



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 14, 2020 – 06:45 pm BST

PDB ID : 2XJN  
Title : Crystal structure of Streptococcus suis Dpr with copper  
Authors : Haikarainen, T.; Thanassoulas, A.; Stavros, P.; Nounesis, G.; Haataja, S.;  
Papageorgiou, A.C.  
Deposited on : 2010-07-06  
Resolution : 2.10 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

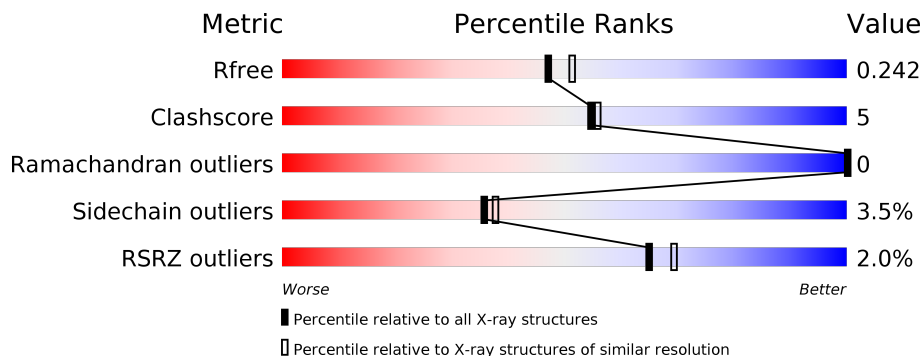
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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.







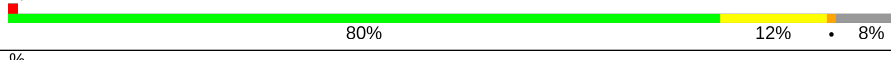
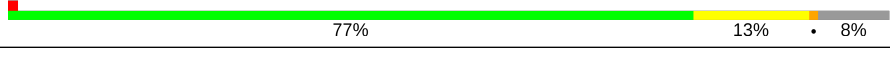
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	A	165	 78% 12% • 9%
1	B	165	 77% 13% • 8%
1	C	165	 83% 6% • 10%
1	D	165	 84% 7% • 8%
1	E	165	 79% 13% 8%
1	F	165	 82% 9% • 8%

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Mol	Chain	Length	Quality of chain
1	G	165	 <p>82% 8% • 8%</p>
1	H	165	 <p>82% 8% • 8%</p>
1	I	165	 <p>78% 13% • 8%</p>
1	J	165	 <p>82% 8% • 8%</p>
1	K	165	 <p>80% 12% • 8%</p>
1	L	165	 <p>77% 13% • 8%</p>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16040 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 DNA PROTECTION DURING STARVATION PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	150	1213	771	200	236	6	0	2	0
1	B	151	1226	781	201	237	7	0	2	0
1	C	149	1212	771	202	233	6	0	2	0
1	D	151	1233	784	204	239	6	0	3	0
1	E	151	1221	777	200	238	6	0	3	0
1	F	151	1218	776	200	236	6	0	1	0
1	G	151	1233	783	205	238	7	0	3	0
1	H	151	1219	775	201	237	6	0	2	0
1	I	151	1220	777	200	237	6	0	2	0
1	J	151	1231	783	201	241	6	0	3	0
1	K	152	1238	787	202	243	6	0	3	0
1	L	151	1237	786	205	240	6	0	3	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Cu	0	0
			1	1		
2	J	1	Total	Cu	0	0
			1	1		

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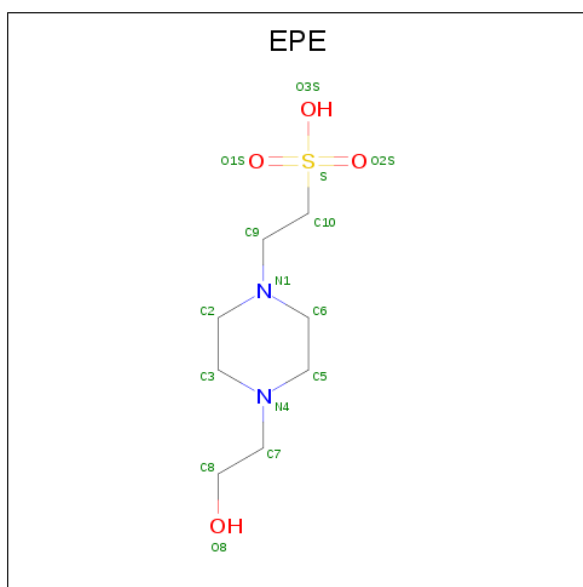
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Cu 1 1	0	0
2	K	1	Total Cu 1 1	0	0
2	E	1	Total Cu 1 1	0	0
2	H	1	Total Cu 1 1	0	0
2	B	1	Total Cu 1 1	0	0
2	I	1	Total Cu 1 1	0	0
2	C	1	Total Cu 1 1	0	0
2	A	1	Total Cu 1 1	0	0
2	L	1	Total Cu 1 1	0	0
2	F	1	Total Cu 1 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Cl 1 1	0	0
3	I	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	E	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	I	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	K	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Ca	0	0
			1	1		
5	J	1	Total	Ca	0	0
			1	1		
5	I	1	Total	Ca	0	0
			1	1		
5	L	1	Total	Ca	0	0
			1	1		
5	F	1	Total	Ca	0	0
			1	1		

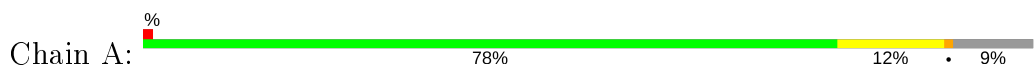
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	110	Total O 110 110	0	0
6	B	122	Total O 122 122	0	0
6	C	90	Total O 90 90	0	0
6	D	129	Total O 129 129	0	0
6	E	87	Total O 87 87	0	0
6	F	107	Total O 107 107	0	0
6	G	100	Total O 100 100	0	0
6	H	92	Total O 92 92	0	0
6	I	110	Total O 110 110	0	0
6	J	90	Total O 90 90	0	0
6	K	129	Total O 129 129	0	0
6	L	91	Total O 91 91	0	0

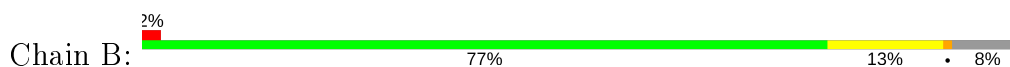
### 3 Residue-property plots [i](#)

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.

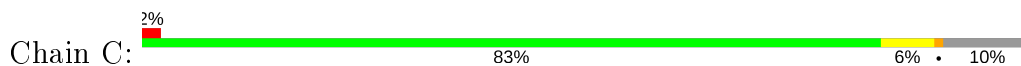
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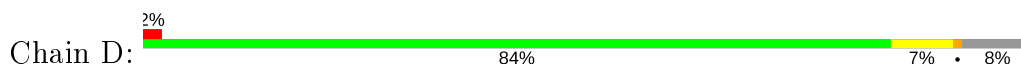
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



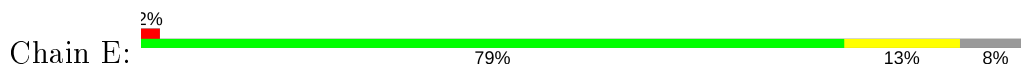
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

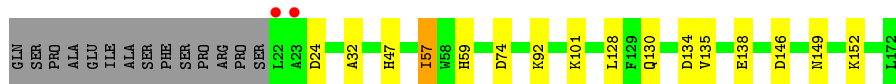
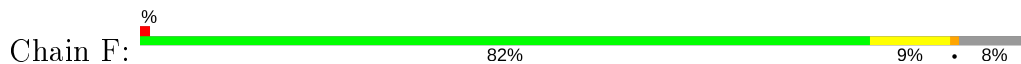


- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

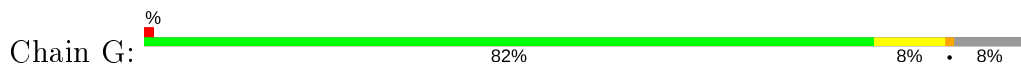




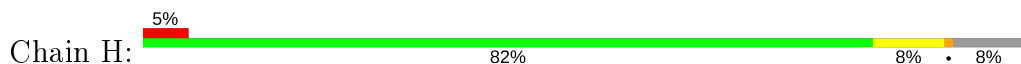
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



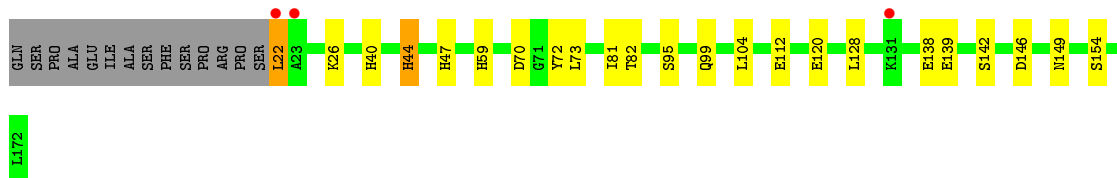
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



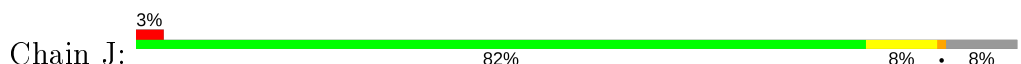
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



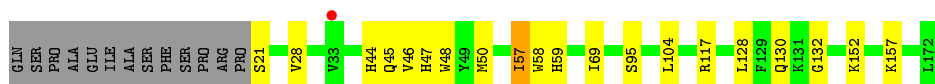
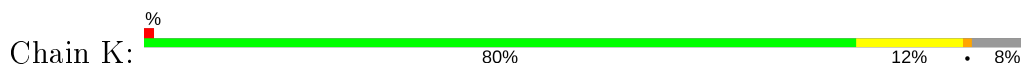
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

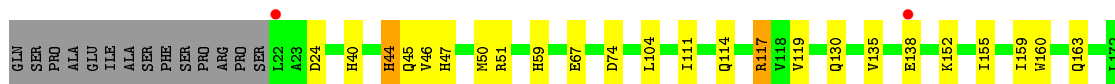


• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.84Å 137.71Å 142.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.76 – 2.10 24.76 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.76-2.10) 98.7 (24.76-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.55 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.4.0078	Depositor
R, $R_{free}$	0.160 , 0.211 0.195 , 0.242	Depositor DCC
$R_{free}$ test set	5932 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.1	Xtrriage
Anisotropy	0.178	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 29.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for -h,l,k	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16040	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.38% 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: CA, EPE, CU, CL

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	0.69	0/1242	0.68	0/1677
1	B	0.71	0/1251	0.69	1/1688 (0.1%)
1	C	0.63	0/1237	0.64	1/1669 (0.1%)
1	D	0.78	1/1262 (0.1%)	0.69	1/1703 (0.1%)
1	E	0.62	0/1250	0.64	0/1689
1	F	0.71	0/1243	0.64	0/1678
1	G	0.64	0/1258	0.65	0/1697
1	H	0.63	0/1244	0.63	0/1680
1	I	0.76	1/1249 (0.1%)	0.68	0/1686
1	J	0.69	0/1260	0.66	1/1701 (0.1%)
1	K	0.73	0/1267	0.69	0/1710
1	L	0.66	0/1262	0.67	1/1703 (0.1%)
All	All	0.69	2/15025 (0.0%)	0.66	5/20281 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	120	GLU	CG-CD	5.45	1.60	1.51
1	I	120	GLU	CG-CD	5.04	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	73	LEU	CA-CB-CG	6.11	129.35	115.30
1	D	69	ILE	CG1-CB-CG2	-5.87	98.49	111.40
1	C	73	LEU	CA-CB-CG	5.72	128.47	115.30
1	B	73	LEU	CA-CB-CG	5.64	128.28	115.30
1	L	51	ARG	NE-CZ-NH2	-5.45	117.58	120.30

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	1213	0	1168	18	0
1	B	1226	0	1187	22	0
1	C	1212	0	1171	7	0
1	D	1233	0	1191	13	0
1	E	1221	0	1170	13	0
1	F	1218	0	1179	13	0
1	G	1233	0	1188	14	0
1	H	1219	0	1169	17	0
1	I	1220	0	1180	13	0
1	J	1231	0	1184	16	0
1	K	1238	0	1191	15	0
1	L	1237	0	1194	22	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
4	B	15	0	17	1	0
4	E	15	0	17	0	0
4	I	15	0	17	0	0
4	K	15	0	17	0	0
5	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	L	1	0	0	0	0
6	A	110	0	0	2	0
6	B	122	0	0	0	0
6	C	90	0	0	1	0
6	D	129	0	0	3	0
6	E	87	0	0	2	0
6	F	107	0	0	1	0
6	G	100	0	0	4	0
6	H	92	0	0	2	0
6	I	110	0	0	3	0
6	J	90	0	0	2	0
6	K	129	0	0	2	0
6	L	91	0	0	0	0
All	All	16040	0	14240	150	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 5.

The worst 5 of 150 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:57:ILE:HD11	1:J:57:ILE:HD11	1.26	1.17
1:L:117[A]:ARG:HG3	1:L:117[A]:ARG:HH21	1.00	1.15
1:B:57:ILE:HD11	1:J:57:ILE:CD1	1.80	1.09
1:D:117[B]:ARG:HG3	1:D:117[B]:ARG:HH11	1.14	1.07
1:A:57:ILE:HD11	1:H:57:ILE:HG13	1.05	1.04

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	A	150/165 (91%)	149 (99%)	1 (1%)	0	100	100
1	B	151/165 (92%)	149 (99%)	2 (1%)	0	100	100
1	C	149/165 (90%)	148 (99%)	1 (1%)	0	100	100
1	D	152/165 (92%)	151 (99%)	1 (1%)	0	100	100
1	E	152/165 (92%)	151 (99%)	1 (1%)	0	100	100
1	F	150/165 (91%)	149 (99%)	1 (1%)	0	100	100
1	G	152/165 (92%)	150 (99%)	2 (1%)	0	100	100
1	H	151/165 (92%)	150 (99%)	1 (1%)	0	100	100
1	I	151/165 (92%)	150 (99%)	1 (1%)	0	100	100
1	J	152/165 (92%)	151 (99%)	1 (1%)	0	100	100
1	K	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
1	L	152/165 (92%)	151 (99%)	1 (1%)	0	100	100
All	All	1815/1980 (92%)	1801 (99%)	14 (1%)	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	130/141 (92%)	125 (96%)	5 (4%)	33	34
1	B	131/141 (93%)	126 (96%)	5 (4%)	33	34
1	C	129/141 (92%)	125 (97%)	4 (3%)	40	43
1	D	132/141 (94%)	129 (98%)	3 (2%)	50	55
1	E	130/141 (92%)	126 (97%)	4 (3%)	40	43
1	F	130/141 (92%)	127 (98%)	3 (2%)	50	55
1	G	131/141 (93%)	127 (97%)	4 (3%)	40	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	129/141 (92%)	127 (98%)	2 (2%)	62	69
1	I	131/141 (93%)	122 (93%)	9 (7%)	15	12
1	J	132/141 (94%)	129 (98%)	3 (2%)	50	55
1	K	133/141 (94%)	125 (94%)	8 (6%)	19	16
1	L	132/141 (94%)	126 (96%)	6 (4%)	27	27
All	All	1570/1692 (93%)	1514 (96%)	56 (4%)	36	36

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	57	ILE
1	I	44	HIS
1	L	104	LEU
1	G	69	ILE
1	H	44	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	145	ASN
1	G	130	GLN
1	L	44	HIS
1	G	31	GLN
1	G	163	GLN

### 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](#)

Of 26 ligands modelled in this entry, 22 are monoatomic - leaving 4 for Mogul analysis.

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
4	EPE	I	1173	-	15,15,15	0.92	1 (6%)	18,20,20	2.31	8 (44%)
4	EPE	K	1173	-	15,15,15	1.27	1 (6%)	18,20,20	2.87	6 (33%)
4	EPE	B	1173	-	15,15,15	0.90	1 (6%)	18,20,20	2.58	6 (33%)
4	EPE	E	1173	-	15,15,15	1.08	1 (6%)	18,20,20	2.05	4 (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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EPE	I	1173	-	-	2/9/19/19	0/1/1/1
4	EPE	K	1173	-	-	4/9/19/19	0/1/1/1
4	EPE	B	1173	-	-	1/9/19/19	0/1/1/1
4	EPE	E	1173	-	-	6/9/19/19	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	1173	EPE	C10-S	4.42	1.83	1.77
4	E	1173	EPE	C10-S	3.71	1.82	1.77
4	I	1173	EPE	C10-S	2.73	1.81	1.77
4	B	1173	EPE	C10-S	2.61	1.81	1.77

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	1173	EPE	O1S-S-C10	8.42	117.06	106.92
4	E	1173	EPE	O1S-S-C10	5.43	113.45	106.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1173	EPE	O2S-S-C10	-5.42	100.39	106.92
4	I	1173	EPE	C5-N4-C3	5.42	121.02	108.83
4	B	1173	EPE	O3S-S-C10	4.89	113.67	105.77

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	K	1173	EPE	C9-C10-S-O2S
4	B	1173	EPE	C8-C7-N4-C5
4	E	1173	EPE	N4-C7-C8-O8
4	K	1173	EPE	C8-C7-N4-C5
4	E	1173	EPE	C9-C10-S-O3S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1173	EPE	1	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	150/165 (90%)	0.10	1 (0%) 87 89	21, 28, 38, 46	0
1	B	151/165 (91%)	0.10	4 (2%) 56 61	18, 24, 39, 71	0
1	C	149/165 (90%)	0.19	3 (2%) 65 69	25, 31, 45, 51	0
1	D	151/165 (91%)	0.04	3 (1%) 65 69	18, 23, 33, 41	0
1	E	151/165 (91%)	0.21	3 (1%) 65 69	27, 33, 49, 74	0
1	F	151/165 (91%)	0.15	2 (1%) 77 80	19, 25, 39, 53	0
1	G	151/165 (91%)	0.11	2 (1%) 77 80	23, 31, 45, 73	0
1	H	151/165 (91%)	0.21	8 (5%) 26 32	22, 30, 48, 57	0
1	I	151/165 (91%)	0.11	3 (1%) 65 69	18, 28, 44, 56	0
1	J	151/165 (91%)	0.11	5 (3%) 46 53	21, 31, 46, 65	0
1	K	152/165 (92%)	-0.00	1 (0%) 87 89	19, 25, 37, 47	0
1	L	151/165 (91%)	0.07	2 (1%) 77 80	22, 31, 45, 52	0
All	All	1810/1980 (91%)	0.12	37 (2%) 65 69	18, 29, 45, 74	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	22	LEU	4.7
1	H	22	LEU	4.5
1	H	23	ALA	4.5
1	F	23	ALA	4.4
1	G	23	ALA	4.1

### 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
5	CA	J	1174	1/1	0.94	0.27	30,30,30,30	0
4	EPE	B	1173	15/15	0.95	0.17	15,23,30,31	0
4	EPE	E	1173	15/15	0.95	0.24	13,21,28,29	0
5	CA	I	1176	1/1	0.95	0.25	26,26,26,26	0
4	EPE	K	1173	15/15	0.96	0.16	13,20,22,23	0
5	CA	L	1174	1/1	0.96	0.27	24,24,24,24	0
4	EPE	I	1173	15/15	0.96	0.17	12,18,27,28	0
5	CA	H	1175	1/1	0.97	0.17	29,29,29,29	0
3	CL	A	1174	1/1	0.97	0.22	19,19,19,19	0
5	CA	F	1174	1/1	0.97	0.15	12,12,12,12	0
2	CU	C	1173	1/1	0.97	0.10	16,16,16,16	1
3	CL	I	1175	1/1	0.97	0.20	22,22,22,22	0
2	CU	L	1173	1/1	0.98	0.08	16,16,16,16	1
3	CL	F	1175	1/1	0.98	0.23	22,22,22,22	0
2	CU	H	1173	1/1	0.98	0.07	16,16,16,16	1
2	CU	E	1174	1/1	0.98	0.11	16,16,16,16	1
2	CU	J	1173	1/1	0.99	0.15	13,13,13,13	1
2	CU	K	1174	1/1	0.99	0.05	15,15,15,15	1
2	CU	D	1173	1/1	0.99	0.04	16,16,16,16	1
2	CU	I	1174	1/1	0.99	0.05	17,17,17,17	1
2	CU	B	1174	1/1	0.99	0.04	16,16,16,16	1
3	CL	H	1174	1/1	0.99	0.22	19,19,19,19	0
3	CL	D	1174	1/1	0.99	0.16	20,20,20,20	0
2	CU	G	1173	1/1	0.99	0.10	18,18,18,18	1
2	CU	F	1173	1/1	0.99	0.16	7,7,7,7	1
2	CU	A	1173	1/1	0.99	0.18	10,10,10,10	1

### 6.5 Other polymers [i](#)

There are no such residues in this entry.