1001	PLR	C5-C4	7.48	1.48	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1001	PLR	C6-N1-C2	2.20	123.24	119.17
3	D	1001	PLR	C6-N1-C2	2.18	123.21	119.17
3	A	1001	PLR	C6-N1-C2	2.16	123.17	119.17
3	C	1001	PLR	C6-N1-C2	2.16	123.17	119.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1001	PLR	C5A-O4P-P-O1P
3	B	1001	PLR	C5A-O4P-P-O2P
3	B	1001	PLR	C5A-O4P-P-O3P
3	B	1001	PLR	C6-C5-C5A-O4P

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	PLR	1	0
3	B	1001	PLR	1	0
3	D	1001	PLR	1	0
3	C	1001	PLR	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	A	444/501 (88%)	-0.39	2 (0%) 91 92	19, 31, 60, 154	0
1	B	443/501 (88%)	-0.34	3 (0%) 87 89	17, 31, 70, 152	0
1	C	443/501 (88%)	-0.39	2 (0%) 91 92	19, 30, 62, 121	0
1	D	443/501 (88%)	-0.36	3 (0%) 87 89	18, 31, 72, 153	0
2	E	74/87 (85%)	3.95	62 (83%) 0 0	89, 152, 191, 192	16 (21%)
All	All	1847/2091 (88%)	-0.20	72 (3%) 39 38	17, 31, 102, 192	16 (0%)

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	44[A]	A	8.3
2	E	31[A]	G	7.6
2	E	9[A]	U	7.6
2	E	61[A]	C	7.6
2	E	62[A]	C	7.3

### 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 monosaccharides 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
4	PO4	B	1002	5/5	0.77	0.32	60,70,84,91	5
4	PO4	D	1002	5/5	0.90	0.30	60,61,82,89	5
4	PO4	A	1002	5/5	0.93	0.09	69,70,81,86	0
4	PO4	C	1002	5/5	0.97	0.07	65,68,80,89	0
3	PLR	C	1001	15/15	0.97	0.15	26,29,36,38	0
3	PLR	B	1001	15/15	0.98	0.14	21,28,32,32	0
3	PLR	A	1001	15/15	0.98	0.16	25,27,33,34	0
3	PLR	D	1001	15/15	0.99	0.15	23,28,32,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.