



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 24, 2026 – 04:16 PM JST

PDB ID : 9WGL / pdb_00009wgl
Title : B. subtilis SufS WT - E. coli SufE variant with deletion of TQHL (residues 112-115)
Authors : Sakurai, R.; Fujishiro, T.
Deposited on : 2025-08-25
Resolution : 2.00 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	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

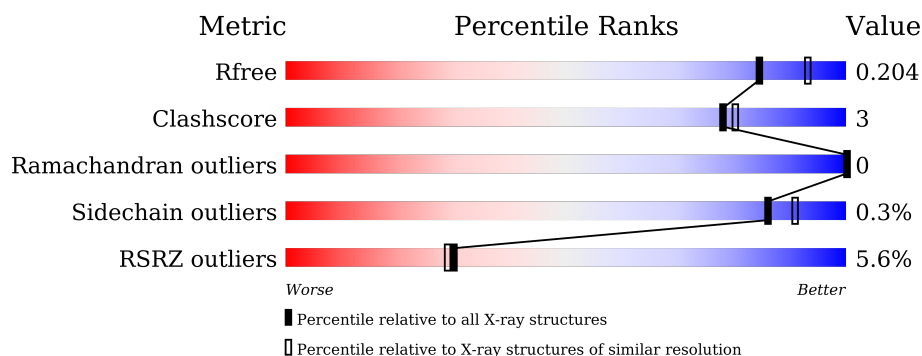
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	419	5% 91% 5% .
1	B	419	4% 91% 5% .
1	C	419	4% 90% 6% .
1	D	419	5% 90% 6% .
2	E	145	7% 84% 10% 6%
2	F	145	7% 87% 7% 6%

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Mol	Chain	Length	Quality of chain
2	G	145	8% 88% 6% 6%
2	H	145	8% 83% 10% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18701 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 Cysteine desulfurase SufS.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	P	S	0	0	0
			3158	2002	531	611	1	13			
1	B	403	Total	C	N	O	P	S	0	0	0
			3156	2000	530	612	1	13			
1	C	402	Total	C	N	O	P	S	0	0	0
			3152	2001	529	608	1	13			
1	D	403	Total	C	N	O	P	S	0	0	0
			3156	2000	530	612	1	13			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP O32164
A	-1	GLY	-	expression tag	UNP O32164
A	0	HIS	-	expression tag	UNP O32164
A	407	VAL	-	expression tag	UNP O32164
A	408	ASP	-	expression tag	UNP O32164
A	409	LEU	-	expression tag	UNP O32164
A	410	GLU	-	expression tag	UNP O32164
A	411	HIS	-	expression tag	UNP O32164
A	412	HIS	-	expression tag	UNP O32164
A	413	HIS	-	expression tag	UNP O32164
A	414	HIS	-	expression tag	UNP O32164
A	415	HIS	-	expression tag	UNP O32164
A	416	HIS	-	expression tag	UNP O32164
B	-2	MET	-	initiating methionine	UNP O32164
B	-1	GLY	-	expression tag	UNP O32164
B	0	HIS	-	expression tag	UNP O32164
B	407	VAL	-	expression tag	UNP O32164
B	408	ASP	-	expression tag	UNP O32164
B	409	LEU	-	expression tag	UNP O32164
B	410	GLU	-	expression tag	UNP O32164
B	411	HIS	-	expression tag	UNP O32164

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Chain	Residue	Modelled	Actual	Comment	Reference
B	412	HIS	-	expression tag	UNP O32164
B	413	HIS	-	expression tag	UNP O32164
B	414	HIS	-	expression tag	UNP O32164
B	415	HIS	-	expression tag	UNP O32164
B	416	HIS	-	expression tag	UNP O32164
C	-2	MET	-	initiating methionine	UNP O32164
C	-1	GLY	-	expression tag	UNP O32164
C	0	HIS	-	expression tag	UNP O32164
C	407	VAL	-	expression tag	UNP O32164
C	408	ASP	-	expression tag	UNP O32164
C	409	LEU	-	expression tag	UNP O32164
C	410	GLU	-	expression tag	UNP O32164
C	411	HIS	-	expression tag	UNP O32164
C	412	HIS	-	expression tag	UNP O32164
C	413	HIS	-	expression tag	UNP O32164
C	414	HIS	-	expression tag	UNP O32164
C	415	HIS	-	expression tag	UNP O32164
C	416	HIS	-	expression tag	UNP O32164
D	-2	MET	-	initiating methionine	UNP O32164
D	-1	GLY	-	expression tag	UNP O32164
D	0	HIS	-	expression tag	UNP O32164
D	407	VAL	-	expression tag	UNP O32164
D	408	ASP	-	expression tag	UNP O32164
D	409	LEU	-	expression tag	UNP O32164
D	410	GLU	-	expression tag	UNP O32164
D	411	HIS	-	expression tag	UNP O32164
D	412	HIS	-	expression tag	UNP O32164
D	413	HIS	-	expression tag	UNP O32164
D	414	HIS	-	expression tag	UNP O32164
D	415	HIS	-	expression tag	UNP O32164
D	416	HIS	-	expression tag	UNP O32164

- Molecule 2 is a protein called Cysteine desulfuration protein SufE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	136	Total	C	N	O	S	0	0	0
			1090	694	192	198	6			
2	F	136	Total	C	N	O	S	0	0	0
			1090	694	192	198	6			
2	G	136	Total	C	N	O	S	0	0	0
			1090	694	192	198	6			
2	H	136	Total	C	N	O	S	0	0	0
			1090	694	192	198	6			

There are 60 discrepancies between the modelled and reference sequences:

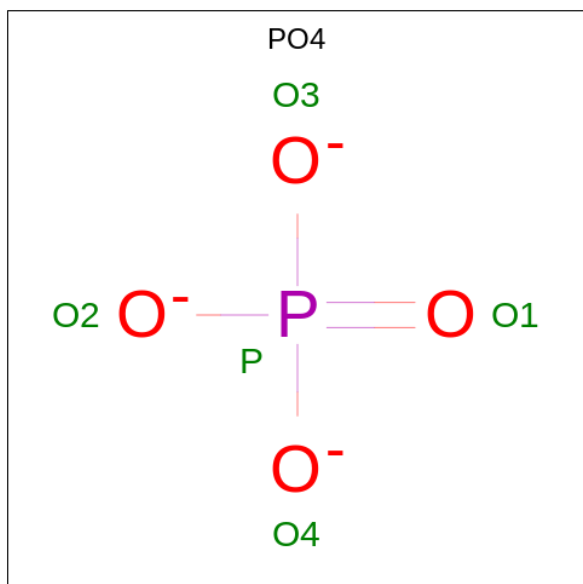
Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	THR	deletion	UNP P76194
E	?	-	GLN	deletion	UNP P76194
E	?	-	HIS	deletion	UNP P76194
E	?	-	LEU	deletion	UNP P76194
E	135	TRP	-	expression tag	UNP P76194
E	136	ALA	-	expression tag	UNP P76194
E	137	ALA	-	expression tag	UNP P76194
E	138	LEU	-	expression tag	UNP P76194
E	139	GLU	-	expression tag	UNP P76194
E	140	HIS	-	expression tag	UNP P76194
E	141	HIS	-	expression tag	UNP P76194
E	142	HIS	-	expression tag	UNP P76194
E	143	HIS	-	expression tag	UNP P76194
E	144	HIS	-	expression tag	UNP P76194
E	145	HIS	-	expression tag	UNP P76194
F	?	-	THR	deletion	UNP P76194
F	?	-	GLN	deletion	UNP P76194
F	?	-	HIS	deletion	UNP P76194
F	?	-	LEU	deletion	UNP P76194
F	135	TRP	-	expression tag	UNP P76194
F	136	ALA	-	expression tag	UNP P76194
F	137	ALA	-	expression tag	UNP P76194
F	138	LEU	-	expression tag	UNP P76194
F	139	GLU	-	expression tag	UNP P76194
F	140	HIS	-	expression tag	UNP P76194
F	141	HIS	-	expression tag	UNP P76194
F	142	HIS	-	expression tag	UNP P76194
F	143	HIS	-	expression tag	UNP P76194
F	144	HIS	-	expression tag	UNP P76194
F	145	HIS	-	expression tag	UNP P76194
G	?	-	THR	deletion	UNP P76194
G	?	-	GLN	deletion	UNP P76194
G	?	-	HIS	deletion	UNP P76194
G	?	-	LEU	deletion	UNP P76194
G	135	TRP	-	expression tag	UNP P76194
G	136	ALA	-	expression tag	UNP P76194
G	137	ALA	-	expression tag	UNP P76194
G	138	LEU	-	expression tag	UNP P76194
G	139	GLU	-	expression tag	UNP P76194
G	140	HIS	-	expression tag	UNP P76194
G	141	HIS	-	expression tag	UNP P76194
G	142	HIS	-	expression tag	UNP P76194

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Chain	Residue	Modelled	Actual	Comment	Reference
G	143	HIS	-	expression tag	UNP P76194
G	144	HIS	-	expression tag	UNP P76194
G	145	HIS	-	expression tag	UNP P76194
H	?	-	THR	deletion	UNP P76194
H	?	-	GLN	deletion	UNP P76194
H	?	-	HIS	deletion	UNP P76194
H	?	-	LEU	deletion	UNP P76194
H	135	TRP	-	expression tag	UNP P76194
H	136	ALA	-	expression tag	UNP P76194
H	137	ALA	-	expression tag	UNP P76194
H	138	LEU	-	expression tag	UNP P76194
H	139	GLU	-	expression tag	UNP P76194
H	140	HIS	-	expression tag	UNP P76194
H	141	HIS	-	expression tag	UNP P76194
H	142	HIS	-	expression tag	UNP P76194
H	143	HIS	-	expression tag	UNP P76194
H	144	HIS	-	expression tag	UNP P76194
H	145	HIS	-	expression tag	UNP P76194

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	291	Total	O	0	0
			291	291		
4	B	314	Total	O	0	0
			314	314		

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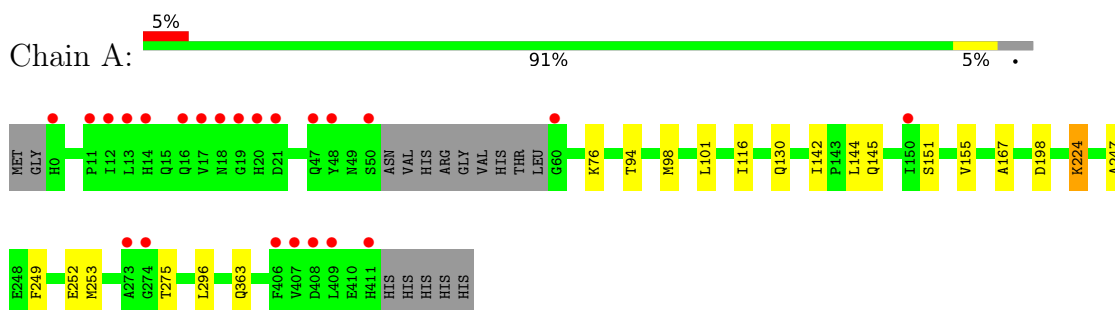
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	350	Total 350	O 350	0	0
4	D	316	Total 316	O 316	0	0
4	E	91	Total 91	O 91	0	0
4	F	93	Total 93	O 93	0	0
4	G	85	Total 85	O 85	0	0
4	H	84	Total 84	O 84	0	0

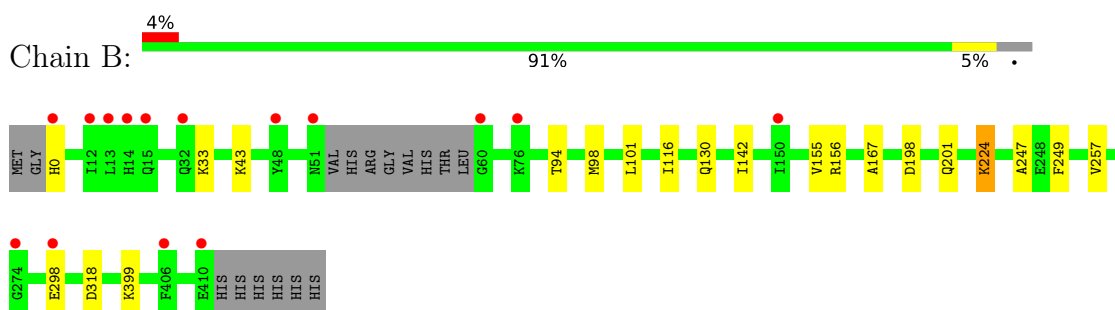
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

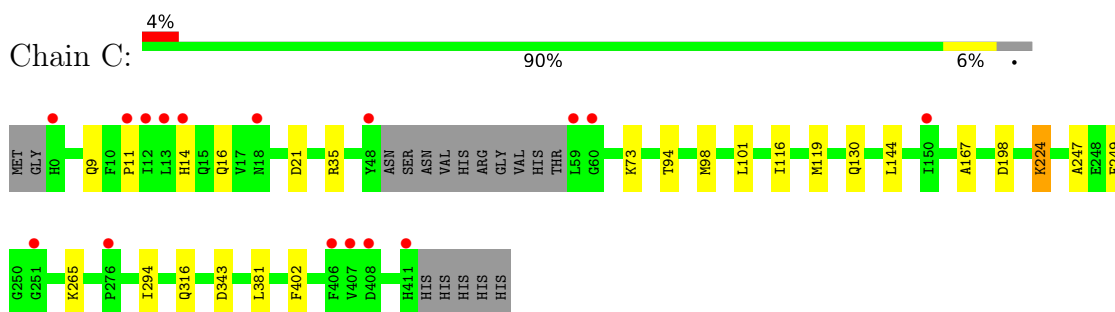
- Molecule 1: Cysteine desulfurase SufS



- Molecule 1: Cysteine desulfurase SufS

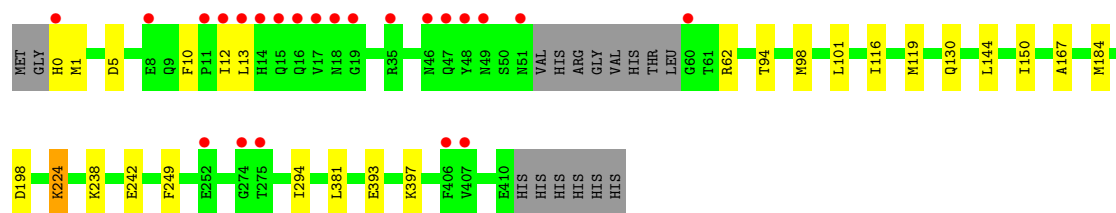


- Molecule 1: Cysteine desulfurase SufS

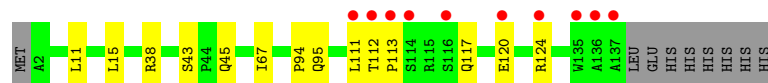
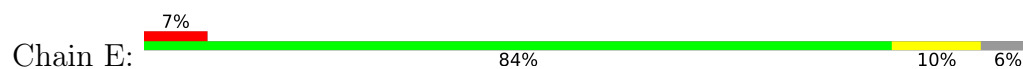


- Molecule 1: Cysteine desulfurase SufS

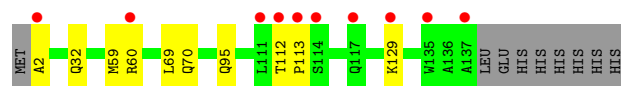
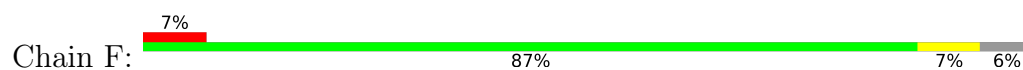




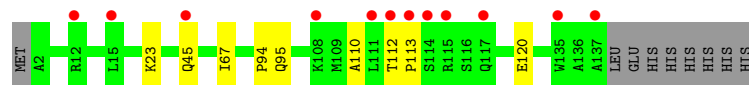
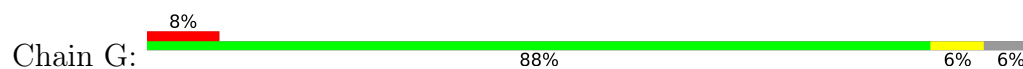
• Molecule 2: Cysteine desulfuration protein SufE



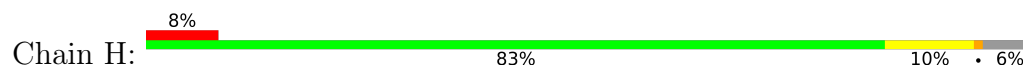
• Molecule 2: Cysteine desulfuration protein SufE



• Molecule 2: Cysteine desulfuration protein SufE



• Molecule 2: Cysteine desulfuration protein SufE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.91Å 126.86Å 126.81Å 90.00° 109.14° 90.00°	Depositor
Resolution (Å)	39.93 – 2.00 39.93 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.8 (39.93-2.00) 98.8 (39.93-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.178 , 0.204 0.178 , 0.204	Depositor DCC
R_{free} test set	11234 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18701	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: LLP, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.16	0/3198	0.39	0/4341
1	B	0.16	0/3195	0.39	0/4337
1	C	0.16	0/3192	0.38	0/4333
1	D	0.17	0/3195	0.39	0/4337
2	E	0.17	0/1110	0.43	0/1502
2	F	0.18	0/1110	0.43	0/1502
2	G	0.20	0/1110	0.41	0/1502
2	H	0.18	0/1110	0.41	0/1502
All	All	0.17	0/17220	0.40	0/23356

There are no bond length outliers.

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	3158	0	3095	14	0
1	B	3156	0	3094	17	0
1	C	3152	0	3095	17	0
1	D	3156	0	3094	17	0
2	E	1090	0	1104	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1090	0	1104	9	0
2	G	1090	0	1104	7	0
2	H	1090	0	1104	9	0
3	A	20	0	0	0	0
3	B	30	0	0	1	0
3	C	20	0	0	0	0
3	D	15	0	0	0	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
4	A	291	0	0	1	0
4	B	314	0	0	2	0
4	C	350	0	0	1	0
4	D	316	0	0	1	0
4	E	91	0	0	2	0
4	F	93	0	0	1	0
4	G	85	0	0	0	0
4	H	84	0	0	1	0
All	All	18701	0	16794	96	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 3.

The worst 5 of 96 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)
2:H:112:THR:HG23	2:H:113:PRO:HD3	1.58	0.84
2:H:23:LYS:NZ	2:H:110:ALA:O	2.21	0.73
2:E:43:SER:HB2	2:E:45:GLN:HE21	1.53	0.72
1:C:16:GLN:NE2	1:C:21:ASP:OD1	2.26	0.68
2:E:112:THR:HG23	2:E:113:PRO:HD3	1.77	0.66

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	398/419 (95%)	391 (98%)	7 (2%)	0	100	100
1	B	398/419 (95%)	391 (98%)	7 (2%)	0	100	100
1	C	397/419 (95%)	390 (98%)	7 (2%)	0	100	100
1	D	398/419 (95%)	391 (98%)	7 (2%)	0	100	100
2	E	134/145 (92%)	131 (98%)	3 (2%)	0	100	100
2	F	134/145 (92%)	131 (98%)	3 (2%)	0	100	100
2	G	134/145 (92%)	131 (98%)	3 (2%)	0	100	100
2	H	134/145 (92%)	132 (98%)	2 (2%)	0	100	100
All	All	2127/2256 (94%)	2088 (98%)	39 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	334/348 (96%)	332 (99%)	2 (1%)	78	85
1	B	334/348 (96%)	334 (100%)	0	100	100
1	C	333/348 (96%)	333 (100%)	0	100	100
1	D	334/348 (96%)	333 (100%)	1 (0%)	86	91
2	E	115/124 (93%)	114 (99%)	1 (1%)	70	78
2	F	115/124 (93%)	115 (100%)	0	100	100
2	G	115/124 (93%)	115 (100%)	0	100	100
2	H	115/124 (93%)	113 (98%)	2 (2%)	53	60
All	All	1795/1888 (95%)	1789 (100%)	6 (0%)	86	91

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	111	LEU
2	H	112	THR
2	H	117	GLN
1	A	296	LEU
1	A	275	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	304	HIS
2	E	64	GLN
2	H	54	GLN
1	D	335	ASN
2	E	46	ASN

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	LLP	C	224	1	23,24,25	1.47	3 (13%)	25,32,34	1.31	3 (12%)
1	LLP	B	224	1	23,24,25	1.46	3 (13%)	25,32,34	1.35	5 (20%)
1	LLP	A	224	1	23,24,25	1.46	4 (17%)	25,32,34	1.05	2 (8%)
1	LLP	D	224	1	23,24,25	1.46	3 (13%)	25,32,34	1.15	3 (12%)

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	LLP	C	224	1	-	1/16/17/19	0/1/1/1
1	LLP	B	224	1	-	2/16/17/19	0/1/1/1
1	LLP	A	224	1	-	1/16/17/19	0/1/1/1
1	LLP	D	224	1	-	1/16/17/19	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)
1	A	224	LLP	C4'-NZ	4.81	1.43	1.27
1	C	224	LLP	C4'-NZ	4.80	1.43	1.27
1	D	224	LLP	C4'-NZ	4.79	1.43	1.27
1	B	224	LLP	C4'-NZ	4.78	1.43	1.27
1	C	224	LLP	C2-N1	2.34	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	224	LLP	C4-C4'-NZ	-3.71	107.27	124.31
1	C	224	LLP	C4-C4'-NZ	-3.44	108.50	124.31
1	C	224	LLP	CE-NZ-C4'	-3.03	109.59	118.90
1	B	224	LLP	CE-NZ-C4'	-2.66	110.75	118.90
1	D	224	LLP	C4-C4'-NZ	-2.53	112.70	124.31

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	224	LLP	C4-C4'-NZ-CE
1	B	224	LLP	C4-C4'-NZ-CE
1	C	224	LLP	C4-C4'-NZ-CE
1	A	224	LLP	C4-C4'-NZ-CE
1	B	224	LLP	C4-C5-C5'-OP4

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	224	LLP	2	0
1	B	224	LLP	3	0
1	A	224	LLP	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	224	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

19 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PO4	A	504	-	4,4,4	1.53	1 (25%)	6,6,6	0.42	0
3	PO4	D	501	-	4,4,4	1.52	1 (25%)	6,6,6	0.46	0
3	PO4	D	502	-	4,4,4	1.53	1 (25%)	6,6,6	0.45	0
3	PO4	B	503	-	4,4,4	1.52	1 (25%)	6,6,6	0.46	0
3	PO4	B	501	-	4,4,4	1.49	1 (25%)	6,6,6	0.43	0
3	PO4	C	501	-	4,4,4	1.49	1 (25%)	6,6,6	0.41	0
3	PO4	F	201	-	4,4,4	1.53	1 (25%)	6,6,6	0.48	0
3	PO4	A	503	-	4,4,4	1.51	1 (25%)	6,6,6	0.44	0
3	PO4	D	503	-	4,4,4	1.48	1 (25%)	6,6,6	0.50	0
3	PO4	B	506	-	4,4,4	1.45	1 (25%)	6,6,6	0.47	0
3	PO4	B	505	-	4,4,4	1.53	1 (25%)	6,6,6	0.44	0
3	PO4	B	502	-	4,4,4	1.53	1 (25%)	6,6,6	0.44	0
3	PO4	C	503	-	4,4,4	1.52	1 (25%)	6,6,6	0.45	0
3	PO4	G	201	-	4,4,4	1.52	1 (25%)	6,6,6	0.43	0
3	PO4	B	504	-	4,4,4	1.51	1 (25%)	6,6,6	0.46	0
3	PO4	A	501	-	4,4,4	1.53	1 (25%)	6,6,6	0.41	0
3	PO4	C	504	-	4,4,4	1.50	1 (25%)	6,6,6	0.45	0
3	PO4	A	502	-	4,4,4	1.53	1 (25%)	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	C	502	-	4,4,4	1.51	1 (25%)	6,6,6	0.48	0

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	PO4	P-O1	2.66	1.57	1.50
3	A	504	PO4	P-O1	2.66	1.57	1.50
3	B	502	PO4	P-O1	2.66	1.57	1.50
3	B	505	PO4	P-O1	2.64	1.57	1.50
3	F	201	PO4	P-O1	2.64	1.57	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	504	PO4	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 ⓘ

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	402/419 (95%)	0.12	23 (5%)	29	28	20, 30, 61, 113	0
1	B	402/419 (95%)	0.05	15 (3%)	45	44	21, 29, 58, 117	0
1	C	401/419 (95%)	-0.01	16 (3%)	42	41	20, 28, 54, 118	0
1	D	402/419 (95%)	0.09	23 (5%)	29	28	19, 28, 61, 118	0
2	E	136/145 (93%)	0.45	10 (7%)	20	19	21, 35, 70, 101	0
2	F	136/145 (93%)	0.45	10 (7%)	20	19	21, 36, 73, 92	0
2	G	136/145 (93%)	0.57	12 (8%)	15	14	24, 38, 73, 108	0
2	H	136/145 (93%)	0.57	12 (8%)	15	14	24, 40, 76, 108	0
All	All	2151/2256 (95%)	0.18	121 (5%)	30	29	19, 31, 64, 118	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	59	LEU	7.5
2	E	113	PRO	7.0
2	H	113	PRO	6.2
1	A	13	LEU	6.0
2	G	113	PRO	6.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	LLP	A	224	24/25	0.94	0.09	20,28,36,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	LLP	B	224	24/25	0.94	0.09	18,28,38,40	0
1	LLP	C	224	24/25	0.94	0.09	18,30,37,39	0
1	LLP	D	224	24/25	0.95	0.08	18,29,35,38	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	PO4	B	506	5/5	0.75	0.21	31,41,78,85	0
3	PO4	D	503	5/5	0.80	0.17	31,39,71,77	0
3	PO4	D	502	5/5	0.83	0.15	73,76,92,93	0
3	PO4	C	501	5/5	0.83	0.18	55,70,81,81	0
3	PO4	G	201	5/5	0.83	0.19	60,67,85,91	0
3	PO4	F	201	5/5	0.84	0.16	38,67,80,86	0
3	PO4	A	502	5/5	0.84	0.14	58,66,75,82	0
3	PO4	B	505	5/5	0.85	0.12	56,62,80,93	0
3	PO4	B	501	5/5	0.87	0.17	54,55,66,88	0
3	PO4	A	501	5/5	0.87	0.14	52,58,75,97	0
3	PO4	A	504	5/5	0.88	0.13	31,40,64,75	0
3	PO4	C	504	5/5	0.88	0.13	30,43,73,80	0
3	PO4	B	504	5/5	0.88	0.15	54,77,84,90	0
3	PO4	C	503	5/5	0.89	0.14	68,70,83,89	0
3	PO4	D	501	5/5	0.89	0.14	52,63,71,72	0
3	PO4	C	502	5/5	0.90	0.15	61,71,75,81	0
3	PO4	A	503	5/5	0.91	0.14	53,67,73,84	0
3	PO4	B	502	5/5	0.91	0.12	61,63,68,71	0
3	PO4	B	503	5/5	0.91	0.11	49,57,70,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.