



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:48 PM GMT

PDB ID : 3S28  
Title : The crystal structure of sucrose synthase-1 in complex with a breakdown product of the UDP-glucose  
Authors : Zheng, Y.; Garavito, R.M.  
Deposited on : 2011-05-16  
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

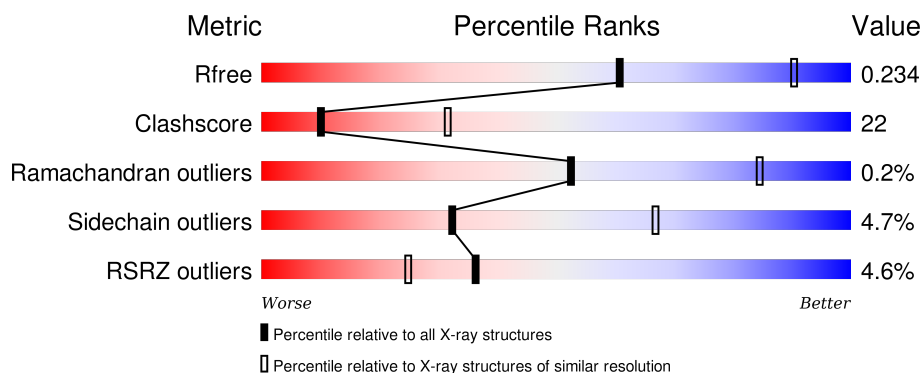
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	816	<div> <div>3%</div> <div>63%</div> <div>30%</div> <div>• •</div> </div>
1	B	816	<div> <div>7%</div> <div>63%</div> <div>30%</div> <div>• •</div> </div>
1	C	816	<div> <div>4%</div> <div>59%</div> <div>35%</div> <div>• •</div> </div>
1	D	816	<div> <div>3%</div> <div>66%</div> <div>28%</div> <div>• •</div> </div>
1	E	816	<div> <div>5%</div> <div>66%</div> <div>26%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	816	
1	G	816	
1	H	816	

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
4	NHF	D	904[B]	-	-	X	-
5	SO4	A	911	-	-	-	X
5	SO4	A	912	-	-	X	-
5	SO4	B	913	-	-	X	X
5	SO4	D	911	-	-	-	X
5	SO4	D	913	-	-	X	-
5	SO4	E	911	-	-	-	X
5	SO4	E	913	-	-	-	X
5	SO4	F	911	-	-	-	X
5	SO4	F	912	-	-	X	-
5	SO4	F	913	-	-	X	-
5	SO4	G	913	-	-	-	X
5	SO4	H	913	-	-	-	X
6	MLA	A	921	-	-	-	X
6	MLA	B	921	-	-	-	X
6	MLA	D	921	-	-	-	X
6	MLA	E	921	-	-	-	X
6	MLA	F	921	-	-	-	X
6	MLA	G	921	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 51388 atoms, of which 264 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 Sucrose synthase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	781	Total	C	N	O	S	0	0	0
			6289	4039	1069	1159	22			
1	B	780	Total	C	N	O	S	0	0	0
			6158	3949	1050	1137	22			
1	C	781	Total	C	N	O	S	0	0	0
			6290	4045	1066	1157	22			
1	D	781	Total	C	N	O	S	0	0	0
			6280	4035	1062	1161	22			
1	E	781	Total	C	N	O	S	0	0	0
			6271	4028	1062	1159	22			
1	F	781	Total	C	N	O	S	0	0	0
			6292	4042	1070	1158	22			
1	G	781	Total	C	N	O	S	0	0	0
			6299	4045	1070	1162	22			
1	H	780	Total	C	N	O	S	0	0	0
			6243	4007	1063	1151	22			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	809	VAL	-	EXPRESSION TAG	UNP P49040
A	810	GLU	-	EXPRESSION TAG	UNP P49040
A	811	HIS	-	EXPRESSION TAG	UNP P49040
A	812	HIS	-	EXPRESSION TAG	UNP P49040
A	813	HIS	-	EXPRESSION TAG	UNP P49040
A	814	HIS	-	EXPRESSION TAG	UNP P49040
A	815	HIS	-	EXPRESSION TAG	UNP P49040
A	816	HIS	-	EXPRESSION TAG	UNP P49040
B	809	VAL	-	EXPRESSION TAG	UNP P49040
B	810	GLU	-	EXPRESSION TAG	UNP P49040
B	811	HIS	-	EXPRESSION TAG	UNP P49040
B	812	HIS	-	EXPRESSION TAG	UNP P49040
B	813	HIS	-	EXPRESSION TAG	UNP P49040

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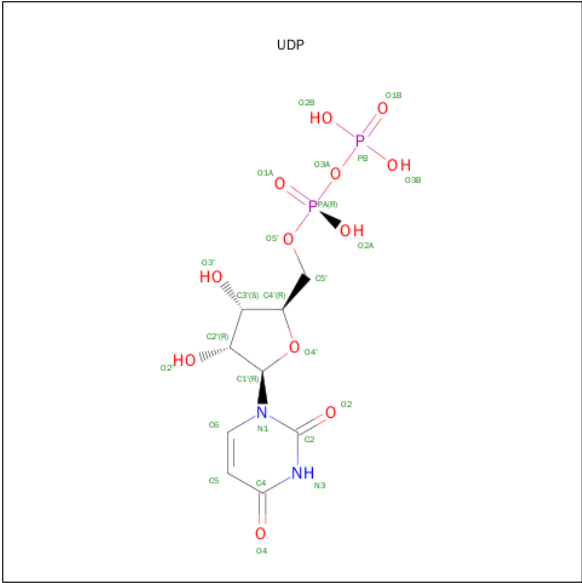
Chain	Residue	Modelled	Actual	Comment	Reference
B	814	HIS	-	EXPRESSION TAG	UNP P49040
B	815	HIS	-	EXPRESSION TAG	UNP P49040
B	816	HIS	-	EXPRESSION TAG	UNP P49040
C	809	VAL	-	EXPRESSION TAG	UNP P49040
C	810	GLU	-	EXPRESSION TAG	UNP P49040
C	811	HIS	-	EXPRESSION TAG	UNP P49040
C	812	HIS	-	EXPRESSION TAG	UNP P49040
C	813	HIS	-	EXPRESSION TAG	UNP P49040
C	814	HIS	-	EXPRESSION TAG	UNP P49040
C	815	HIS	-	EXPRESSION TAG	UNP P49040
C	816	HIS	-	EXPRESSION TAG	UNP P49040
D	809	VAL	-	EXPRESSION TAG	UNP P49040
D	810	GLU	-	EXPRESSION TAG	UNP P49040
D	811	HIS	-	EXPRESSION TAG	UNP P49040
D	812	HIS	-	EXPRESSION TAG	UNP P49040
D	813	HIS	-	EXPRESSION TAG	UNP P49040
D	814	HIS	-	EXPRESSION TAG	UNP P49040
D	815	HIS	-	EXPRESSION TAG	UNP P49040
D	816	HIS	-	EXPRESSION TAG	UNP P49040
E	809	VAL	-	EXPRESSION TAG	UNP P49040
E	810	GLU	-	EXPRESSION TAG	UNP P49040
E	811	HIS	-	EXPRESSION TAG	UNP P49040
E	812	HIS	-	EXPRESSION TAG	UNP P49040
E	813	HIS	-	EXPRESSION TAG	UNP P49040
E	814	HIS	-	EXPRESSION TAG	UNP P49040
E	815	HIS	-	EXPRESSION TAG	UNP P49040
E	816	HIS	-	EXPRESSION TAG	UNP P49040
F	809	VAL	-	EXPRESSION TAG	UNP P49040
F	810	GLU	-	EXPRESSION TAG	UNP P49040
F	811	HIS	-	EXPRESSION TAG	UNP P49040
F	812	HIS	-	EXPRESSION TAG	UNP P49040
F	813	HIS	-	EXPRESSION TAG	UNP P49040
F	814	HIS	-	EXPRESSION TAG	UNP P49040
F	815	HIS	-	EXPRESSION TAG	UNP P49040
F	816	HIS	-	EXPRESSION TAG	UNP P49040
G	809	VAL	-	EXPRESSION TAG	UNP P49040
G	810	GLU	-	EXPRESSION TAG	UNP P49040
G	811	HIS	-	EXPRESSION TAG	UNP P49040
G	812	HIS	-	EXPRESSION TAG	UNP P49040
G	813	HIS	-	EXPRESSION TAG	UNP P49040
G	814	HIS	-	EXPRESSION TAG	UNP P49040
G	815	HIS	-	EXPRESSION TAG	UNP P49040

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Chain	Residue	Modelled	Actual	Comment	Reference
G	816	HIS	-	EXPRESSION TAG	UNP P49040
H	809	VAL	-	EXPRESSION TAG	UNP P49040
H	810	GLU	-	EXPRESSION TAG	UNP P49040
H	811	HIS	-	EXPRESSION TAG	UNP P49040
H	812	HIS	-	EXPRESSION TAG	UNP P49040
H	813	HIS	-	EXPRESSION TAG	UNP P49040
H	814	HIS	-	EXPRESSION TAG	UNP P49040
H	815	HIS	-	EXPRESSION TAG	UNP P49040
H	816	HIS	-	EXPRESSION TAG	UNP P49040

- Molecule 2 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>12</sub>P<sub>2</sub>).



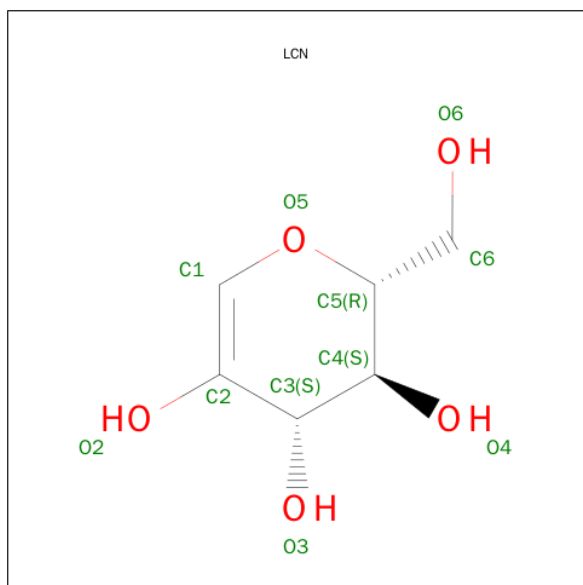
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	B	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	C	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	D	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	E	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	F	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		
2	G	1	Total	C	H	N	O	P	0	0
			36	9	11	2	12	2		

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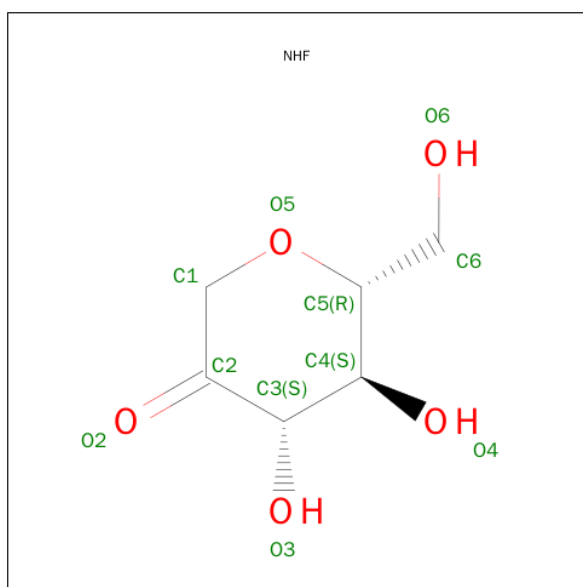
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	H	N	O	P	
			36	9	11	2	12	2	
								0	0

- Molecule 3 is SUGAR (1,5-ANHYDRO-D-ARABINO-HEX-1-ENITOL) (three-letter code: LCN) (formula: C<sub>6</sub>H<sub>10</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	1
			21	6	10	5		
3	B	1	Total	C	H	O	0	1
			21	6	10	5		
3	C	1	Total	C	H	O	0	1
			21	6	10	5		
3	D	1	Total	C	H	O	0	1
			21	6	10	5		
3	E	1	Total	C	H	O	0	1
			21	6	10	5		
3	F	1	Total	C	H	O	0	1
			21	6	10	5		
3	G	1	Total	C	H	O	0	1
			21	6	10	5		
3	H	1	Total	C	H	O	0	1
			21	6	10	5		

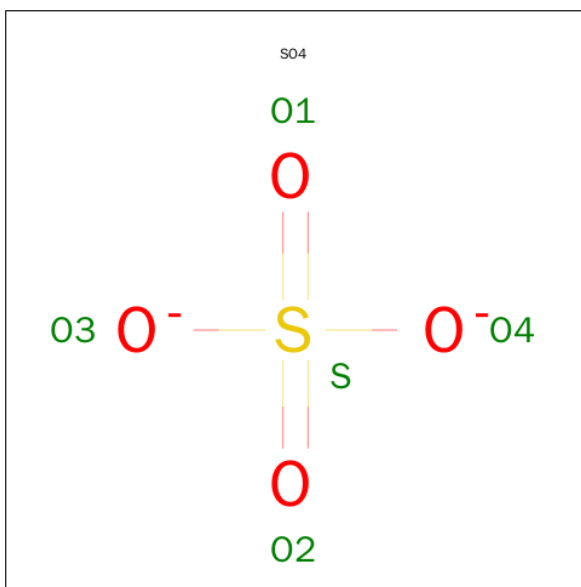
- Molecule 4 is SUGAR (1,5-ANHYDRO-D-FRUCTOSE) (three-letter code: NHF) (formula: C<sub>6</sub>H<sub>10</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	1
			21	6	10	5		
4	B	1	Total	C	H	O	0	1
			21	6	10	5		
4	C	1	Total	C	H	O	0	1
			21	6	10	5		
4	D	1	Total	C	H	O	0	1
			21	6	10	5		
4	E	1	Total	C	H	O	0	1
			21	6	10	5		
4	F	1	Total	C	H	O	0	1
			21	6	10	5		
4	G	1	Total	C	H	O	0	1
			21	6	10	5		
4	H	1	Total	C	H	O	0	1
			21	6	10	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).





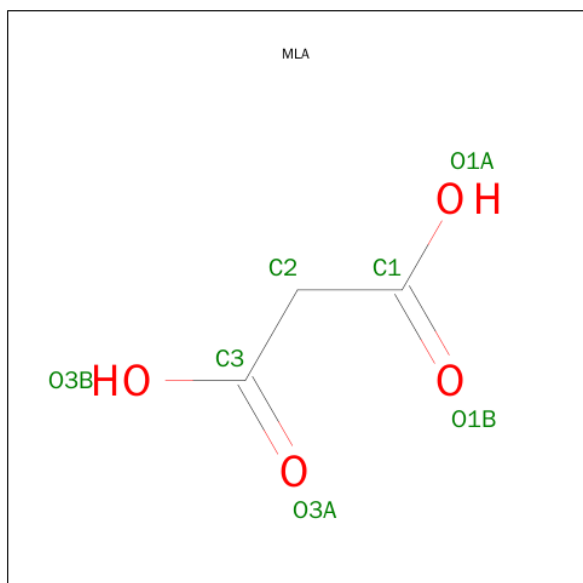
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MALONIC ACID (three-letter code: MLA) (formula:  $C_3H_4O_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			9	3	2	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	0	0
			9	3	2	4		
6	C	1	Total	C	H	O	0	0
			9	3	2	4		
6	D	1	Total	C	H	O	0	0
			9	3	2	4		
6	E	1	Total	C	H	O	0	0
			9	3	2	4		
6	F	1	Total	C	H	O	0	0
			9	3	2	4		
6	G	1	Total	C	H	O	0	0
			9	3	2	4		
6	H	1	Total	C	H	O	0	0
			9	3	2	4		

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	1	Total	K	0	0
			1	1		
7	D	1	Total	K	0	0
			1	1		
7	E	1	Total	K	0	0
			1	1		
7	H	1	Total	K	0	0
			1	1		
7	B	1	Total	K	0	0
			1	1		
7	C	1	Total	K	0	0
			1	1		
7	A	1	Total	K	0	0
			1	1		
7	F	1	Total	K	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	69	Total	O	0	0
			69	69		
8	B	55	Total	O	0	0
			55	55		

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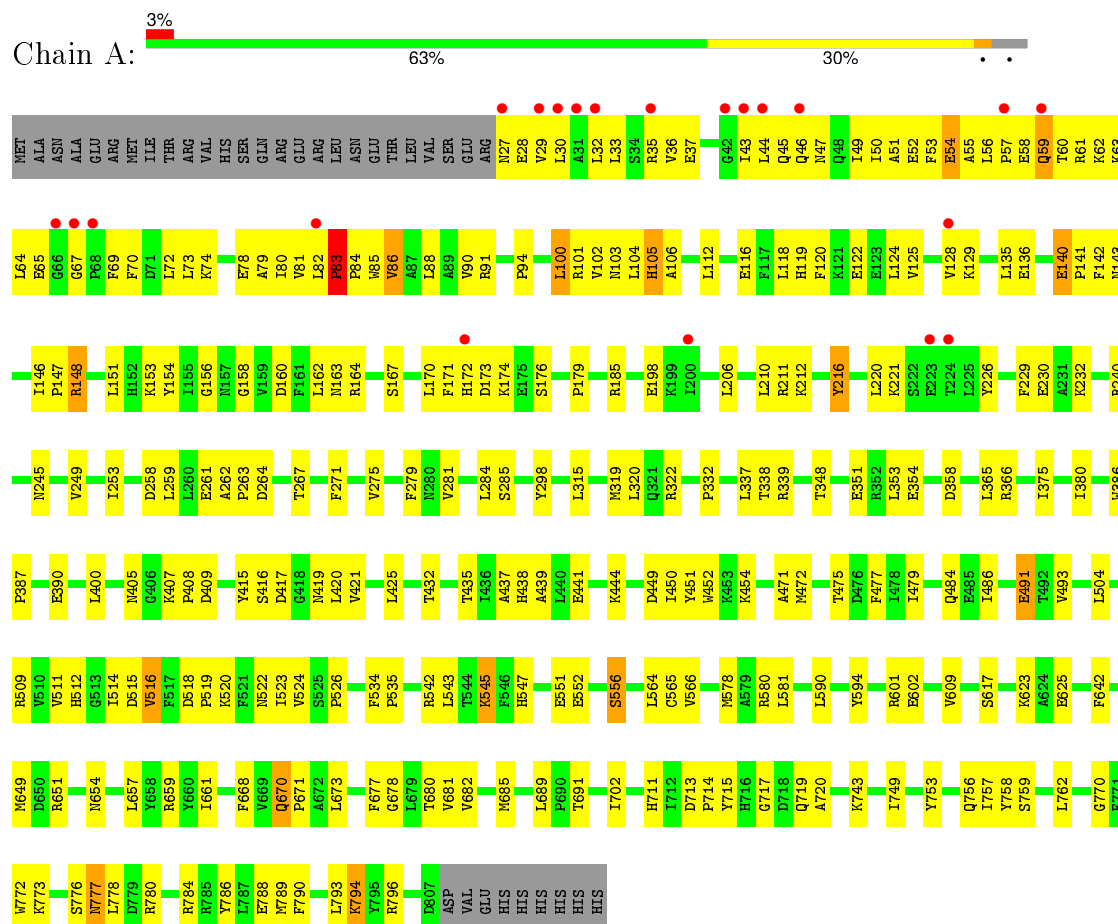
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	24	Total 24	O 24	0	0
8	D	54	Total 54	O 54	0	0
8	E	50	Total 50	O 50	0	0
8	F	79	Total 79	O 79	0	0
8	G	62	Total 62	O 62	0	0
8	H	49	Total 49	O 49	0	0

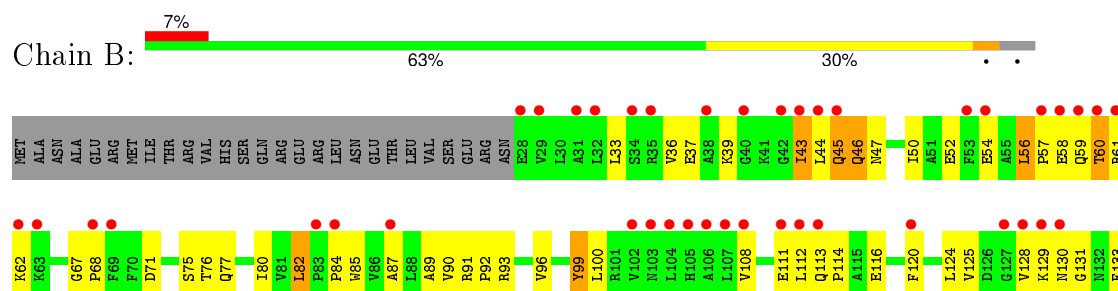
### 3 Residue-property plots

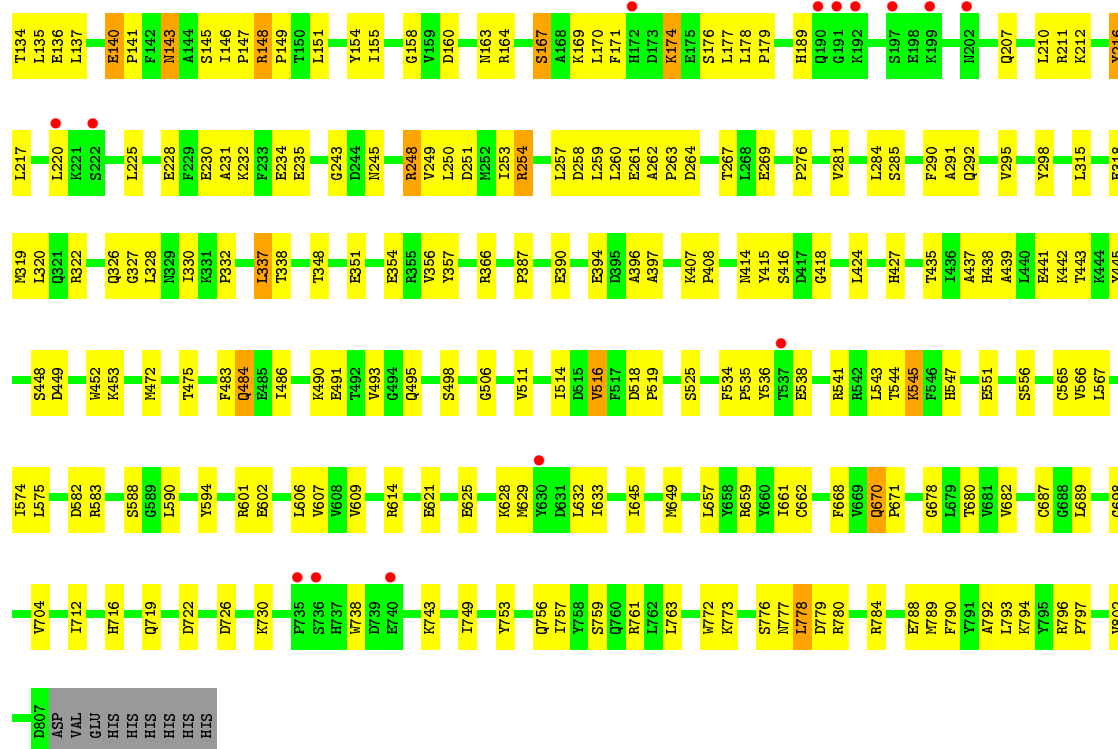
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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: Sucrose synthase 1

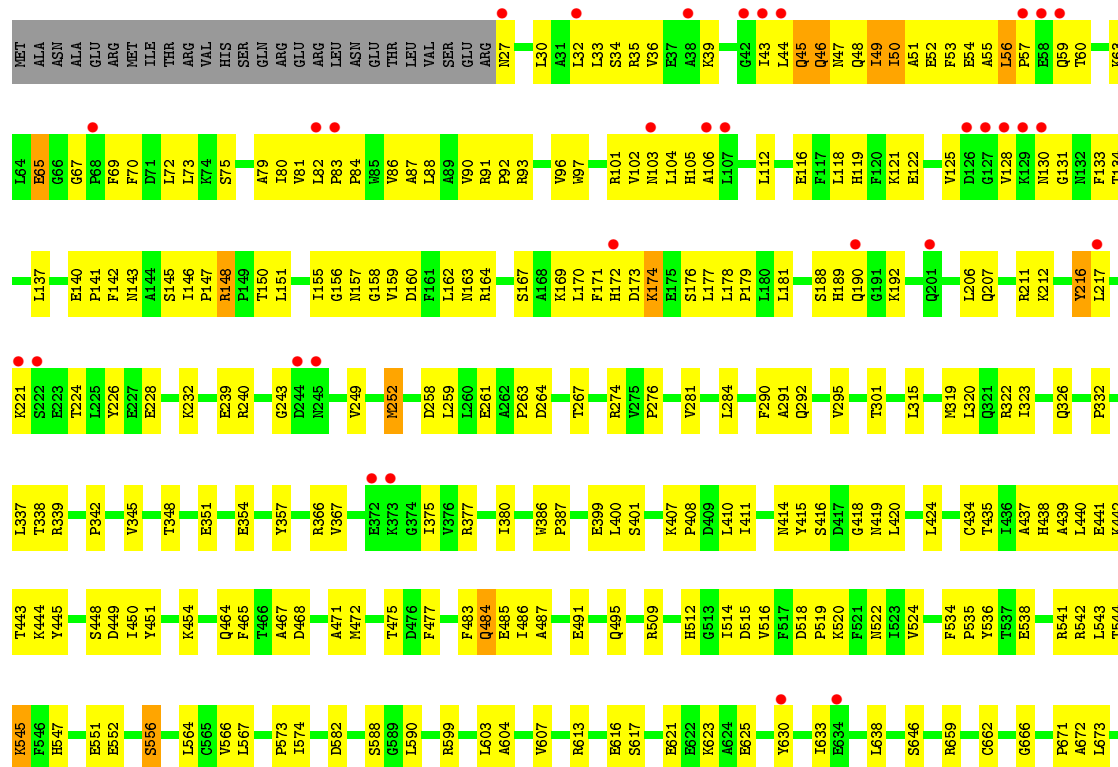


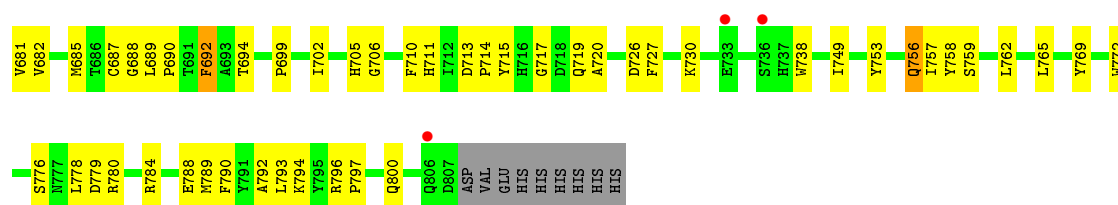
#### • Molecule 1: Sucrose synthase 1



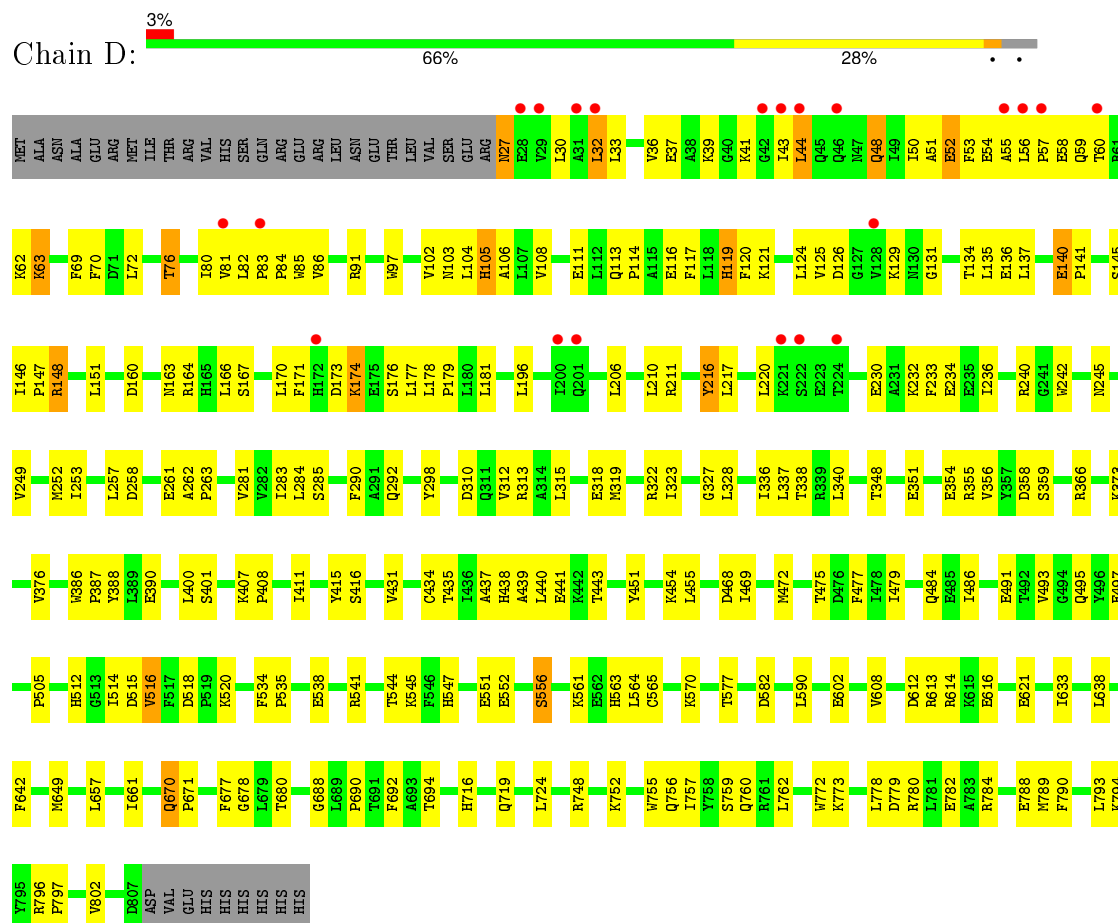


### • Molecule 1: Sucrose synthase 1

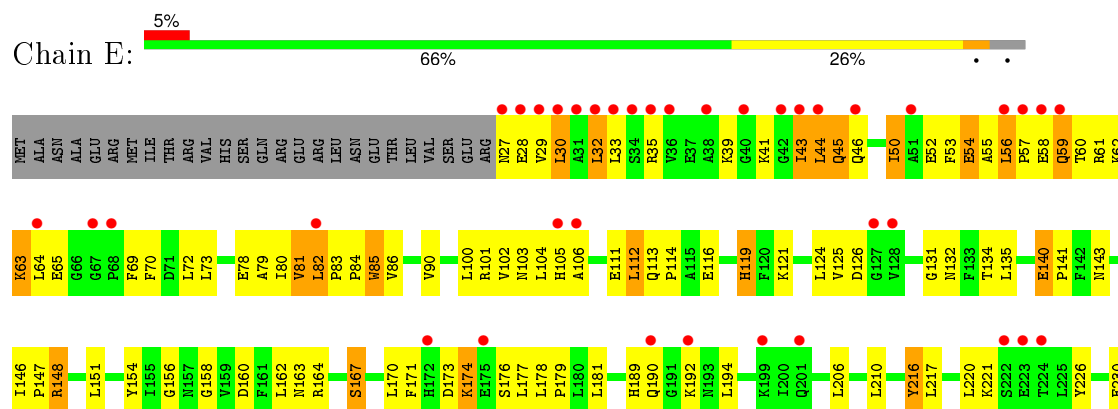


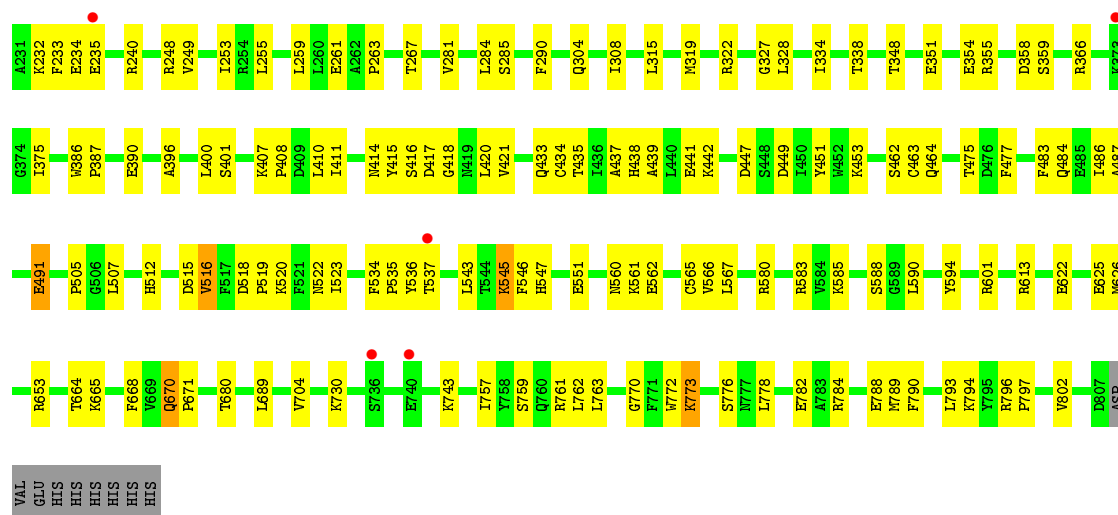


● Molecule 1: Sucrose synthase 1

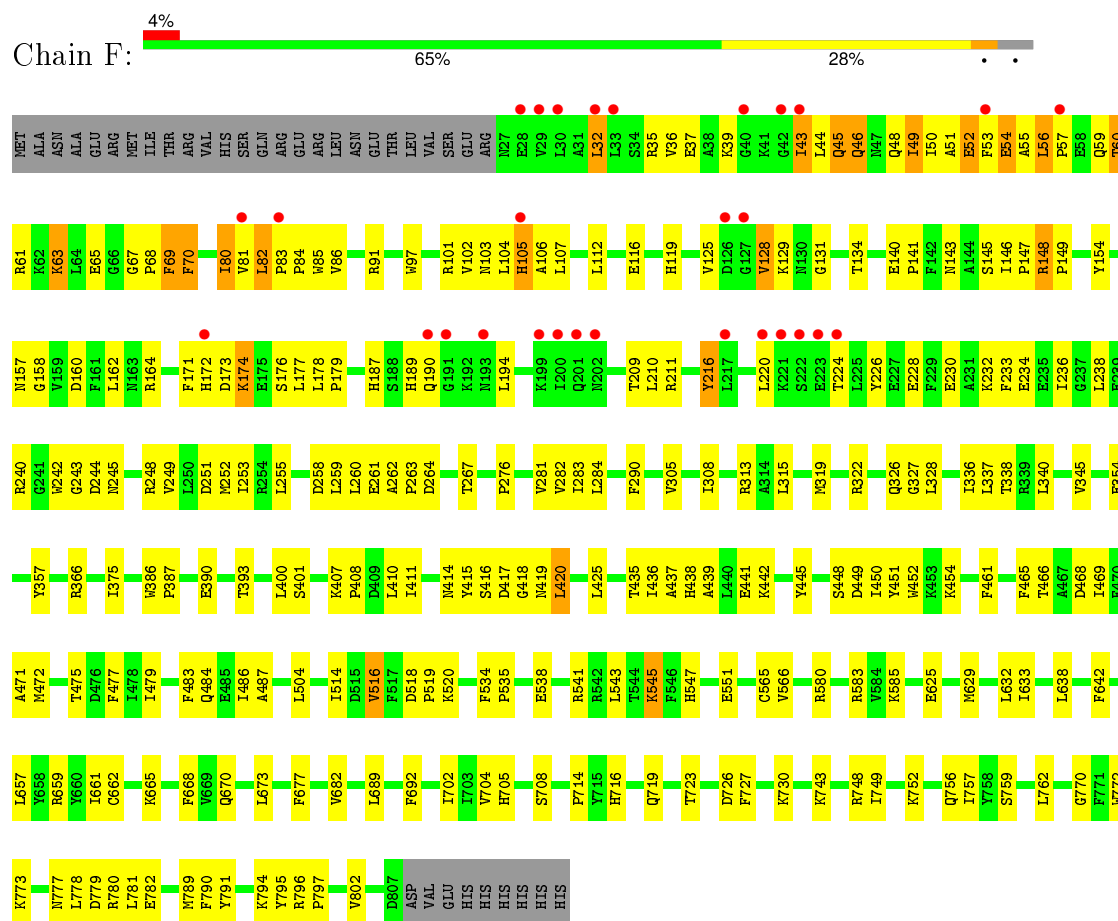


● Molecule 1: Sucrose synthase 1

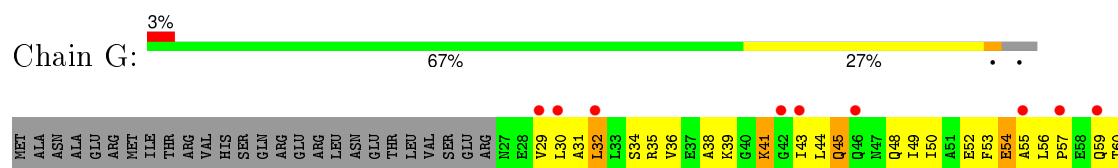




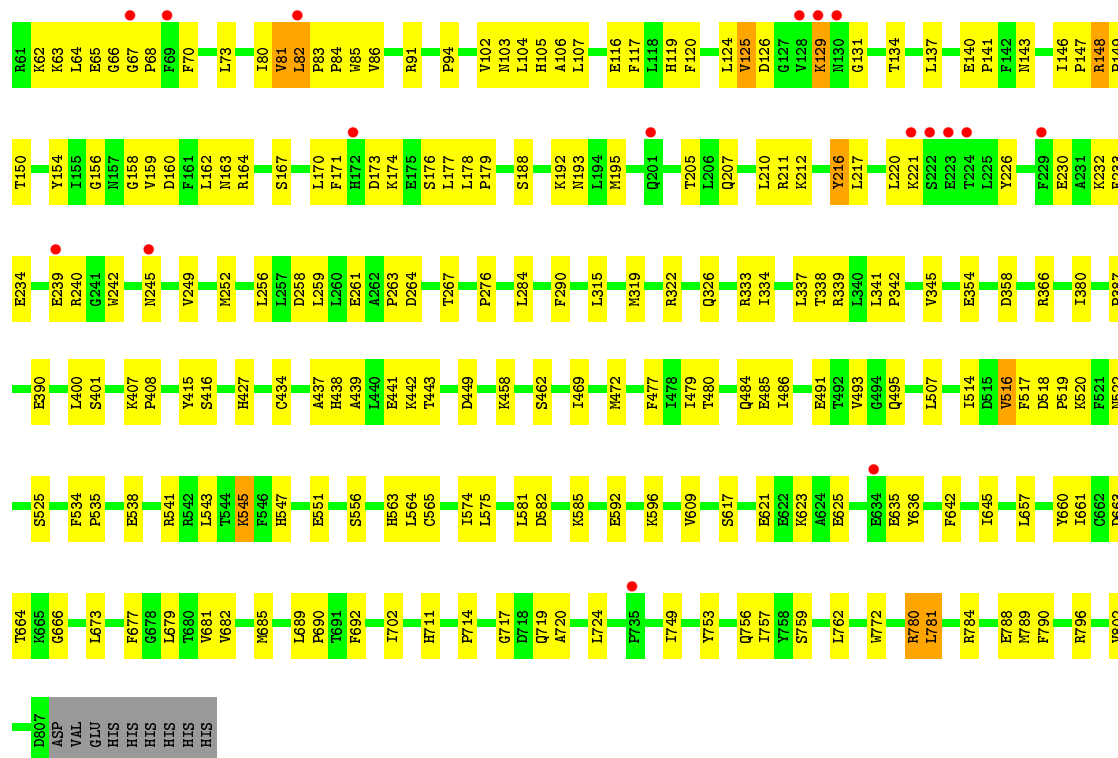
• Molecule 1: Sucrose synthase 1



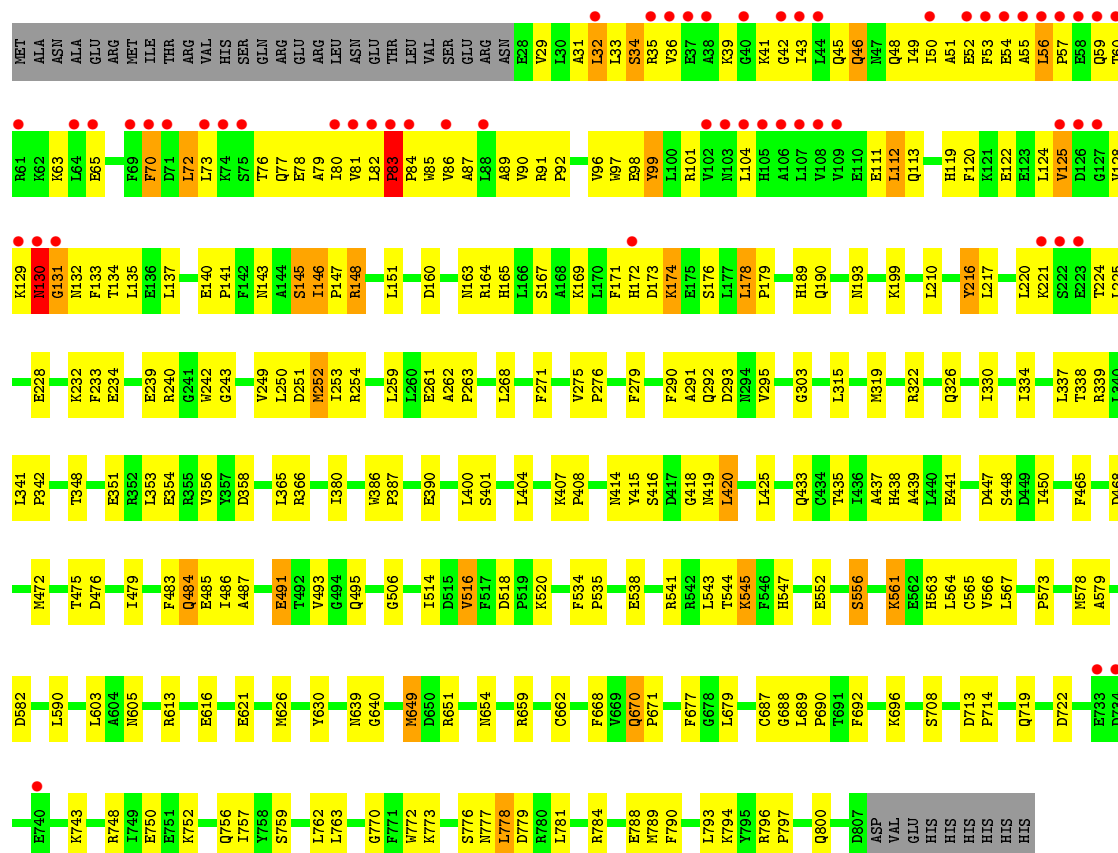
• Molecule 1: Sucrose synthase 1







• Molecule 1: Sucrose synthase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	276.75Å 261.88Å 160.19Å 90.00° 108.70° 90.00°	Depositor
Resolution (Å)	24.98 – 2.80 50.06 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (24.98-2.80) 99.7 (50.06-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.98 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.188 , 0.236 0.188 , 0.234	Depositor DCC
$R_{free}$ test set	13252 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.7	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 50.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	4 of 263585 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	51388	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.65 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.1188e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UDP, NHF, K, MLA, SO4, LCN

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	0.37	0/6436	0.56	1/8714 (0.0%)
1	B	0.35	0/6304	0.58	1/8549 (0.0%)
1	C	0.33	0/6437	0.53	0/8718
1	D	0.36	0/6427	0.56	1/8707 (0.0%)
1	E	0.35	0/6417	0.56	0/8693
1	F	0.38	0/6439	0.58	0/8719
1	G	0.36	0/6446	0.57	0/8728
1	H	0.35	0/6390	0.55	0/8655
All	All	0.36	0/51296	0.56	3/69483 (0.0%)

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	A	0	1
1	B	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	3
All	All	0	8

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	678	GLY	N-CA-C	5.35	126.48	113.10
1	B	678	GLY	N-CA-C	5.33	126.43	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	678	GLY	N-CA-C	5.11	125.88	113.10

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	PRO	Peptide
1	B	71	ASP	Peptide
1	E	81	VAL	Peptide
1	F	82	LEU	Peptide
1	G	81	VAL	Peptide

## 5.2 Too-close contacts

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	6289	0	6220	285	0
1	B	6158	0	5959	298	0
1	C	6290	0	6242	314	0
1	D	6280	0	6206	274	0
1	E	6271	0	6194	266	0
1	F	6292	0	6234	285	0
1	G	6299	0	6240	268	0
1	H	6243	0	6130	322	0
2	A	25	11	11	3	0
2	B	25	11	11	1	0
2	C	25	11	11	0	0
2	D	25	11	11	4	0
2	E	25	11	11	1	0
2	F	25	11	11	1	0
2	G	25	11	11	4	0
2	H	25	11	11	4	0
3	A	11	10	10	1	0
3	B	11	10	10	0	0
3	C	11	10	10	0	0
3	D	11	10	10	1	0
3	E	11	10	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	11	10	10	1	0
3	G	11	10	10	1	0
3	H	11	10	10	0	0
4	A	11	10	10	2	0
4	B	11	10	10	2	0
4	C	11	10	10	1	0
4	D	11	10	10	6	0
4	E	11	10	10	2	0
4	F	11	10	10	0	0
4	G	11	10	10	1	0
4	H	11	10	10	4	0
5	A	15	0	0	3	0
5	B	15	0	0	5	0
5	C	15	0	0	1	0
5	D	15	0	0	2	0
5	E	15	0	0	1	0
5	F	15	0	0	5	0
5	G	15	0	0	2	0
5	H	15	0	0	1	0
6	A	7	2	2	0	0
6	B	7	2	2	0	0
6	C	7	2	2	0	0
6	D	7	2	2	0	0
6	E	7	2	2	1	0
6	F	7	2	2	1	0
6	G	7	2	2	0	0
6	H	7	2	2	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	H	1	0	0	0	0
8	A	69	0	0	0	0
8	B	55	0	0	2	0
8	C	24	0	0	0	0
8	D	54	0	0	1	0
8	E	50	0	0	1	0
8	F	79	0	0	2	0
8	G	62	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	49	0	0	1	0
All	All	51124	264	49689	2198	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 22.

The worst 5 of 2198 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:GLN:HG2	1:B:50:ILE:CB	1.66	1.25
1:E:789:MET:HB3	1:H:789:MET:CE	1.68	1.22
1:F:789:MET:CE	1:G:789:MET:HB3	1.71	1.21
1:G:66:GLY:C	1:G:68:PRO:HD3	1.60	1.19
1:H:82:LEU:HB2	1:H:83:PRO:HD2	1.20	1.19

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	779/816 (96%)	741 (95%)	37 (5%)	1 (0%)	56	87
1	B	778/816 (95%)	724 (93%)	52 (7%)	2 (0%)	46	79
1	C	779/816 (96%)	739 (95%)	40 (5%)	0	100	100
1	D	779/816 (96%)	741 (95%)	38 (5%)	0	100	100
1	E	779/816 (96%)	742 (95%)	35 (4%)	2 (0%)	46	79
1	F	779/816 (96%)	737 (95%)	39 (5%)	3 (0%)	39	74
1	G	779/816 (96%)	743 (95%)	36 (5%)	0	100	100
1	H	778/816 (95%)	736 (95%)	40 (5%)	2 (0%)	46	79
All	All	6230/6528 (95%)	5903 (95%)	317 (5%)	10 (0%)	52	84

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	29	VAL
1	B	56	LEU
1	F	63	LYS
1	A	83	PRO
1	E	63	LYS

### 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	670/718 (93%)	644 (96%)	26 (4%)	39	74
1	B	635/718 (88%)	600 (94%)	35 (6%)	27	59
1	C	673/718 (94%)	649 (96%)	24 (4%)	42	76
1	D	671/718 (94%)	640 (95%)	31 (5%)	33	67
1	E	668/718 (93%)	633 (95%)	35 (5%)	29	62
1	F	672/718 (94%)	641 (95%)	31 (5%)	33	67
1	G	674/718 (94%)	647 (96%)	27 (4%)	38	73
1	H	658/718 (92%)	615 (94%)	43 (6%)	21	52
All	All	5321/5744 (93%)	5069 (95%)	252 (5%)	32	67

5 of 252 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	759	SER
1	E	484	GLN
1	H	484	GLN
1	E	32	LEU
1	E	119	HIS

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

Mol	Chain	Res	Type
1	C	512	HIS
1	E	190	GLN
1	H	59	GLN
1	D	46	GLN
1	D	103	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 8 are monoatomic - leaving 56 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	UDP	A	901	-	18,26,26	1.02	0	23,40,40	0.94	1 (4%)
3	LCN	A	903[A]	-	10,11,11	2.15	4 (40%)	9,15,15	2.38	2 (22%)
4	NHF	A	904[B]	-	11,11,11	1.67	4 (36%)	8,15,15	0.73	0
5	SO4	A	911	-	4,4,4	0.16	0	6,6,6	0.33	0
5	SO4	A	912	-	4,4,4	0.13	0	6,6,6	0.14	0
5	SO4	A	913	-	4,4,4	0.07	0	6,6,6	0.13	0
6	MLA	A	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	B	901	-	18,26,26	0.99	0	23,40,40	1.00	1 (4%)
3	LCN	B	903[A]	-	10,11,11	2.09	4 (40%)	9,15,15	2.75	3 (33%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NHF	B	904[B]	-	11,11,11	1.88	4 (36%)	8,15,15	0.78	0
5	SO4	B	911	-	4,4,4	0.23	0	6,6,6	0.16	0
5	SO4	B	912	-	4,4,4	0.09	0	6,6,6	0.17	0
5	SO4	B	913	-	4,4,4	0.07	0	6,6,6	0.24	0
6	MLA	B	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	C	901	-	18,26,26	0.95	0	23,40,40	0.91	1 (4%)
3	LCN	C	903[A]	-	10,11,11	2.14	4 (40%)	9,15,15	2.52	2 (22%)
4	NHF	C	904[B]	-	11,11,11	1.82	5 (45%)	8,15,15	0.64	0
5	SO4	C	911	-	4,4,4	0.07	0	6,6,6	0.28	0
5	SO4	C	912	-	4,4,4	0.08	0	6,6,6	0.17	0
5	SO4	C	913	-	4,4,4	0.08	0	6,6,6	0.12	0
6	MLA	C	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	D	901	-	18,26,26	1.07	0	23,40,40	1.03	2 (8%)
3	LCN	D	903[A]	-	10,11,11	2.06	3 (30%)	9,15,15	2.42	2 (22%)
4	NHF	D	904[B]	-	11,11,11	1.80	3 (27%)	8,15,15	1.03	0
5	SO4	D	911	-	4,4,4	0.07	0	6,6,6	0.29	0
5	SO4	D	912	-	4,4,4	0.08	0	6,6,6	0.30	0
5	SO4	D	913	-	4,4,4	0.10	0	6,6,6	0.10	0
6	MLA	D	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	E	901	-	18,26,26	0.96	0	23,40,40	1.08	1 (4%)
3	LCN	E	903[A]	-	10,11,11	1.99	2 (20%)	9,15,15	1.90	2 (22%)
4	NHF	E	904[B]	-	11,11,11	1.77	3 (27%)	8,15,15	0.63	0
5	SO4	E	911	-	4,4,4	0.12	0	6,6,6	0.25	0
5	SO4	E	912	-	4,4,4	0.04	0	6,6,6	0.06	0
5	SO4	E	913	-	4,4,4	0.04	0	6,6,6	0.11	0
6	MLA	E	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	F	901	-	18,26,26	1.00	1 (5%)	23,40,40	0.98	1 (4%)
3	LCN	F	903[A]	-	10,11,11	2.11	3 (30%)	9,15,15	2.67	3 (33%)
4	NHF	F	904[B]	-	11,11,11	1.84	3 (27%)	8,15,15	0.68	0
5	SO4	F	911	-	4,4,4	0.15	0	6,6,6	0.25	0
5	SO4	F	912	-	4,4,4	0.12	0	6,6,6	0.16	0
5	SO4	F	913	-	4,4,4	0.06	0	6,6,6	0.16	0
6	MLA	F	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	G	901	-	18,26,26	1.04	0	23,40,40	0.82	1 (4%)
3	LCN	G	903[A]	-	10,11,11	2.11	4 (40%)	9,15,15	2.54	2 (22%)
4	NHF	G	904[B]	-	11,11,11	1.84	4 (36%)	8,15,15	0.55	0
5	SO4	G	911	-	4,4,4	0.14	0	6,6,6	0.16	0
5	SO4	G	912	-	4,4,4	0.08	0	6,6,6	0.09	0
5	SO4	G	913	-	4,4,4	0.07	0	6,6,6	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	MLA	G	921	-	0,6,6	0.00	-	0,7,7	0.00	-
2	UDP	H	901	-	18,26,26	1.00	0	23,40,40	0.75	0
3	LCN	H	903[A]	-	10,11,11	2.00	3 (30%)	9,15,15	2.24	2 (22%)
4	NHF	H	904[B]	-	11,11,11	1.73	2 (18%)	8,15,15	0.54	0
5	SO4	H	911	-	4,4,4	0.16	0	6,6,6	0.17	0
5	SO4	H	912	-	4,4,4	0.07	0	6,6,6	0.13	0
5	SO4	H	913	-	4,4,4	0.09	0	6,6,6	0.19	0
6	MLA	H	921	-	0,6,6	0.00	-	0,7,7	0.00	-

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	UDP	A	901	-	-	0/12/32/32	0/2/2/2
3	LCN	A	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	A	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	A	911	-	-	0/0/0/0	0/0/0/0
5	SO4	A	912	-	-	0/0/0/0	0/0/0/0
5	SO4	A	913	-	-	0/0/0/0	0/0/0/0
6	MLA	A	921	-	-	0/0/4/4	0/0/0/0
2	UDP	B	901	-	-	0/12/32/32	0/2/2/2
3	LCN	B	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	B	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	B	911	-	-	0/0/0/0	0/0/0/0
5	SO4	B	912	-	-	0/0/0/0	0/0/0/0
5	SO4	B	913	-	-	0/0/0/0	0/0/0/0
6	MLA	B	921	-	-	0/0/4/4	0/0/0/0
2	UDP	C	901	-	-	0/12/32/32	0/2/2/2
3	LCN	C	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	C	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	C	911	-	-	0/0/0/0	0/0/0/0
5	SO4	C	912	-	-	0/0/0/0	0/0/0/0
5	SO4	C	913	-	-	0/0/0/0	0/0/0/0
6	MLA	C	921	-	-	0/0/4/4	0/0/0/0
2	UDP	D	901	-	-	0/12/32/32	0/2/2/2
3	LCN	D	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	D	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	D	911	-	-	0/0/0/0	0/0/0/0
5	SO4	D	912	-	-	0/0/0/0	0/0/0/0
5	SO4	D	913	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MLA	D	921	-	-	0/0/4/4	0/0/0/0
2	UDP	E	901	-	-	0/12/32/32	0/2/2/2
3	LCN	E	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	E	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	E	911	-	-	0/0/0/0	0/0/0/0
5	SO4	E	912	-	-	0/0/0/0	0/0/0/0
5	SO4	E	913	-	-	0/0/0/0	0/0/0/0
6	MLA	E	921	-	-	0/0/4/4	0/0/0/0
2	UDP	F	901	-	-	0/12/32/32	0/2/2/2
3	LCN	F	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	F	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	F	911	-	-	0/0/0/0	0/0/0/0
5	SO4	F	912	-	-	0/0/0/0	0/0/0/0
5	SO4	F	913	-	-	0/0/0/0	0/0/0/0
6	MLA	F	921	-	-	0/0/4/4	0/0/0/0
2	UDP	G	901	-	-	0/12/32/32	0/2/2/2
3	LCN	G	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	G	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	G	911	-	-	0/0/0/0	0/0/0/0
5	SO4	G	912	-	-	0/0/0/0	0/0/0/0
5	SO4	G	913	-	-	0/0/0/0	0/0/0/0
6	MLA	G	921	-	-	0/0/4/4	0/0/0/0
2	UDP	H	901	-	-	0/12/32/32	0/2/2/2
3	LCN	H	903[A]	-	-	0/2/19/19	0/1/1/1
4	NHF	H	904[B]	-	-	0/2/19/19	0/1/1/1
5	SO4	H	911	-	-	0/0/0/0	0/0/0/0
5	SO4	H	912	-	-	0/0/0/0	0/0/0/0
5	SO4	H	913	-	-	0/0/0/0	0/0/0/0
6	MLA	H	921	-	-	0/0/4/4	0/0/0/0

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	903[A]	LCN	O5-C5	-4.82	1.39	1.45
3	C	903[A]	LCN	O5-C5	-4.69	1.39	1.45
3	E	903[A]	LCN	O5-C5	-4.67	1.39	1.45
3	G	903[A]	LCN	O5-C5	-4.65	1.39	1.45
3	H	903[A]	LCN	O5-C5	-4.62	1.39	1.45

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	901	UDP	PA-O3A-PB	-3.56	120.74	132.67
2	D	901	UDP	PA-O3A-PB	-3.10	122.28	132.67
2	B	901	UDP	PA-O3A-PB	-2.96	122.75	132.67
2	A	901	UDP	PA-O3A-PB	-2.62	123.88	132.67
2	F	901	UDP	PA-O3A-PB	-2.52	124.23	132.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

32 monomers are involved in 56 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	UDP	3	0
3	A	903[A]	LCN	1	0
4	A	904[B]	NHF	2	0
5	A	912	SO4	2	0
5	A	913	SO4	1	0
2	B	901	UDP	1	0
4	B	904[B]	NHF	2	0
5	B	912	SO4	1	0
5	B	913	SO4	4	0
4	C	904[B]	NHF	1	0
5	C	913	SO4	1	0
2	D	901	UDP	4	0
3	D	903[A]	LCN	1	0
4	D	904[B]	NHF	6	0
5	D	913	SO4	2	0
2	E	901	UDP	1	0
4	E	904[B]	NHF	2	0
5	E	912	SO4	1	0
6	E	921	MLA	1	0
2	F	901	UDP	1	0
3	F	903[A]	LCN	1	0
5	F	912	SO4	2	0
5	F	913	SO4	3	0
6	F	921	MLA	1	0
2	G	901	UDP	4	0
3	G	903[A]	LCN	1	0
4	G	904[B]	NHF	1	0
5	G	912	SO4	1	0
5	G	913	SO4	1	0
2	H	901	UDP	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	904[B]	NHF	4	0
5	H	913	SO4	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, 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	781/816 (95%)	-0.29	21 (2%) 58 45	19, 34, 105, 147	0
1	B	780/816 (95%)	-0.02	55 (7%) 19 10	23, 43, 130, 171	0
1	C	781/816 (95%)	-0.08	35 (4%) 37 26	30, 52, 101, 141	0
1	D	781/816 (95%)	-0.31	21 (2%) 58 45	22, 35, 92, 136	0
1	E	781/816 (95%)	-0.16	43 (5%) 29 18	23, 39, 116, 147	0
1	F	781/816 (95%)	-0.30	29 (3%) 45 33	17, 33, 84, 128	0
1	G	781/816 (95%)	-0.27	26 (3%) 50 38	22, 39, 81, 126	0
1	H	780/816 (95%)	-0.03	56 (7%) 18 10	26, 43, 127, 156	0
All	All	6246/6528 (95%)	-0.18	286 (4%) 36 25	17, 41, 105, 171	0

The worst 5 of 286 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	60	THR	11.8
1	H	83	PRO	8.9
1	B	106	ALA	8.8
1	C	106	ALA	7.6
1	B	58	GLU	7.5

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 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
5	SO4	H	913	5/5	0.87	0.47	6.30	81,87,102,115	0
5	SO4	B	913	5/5	0.94	0.38	5.73	68,71,80,95	0
6	MLA	E	921	7/7	0.94	0.28	4.36	42,50,55,56	0
6	MLA	G	921	7/7	0.94	0.31	4.26	58,62,74,74	0
5	SO4	A	911	5/5	0.95	0.20	3.81	35,43,59,63	0
5	SO4	D	911	5/5	0.96	0.22	3.75	43,47,64,77	0
6	MLA	A	921	7/7	0.98	0.24	3.08	31,38,42,42	0
5	SO4	E	913	5/5	0.95	0.28	2.96	56,63,79,86	0
5	SO4	E	911	5/5	0.96	0.20	2.80	44,48,60,65	0
5	SO4	F	911	5/5	0.95	0.18	2.73	42,42,63,71	0
6	MLA	B	921	7/7	0.92	0.21	2.72	51,58,61,61	0
5	SO4	G	913	5/5	0.93	0.21	2.41	59,63,84,96	0
6	MLA	F	921	7/7	0.97	0.22	2.20	33,38,42,43	0
6	MLA	D	921	7/7	0.97	0.22	2.08	33,40,44,46	0
6	MLA	H	921	7/7	0.91	0.27	1.86	52,61,68,70	0
6	MLA	C	921	7/7	0.93	0.31	1.75	70,73,87,91	0
5	SO4	A	913	5/5	0.98	0.19	1.71	44,50,74,74	0
5	SO4	B	911	5/5	0.93	0.17	1.53	45,47,65,81	0
5	SO4	D	913	5/5	0.95	0.22	1.37	46,47,69,73	0
5	SO4	H	911	5/5	0.97	0.17	1.31	44,47,65,70	0
5	SO4	F	913	5/5	0.97	0.18	0.75	49,51,53,70	0
3	LCN	D	903[A]	11/11	0.95	0.16	0.35	24,27,32,32	21
7	K	D	931	1/1	0.91	0.24	0.33	72,72,72,72	0
2	UDP	H	901	25/25	0.98	0.18	0.28	28,34,41,44	0
2	UDP	C	901	25/25	0.98	0.17	0.25	32,41,49,54	0
7	K	C	931	1/1	0.95	0.25	0.22	81,81,81,81	0
7	K	B	931	1/1	0.81	0.25	0.20	83,83,83,83	0
7	K	F	931	1/1	0.76	0.21	0.05	82,82,82,82	0
5	SO4	G	911	5/5	0.98	0.13	-0.03	35,41,56,61	0
2	UDP	E	901	25/25	0.99	0.17	-0.15	21,27,35,38	0
2	UDP	D	901	25/25	0.99	0.15	-0.40	22,28,34,39	0
3	LCN	G	903[A]	11/11	0.97	0.16	-0.53	25,28,33,34	21
4	NHF	G	904[B]	11/11	0.97	0.16	-0.61	26,27,32,33	21
2	UDP	G	901	25/25	0.99	0.15	-0.62	20,28,34,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
7	K	G	931	1/1	0.82	0.20	-0.64	74,74,74,74	0
2	UDP	B	901	25/25	0.99	0.14	-0.67	23,31,37,43	0
7	K	A	931	1/1	0.95	0.15	-0.80	61,61,61,61	0
5	SO4	C	911	5/5	0.97	0.14	-0.83	48,51,70,71	0
2	UDP	F	901	25/25	0.99	0.15	-0.85	16,23,29,34	0
4	NHF	E	904[B]	11/11	0.96	0.15	-0.93	27,29,34,35	21
4	NHF	B	904[B]	11/11	0.98	0.15	-0.95	29,32,37,38	21
3	LCN	B	903[A]	11/11	0.98	0.15	-1.03	29,32,37,39	21
2	UDP	A	901	25/25	0.99	0.14	-1.06	18,23,29,32	0
4	NHF	D	904[B]	11/11	0.97	0.14	-1.20	24,27,32,32	21
4	NHF	C	904[B]	11/11	0.98	0.13	-1.36	37,38,45,47	21
3	LCN	C	903[A]	11/11	0.97	0.13	-1.46	36,39,46,48	21
4	NHF	F	904[B]	11/11	0.99	0.14	-1.54	24,25,30,32	21
3	LCN	A	903[A]	11/11	0.96	0.14	-1.64	23,25,29,30	21
3	LCN	E	903[A]	11/11	0.98	0.14	-1.65	26,30,35,36	21
7	K	H	931	1/1	0.95	0.13	-1.89	69,69,69,69	0
3	LCN	H	903[A]	11/11	0.95	0.13	-1.97	32,34,41,41	21
4	NHF	H	904[B]	11/11	0.97	0.13	-1.97	32,34,40,41	21
3	LCN	F	903[A]	11/11	0.98	0.13	-2.19	23,27,31,33	21
7	K	E	931	1/1	0.69	0.12	-2.23	73,73,73,73	0
4	NHF	A	904[B]	11/11	0.98	0.10	-3.88	23,25,29,30	21
5	SO4	D	912	5/5	0.90	0.22	-	59,77,86,101	0
5	SO4	F	912	5/5	0.96	0.15	-	55,58,68,85	0
5	SO4	A	912	5/5	0.92	0.15	-	51,56,69,85	0
5	SO4	H	912	5/5	0.93	0.23	-	70,77,86,105	0
5	SO4	E	912	5/5	0.96	0.16	-	57,62,70,86	0
5	SO4	C	912	5/5	0.82	0.36	-	84,89,106,115	0
5	SO4	G	912	5/5	0.95	0.23	-	59,69,86,94	0
5	SO4	C	913	5/5	0.88	0.31	-	81,84,103,107	0
5	SO4	B	912	5/5	0.92	0.17	-	70,76,90,106	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.