



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:18 PM GMT

PDB ID : 4XS8  
Title : Salmonella typhimurium AhpC E49Q mutant  
Authors : Perkins, A.; Nelson, K.; Parsonage, D.; Poole, L.; Karplus, P.A.  
Deposited on : 2015-01-22  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

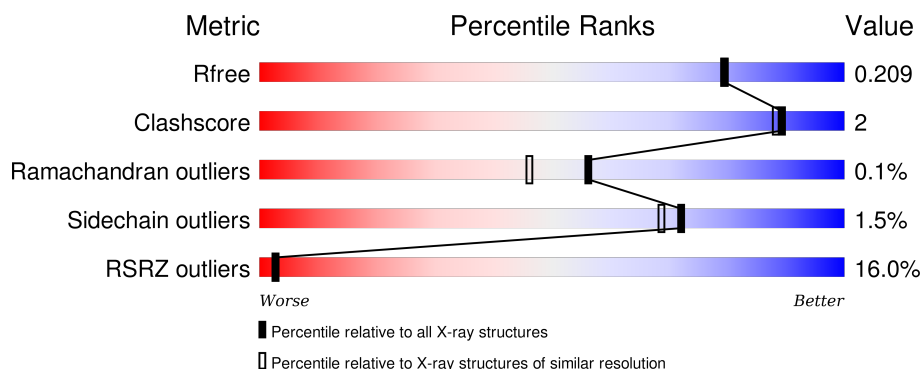
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	186	<div> <div>12%</div> <div>82%</div> <div>6% • 11%</div> </div>
1	C	186	<div> <div>11%</div> <div>82%</div> <div>5% 12%</div> </div>
1	D	186	<div> <div>10%</div> <div>84%</div> <div>• • 12%</div> </div>
1	E	186	<div> <div>27%</div> <div>78%</div> <div>9% 13%</div> </div>
2	B	186	<div> <div>9%</div> <div>83%</div> <div>5% 12%</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
3	CL	A	203	-	-	-	X
3	CL	B	204[A]	-	-	-	X
3	CL	B	204[B]	-	-	-	X
3	CL	E	202[A]	-	-	-	X
3	CL	E	202[B]	-	-	-	X
4	K	D	202	-	-	-	X
5	NA	B	203	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13517 atoms, of which 6356 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 Alkyl hydroperoxide reductase subunit C.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	165	Total	C	H	N	O	S	0	6	0
			2607	840	1282	222	259	4			
1	C	163	Total	C	H	N	O	S	0	7	0
			2586	836	1265	219	263	3			
1	D	164	Total	C	H	N	O	S	0	4	0
			2573	831	1263	219	257	3			
1	E	162	Total	C	H	N	O	S	0	0	0
			2496	807	1224	214	248	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	GLN	GLU	engineered mutation	UNP P0A251
C	49	GLN	GLU	engineered mutation	UNP P0A251
D	49	GLN	GLU	engineered mutation	UNP P0A251
E	49	GLN	GLU	engineered mutation	UNP P0A251

- Molecule 2 is a protein called Alkyl hydroperoxide reductase subunit C.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	164	Total	C	H	N	O	S	0	13	0
			2693	873	1322	227	267	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	49	GLN	GLU	engineered mutation	UNP P0A251

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Cl 3 3	0	1
3	A	2	Total Cl 2 2	0	0
3	D	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	E	2	Total Cl 3 3	0	1

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total K 1 1	0	0
4	A	1	Total K 1 1	0	0
4	D	1	Total K 1 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0

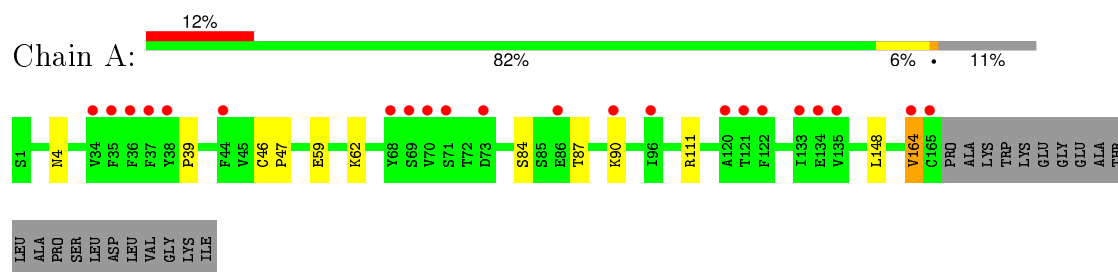
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	128	Total O 129 129	0	1
6	B	137	Total O 140 140	0	3
6	C	124	Total O 126 126	0	2
6	D	121	Total O 122 122	0	1
6	E	31	Total O 31 31	0	0

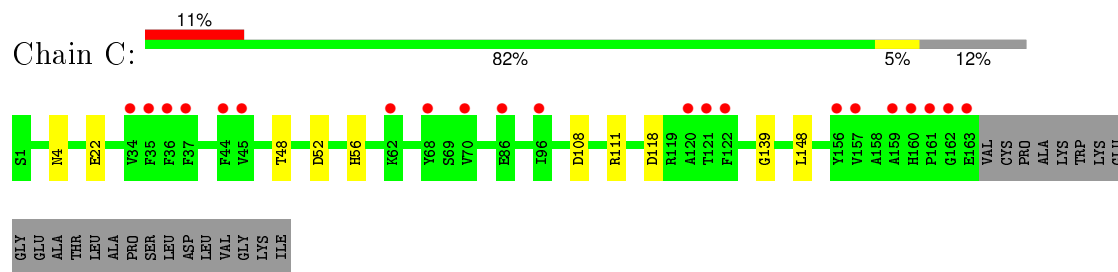
### 3 Residue-property plots

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

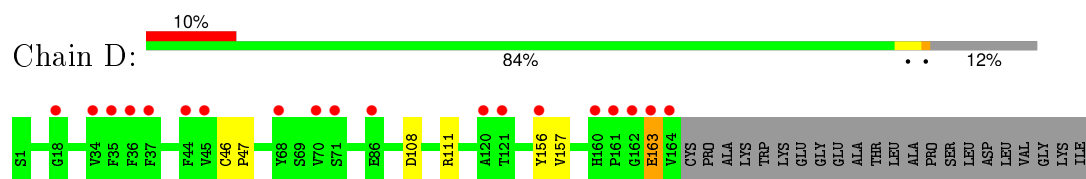
- Molecule 1: Alkyl hydroperoxide reductase subunit C



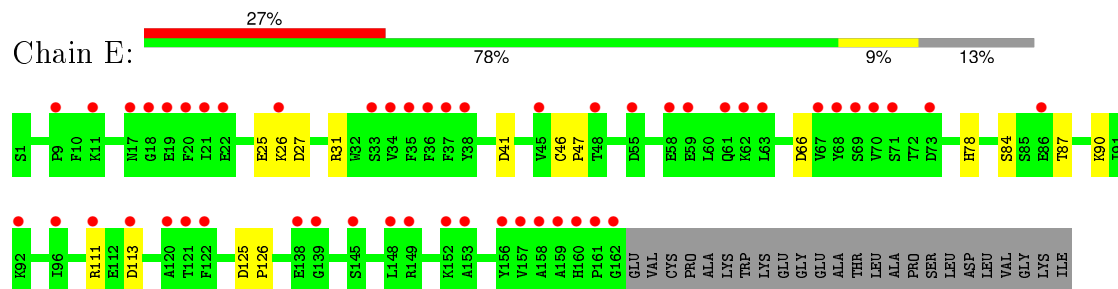
- Molecule 1: Alkyl hydroperoxide reductase subunit C



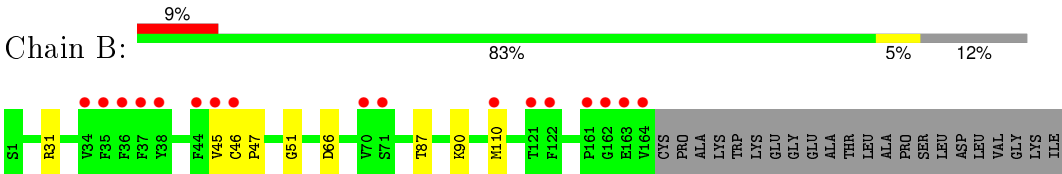
- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 2: Alkyl hydroperoxide reductase subunit C



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.90Å 171.95Å 135.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.26 – 1.90 27.97 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (27.26-1.90) 99.9 (27.97-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 1.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.172 , 0.205 0.183 , 0.209	Depositor DCC
$R_{free}$ test set	5790 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.6	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 63.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 116315 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	13517	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, CSO, K, 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	0.65	0/1370	0.66	0/1854
1	C	0.61	0/1365	0.66	0/1848
1	D	0.53	0/1347	0.60	0/1824
1	E	0.38	0/1293	0.54	0/1750
2	B	0.63	0/1428	0.72	1/1938 (0.1%)
All	All	0.57	0/6803	0.64	1/9214 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	110	MET	CG-SD-CE	-9.77	84.57	100.20

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	1325	1282	1254	6	0
1	C	1321	1265	1238	5	0
1	D	1310	1263	1247	4	0
1	E	1272	1224	1228	7	0
2	B	1371	1322	1298	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2	0	0	1	0
3	B	3	0	0	2	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	3	0	0	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	B	1	0	0	0	0
6	A	129	0	0	2	0
6	B	140	0	0	4	0
6	C	126	0	0	2	0
6	D	122	0	0	2	0
6	E	31	0	0	0	0
All	All	7161	6356	6265	31	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 2.

All (31) 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)
3:A:203:CL:CL	6:A:303:HOH:O	2.23	0.93
2:B:46[B]:CYS:SG	6:B:410:HOH:O	2.16	0.92
1:A:4[B]:ASN:ND2	6:A:426:HOH:O	2.14	0.79
3:B:204[A]:CL:CL	6:B:392[A]:HOH:O	2.37	0.78
6:D:396[A]:HOH:O	3:E:202[A]:CL:CL	2.42	0.73
1:D:108[A]:ASP:OD2	6:D:375:HOH:O	2.06	0.72
1:C:108[A]:ASP:OD2	6:C:401:HOH:O	2.08	0.69
1:E:111:ARG:NH1	1:E:113:ASP:OD1	2.27	0.68
1:E:25:GLU:OE2	1:E:26:LYS:NZ	2.27	0.67
1:E:87:THR:O	1:E:90:LYS:HG2	2.08	0.54
3:B:204[B]:CL:CL	6:B:392[B]:HOH:O	2.57	0.51
1:A:164:VAL:HG21	2:B:45[A]:VAL:HG12	1.94	0.49
2:B:31:ARG:NH2	6:B:301:HOH:O	2.47	0.48
1:D:156:TYR:OH	1:D:163:GLU:OE1	2.31	0.47
1:A:59:GLU:O	1:A:62[B]:LYS:HG2	2.15	0.47
2:B:87:THR:O	2:B:90:LYS:HG2	2.15	0.46
1:C:111:ARG:HG2	1:C:118:ASP:OD1	2.15	0.46
1:E:46:CSO:N	1:E:47:PRO:HD2	2.32	0.44
1:A:39:PRO:HD2	1:A:46:CSO:SG	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:31:ARG:NH1	1:E:66:ASP:OD1	2.53	0.42
2:B:46[B]:CYS:N	2:B:47[B]:PRO:HD2	2.36	0.41
1:C:139:GLY:HA3	1:D:157:VAL:HG11	2.03	0.41
1:C:52[B]:ASP:O	1:C:56:HIS:HD2	2.04	0.41
1:A:87:THR:O	1:A:90:LYS:HG2	2.21	0.40
1:E:41:ASP:OD2	1:E:78:HIS:ND1	2.50	0.40
1:D:46:CSO:N	1:D:47:PRO:CD	2.84	0.40
1:C:48:THR:HG23	6:C:403:HOH:O	2.20	0.40
2:B:47[B]:PRO:O	2:B:51:GLY:N	2.53	0.40
2:B:31:ARG:HD3	2:B:66:ASP:OD2	2.22	0.40
1:A:46:CSO:N	1:A:47:PRO:HD2	2.36	0.40
1:E:125:ASP:HB2	1:E:126:PRO:CD	2.51	0.40

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	168/186 (90%)	167 (99%)	1 (1%)	0	100	100
1	C	167/186 (90%)	165 (99%)	2 (1%)	0	100	100
1	D	165/186 (89%)	162 (98%)	2 (1%)	1 (1%)	30	17
1	E	159/186 (86%)	156 (98%)	3 (2%)	0	100	100
2	B	175/186 (94%)	173 (99%)	2 (1%)	0	100	100
All	All	834/930 (90%)	823 (99%)	10 (1%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	163	GLU

### 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	143/153 (94%)	139 (97%)	4 (3%)	51	41
1	C	142/153 (93%)	138 (97%)	4 (3%)	51	41
1	D	140/153 (92%)	139 (99%)	1 (1%)	88	88
1	E	133/153 (87%)	131 (98%)	2 (2%)	72	69
2	B	150/154 (97%)	150 (100%)	0	100	100
All	All	708/766 (92%)	697 (98%)	11 (2%)	72	66

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	SER
1	A	111	ARG
1	A	148	LEU
1	A	164	VAL
1	C	4	ASN
1	C	22[A]	GLU
1	C	22[B]	GLU
1	C	148	LEU
1	D	111	ARG
1	E	27	ASP
1	E	84	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	56	HIS
1	D	160	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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$
1	CSO	A	46	1	3,6,7	0.80	0	2,6,8	2.01	1 (50%)
1	CSO	C	46	1	3,6,7	0.59	0	2,6,8	2.00	1 (50%)
1	CSO	D	46	1	3,6,7	0.76	0	2,6,8	2.08	1 (50%)
1	CSO	E	46	1	3,6,7	0.63	0	2,6,8	1.88	1 (50%)

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
1	CSO	A	46	1	-	0/1/5/7	0/0/0/0
1	CSO	C	46	1	-	0/1/5/7	0/0/0/0
1	CSO	D	46	1	-	0/1/5/7	0/0/0/0
1	CSO	E	46	1	-	0/1/5/7	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	46	CSO	O-C-CA	-2.52	118.97	125.72
1	C	46	CSO	O-C-CA	-2.51	119.00	125.72
1	A	46	CSO	O-C-CA	-2.50	119.02	125.72
1	E	46	CSO	O-C-CA	-2.37	119.36	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	46	CSO	2	0
1	D	46	CSO	1	0
1	E	46	CSO	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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

### 6.1 Protein, DNA and RNA chains

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	164/186 (88%)	0.40	22 (13%) 4 5	27, 45, 85, 143	0
1	C	162/186 (87%)	0.47	21 (12%) 5 5	29, 48, 84, 154	0
1	D	163/186 (87%)	0.47	19 (11%) 6 7	36, 50, 86, 152	0
1	E	161/186 (86%)	1.30	51 (31%) 1 0	48, 77, 110, 133	0
2	B	164/186 (88%)	0.36	17 (10%) 8 9	28, 43, 78, 151	0
All	All	814/930 (87%)	0.60	130 (15%) 3 3	27, 52, 99, 154	0

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	164	VAL	10.4
2	B	164	VAL	8.4
1	E	156	TYR	7.1
1	E	159	ALA	6.7
2	B	162	GLY	6.4
1	D	163	GLU	6.0
1	D	162	GLY	5.8
1	E	36	PHE	5.8
1	E	161	PRO	5.7
1	E	70	VAL	5.7
2	B	46[A]	CYS	5.7
1	E	45	VAL	5.6
1	E	160	HIS	5.5
1	E	35	PHE	5.3
1	E	157	VAL	5.3
1	C	44	PHE	5.0
1	E	38	TYR	4.9
2	B	163	GLU	4.9
1	C	162	GLY	4.8
1	E	34	VAL	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	37	PHE	4.5
1	C	156	TYR	4.5
1	E	162	GLY	4.5
1	A	70	VAL	4.4
2	B	44[A]	PHE	4.3
1	C	163	GLU	4.3
1	C	45	VAL	4.2
1	D	44	PHE	4.2
1	E	37	PHE	4.2
1	E	58	GLU	4.1
1	D	161	PRO	4.0
1	E	69	SER	4.0
1	E	148	LEU	3.8
1	E	122	PHE	3.8
1	E	62	LYS	3.8
1	A	122	PHE	3.7
1	D	45	VAL	3.7
1	E	121	THR	3.7
1	A	165	CYS	3.7
1	E	18	GLY	3.6
1	A	120	ALA	3.6
1	E	138	GLU	3.6
1	E	120	ALA	3.5
1	C	70	VAL	3.5
1	D	86	GLU	3.5
1	C	157	VAL	3.5
1	C	161	PRO	3.4
1	A	164	VAL	3.4
1	C	35	PHE	3.4
1	C	37	PHE	3.4
1	A	35	PHE	3.4
1	A	44	PHE	3.3
1	E	158	ALA	3.3
1	C	68	TYR	3.3
1	A	36	PHE	3.3
1	C	159	ALA	3.2
1	E	67	VAL	3.2
1	D	70	VAL	3.2
1	A	96	ILE	3.1
1	E	68	TYR	3.1
1	E	20	PHE	3.1
1	C	160	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
1	E	152	LYS	3.1
1	C	34	VAL	3.0
1	D	18	GLY	3.0
2	B	37	PHE	3.0
1	E	149	ARG	3.0
1	E	153	ALA	3.0
1	E	26	LYS	2.9
1	E	71	SER	2.9
1	A	121	THR	2.9
1	E	96	ILE	2.9
1	D	35	PHE	2.9
1	D	36	PHE	2.9
2	B	35	PHE	2.8
1	C	86[A]	GLU	2.8
1	E	145	SER	2.8
2	B	70	VAL	2.8
1	C	122	PHE	2.8
1	C	121	THR	2.7
1	D	160	HIS	2.7
1	A	69	SER	2.7
1	D	156	TYR	2.7
1	E	111	ARG	2.7
2	B	161	PRO	2.6
1	E	21	ILE	2.6
1	C	62	LYS	2.6
1	D	121	THR	2.6
1	E	63	LEU	2.6
1	D	34	VAL	2.6
1	D	68	TYR	2.6
1	D	37	PHE	2.5
1	A	71	SER	2.5
1	A	34	VAL	2.5
1	A	38	TYR	2.5
1	E	11	LYS	2.5
1	E	86	GLU	2.5
1	A	133	ILE	2.5
1	A	68	TYR	2.5
2	B	38	TYR	2.4
2	B	122	PHE	2.4
2	B	36	PHE	2.4
1	D	120	ALA	2.4
1	A	73	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	17	ASN	2.3
1	E	139	GLY	2.3
1	D	71	SER	2.3
1	E	19	GLU	2.3
1	E	73	ASP	2.3
1	E	113	ASP	2.3
2	B	110	MET	2.2
1	C	36	PHE	2.2
2	B	45[A]	VAL	2.2
1	E	59	GLU	2.2
1	A	90	LYS	2.2
1	E	33	SER	2.2
2	B	71	SER	2.2
1	C	120	ALA	2.2
1	E	9	PRO	2.1
1	C	96	ILE	2.1
1	E	48	THR	2.1
1	E	61	GLN	2.1
1	A	86	GLU	2.1
1	A	135	VAL	2.1
2	B	34	VAL	2.1
1	E	92	LYS	2.1
2	B	121	THR	2.1
1	A	134	GLU	2.1
1	E	22	GLU	2.0
1	E	55	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	CSO	E	46	7/8	0.87	0.18	-	52,97,109,213	1
1	CSO	C	46	7/8	0.80	0.20	-	45,68,101,229	1
1	CSO	A	46	7/8	0.82	0.21	-	47,86,117,197	2
1	CSO	D	46	7/8	0.91	0.14	-	52,75,97,191	1

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	CL	A	203	1/1	-0.32	2.22	231.44	272,272,272,272	1
3	CL	E	202[A]	1/1	0.66	1.44	57.68	260,260,260,260	1
3	CL	E	202[B]	1/1	0.66	1.44	52.40	224,224,224,224	1
3	CL	B	204[A]	1/1	0.68	0.66	29.23	232,232,232,232	1
3	CL	B	204[B]	1/1	0.68	0.66	11.78	196,196,196,196	1
5	NA	B	203	1/1	0.40	0.34	4.62	92,92,92,92	0
4	K	D	202	1/1	0.60	0.34	3.53	102,102,102,102	0
4	K	B	202	1/1	0.95	0.19	0.52	72,72,72,72	0
3	CL	A	201	1/1	1.00	0.10	-0.51	43,43,43,43	0
3	CL	E	201	1/1	0.97	0.07	-0.78	70,70,70,70	0
3	CL	B	201	1/1	1.00	0.08	-0.80	44,44,44,44	0
3	CL	D	201	1/1	0.97	0.07	-1.44	52,52,52,52	0
3	CL	C	201	1/1	0.99	0.05	-1.55	50,50,50,50	0
4	K	A	202	1/1	0.90	0.18	-	79,79,79,79	1

### 6.5 Other polymers ⓘ

There are no such residues in this entry.