



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:28 am GMT

PDB ID : 4XTS
Title : Salmonella typhimurium AhpC T43A mutant
Authors : Perkins, A.; Nelson, K.; Parsonage, D.; Poole, L.; Karplus, P.A.
Deposited on : 2015-01-24
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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

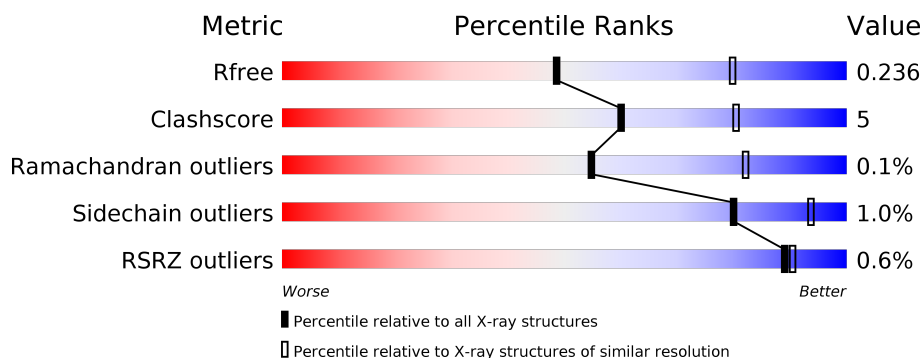
1 Overall quality at a glance

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.




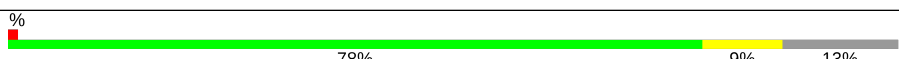
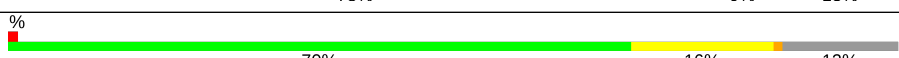
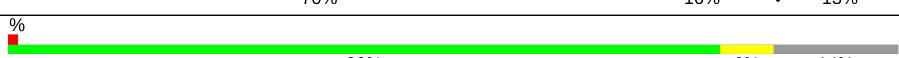
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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 ≥ 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 style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 77%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 77% 9% • 14% </div> </div>
1	B	186	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 18%, green 69%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 69% 18% 13% </div> </div>
1	C	186	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 73%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 73% 14% • 13% </div> </div>
1	D	186	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 74%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 74% 12% • 13% </div> </div>
1	E	186	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 9%, green 75%, grey 14%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 75% 9% • 14% </div> </div>
1	F	186	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 7%, green 78%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: small;"> % 78% 7% • 13% </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	186	
1	H	186	
1	I	186	
1	J	186	
1	K	186	
1	L	186	
1	M	186	
1	N	186	
1	O	186	
1	P	186	
1	Q	186	
1	R	186	
1	S	186	
1	T	186	

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	CL	A	201	-	-	-	X
2	CL	B	201	-	-	-	X
2	CL	E	201	-	-	-	X
2	CL	G	201	-	-	-	X
2	CL	K	201	-	-	-	X
2	CL	K	202	-	-	-	X
2	CL	M	201	-	-	-	X
2	CL	N	201	-	-	-	X
2	CL	O	201	-	-	-	X
2	CL	S	201	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25877 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 Alkyl hydroperoxide reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	0	0	0
			1261	804	211	243	3			
1	B	162	Total	C	N	O	S	0	1	0
			1281	816	213	249	3			
1	C	162	Total	C	N	O	S	0	1	0
			1283	816	214	250	3			
1	D	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	E	160	Total	C	N	O	S	0	1	0
			1272	809	212	248	3			
1	F	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	G	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	H	161	Total	C	N	O	S	0	1	0
			1276	813	212	248	3			
1	I	161	Total	C	N	O	S	0	1	0
			1276	813	212	248	3			
1	J	161	Total	C	N	O	S	0	2	0
			1288	819	217	248	4			
1	K	160	Total	C	N	O	S	0	0	0
			1264	805	211	245	3			
1	L	162	Total	C	N	O	S	0	0	0
			1275	812	213	247	3			
1	M	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	N	160	Total	C	N	O	S	0	0	0
			1261	804	211	243	3			
1	O	160	Total	C	N	O	S	0	0	0
			1264	805	211	245	3			
1	P	160	Total	C	N	O	S	0	0	0
			1264	805	211	245	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	R	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	S	161	Total	C	N	O	S	0	0	0
			1271	810	212	246	3			
1	T	160	Total	C	N	O	S	0	0	0
			1264	805	211	245	3			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	ALA	THR	engineered mutation	UNP P0A251
B	43	ALA	THR	engineered mutation	UNP P0A251
C	43	ALA	THR	engineered mutation	UNP P0A251
D	43	ALA	THR	engineered mutation	UNP P0A251
E	43	ALA	THR	engineered mutation	UNP P0A251
F	43	ALA	THR	engineered mutation	UNP P0A251
G	43	ALA	THR	engineered mutation	UNP P0A251
H	43	ALA	THR	engineered mutation	UNP P0A251
I	43	ALA	THR	engineered mutation	UNP P0A251
J	43	ALA	THR	engineered mutation	UNP P0A251
K	43	ALA	THR	engineered mutation	UNP P0A251
L	43	ALA	THR	engineered mutation	UNP P0A251
M	43	ALA	THR	engineered mutation	UNP P0A251
N	43	ALA	THR	engineered mutation	UNP P0A251
O	43	ALA	THR	engineered mutation	UNP P0A251
P	43	ALA	THR	engineered mutation	UNP P0A251
Q	43	ALA	THR	engineered mutation	UNP P0A251
R	43	ALA	THR	engineered mutation	UNP P0A251
S	43	ALA	THR	engineered mutation	UNP P0A251
T	43	ALA	THR	engineered mutation	UNP P0A251

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total 1	Cl 1	0	0
2	K	2	Total 2	Cl 2	0	0
2	E	1	Total 1	Cl 1	0	0
2	H	2	Total 2	Cl 2	0	0
2	B	1	Total 1	Cl 1	0	0
2	I	1	Total 1	Cl 1	0	0
2	C	2	Total 2	Cl 2	0	0
2	A	2	Total 2	Cl 2	0	0
2	T	1	Total 1	Cl 1	0	0
2	N	1	Total 1	Cl 1	0	0
2	O	2	Total 2	Cl 2	0	0
2	R	2	Total 2	Cl 2	0	0
2	L	2	Total 2	Cl 2	0	0
2	S	1	Total 1	Cl 1	0	0
2	F	1	Total 1	Cl 1	0	0
2	M	1	Total 1	Cl 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total 15	O 15	0	0
3	B	11	Total 11	O 11	0	0
3	C	27	Total 27	O 27	0	0

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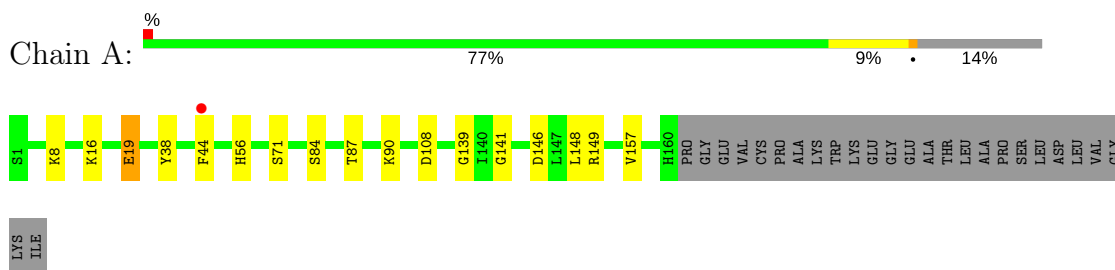
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	27	Total 27	O 27	0	0
3	E	32	Total 32	O 32	0	0
3	F	27	Total 28	O 28	0	1
3	G	21	Total 21	O 21	0	0
3	H	25	Total 25	O 25	0	0
3	I	12	Total 12	O 12	0	0
3	J	29	Total 29	O 29	0	0
3	K	15	Total 16	O 16	0	1
3	L	22	Total 23	O 23	0	1
3	M	9	Total 9	O 9	0	0
3	N	25	Total 26	O 26	0	1
3	O	16	Total 16	O 16	0	0
3	P	17	Total 17	O 17	0	0
3	Q	22	Total 22	O 22	0	0
3	R	15	Total 15	O 15	0	0
3	S	23	Total 23	O 23	0	0
3	T	30	Total 30	O 30	0	0

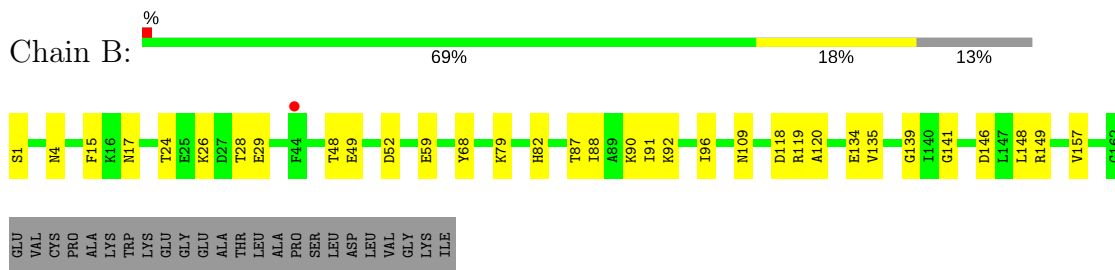
3 Residue-property plots

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

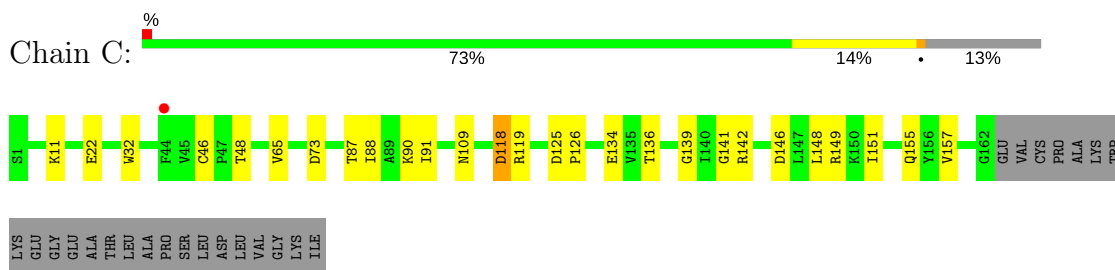
• Molecule 1: Alkyl hydroperoxide reductase subunit C



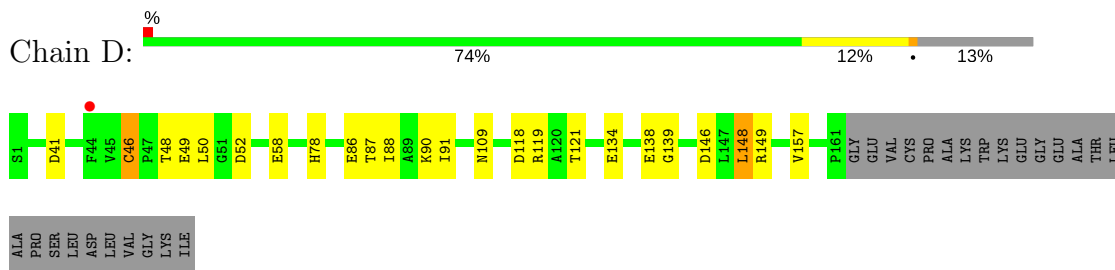
• Molecule 1: Alkyl hydroperoxide reductase subunit C



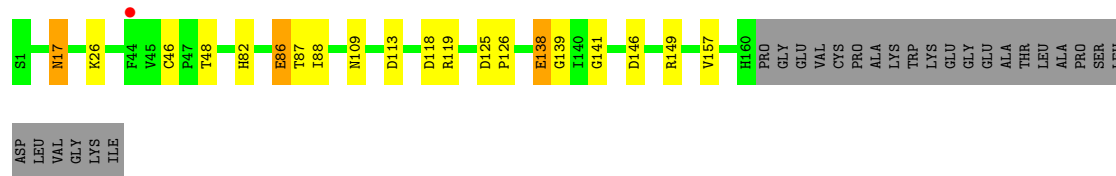
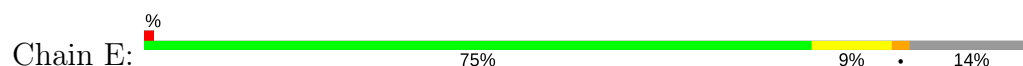
• Molecule 1: Alkyl hydroperoxide reductase subunit C



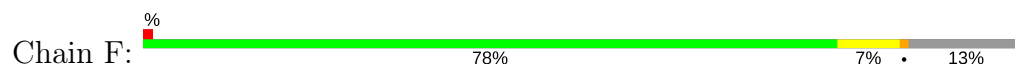
• Molecule 1: Alkyl hydroperoxide reductase subunit C



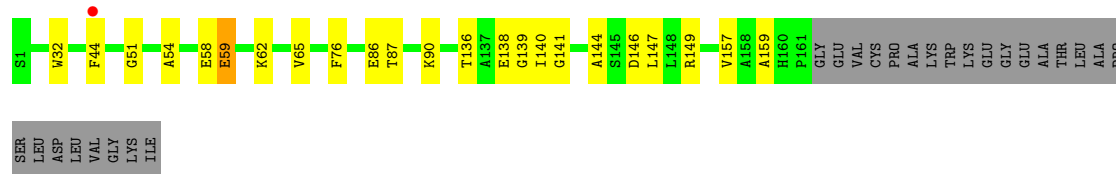
● Molecule 1: Alkyl hydroperoxide reductase subunit C



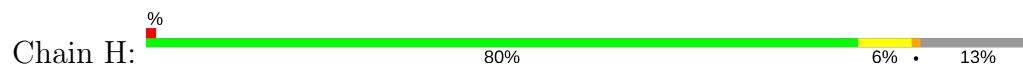
● Molecule 1: Alkyl hydroperoxide reductase subunit C



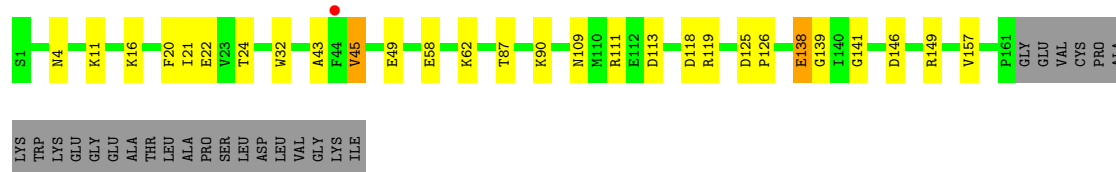
● Molecule 1: Alkyl hydroperoxide reductase subunit C



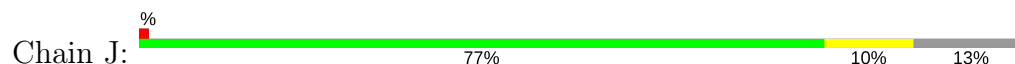
● Molecule 1: Alkyl hydroperoxide reductase subunit C



● Molecule 1: Alkyl hydroperoxide reductase subunit C



● Molecule 1: Alkyl hydroperoxide reductase subunit C



GLY
LYS
ILE


- Molecule 1: Alkyl hydroperoxide reductase subunit C

Chain K:  74% 10% 14%

S1 T24 E25 K26 C46 P47 T48 E58 E59 L60 Q61 K62 N109 D118 R119 T136 A137 E138 G139 I140 G141 D146 R149 Y156 V157 A158 A159 H160 PRO GLY GLU VAL CYS VAL PRO ALA LYS TRP LYS GLY GLU ALA THR ALA PRO SER LEU ASP LEU VAL

GLY
LYS
ILE

- Molecule 1: Alkyl hydroperoxide reductase subunit C

Chain L:  % 78% 9% 13%


S1 D41 C46 E49 V65 H78 H82 I88 I96 R119 T136 A137 E138 G139 I140 G141 D146 R149 K150 I151 V157 G162 VAL CYS PRO ALA LYS TRP LYS GLU GLY ALA THR LEU ALA PRO SER LEU ASP LEU VAL GLY ILE

- Molecule 1: Alkyl hydroperoxide reductase subunit C

Chain M:  % 70% 16% 13%

S1 K11 K16 E19 E22 K26 D41 F44 V45 C46 P47 V63 E59 L63 H78 H82 E86 T87 I88 A89 K90 I91 K92 M109 R110 R111 E112 D113 D118 R119 A120 T121 D125 P126 E134 E138 G139 D146 R149 V157 P161 GLY VAL CYS PRO ALA TRP LYS LYS GLY ALA THR LEU PRO SER ASP LEU VAL GLY ILE

- Molecule 1: Alkyl hydroperoxide reductase subunit C

Chain N:  % 80% 6% 14%

S1 F44 L50 T87 K90 I91 M109 D118 E138 G139 I140 G141 S145 V157 H160 PRO GLY VAL CYS PRO ALA LYS TRP LYS GLU GLU ALA THR LEU PRO SER LEU ASP VAL GLY ILE

- Molecule 1: Alkyl hydroperoxide reductase subunit C

Chain O:  71% 14% 14%

S1 A43 F44 V45 C46 P47 T48 E49 E59 L63 S71 R111 E112 D113 R119 V123 V124 D125 P126 A132 T133 E134 V135 T136 A137 E138 G139 I140 G141 R142 D146 L147 L148 R149 K152 V157 A158 A159 H160 PRO GLY GLU VAL CYS PRO ALA LYS TRP LYS

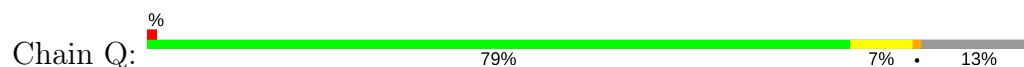
GLU
GLY
ALA
THR
LEU
ALA
PRO
SER
LEU
ASP
LEU
VAL
GLY
LYS
ILE

- Molecule 1: Alkyl hydroperoxide reductase subunit C

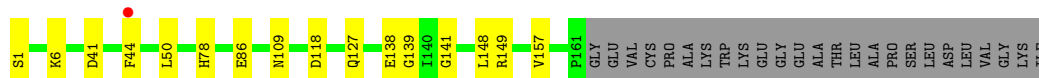
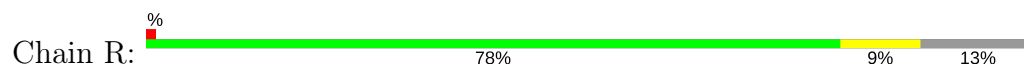
Chain P:  % 77% 8% 14%



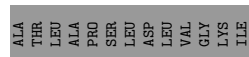
- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	107.65Å 109.45Å 119.04Å 93.33° 110.02° 114.00°	Depositor
Resolution (Å)	63.51 – 2.70 63.51 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.8 (63.51-2.70) 88.2 (63.51-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.190 , 0.245 0.177 , 0.236	Depositor DCC
R_{free} test set	5944 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	25877	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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:
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	0.57	0/1290	0.81	1/1747 (0.1%)
1	B	0.53	0/1314	0.82	0/1780
1	C	0.54	0/1313	0.77	0/1779
1	D	0.61	0/1301	0.86	2/1763 (0.1%)
1	E	0.66	1/1301 (0.1%)	0.82	2/1762 (0.1%)
1	F	0.60	0/1301	0.90	5/1763 (0.3%)
1	G	0.63	0/1301	0.83	0/1763
1	H	0.59	0/1309	0.84	3/1774 (0.2%)
1	I	0.60	0/1309	0.84	1/1774 (0.1%)
1	J	0.60	0/1318	0.80	1/1786 (0.1%)
1	K	0.58	0/1293	0.83	4/1751 (0.2%)
1	L	0.56	0/1305	0.77	1/1768 (0.1%)
1	M	0.57	0/1301	0.82	0/1763
1	N	0.54	0/1290	0.77	0/1747
1	O	0.59	0/1293	0.82	1/1751 (0.1%)
1	P	0.57	0/1293	0.79	2/1751 (0.1%)
1	Q	0.60	1/1301 (0.1%)	0.84	1/1763 (0.1%)
1	R	0.53	0/1301	0.82	2/1763 (0.1%)
1	S	0.65	0/1301	0.97	5/1763 (0.3%)
1	T	0.60	0/1293	0.83	2/1751 (0.1%)
All	All	0.59	2/26028 (0.0%)	0.83	33/35262 (0.1%)

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	M	0	1
1	S	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	86	GLU	CB-CG	5.33	1.62	1.52
1	Q	86	GLU	CG-CD	5.21	1.59	1.51

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	146	ASP	CB-CG-OD2	-9.26	109.97	118.30
1	F	44	PHE	CB-CG-CD1	-9.02	114.49	120.80
1	S	146	ASP	CB-CG-OD1	8.20	125.68	118.30
1	F	44	PHE	CB-CG-CD2	8.06	126.44	120.80
1	S	45	VAL	CG1-CB-CG2	-7.56	98.81	110.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	19	GLU	Sidechain
1	S	43	ALA	Peptide

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	1261	0	1219	13	0
1	B	1281	0	1237	22	0
1	C	1283	0	1234	17	0
1	D	1271	0	1228	16	0
1	E	1272	0	1224	18	0
1	F	1271	0	1228	11	0
1	G	1271	0	1228	24	0
1	H	1276	0	1232	11	0
1	I	1276	0	1232	22	0
1	J	1288	0	1245	17	0
1	K	1264	0	1221	18	0
1	L	1275	0	1231	12	0
1	M	1271	0	1228	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	1261	0	1219	9	0
1	O	1264	0	1221	19	0
1	P	1264	0	1221	10	0
1	Q	1271	0	1228	8	0
1	R	1271	0	1228	13	0
1	S	1271	0	1228	25	0
1	T	1264	0	1221	15	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	2	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	2	0	0	0	0
2	I	1	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	2	0	0	0	0
2	P	1	0	0	0	0
2	R	2	0	0	1	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
3	A	15	0	0	0	0
3	B	11	0	0	1	0
3	C	27	0	0	1	0
3	D	27	0	0	0	0
3	E	32	0	0	0	0
3	F	28	0	0	0	0
3	G	21	0	0	0	0
3	H	25	0	0	0	0
3	I	12	0	0	0	0
3	J	29	0	0	0	0
3	K	16	0	0	0	0
3	L	23	0	0	0	0
3	M	9	0	0	0	0
3	N	26	0	0	0	0
3	O	16	0	0	0	0
3	P	17	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Q	22	0	0	1	0
3	R	15	0	0	0	0
3	S	23	0	0	1	0
3	T	30	0	0	2	0
All	All	25877	0	24553	267	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 267 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:H:157:VAL:HG11	1:I:139:GLY:HA3	1.43	1.00
1:S:4:ASN:ND2	3:S:311:HOH:O	1.98	0.96
1:A:157:VAL:HG11	1:B:139:GLY:HA3	1.48	0.95
1:F:157:VAL:HG11	1:G:139:GLY:HA3	1.46	0.93
1:C:146:ASP:OD1	1:C:149:ARG:NH1	2.03	0.92

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	158/186 (85%)	155 (98%)	3 (2%)	0	100	100
1	B	161/186 (87%)	160 (99%)	1 (1%)	0	100	100
1	C	161/186 (87%)	158 (98%)	3 (2%)	0	100	100
1	D	159/186 (86%)	157 (99%)	2 (1%)	0	100	100
1	E	159/186 (86%)	156 (98%)	2 (1%)	1 (1%)	28	56
1	F	159/186 (86%)	156 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	159/186 (86%)	156 (98%)	3 (2%)	0	100	100
1	H	160/186 (86%)	157 (98%)	3 (2%)	0	100	100
1	I	160/186 (86%)	157 (98%)	3 (2%)	0	100	100
1	J	161/186 (87%)	159 (99%)	2 (1%)	0	100	100
1	K	158/186 (85%)	155 (98%)	3 (2%)	0	100	100
1	L	160/186 (86%)	157 (98%)	3 (2%)	0	100	100
1	M	159/186 (86%)	156 (98%)	3 (2%)	0	100	100
1	N	158/186 (85%)	155 (98%)	3 (2%)	0	100	100
1	O	158/186 (85%)	155 (98%)	3 (2%)	0	100	100
1	P	158/186 (85%)	156 (99%)	2 (1%)	0	100	100
1	Q	159/186 (86%)	156 (98%)	3 (2%)	0	100	100
1	R	159/186 (86%)	156 (98%)	3 (2%)	0	100	100
1	S	159/186 (86%)	155 (98%)	3 (2%)	1 (1%)	28	56
1	T	158/186 (85%)	155 (98%)	2 (1%)	1 (1%)	28	56
All	All	3183/3720 (86%)	3127 (98%)	53 (2%)	3 (0%)	55	82

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	T	138	GLU
1	E	17	ASN
1	S	44	PHE

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	132/153 (86%)	130 (98%)	2 (2%)	70	90
1	B	135/153 (88%)	132 (98%)	3 (2%)	57	84
1	C	135/153 (88%)	133 (98%)	2 (2%)	70	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	134/153 (88%)	131 (98%)	3 (2%)	57	84
1	E	134/153 (88%)	134 (100%)	0	100	100
1	F	134/153 (88%)	133 (99%)	1 (1%)	87	96
1	G	134/153 (88%)	133 (99%)	1 (1%)	87	96
1	H	135/153 (88%)	134 (99%)	1 (1%)	87	96
1	I	135/153 (88%)	133 (98%)	2 (2%)	70	90
1	J	136/153 (89%)	134 (98%)	2 (2%)	70	90
1	K	133/153 (87%)	132 (99%)	1 (1%)	85	95
1	L	134/153 (88%)	134 (100%)	0	100	100
1	M	134/153 (88%)	132 (98%)	2 (2%)	70	90
1	N	132/153 (86%)	131 (99%)	1 (1%)	85	95
1	O	133/153 (87%)	131 (98%)	2 (2%)	70	90
1	P	133/153 (87%)	131 (98%)	2 (2%)	70	90
1	Q	134/153 (88%)	134 (100%)	0	100	100
1	R	134/153 (88%)	134 (100%)	0	100	100
1	S	134/153 (88%)	131 (98%)	3 (2%)	57	84
1	T	133/153 (87%)	132 (99%)	1 (1%)	85	95
All	All	2678/3060 (88%)	2649 (99%)	29 (1%)	80	93

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	4	ASN
1	J	46[B]	CYS
1	S	84	SER
1	I	45	VAL
1	K	62	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	13	GLN
1	L	78	HIS
1	T	56	HIS
1	T	82	HIS

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 27 ligands modelled in this entry, 27 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, 95th 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 ²)	Q<0.9
1	A	160/186 (86%)	-0.44	1 (0%) 89 90	26, 44, 72, 107	0
1	B	162/186 (87%)	-0.49	1 (0%) 89 90	26, 45, 80, 120	0
1	C	162/186 (87%)	-0.51	1 (0%) 89 90	23, 38, 73, 134	0
1	D	161/186 (86%)	-0.50	1 (0%) 89 90	23, 38, 73, 134	0
1	E	160/186 (86%)	-0.42	1 (0%) 89 90	23, 35, 68, 129	0
1	F	161/186 (86%)	-0.54	1 (0%) 89 90	23, 38, 70, 153	0
1	G	161/186 (86%)	-0.48	1 (0%) 89 90	23, 40, 74, 138	0
1	H	161/186 (86%)	-0.51	1 (0%) 89 90	22, 36, 69, 121	0
1	I	161/186 (86%)	-0.41	1 (0%) 89 90	24, 46, 79, 121	0
1	J	161/186 (86%)	-0.47	1 (0%) 89 90	23, 35, 68, 122	0
1	K	160/186 (86%)	-0.36	0 100 100	27, 50, 86, 119	0
1	L	162/186 (87%)	-0.45	1 (0%) 89 90	26, 44, 82, 114	0
1	M	161/186 (86%)	-0.27	2 (1%) 79 80	26, 55, 89, 121	0
1	N	160/186 (86%)	-0.46	1 (0%) 89 90	24, 41, 73, 127	0
1	O	160/186 (86%)	-0.38	0 100 100	26, 47, 78, 113	0
1	P	160/186 (86%)	-0.40	1 (0%) 89 90	29, 47, 83, 138	0
1	Q	161/186 (86%)	-0.43	1 (0%) 89 90	29, 44, 77, 139	0
1	R	161/186 (86%)	-0.38	1 (0%) 89 90	30, 56, 91, 150	0
1	S	161/186 (86%)	-0.38	2 (1%) 79 80	26, 40, 78, 140	0
1	T	160/186 (86%)	-0.49	0 100 100	26, 39, 73, 108	0
All	All	3216/3720 (86%)	-0.44	19 (0%) 89 90	22, 43, 80, 153	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	44	PHE	6.3
1	P	44	PHE	5.8
1	Q	44	PHE	4.1
1	B	44	PHE	4.0
1	E	44	PHE	3.8

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. 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, 95th 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 ²)	Q<0.9
2	CL	N	201	1/1	0.84	0.40	16.22	104,104,104,104	0
2	CL	B	201	1/1	0.95	0.29	7.42	71,71,71,71	0
2	CL	A	201	1/1	0.92	0.24	7.05	85,85,85,85	0
2	CL	M	201	1/1	0.92	0.26	5.09	80,80,80,80	0
2	CL	K	201	1/1	0.78	0.21	4.66	90,90,90,90	0
2	CL	O	201	1/1	0.82	0.23	4.16	72,72,72,72	0
2	CL	S	201	1/1	0.80	0.24	4.07	73,73,73,73	0
2	CL	K	202	1/1	0.77	0.19	2.68	83,83,83,83	0
2	CL	E	201	1/1	0.83	0.17	2.67	75,75,75,75	0
2	CL	G	201	1/1	0.98	0.20	2.41	67,67,67,67	0
2	CL	J	202	1/1	0.98	0.17	1.17	57,57,57,57	0
2	CL	T	201	1/1	0.86	0.16	1.05	68,68,68,68	0
2	CL	R	201	1/1	0.85	0.16	0.86	89,89,89,89	0
2	CL	L	201	1/1	0.91	0.14	-0.03	72,72,72,72	0
2	CL	R	202	1/1	0.84	0.13	-0.07	75,75,75,75	0
2	CL	O	202	1/1	0.93	0.11	-0.72	74,74,74,74	0
2	CL	C	201	1/1	0.87	0.12	-0.91	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CL	H	201	1/1	0.97	0.12	-1.21	74,74,74,74	0
2	CL	H	202	1/1	0.84	0.10	-1.27	78,78,78,78	0
2	CL	L	202	1/1	0.89	0.10	-1.30	78,78,78,78	0
2	CL	D	201	1/1	0.96	0.12	-1.45	67,67,67,67	0
2	CL	F	201	1/1	0.94	0.10	-1.52	68,68,68,68	0
2	CL	A	202	1/1	0.94	0.11	-1.77	65,65,65,65	0
2	CL	P	201	1/1	0.97	0.11	-1.90	62,62,62,62	0
2	CL	J	201	1/1	0.93	0.09	-3.45	65,65,65,65	0
2	CL	I	201	1/1	0.94	0.09	-3.65	61,61,61,61	0
2	CL	C	202	1/1	0.94	0.05	-4.70	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.