



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 25, 2024 – 06:07 PM EST

PDB ID : 3G8W
Title : Crystal structure of a probable acetyltransferase from *Staphylococcus epidermidis* ATCC 12228
Authors : Tan, K.; Sather, A.; Marshall, N.; Clancy, S.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2009-02-12
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

<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>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

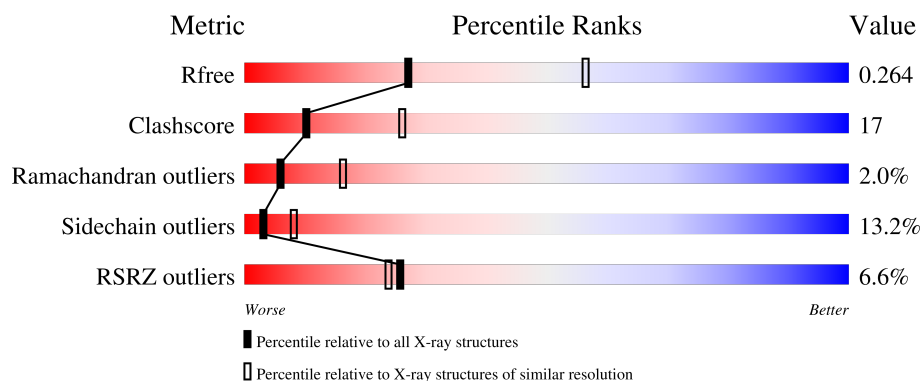
1 Overall quality at a glance

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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	169	<div> <div>2%</div> <div>62%</div> <div>30%</div> <div>• •</div> </div>
1	B	169	<div> <div>11%</div> <div>63%</div> <div>28%</div> <div>7%</div> <div>•</div> </div>
1	C	169	<div> <div>4%</div> <div>55%</div> <div>35%</div> <div>6%</div> <div>•</div> </div>
1	D	169	<div> <div>8%</div> <div>57%</div> <div>32%</div> <div>6%</div> <div>5%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NHE	C	171	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5447 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.

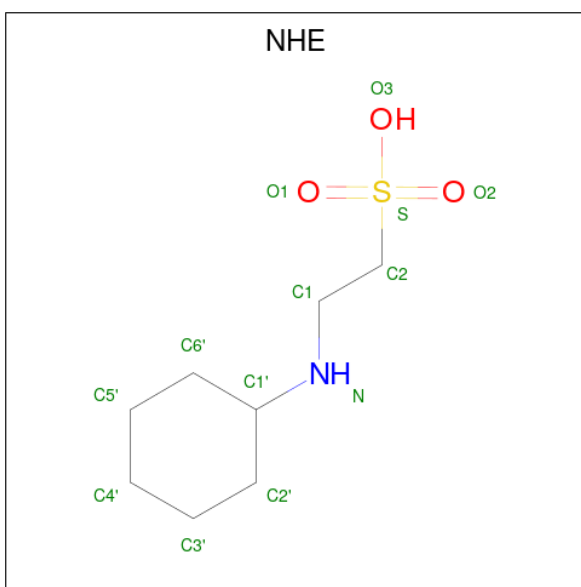
- Molecule 1 is a protein called Lactococcal prophage ps3 protein 05.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	Se	0	0	0
			1342	855	223	259	2	3			
1	B	164	Total	C	N	O	S	Se	0	0	0
			1348	859	225	259	2	3			
1	C	162	Total	C	N	O	S	Se	0	0	0
			1338	853	223	257	2	3			
1	D	161	Total	C	N	O	S	Se	0	0	0
			1229	777	211	236	2	3			

There are 12 discrepancies between the modelled and reference sequences:

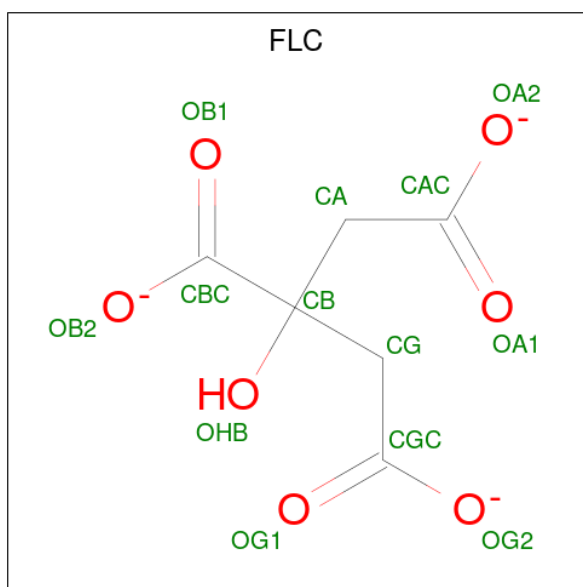
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q8CPX3
A	-1	ASN	-	expression tag	UNP Q8CPX3
A	0	ALA	-	expression tag	UNP Q8CPX3
B	-2	SER	-	expression tag	UNP Q8CPX3
B	-1	ASN	-	expression tag	UNP Q8CPX3
B	0	ALA	-	expression tag	UNP Q8CPX3
C	-2	SER	-	expression tag	UNP Q8CPX3
C	-1	ASN	-	expression tag	UNP Q8CPX3
C	0	ALA	-	expression tag	UNP Q8CPX3
D	-2	SER	-	expression tag	UNP Q8CPX3
D	-1	ASN	-	expression tag	UNP Q8CPX3
D	0	ALA	-	expression tag	UNP Q8CPX3

- Molecule 2 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: C₈H₁₇NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
2	D	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			13	6	7		

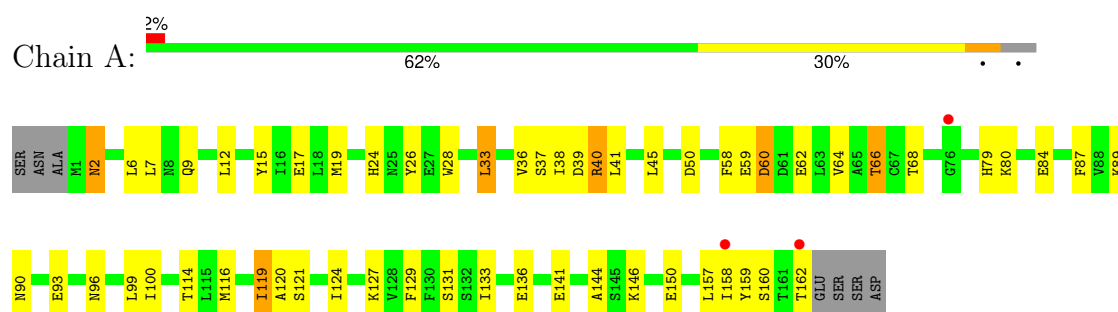
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	O	0	0
			7	7		
4	B	5	Total	O	0	0
			5	5		
4	C	8	Total	O	0	0
			8	8		
4	D	1	Total	O	0	0
			1	1		

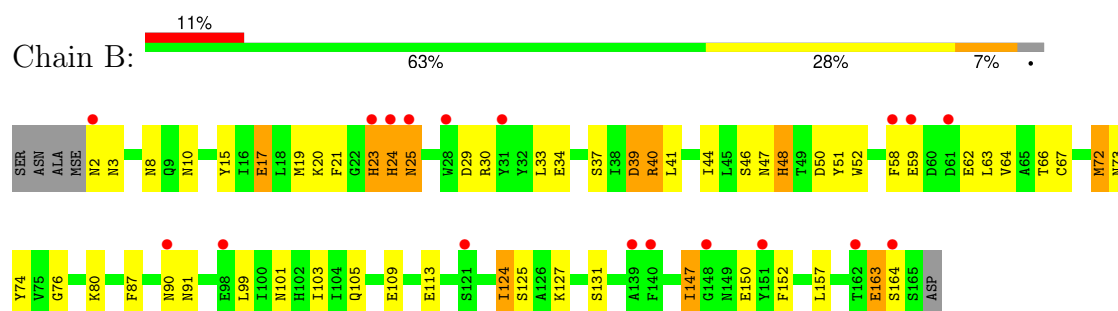
3 Residue-property plots [i](#)

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. 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. 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.

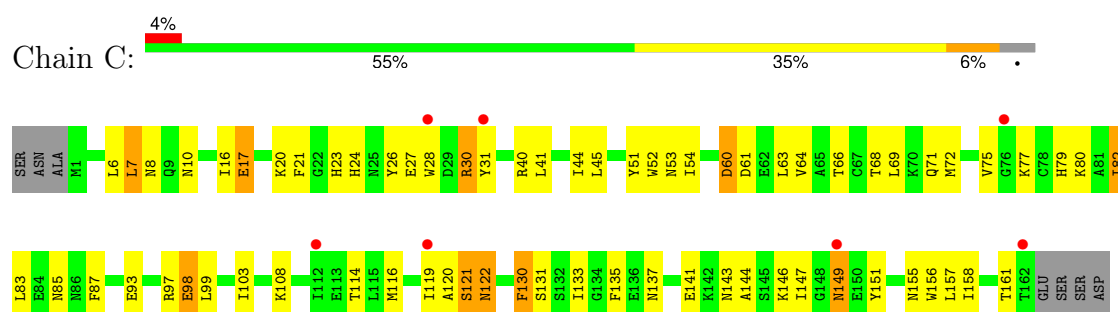
- Molecule 1: Lactococcal prophage ps3 protein 05



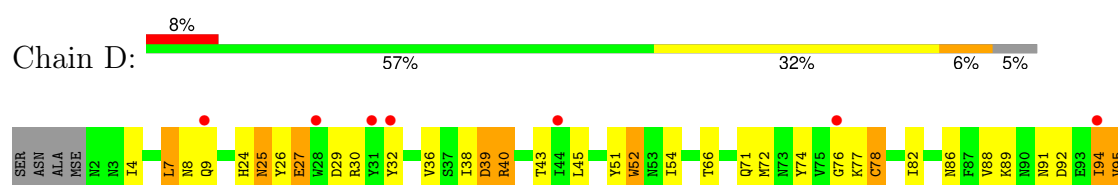
- Molecule 1: Lactococcal prophage ps3 protein 05



- Molecule 1: Lactococcal prophage ps3 protein 05



- Molecule 1: Lactococcal prophage ps3 protein 05





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	96.96Å 110.41Å 220.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.39 – 2.70 49.39 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.39-2.70) 98.9 (49.39-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.04 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0054	Depositor
R, R_{free}	0.213 , 0.256 0.219 , 0.264	Depositor DCC
R_{free} test set	1639 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	74.6	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 83.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5447	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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: NHE, FLC

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	0.89	0/1367	0.86	0/1845
1	B	0.69	0/1373	0.72	0/1853
1	C	0.84	2/1363 (0.1%)	0.82	0/1840
1	D	0.54	0/1249	0.67	0/1695
All	All	0.75	2/5352 (0.0%)	0.77	0/7233

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	17	GLU	CG-CD	5.16	1.59	1.51
1	C	130	PHE	CE2-CZ	5.08	1.47	1.37

There are no bond angle outliers.

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	1342	0	1283	38	0
1	B	1348	0	1286	44	0
1	C	1338	0	1279	48	0
1	D	1229	0	1099	50	0
2	A	39	0	50	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	39	0	51	3	0
2	C	65	0	85	18	0
2	D	13	0	17	2	0
3	C	13	0	5	3	0
4	A	7	0	0	0	0
4	B	5	0	0	2	0
4	C	8	0	0	1	0
4	D	1	0	0	0	0
All	All	5447	0	5155	179	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 17.

The worst 5 of 179 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:A:116:MSE:HE1	2:B:168:NHE:HC11	1.33	1.05
1:A:19:MSE:HE2	1:A:87:PHE:CE2	1.94	1.01
1:B:23:HIS:HB2	1:B:87:PHE:HD1	1.28	0.99
1:B:23:HIS:HB2	1:B:87:PHE:CD1	2.08	0.88
1:A:89:LYS:O	1:A:90:ASN:HB2	1.70	0.88

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	160/169 (95%)	154 (96%)	5 (3%)	1 (1%)	22	45
1	B	162/169 (96%)	144 (89%)	14 (9%)	4 (2%)	4	12
1	C	160/169 (95%)	149 (93%)	11 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	159/169 (94%)	135 (85%)	16 (10%)	8 (5%)	1	3
All	All	641/676 (95%)	582 (91%)	46 (7%)	13 (2%)	6	16

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	24	HIS
1	B	164	SER
1	D	39	ASP
1	D	89	LYS
1	B	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	147/150 (98%)	128 (87%)	19 (13%)	3	8
1	B	147/150 (98%)	128 (87%)	19 (13%)	3	8
1	C	146/150 (97%)	128 (88%)	18 (12%)	4	9
1	D	120/150 (80%)	102 (85%)	18 (15%)	2	6
All	All	560/600 (93%)	486 (87%)	74 (13%)	3	8

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	8	ASN
1	D	142	LYS
1	D	29	ASP
1	D	95	VAL
1	B	40	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	96	ASN
1	D	102	HIS
1	D	149	ASN
1	B	101	ASN
1	B	90	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NHE	A	169	-	13,13,13	1.85	1 (7%)	16,17,17	2.02	6 (37%)
2	NHE	B	167	-	13,13,13	2.15	1 (7%)	16,17,17	1.64	3 (18%)
2	NHE	A	168	-	13,13,13	2.28	1 (7%)	16,17,17	1.62	2 (12%)
2	NHE	C	167	-	13,13,13	1.63	1 (7%)	16,17,17	1.98	7 (43%)
2	NHE	A	167	-	13,13,13	1.42	1 (7%)	16,17,17	2.92	9 (56%)
2	NHE	B	168	-	13,13,13	2.11	1 (7%)	16,17,17	1.84	4 (25%)
2	NHE	C	168	-	13,13,13	2.50	1 (7%)	16,17,17	1.50	4 (25%)
2	NHE	B	169	-	13,13,13	2.11	1 (7%)	16,17,17	1.58	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FLC	C	172	-	12,12,12	1.37	1 (8%)	17,17,17	1.05	2 (11%)
2	NHE	D	167	-	13,13,13	2.08	1 (7%)	16,17,17	1.56	2 (12%)
2	NHE	C	171	-	13,13,13	2.30	1 (7%)	16,17,17	1.45	3 (18%)
2	NHE	C	169	-	13,13,13	2.04	1 (7%)	16,17,17	2.33	5 (31%)
2	NHE	C	170	-	13,13,13	2.46	1 (7%)	16,17,17	1.60	3 (18%)

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
2	NHE	A	169	-	-	4/7/15/15	0/1/1/1
2	NHE	B	167	-	-	3/7/15/15	0/1/1/1
2	NHE	A	168	-	-	1/7/15/15	0/1/1/1
2	NHE	C	167	-	-	6/7/15/15	0/1/1/1
2	NHE	A	167	-	-	7/7/15/15	0/1/1/1
2	NHE	B	168	-	-	5/7/15/15	0/1/1/1
2	NHE	C	168	-	-	1/7/15/15	0/1/1/1
2	NHE	B	169	-	-	3/7/15/15	0/1/1/1
3	FLC	C	172	-	-	0/16/16/16	-
2	NHE	D	167	-	-	6/7/15/15	0/1/1/1
2	NHE	C	171	-	-	4/7/15/15	0/1/1/1
2	NHE	C	169	-	-	2/7/15/15	0/1/1/1
2	NHE	C	170	-	-	1/7/15/15	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	168	NHE	C2-S	-8.63	1.65	1.77
2	C	170	NHE	C2-S	-8.27	1.66	1.77
2	C	171	NHE	C2-S	-7.97	1.66	1.77
2	A	168	NHE	C2-S	-7.78	1.66	1.77
2	B	167	NHE	C2-S	-7.35	1.67	1.77

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	169	NHE	O2-S-C2	6.35	116.33	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	167	NHE	C1-N-C1'	5.97	125.68	114.18
2	A	168	NHE	C1-N-C1'	4.87	123.56	114.18
2	A	167	NHE	O2-S-C2	4.81	114.00	106.73
2	B	168	NHE	C1-N-C1'	4.49	122.82	114.18

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	168	NHE	C6'-C1'-N-C1
2	A	169	NHE	C6'-C1'-N-C1
2	A	169	NHE	N-C1-C2-S
2	B	167	NHE	C2'-C1'-N-C1
2	B	167	NHE	N-C1-C2-S

There are no ring outliers.

11 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	169	NHE	2	0
2	B	167	NHE	1	0
2	A	168	NHE	1	0
2	B	168	NHE	1	0
2	C	168	NHE	4	0
2	B	169	NHE	1	0
3	C	172	FLC	3	0
2	D	167	NHE	2	0
2	C	171	NHE	9	0
2	C	169	NHE	2	0
2	C	170	NHE	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

Warning: The R factor obtained from EDS is 0.2728, which does not match the depositor's R factor of 0.21323. Please interpret the results in this section carefully.

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	158/169 (93%)	0.31	3 (1%) 66 65	24, 42, 55, 67	0
1	B	161/169 (95%)	0.74	18 (11%) 11 11	37, 49, 74, 87	0
1	C	158/169 (93%)	0.30	7 (4%) 39 38	24, 38, 49, 54	0
1	D	158/169 (93%)	0.88	14 (8%) 17 16	17, 31, 64, 67	0
All	All	635/676 (93%)	0.56	42 (6%) 26 24	17, 41, 64, 87	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	162	THR	5.0
1	D	28	TRP	4.8
1	B	23	HIS	4.2
1	D	31	TYR	4.1
1	D	121	SER	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 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, 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	B-factors(Å ²)	Q<0.9
3	FLC	C	172	13/13	0.73	0.24	92,94,94,94	13
2	NHE	D	167	13/13	0.76	0.51	104,105,108,108	13
2	NHE	C	171	13/13	0.81	0.39	86,87,88,88	13
2	NHE	C	169	13/13	0.83	0.23	82,83,85,86	13
2	NHE	A	167	13/13	0.86	0.20	66,67,78,78	13
2	NHE	C	167	13/13	0.88	0.23	75,76,85,85	13
2	NHE	C	168	13/13	0.88	0.20	89,90,91,91	13
2	NHE	B	169	13/13	0.88	0.25	85,86,91,91	13
2	NHE	B	168	13/13	0.89	0.20	84,86,92,92	13
2	NHE	B	167	13/13	0.89	0.23	121,121,122,122	13
2	NHE	A	169	13/13	0.90	0.24	85,87,88,89	13
2	NHE	C	170	13/13	0.91	0.20	79,80,83,83	13
2	NHE	A	168	13/13	0.95	0.14	77,79,82,83	13

6.5 Other polymers [i](#)

There are no such residues in this entry.