



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:24 PM GMT

PDB ID : 4I4Z  
Title : Synechocystis sp. PCC 6803 1,4-dihydroxy-2-naphthoyl-coenzyme A synthase (MenB) in complex with salicylyl-CoA  
Authors : Song, H.G.; Sun, Y.R.; Li, J.; Li, Y.; Jiang, M.; Zhou, J.H.; Guo, Z.H.  
Deposited on : 2012-11-28  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (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

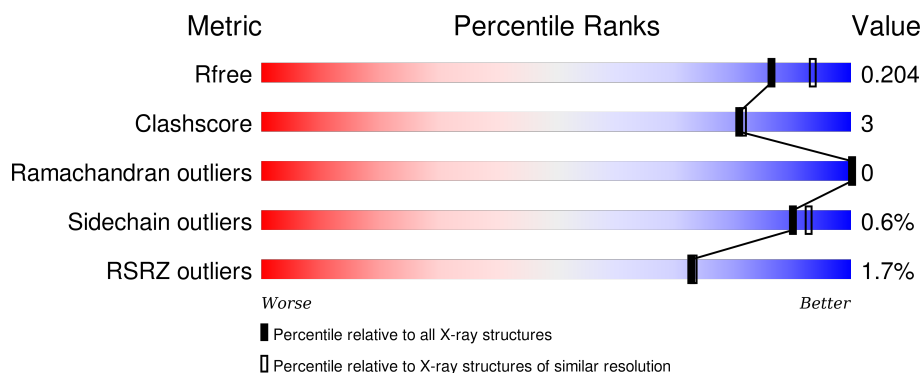
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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 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	275	<div> <div>94%</div> <div>6%</div> </div>
1	B	275	<div> <div>%</div> <div>95%</div> <div>5%</div> </div>
1	C	275	<div> <div>94%</div> <div>5%</div> </div>
1	D	275	<div> <div>97%</div> <div>.</div> </div>
1	E	275	<div> <div>96%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	275	
1	G	275	
1	H	275	
1	I	275	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BCT	B	302	-	-	-	X
3	BCT	C	302	-	-	-	X
3	BCT	E	302	-	-	-	X
3	BCT	F	302	-	-	-	X
3	BCT	G	302	-	-	-	X
3	BCT	H	302	-	-	-	X
4	MLI	C	303	-	-	-	X
4	MLI	I	303	-	-	-	X

## 2 Entry composition

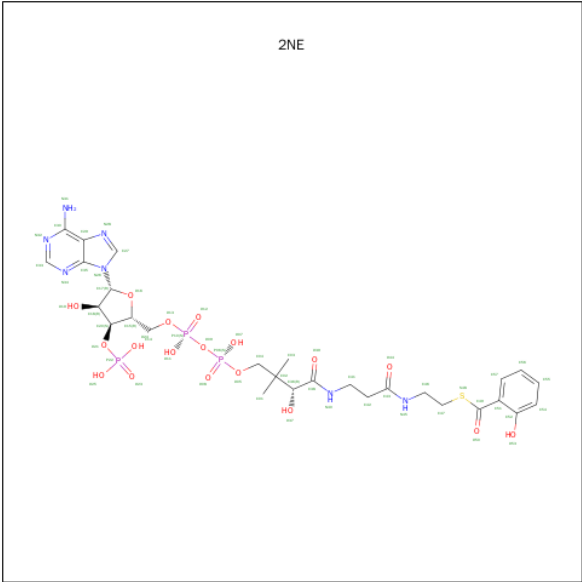
There are 5 unique types of molecules in this entry. The entry contains 20593 atoms, of which 4 are hydrogens and 0 are deuteriums.

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 Naphthoate synthase.

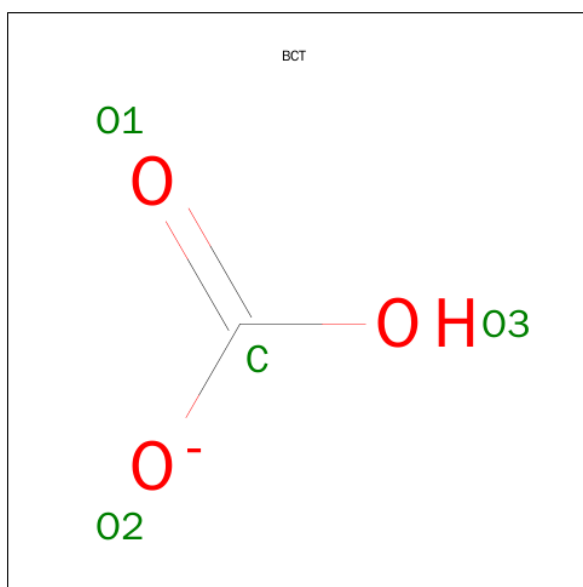
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2135	1354	375	395	11			
1	B	274	Total	C	N	O	S	0	0	0
			2120	1346	374	390	10			
1	C	275	Total	C	N	O	S	0	1	0
			2142	1359	378	394	11			
1	D	275	Total	C	N	O	S	0	2	0
			2144	1361	377	395	11			
1	E	275	Total	C	N	O	S	0	0	0
			2125	1350	370	394	11			
1	F	275	Total	C	N	O	S	0	0	0
			2120	1348	370	391	11			
1	G	275	Total	C	N	O	S	0	0	0
			2121	1347	372	391	11			
1	H	275	Total	C	N	O	S	0	0	0
			2109	1341	364	393	11			
1	I	275	Total	C	N	O	S	0	0	0
			2127	1349	374	393	11			

- Molecule 2 is SALICYLYL COA (three-letter code: 2NE) (formula:  $C_{28}H_{40}N_7O_{18}P_3S$ ).



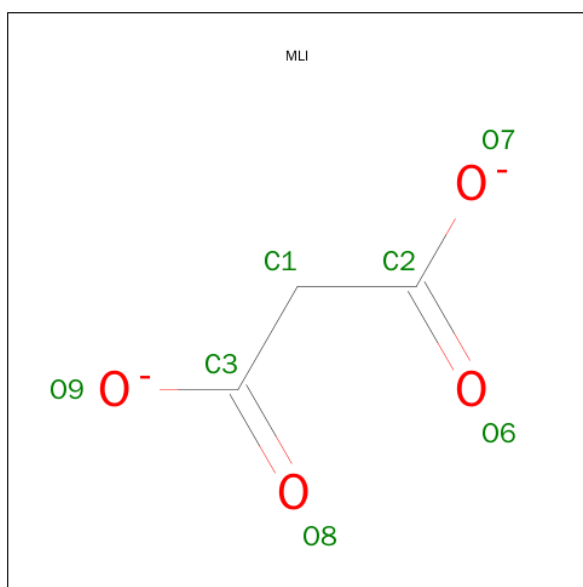
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	G	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	H	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		
2	I	1	Total	C	N	O	P	S	0	0
			57	28	7	18	3	1		

- Molecule 3 is BICARBONATE ION (three-letter code: BCT) (formula: CHO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	1	3		
3	B	1	Total	C	O	0	0
			4	1	3		
3	C	1	Total	C	O	0	0
			4	1	3		
3	D	1	Total	C	O	0	0
			4	1	3		
3	E	1	Total	C	O	0	0
			4	1	3		
3	F	1	Total	C	O	0	0
			4	1	3		
3	G	1	Total	C	O	0	0
			4	1	3		
3	H	1	Total	C	O	0	0
			4	1	3		
3	I	1	Total	C	O	0	0
			4	1	3		

- Molecule 4 is MALONATE ION (three-letter code: MLI) (formula: C<sub>3</sub>H<sub>2</sub>O<sub>4</sub>).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	114	Total	O	0	0
			114	114		
5	B	89	Total	O	0	0
			89	89		
5	C	132	Total	O	0	0
			132	132		
5	D	103	Total	O	0	0
			103	103		
5	E	120	Total	O	0	0
			120	120		
5	F	104	Total	O	0	0
			104	104		
5	G	62	Total	O	0	0
			62	62		
5	H	60	Total	O	0	0
			60	60		
5	I	99	Total	O	0	0
			99	99		

### 3 Residue-property plots

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

- Molecule 1: Naphthoate synthase

Chain A: 



- Molecule 1: Naphthoate synthase

Chain B: 



- Molecule 1: Naphthoate synthase

Chain C: 



- Molecule 1: Naphthoate synthase

Chain D: 



- Molecule 1: Naphthoate synthase

Chain E: 



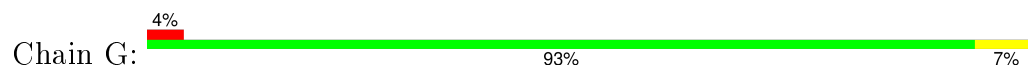
- Molecule 1: Naphthoate synthase

Chain F: 

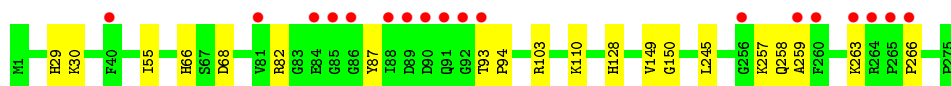
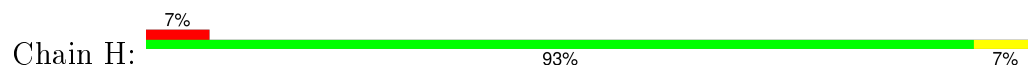




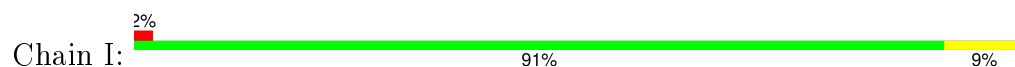
- Molecule 1: Naphthoate synthase



- Molecule 1: Naphthoate synthase



- Molecule 1: Naphthoate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.21Å 139.21Å 220.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.67 – 2.00 42.13 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.67-2.00) 99.7 (42.13-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.88 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.198 , 0.221 0.170 , 0.204	Depositor DCC
$R_{free}$ test set	8393 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.7	EDS
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 166972 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	20593	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.70% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCT, MLI, 2NE

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	0/2183	0.51	0/2951
1	B	0.36	0/2168	0.52	0/2932
1	C	0.41	0/2191	0.52	0/2962
1	D	0.38	0/2194	0.50	0/2968
1	E	0.39	0/2173	0.52	0/2939
1	F	0.39	0/2168	0.52	0/2932
1	G	0.34	0/2169	0.50	0/2934
1	H	0.33	0/2157	0.51	0/2921
1	I	0.37	0/2173	0.52	0/2937
All	All	0.37	0/19576	0.51	0/26476

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

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	2135	0	2101	19	0
1	B	2120	0	2083	10	0
1	C	2142	0	2105	24	0
1	D	2144	0	2093	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2125	0	2081	10	1
1	F	2120	0	2080	17	0
1	G	2121	0	2082	16	0
1	H	2109	0	2049	12	2
1	I	2127	0	2086	19	1
2	A	57	0	37	2	0
2	B	57	0	35	2	0
2	C	57	0	35	1	0
2	D	57	0	35	3	0
2	E	57	0	35	2	0
2	F	57	0	35	2	0
2	G	57	0	35	5	0
2	H	57	0	35	4	1
2	I	57	0	35	4	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	4	0	1	0	0
3	D	4	0	0	0	0
3	E	4	0	1	0	0
3	F	4	0	1	0	0
3	G	4	0	1	1	0
3	H	4	0	0	0	0
3	I	4	0	0	0	0
4	C	7	2	2	0	0
4	I	7	2	2	0	0
5	A	114	0	0	1	0
5	B	89	0	0	0	0
5	C	132	0	0	2	0
5	D	103	0	0	3	0
5	E	120	0	0	1	0
5	F	104	0	0	2	0
5	G	62	0	0	2	0
5	H	60	0	0	0	0
5	I	99	0	0	3	0
All	All	20589	4	19085	127	3

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.

All (127) 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:C:82:ARG:HG2	1:E:257:LYS:HD3	1.29	1.11
2:I:301:2NE:O50	2:I:301:2NE:H33	1.78	0.83
1:I:53:ASN:O	1:I:54:ARG:N	2.14	0.80
1:I:149:VAL:HG21	2:I:301:2NE:H35	1.64	0.78
1:H:257:LYS:HE3	1:H:258:GLN:OE1	1.83	0.77
1:C:82:ARG:HD2	5:C:414:HOH:O	1.84	0.76
1:G:89:ASP:OD2	1:G:93:THR:HG23	1.84	0.76
1:A:103:ARG:NH2	1:F:238:GLU:OE2	2.18	0.75
1:C:82:ARG:HG2	1:E:257:LYS:CD	2.14	0.72
1:C:5:ILE:HD12	1:C:15:TYR:CD2	2.23	0.72
1:C:238:GLU:OE2	1:E:103:ARG:NH2	2.21	0.71
2:G:301:2NE:O53	3:G:302:BCT:O1	2.09	0.71
1:I:53:ASN:CA	1:I:54:ARG:N	2.55	0.69
2:H:301:2NE:H33	2:H:301:2NE:O50	1.91	0.69
1:G:203:GLU:OE2	5:G:454:HOH:O	2.11	0.68
1:F:103:ARG:NH2	5:F:437:HOH:O	2.27	0.66
1:G:41:GLU:OE2	5:G:428:HOH:O	2.12	0.66
1:B:103:ARG:NH2	1:D:238:GLU:OE2	2.29	0.64
1:A:103:ARG:NH1	1:F:103:ARG:NH1	2.45	0.64
1:C:103:ARG:NH2	1:E:238:GLU:OE2	2.31	0.63
1:G:89:ASP:CG	1:G:93:THR:HG23	2.19	0.63
1:I:2:ASP:OD2	1:I:4:HIS:NE2	2.32	0.62
1:G:210:GLU:O	1:G:214:LYS:NZ	2.29	0.60
1:F:103:ARG:HD2	5:F:437:HOH:O	2.02	0.59
1:I:53:ASN:CA	1:I:53:ASN:O	2.51	0.59
1:H:149:VAL:HG21	2:H:301:2NE:H34	1.85	0.59
2:D:301:2NE:C54	5:D:440:HOH:O	2.49	0.59
1:A:149:VAL:HG21	2:A:301:2NE:H32	1.84	0.58
1:G:16:LYS:NZ	1:G:52:ASP:OD2	2.23	0.58
1:C:5:ILE:N	1:C:5:ILE:CD1	2.66	0.58
1:D:245:LEU:HD23	1:D:245:LEU:C	2.24	0.57
1:C:5:ILE:HD11	1:C:15:TYR:HE2	1.70	0.56
2:D:301:2NE:H37	5:D:440:HOH:O	2.07	0.55
1:C:5:ILE:CD1	1:C:15:TYR:CE2	2.90	0.54
1:A:103:ARG:HH11	1:F:103:ARG:NH1	2.06	0.54
1:B:149:VAL:HG21	2:B:301:2NE:H32	1.90	0.54
1:C:5:ILE:HD12	1:C:15:TYR:HD2	1.72	0.54
1:G:31:ARG:NH2	2:G:301:2NE:O09	2.41	0.53
1:E:55:ILE:O	1:E:110:LYS:HD2	2.09	0.53
1:C:183:GLN:HG3	5:C:428:HOH:O	2.08	0.52
1:B:79:GLN:NE2	2:B:301:2NE:H35	2.25	0.51
2:H:301:2NE:O39	2:H:301:2NE:H3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:245:LEU:C	1:I:245:LEU:HD23	2.31	0.51
1:B:199:ARG:O	1:B:199:ARG:HG3	2.11	0.50
1:B:184:GLU:HG2	1:B:187:ARG:HH22	1.76	0.50
1:H:66:HIS:HB3	1:H:68:ASP:OD1	2.12	0.49
1:I:31:ARG:NH1	1:I:70:LYS:HG3	2.27	0.49
1:I:251:GLU:HG3	1:I:252:GLU:N	2.27	0.49
2:F:301:2NE:O50	2:F:301:2NE:H33	2.11	0.49
1:B:103:ARG:HH11	1:D:103:ARG:HH21	1.60	0.48
1:A:7:LYS:HG3	1:A:8:HIS:N	2.28	0.48
2:E:301:2NE:O13	2:E:301:2NE:H15	2.13	0.48
1:C:5:ILE:HD11	1:C:15:TYR:CE2	2.47	0.48
1:E:199:ARG:HG3	1:E:199:ARG:O	2.14	0.48
1:A:103:ARG:HH21	1:F:238:GLU:HG3	1.78	0.48
1:G:31:ARG:HH21	2:G:301:2NE:P06	2.36	0.47
1:G:79:GLN:NE2	2:G:301:2NE:H35	2.28	0.47
1:B:137:ALA:HA	1:B:195:VAL:O	2.14	0.47
1:F:90:ASP:HB3	1:H:29:HIS:HD2	1.79	0.47
1:A:187:ARG:NH1	5:A:497:HOH:O	1.84	0.47
1:C:137:ALA:HA	1:C:195:VAL:O	2.14	0.47
1:I:251:GLU:CG	5:I:449:HOH:O	2.63	0.47
1:G:199:ARG:O	1:G:199:ARG:HG3	2.15	0.46
1:C:5:ILE:N	1:C:5:ILE:HD12	2.31	0.46
1:I:147:PRO:HD2	1:I:177:CYS:SG	2.55	0.46
1:A:103:ARG:NH2	1:F:238:GLU:HG3	2.31	0.46
1:I:77:GLY:HA3	2:I:301:2NE:H40	1.98	0.46
1:C:55:ILE:O	1:C:110:LYS:HD2	2.16	0.46
1:H:82:ARG:NH1	1:H:150:GLY:O	2.49	0.46
1:A:199:ARG:HG3	1:A:199:ARG:O	2.16	0.46
1:F:137:ALA:HB1	1:F:197:VAL:HA	1.98	0.45
1:A:245:LEU:C	1:A:245:LEU:HD23	2.36	0.45
1:C:5:ILE:HD12	1:C:15:TYR:CE2	2.49	0.45
1:A:103:ARG:NH1	1:F:103:ARG:HH11	2.14	0.45
1:G:137:ALA:HB1	1:G:197:VAL:HG22	1.99	0.45
1:A:103:ARG:NH2	1:F:238:GLU:CG	2.81	0.44
1:H:245:LEU:C	1:H:245:LEU:HD23	2.38	0.44
1:H:87:TYR:OH	2:H:301:2NE:S48	2.75	0.44
1:I:267:ASP:OD1	1:I:269:SER:OG	2.27	0.44
1:G:89:ASP:OD2	1:G:93:THR:CG2	2.60	0.44
1:A:86:GLY:HA2	1:F:248:TYR:HD2	1.81	0.44
1:H:55:ILE:O	1:H:110:LYS:HD2	2.18	0.44
2:D:301:2NE:H15	2:D:301:2NE:O13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:29:HIS:CD2	1:H:30:LYS:HG2	2.52	0.44
1:B:55:ILE:O	1:B:110:LYS:HD2	2.18	0.43
1:C:7:LYS:HD3	1:C:9:TYR:OH	2.18	0.43
1:F:55:ILE:O	1:F:110:LYS:HD2	2.18	0.43
1:F:149:VAL:HG21	2:F:301:2NE:H35	2.01	0.43
1:A:66:HIS:CG	1:A:67:SER:H	2.37	0.43
1:D:70:LYS:HA	1:D:70:LYS:HD2	1.80	0.43
1:E:245:LEU:C	1:E:245:LEU:HD23	2.38	0.43
1:I:251:GLU:HG2	5:I:449:HOH:O	2.18	0.43
1:E:137:ALA:HA	1:E:195:VAL:O	2.18	0.43
1:B:248:TYR:HD2	1:D:86:GLY:HA2	1.84	0.43
1:I:11:ASP:HB2	1:I:41:GLU:OE1	2.18	0.42
1:A:210:GLU:O	1:A:214:LYS:NZ	2.50	0.42
1:C:199:ARG:HG3	1:C:199:ARG:O	2.20	0.42
2:C:301:2NE:H15	2:C:301:2NE:O13	2.19	0.42
1:C:103:ARG:NH2	1:E:238:GLU:HG3	2.35	0.42
1:G:93:THR:HA	1:G:94:PRO:HD3	1.86	0.42
1:A:274:LEU:HB3	1:A:275:PRO:HD2	2.02	0.42
1:A:103:ARG:HH21	1:F:238:GLU:CG	2.32	0.42
1:C:103:ARG:HH21	1:E:238:GLU:HG3	1.84	0.41
1:I:251:GLU:HG3	5:I:449:HOH:O	2.20	0.41
1:D:202:GLU:OE1	5:D:435:HOH:O	2.21	0.41
1:I:19:GLY:HA2	1:I:54:ARG:O	2.20	0.41
1:G:35:ARG:HG2	1:G:38:THR:OG1	2.20	0.41
1:A:59:LEU:HD13	1:A:115:LEU:HD11	2.02	0.41
1:I:27:ARG:NH2	1:I:78:ASP:OD2	2.37	0.41
1:H:259:ALA:CB	1:H:266:PRO:HA	2.49	0.41
1:G:149:VAL:HG21	2:G:301:2NE:H32	2.02	0.41
1:H:93:THR:HA	1:H:94:PRO:HD3	1.98	0.41
1:D:27:ARG:NH2	1:D:78:ASP:OD2	2.40	0.41
1:H:257:LYS:HB3	1:H:257:LYS:HE2	1.69	0.41
1:F:93:THR:HA	1:F:94:PRO:HD3	1.92	0.41
1:C:93:THR:HA	1:C:94:PRO:HD3	1.91	0.41
2:E:301:2NE:C54	5:E:414:HOH:O	2.68	0.41
1:I:149:VAL:CG2	2:I:301:2NE:H35	2.43	0.41
1:B:82:ARG:NH1	1:B:150:GLY:O	2.54	0.40
1:F:245:LEU:C	1:F:245:LEU:HD23	2.42	0.40
2:A:301:2NE:O13	2:A:301:2NE:H15	2.21	0.40
1:A:66:HIS:CG	1:A:67:SER:N	2.89	0.40
1:G:125:HIS:CD2	1:G:142:PHE:HB3	2.56	0.40
1:I:268:PHE:HA	1:I:271:TYR:HD2	1.86	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:263:LYS:NZ	2:H:301:2NE:O25[6_554]	1.59	0.61
1:H:103:ARG:NH2	1:H:103:ARG:NH2[6_554]	2.05	0.15
1:E:26:ASN:ND2	1:I:91:GLN:OE1[1_655]	2.16	0.04

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	273/275 (99%)	266 (97%)	7 (3%)	0	100	100
1	B	272/275 (99%)	266 (98%)	6 (2%)	0	100	100
1	C	274/275 (100%)	268 (98%)	6 (2%)	0	100	100
1	D	275/275 (100%)	269 (98%)	6 (2%)	0	100	100
1	E	273/275 (99%)	267 (98%)	6 (2%)	0	100	100
1	F	273/275 (99%)	267 (98%)	6 (2%)	0	100	100
1	G	273/275 (99%)	267 (98%)	6 (2%)	0	100	100
1	H	273/275 (99%)	266 (97%)	7 (3%)	0	100	100
1	I	271/275 (98%)	265 (98%)	6 (2%)	0	100	100
All	All	2457/2475 (99%)	2401 (98%)	56 (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	218/218 (100%)	217 (100%)	1 (0%)	92	94
1	B	215/218 (99%)	214 (100%)	1 (0%)	92	94
1	C	218/218 (100%)	216 (99%)	2 (1%)	84	88
1	D	217/218 (100%)	216 (100%)	1 (0%)	92	94
1	E	215/218 (99%)	214 (100%)	1 (0%)	92	94
1	F	214/218 (98%)	213 (100%)	1 (0%)	92	94
1	G	215/218 (99%)	213 (99%)	2 (1%)	84	88
1	H	212/218 (97%)	211 (100%)	1 (0%)	92	94
1	I	216/218 (99%)	215 (100%)	1 (0%)	92	94
All	All	1940/1962 (99%)	1929 (99%)	11 (1%)	90	93

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

Mol	Chain	Res	Type
1	A	128	HIS
1	B	128	HIS
1	C	5	ILE
1	C	128	HIS
1	D	128	HIS
1	E	128	HIS
1	F	128	HIS
1	G	93	THR
1	G	128	HIS
1	H	128	HIS
1	I	128	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	29	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

20 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	2NE	A	301	-	50,60,60	2.14	9 (18%)	65,89,89	2.22	13 (20%)
3	BCT	A	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	B	301	-	50,60,60	2.09	14 (28%)	65,89,89	2.44	17 (26%)
3	BCT	B	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	C	301	-	50,60,60	2.15	17 (34%)	65,89,89	2.47	12 (18%)
3	BCT	C	302	-	0,3,3	0.00	-	0,3,3	0.00	-
4	MLI	C	303	-	0,6,6	0.00	-	0,7,7	0.00	-
2	2NE	D	301	-	50,60,60	2.14	15 (30%)	65,89,89	2.61	13 (20%)
3	BCT	D	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	E	301	-	50,60,60	2.09	15 (30%)	65,89,89	2.23	14 (21%)
3	BCT	E	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	F	301	-	50,60,60	2.13	14 (28%)	65,89,89	2.19	13 (20%)
3	BCT	F	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	G	301	-	50,60,60	2.04	13 (26%)	65,89,89	2.56	16 (24%)
3	BCT	G	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	H	301	-	50,60,60	1.99	9 (18%)	65,89,89	2.66	18 (27%)
3	BCT	H	302	-	0,3,3	0.00	-	0,3,3	0.00	-
2	2NE	I	301	-	50,60,60	2.17	17 (34%)	65,89,89	2.62	15 (23%)
3	BCT	I	302	-	0,3,3	0.00	-	0,3,3	0.00	-
4	MLI	I	303	-	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	2NE	A	301	-	-	0/50/71/71	0/4/4/4
3	BCT	A	302	-	-	0/0/0/0	0/0/0/0
2	2NE	B	301	-	-	0/50/71/71	0/4/4/4
3	BCT	B	302	-	-	0/0/0/0	0/0/0/0
2	2NE	C	301	-	-	0/50/71/71	0/4/4/4
3	BCT	C	302	-	-	0/0/0/0	0/0/0/0
4	MLI	C	303	-	-	0/0/4/4	0/0/0/0
2	2NE	D	301	-	-	0/50/71/71	0/4/4/4
3	BCT	D	302	-	-	0/0/0/0	0/0/0/0
2	2NE	E	301	-	-	0/50/71/71	0/4/4/4
3	BCT	E	302	-	-	0/0/0/0	0/0/0/0
2	2NE	F	301	-	-	0/50/71/71	0/4/4/4
3	BCT	F	302	-	-	0/0/0/0	0/0/0/0
2	2NE	G	301	-	-	0/50/71/71	0/4/4/4
3	BCT	G	302	-	-	0/0/0/0	0/0/0/0
2	2NE	H	301	-	-	0/50/71/71	0/4/4/4
3	BCT	H	302	-	-	0/0/0/0	0/0/0/0
2	2NE	I	301	-	-	0/50/71/71	0/4/4/4
3	BCT	I	302	-	-	0/0/0/0	0/0/0/0
4	MLI	I	303	-	-	0/0/4/4	0/0/0/0

All (123) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	2NE	C18-C20	-5.38	1.40	1.53
2	C	301	2NE	C18-C20	-5.25	1.41	1.53
2	G	301	2NE	C18-C20	-5.13	1.41	1.53
2	I	301	2NE	C18-C20	-5.13	1.41	1.53
2	A	301	2NE	C18-C20	-5.04	1.41	1.53
2	H	301	2NE	C18-C20	-4.95	1.41	1.53
2	F	301	2NE	O37-C36	-4.84	1.32	1.42
2	D	301	2NE	C18-C20	-4.67	1.42	1.53
2	E	301	2NE	C18-C20	-4.66	1.42	1.53
2	F	301	2NE	C18-C20	-4.61	1.42	1.53
2	D	301	2NE	O37-C36	-4.21	1.33	1.42
2	E	301	2NE	O37-C36	-4.14	1.33	1.42
2	I	301	2NE	O37-C36	-4.11	1.34	1.42
2	B	301	2NE	O37-C36	-3.98	1.34	1.42
2	G	301	2NE	O37-C36	-3.75	1.34	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	2NE	O37-C36	-3.65	1.34	1.42
2	D	301	2NE	C20-C15	-3.62	1.42	1.52
2	H	301	2NE	O37-C36	-3.50	1.35	1.42
2	C	301	2NE	P06-O07	-3.34	1.40	1.54
2	E	301	2NE	C20-C15	-3.32	1.43	1.52
2	G	301	2NE	C20-C15	-3.27	1.43	1.52
2	D	301	2NE	P06-O07	-3.26	1.41	1.54
2	I	301	2NE	P06-O07	-3.26	1.41	1.54
2	D	301	2NE	P10-O11	-3.20	1.41	1.54
2	F	301	2NE	C20-C15	-3.16	1.43	1.52
2	C	301	2NE	C20-C15	-3.15	1.43	1.52
2	B	301	2NE	C20-C15	-3.11	1.43	1.52
2	I	301	2NE	C20-C15	-3.10	1.43	1.52
2	I	301	2NE	P22-O25	-3.09	1.43	1.54
2	H	301	2NE	C20-C15	-3.08	1.43	1.52
2	E	301	2NE	P22-O25	-3.08	1.43	1.54
2	F	301	2NE	P10-O11	-2.93	1.42	1.54
2	I	301	2NE	P22-O24	-2.91	1.44	1.54
2	E	301	2NE	P06-O07	-2.90	1.42	1.54
2	I	301	2NE	P10-O11	-2.90	1.42	1.54
2	C	301	2NE	P22-O25	-2.89	1.44	1.54
2	C	301	2NE	P10-O11	-2.86	1.42	1.54
2	E	301	2NE	P10-O11	-2.86	1.42	1.54
2	C	301	2NE	P22-O24	-2.78	1.44	1.54
2	D	301	2NE	P22-O23	-2.71	1.42	1.51
2	B	301	2NE	P22-O25	-2.70	1.45	1.54
2	F	301	2NE	P06-O07	-2.67	1.43	1.54
2	F	301	2NE	P22-O23	-2.61	1.42	1.51
2	B	301	2NE	P06-O07	-2.55	1.44	1.54
2	D	301	2NE	P22-O25	-2.52	1.45	1.54
2	C	301	2NE	O39-C38	-2.51	1.18	1.23
2	E	301	2NE	P22-O24	-2.50	1.45	1.54
2	D	301	2NE	O39-C38	-2.48	1.18	1.23
2	E	301	2NE	O39-C38	-2.44	1.18	1.23
2	F	301	2NE	P22-O24	-2.40	1.46	1.54
2	A	301	2NE	C20-C15	-2.39	1.45	1.52
2	G	301	2NE	P06-O07	-2.36	1.44	1.54
2	G	301	2NE	P10-O11	-2.36	1.44	1.54
2	G	301	2NE	C42-C43	-2.34	1.46	1.51
2	F	301	2NE	P22-O25	-2.34	1.46	1.54
2	D	301	2NE	C27-N28	-2.33	1.30	1.34
2	I	301	2NE	C29-N28	-2.33	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	2NE	P22-O23	-2.31	1.43	1.51
2	C	301	2NE	O50-C49	-2.30	1.17	1.21
2	G	301	2NE	P22-O25	-2.30	1.46	1.54
2	A	301	2NE	O37-C36	-2.27	1.37	1.42
2	D	301	2NE	P22-O21	-2.23	1.53	1.60
2	B	301	2NE	P10-O11	-2.21	1.45	1.54
2	I	301	2NE	O39-C38	-2.18	1.19	1.23
2	E	301	2NE	P10-O12	-2.17	1.43	1.51
2	B	301	2NE	C35-N34	-2.16	1.32	1.35
2	G	301	2NE	P22-O24	-2.14	1.47	1.54
2	I	301	2NE	P22-O23	-2.14	1.44	1.51
2	C	301	2NE	P06-O08	-2.13	1.43	1.51
2	I	301	2NE	C35-N34	-2.12	1.32	1.35
2	D	301	2NE	P22-O24	-2.10	1.47	1.54
2	E	301	2NE	C35-N34	-2.10	1.32	1.35
2	B	301	2NE	P22-O23	-2.10	1.44	1.51
2	B	301	2NE	C29-N28	-2.05	1.32	1.39
2	C	301	2NE	C29-N28	-2.04	1.32	1.39
2	G	301	2NE	C46-N45	-2.03	1.41	1.46
2	F	301	2NE	C30-N31	2.00	1.41	1.34
2	E	301	2NE	C49-S48	2.03	1.80	1.76
2	A	301	2NE	C51-C49	2.05	1.52	1.50
2	I	301	2NE	C30-N31	2.11	1.41	1.34
2	B	301	2NE	C30-N31	2.16	1.41	1.34
2	H	301	2NE	O16-C15	2.17	1.50	1.45
2	H	301	2NE	C51-C49	2.21	1.52	1.50
2	F	301	2NE	O53-C52	2.24	1.41	1.36
2	C	301	2NE	C30-N31	2.27	1.41	1.34
2	H	301	2NE	C30-N31	2.34	1.42	1.34
2	A	301	2NE	O16-C15	2.36	1.50	1.45
2	E	301	2NE	C30-N31	2.43	1.42	1.34
2	G	301	2NE	C30-N31	2.53	1.42	1.34
2	C	301	2NE	C49-S48	2.72	1.82	1.76
2	I	301	2NE	C51-C49	2.96	1.53	1.50
2	B	301	2NE	C51-C49	3.13	1.54	1.50
2	I	301	2NE	C49-S48	3.16	1.83	1.76
2	F	301	2NE	C49-S48	3.18	1.83	1.76
2	G	301	2NE	C43-N45	3.22	1.41	1.33
2	D	301	2NE	C43-N45	3.40	1.41	1.33
2	D	301	2NE	C49-S48	3.47	1.83	1.76
2	A	301	2NE	C30-N31	3.57	1.46	1.34
2	I	301	2NE	C43-N45	3.60	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	2NE	C43-N45	3.87	1.42	1.33
2	B	301	2NE	C43-N45	4.13	1.43	1.33
2	F	301	2NE	C43-N45	4.21	1.43	1.33
2	E	301	2NE	C43-N45	4.21	1.43	1.33
2	E	301	2NE	C38-N40	4.40	1.42	1.33
2	H	301	2NE	C43-N45	4.43	1.44	1.33
2	C	301	2NE	O16-C17	4.45	1.46	1.41
2	G	301	2NE	C38-N40	4.62	1.43	1.33
2	I	301	2NE	C38-N40	4.65	1.43	1.33
2	I	301	2NE	O16-C17	4.73	1.47	1.41
2	E	301	2NE	O16-C17	4.75	1.47	1.41
2	F	301	2NE	O16-C17	4.83	1.47	1.41
2	D	301	2NE	O16-C17	4.85	1.47	1.41
2	C	301	2NE	C38-N40	4.88	1.43	1.33
2	D	301	2NE	C38-N40	4.91	1.43	1.33
2	B	301	2NE	C38-N40	4.98	1.44	1.33
2	F	301	2NE	C38-N40	5.30	1.44	1.33
2	B	301	2NE	O16-C17	5.43	1.48	1.41
2	A	301	2NE	C43-N45	5.65	1.46	1.33
2	H	301	2NE	C38-N40	5.84	1.45	1.33
2	G	301	2NE	O16-C17	6.22	1.49	1.41
2	H	301	2NE	O16-C17	6.61	1.49	1.41
2	A	301	2NE	C38-N40	6.78	1.47	1.33
2	A	301	2NE	O16-C17	8.41	1.51	1.41

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	2NE	O50-C49-C51	-10.34	106.67	123.28
2	A	301	2NE	N34-C33-N32	-9.45	121.66	128.89
2	H	301	2NE	N34-C33-N32	-9.21	121.85	128.89
2	G	301	2NE	N34-C33-N32	-7.73	122.98	128.89
2	B	301	2NE	N34-C33-N32	-7.63	123.05	128.89
2	D	301	2NE	N34-C33-N32	-7.42	123.21	128.89
2	B	301	2NE	C15-O16-C17	-7.19	101.82	109.72
2	C	301	2NE	N34-C33-N32	-7.10	123.46	128.89
2	I	301	2NE	C15-O16-C17	-6.93	102.10	109.72
2	D	301	2NE	C15-O16-C17	-6.81	102.23	109.72
2	A	301	2NE	C15-O16-C17	-6.81	102.24	109.72
2	G	301	2NE	C15-O16-C17	-6.67	102.39	109.72
2	C	301	2NE	C15-O16-C17	-6.63	102.44	109.72
2	I	301	2NE	N34-C33-N32	-6.56	123.87	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	2NE	O50-C49-C51	-6.47	112.88	123.28
2	F	301	2NE	O50-C49-C51	-6.46	112.90	123.28
2	H	301	2NE	P06-O09-P10	-6.44	114.64	132.73
2	F	301	2NE	N34-C33-N32	-6.41	123.98	128.89
2	E	301	2NE	C15-O16-C17	-6.16	102.95	109.72
2	E	301	2NE	N34-C33-N32	-6.14	124.20	128.89
2	E	301	2NE	O50-C49-C51	-5.81	113.95	123.28
2	G	301	2NE	O50-C49-C51	-5.80	113.96	123.28
2	H	301	2NE	C15-O16-C17	-5.78	103.37	109.72
2	I	301	2NE	O50-C49-C51	-5.22	114.90	123.28
2	F	301	2NE	C15-O16-C17	-5.11	104.10	109.72
2	C	301	2NE	C35-C29-N28	-4.87	105.00	109.48
2	E	301	2NE	C35-C29-N28	-4.74	105.12	109.48
2	B	301	2NE	O50-C49-C51	-4.73	115.67	123.28
2	G	301	2NE	O50-C49-S48	-4.57	116.55	122.37
2	G	301	2NE	C41-C42-C43	-4.41	105.04	112.31
2	G	301	2NE	P06-O09-P10	-4.30	120.67	132.73
2	F	301	2NE	C35-C29-N28	-4.06	105.75	109.48
2	D	301	2NE	C46-C47-S48	-3.77	101.27	111.36
2	A	301	2NE	C41-C42-C43	-3.76	106.11	112.31
2	C	301	2NE	P06-O09-P10	-3.62	122.55	132.73
2	B	301	2NE	P06-O09-P10	-3.59	122.66	132.73
2	H	301	2NE	O50-C49-S48	-3.57	117.82	122.37
2	I	301	2NE	C35-C29-N28	-3.54	106.22	109.48
2	A	301	2NE	C41-N40-C38	-3.52	115.56	122.53
2	H	301	2NE	C18-C17-N26	-3.48	108.97	114.29
2	G	301	2NE	C46-C47-S48	-3.45	102.12	111.36
2	E	301	2NE	P06-O09-P10	-3.16	123.87	132.73
2	H	301	2NE	P22-O21-C20	-3.12	114.08	121.56
2	H	301	2NE	C41-N40-C38	-3.12	116.36	122.53
2	H	301	2NE	O50-C49-C51	-3.08	118.33	123.28
2	I	301	2NE	P06-O09-P10	-3.05	124.16	132.73
2	B	301	2NE	C35-C29-N28	-3.03	106.69	109.48
2	A	301	2NE	O39-C38-N40	-3.00	117.07	123.08
2	D	301	2NE	C35-C29-N28	-2.94	106.78	109.48
2	G	301	2NE	C35-C29-N28	-2.92	106.79	109.48
2	F	301	2NE	P06-O09-P10	-2.92	124.54	132.73
2	C	301	2NE	O50-C49-S48	-2.91	118.66	122.37
2	A	301	2NE	C46-N45-C43	-2.87	117.14	122.79
2	B	301	2NE	C46-N45-C43	-2.87	117.14	122.79
2	F	301	2NE	C46-C47-S48	-2.82	103.81	111.36
2	E	301	2NE	O37-C36-C38	-2.77	104.04	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	2NE	P06-O09-P10	-2.75	125.00	132.73
2	B	301	2NE	O50-C49-S48	-2.72	118.90	122.37
2	A	301	2NE	C35-C29-N28	-2.72	106.98	109.48
2	A	301	2NE	P06-O09-P10	-2.68	125.21	132.73
2	E	301	2NE	C46-C47-S48	-2.62	104.34	111.36
2	I	301	2NE	C46-C47-S48	-2.58	104.46	111.36
2	G	301	2NE	O11-P10-O12	-2.57	98.58	112.53
2	D	301	2NE	O25-P22-O23	-2.55	102.37	110.58
2	B	301	2NE	O39-C38-N40	-2.55	117.97	123.08
2	D	301	2NE	O37-C36-C38	-2.55	104.54	110.38
2	G	301	2NE	C46-N45-C43	-2.54	117.80	122.79
2	H	301	2NE	C35-C29-N28	-2.46	107.21	109.48
2	I	301	2NE	O50-C49-S48	-2.45	119.25	122.37
2	A	301	2NE	C46-C47-S48	-2.43	104.86	111.36
2	C	301	2NE	C46-C47-S48	-2.39	104.97	111.36
2	H	301	2NE	C03-C02-C04	-2.28	105.55	108.50
2	B	301	2NE	C46-C47-S48	-2.22	105.41	111.36
2	I	301	2NE	O39-C38-N40	-2.21	118.66	123.08
2	G	301	2NE	C42-C41-N40	-2.11	107.25	111.88
2	B	301	2NE	C41-C42-C43	-2.07	108.90	112.31
2	G	301	2NE	C41-N40-C38	-2.07	118.44	122.53
2	H	301	2NE	O39-C38-N40	-2.04	118.99	123.08
2	E	301	2NE	O07-P06-O09	2.00	114.18	105.09
2	C	301	2NE	O09-P10-O13	2.02	108.30	102.94
2	I	301	2NE	C57-C51-C49	2.06	124.43	119.88
2	D	301	2NE	C20-C18-C17	2.08	104.96	99.98
2	B	301	2NE	C03-C02-C36	2.09	113.16	109.34
2	H	301	2NE	O25-P22-O24	2.10	115.39	107.38
2	D	301	2NE	C47-S48-C49	2.14	102.31	99.59
2	G	301	2NE	O11-P10-O09	2.16	114.88	105.09
2	H	301	2NE	O09-P10-O13	2.16	108.67	102.94
2	A	301	2NE	O09-P06-O05	2.22	108.82	102.94
2	E	301	2NE	C20-C18-C17	2.25	105.38	99.98
2	B	301	2NE	C20-C18-C17	2.31	105.51	99.98
2	H	301	2NE	C20-C18-C17	2.31	105.52	99.98
2	E	301	2NE	C47-C46-N45	2.37	117.09	112.36
2	D	301	2NE	O09-P10-O13	2.37	109.23	102.94
2	E	301	2NE	O09-P10-O13	2.39	109.27	102.94
2	C	301	2NE	C20-C18-C17	2.44	105.84	99.98
2	F	301	2NE	O07-P06-O09	2.45	116.22	105.09
2	A	301	2NE	C42-C43-N45	2.59	120.95	116.46
2	B	301	2NE	C47-C46-N45	2.60	117.56	112.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	2NE	O09-P10-O13	2.66	109.99	102.94
2	F	301	2NE	C20-C18-C17	2.67	106.38	99.98
2	H	301	2NE	C01-C02-C04	2.79	112.12	108.50
2	I	301	2NE	C20-C18-C17	2.80	106.70	99.98
2	E	301	2NE	O09-P06-O05	2.94	110.73	102.94
2	I	301	2NE	O09-P10-O13	2.94	110.75	102.94
2	C	301	2NE	O21-P22-O23	3.09	114.83	107.11
2	F	301	2NE	C47-C46-N45	3.38	119.12	112.36
2	D	301	2NE	O09-P06-O05	3.42	112.00	102.94
2	I	301	2NE	C46-N45-C43	3.45	129.58	122.79
2	A	301	2NE	C51-C49-S48	3.59	119.38	115.22
2	F	301	2NE	O09-P06-O05	3.70	112.74	102.94
2	G	301	2NE	O09-P06-O05	3.74	112.86	102.94
2	B	301	2NE	O09-P06-O05	4.03	113.63	102.94
2	C	301	2NE	C47-S48-C49	4.18	104.90	99.59
2	F	301	2NE	C46-N45-C43	4.36	131.37	122.79
2	I	301	2NE	O09-P06-O05	4.44	114.72	102.94
2	E	301	2NE	C47-S48-C49	4.97	105.92	99.59
2	G	301	2NE	C47-S48-C49	5.04	106.00	99.59
2	H	301	2NE	O09-P06-O05	5.04	116.32	102.94
2	F	301	2NE	C51-C49-S48	5.34	121.41	115.22
2	H	301	2NE	C51-C49-S48	6.73	123.02	115.22
2	F	301	2NE	C47-S48-C49	6.91	108.39	99.59
2	A	301	2NE	C47-S48-C49	6.97	108.46	99.59
2	B	301	2NE	C47-S48-C49	7.50	109.13	99.59
2	I	301	2NE	C51-C49-S48	8.37	124.92	115.22
2	B	301	2NE	C51-C49-S48	8.66	125.26	115.22
2	E	301	2NE	C51-C49-S48	9.25	125.94	115.22
2	G	301	2NE	C51-C49-S48	9.99	126.80	115.22
2	H	301	2NE	C47-S48-C49	10.40	112.83	99.59
2	I	301	2NE	C47-S48-C49	10.60	113.08	99.59
2	D	301	2NE	C51-C49-S48	11.18	128.19	115.22
2	C	301	2NE	C51-C49-S48	11.33	128.36	115.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	2NE	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	2NE	2	0
2	C	301	2NE	1	0
2	D	301	2NE	3	0
2	E	301	2NE	2	0
2	F	301	2NE	2	0
2	G	301	2NE	5	0
3	G	302	BCT	1	0
2	H	301	2NE	4	1
2	I	301	2NE	4	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	275/275 (100%)	-0.31	1 (0%) 93 93	21, 34, 53, 65	0
1	B	274/275 (99%)	-0.28	4 (1%) 76 77	21, 37, 58, 76	0
1	C	275/275 (100%)	-0.51	0 100 100	21, 29, 49, 68	0
1	D	275/275 (100%)	-0.28	0 100 100	20, 32, 53, 69	0
1	E	275/275 (100%)	-0.39	0 100 100	22, 31, 51, 67	0
1	F	275/275 (100%)	-0.37	4 (1%) 76 77	20, 31, 52, 85	0
1	G	275/275 (100%)	0.05	10 (3%) 46 48	27, 45, 67, 88	0
1	H	275/275 (100%)	0.02	18 (6%) 22 23	27, 40, 76, 101	0
1	I	275/275 (100%)	-0.22	5 (1%) 71 72	25, 34, 58, 77	0
All	All	2474/2475 (99%)	-0.25	42 (1%) 73 73	20, 34, 61, 101	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	90	ASP	5.3
1	H	256	GLY	4.8
1	H	91	GLN	4.7
1	G	3	TRP	4.4
1	H	84	GLU	4.2
1	G	91	GLN	4.1
1	H	260	PHE	3.9
1	G	1	MET	3.6
1	H	85	GLY	3.5
1	F	91	GLN	3.2
1	G	90	ASP	3.2
1	H	92	GLY	3.2
1	H	265	PRO	3.1
1	I	265	PRO	3.1
1	H	263	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	3	TRP	3.0
1	H	88	ILE	2.9
1	B	5	ILE	2.8
1	B	91	GLN	2.6
1	H	40	PHE	2.6
1	H	266	PRO	2.6
1	H	93	THR	2.5
1	G	67	SER	2.4
1	F	90	ASP	2.3
1	H	89	ASP	2.3
1	F	265	PRO	2.3
1	F	1	MET	2.3
1	I	261	LEU	2.2
1	G	236	LEU	2.2
1	I	54	ARG	2.2
1	G	70	LYS	2.2
1	H	264	ARG	2.2
1	G	69	GLY	2.2
1	H	81	VAL	2.2
1	H	86	GLY	2.1
1	I	259	ALA	2.1
1	G	2	ASP	2.1
1	B	90	ASP	2.1
1	H	259	ALA	2.1
1	I	234	ALA	2.1
1	B	67	SER	2.1
1	G	196	PRO	2.1

## 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	BCT	H	302	4/4	0.93	0.28	10.63	52,63,63,70	0
3	BCT	B	302	4/4	0.96	0.16	5.93	35,50,56,61	0
4	MLI	C	303	7/7	0.76	0.30	5.43	40,56,69,69	0
3	BCT	E	302	4/4	0.94	0.14	5.20	36,45,50,56	0
3	BCT	F	302	4/4	0.95	0.14	3.94	32,37,46,49	0
4	MLI	I	303	7/7	0.84	0.26	3.88	45,52,60,67	0
3	BCT	C	302	4/4	0.95	0.17	3.75	31,38,44,51	0
3	BCT	G	302	4/4	0.86	0.17	2.91	51,63,66,69	0
3	BCT	A	302	4/4	0.95	0.11	1.75	36,53,56,61	0
2	2NE	E	301	57/57	0.94	0.14	1.55	27,44,77,84	0
2	2NE	A	301	57/57	0.92	0.16	1.52	30,47,76,97	0
2	2NE	B	301	57/57	0.91	0.16	1.32	35,49,84,92	0
2	2NE	H	301	57/57	0.75	0.24	1.25	40,89,101,133	57
2	2NE	G	301	57/57	0.90	0.15	1.09	36,62,99,100	0
3	BCT	I	302	4/4	0.96	0.10	0.59	35,47,52,55	0
3	BCT	D	302	4/4	0.98	0.09	0.54	30,42,48,56	0
2	2NE	D	301	57/57	0.96	0.10	0.52	26,37,84,125	0
2	2NE	C	301	57/57	0.95	0.10	0.46	22,37,68,97	0
2	2NE	I	301	57/57	0.95	0.10	0.38	26,38,70,136	0
2	2NE	F	301	57/57	0.95	0.09	0.14	24,35,79,102	0

## 6.5 Other polymers

There are no such residues in this entry.