



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2017 – 09:44 PM EDT

PDB ID : 3QHO
Title : Crystal analysis of the complex structure, Y299F-cellobiotetraose, of endocellulase from pyrococcus horikoshii
Authors : Kim, H.-W.; Ishikawa, K.
Deposited on : unknown
Resolution : 1.65 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

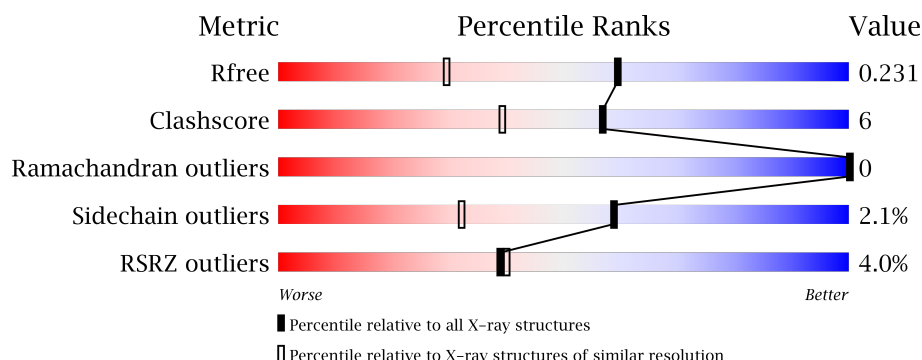
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1368 (1.66-1.66)
Clashscore	112137	1468 (1.66-1.66)
Ramachandran outliers	110173	1438 (1.66-1.66)
Sidechain outliers	110143	1438 (1.66-1.66)
RSRZ outliers	101464	1371 (1.66-1.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	458	<div> <div>2%</div> <div>68% 13% 18%</div> </div>
1	B	458	<div> <div>2%</div> <div>72% 10% 18%</div> </div>
1	C	458	<div> <div>5%</div> <div>71% 12% 18%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	C	462	-	-	X	-

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 9884 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.

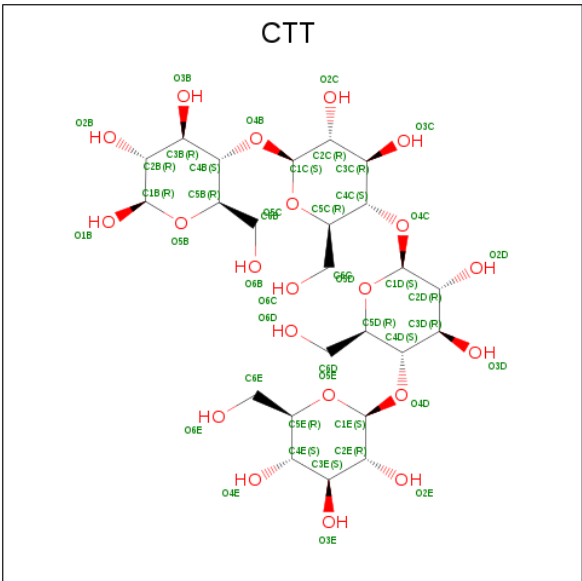
- Molecule 1 is a protein called 458aa long hypothetical endo-1,4-beta-glucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			3070	2002	502	556	10			
1	B	377	Total	C	N	O	S	0	2	0
			3089	2013	506	560	10			
1	C	377	Total	C	N	O	S	0	2	0
			3085	2010	504	560	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	299	PHE	TYR	ENGINEERED MUTATION	UNP O58925
B	299	PHE	TYR	ENGINEERED MUTATION	UNP O58925
C	299	PHE	TYR	ENGINEERED MUTATION	UNP O58925

- Molecule 2 is beta-D-glucopyranosyl-(1->4)-beta-D-glucopyranosyl-(1->4)-beta-D-glucopyranosyl-(1->4)-beta-D-glucopyranose (three-letter code: CTT) (formula: C₂₄H₄₂O₂₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			45	24	21		
2	B	1	Total	C	O	0	0
			45	24	21		
2	C	1	Total	C	O	0	0
			45	24	21		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	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		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	190	Total	O	0	0
			190	190		
4	B	160	Total	O	0	0
			160	160		

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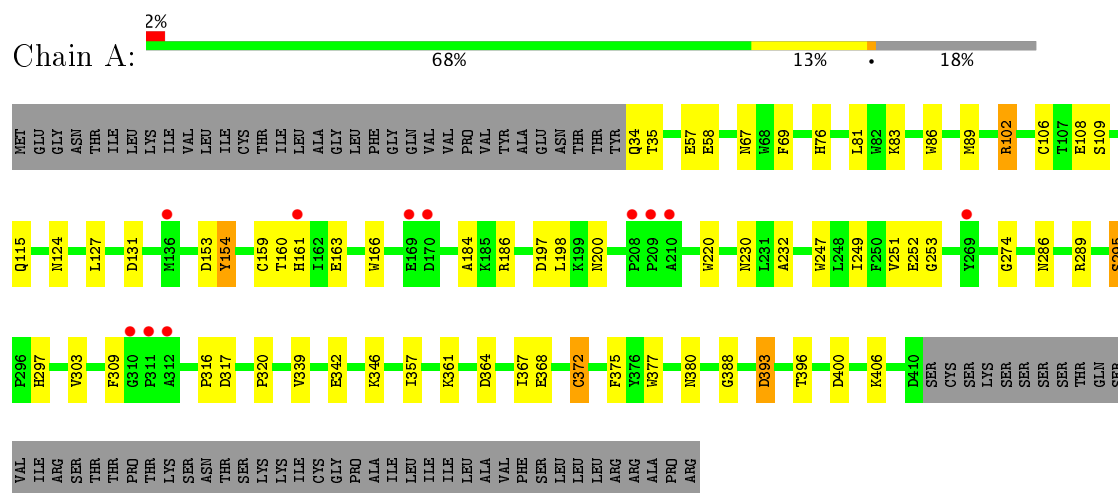
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	130	Total	O	0	0
			130	130		

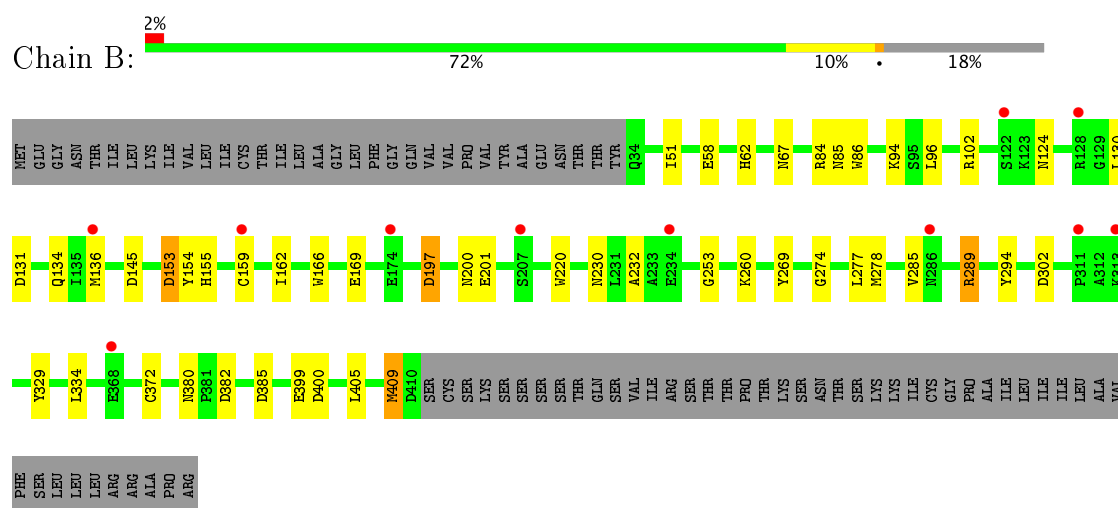
3 Residue-property plots [i](#)

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

- Molecule 1: 458aa long hypothetical endo-1,4-beta-glucanase

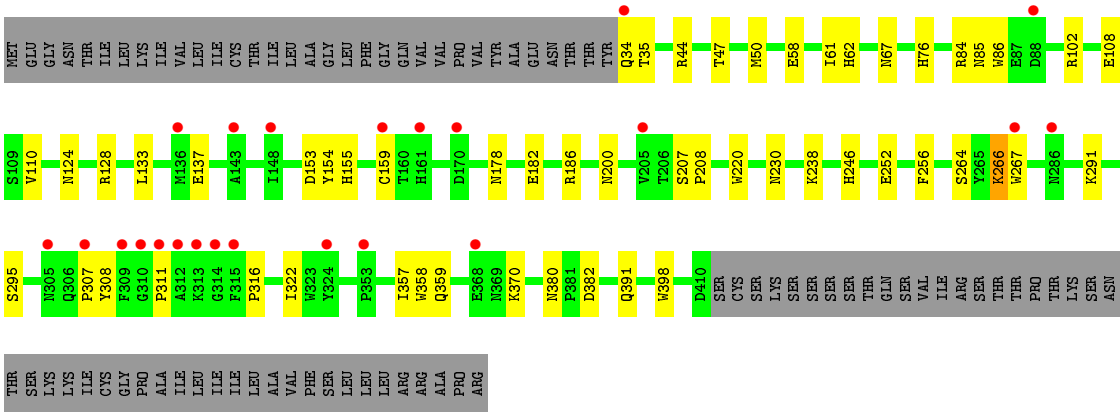


- Molecule 1: 458aa long hypothetical endo-1,4-beta-glucanase



- Molecule 1: 458aa long hypothetical endo-1,4-beta-glucanase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	161.16Å 58.53Å 138.32Å 90.00° 109.24° 90.00°	Depositor
Resolution (Å)	33.67 – 1.65 40.26 – 1.63	Depositor EDS
% Data completeness (in resolution range)	94.8 (33.67-1.65) 92.3 (40.26-1.63)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 1.63Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.187 , 0.227 0.196 , 0.231	Depositor DCC
R_{free} test set	6965 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.537	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 49.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9884	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: CTT, 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	1.28	12/3181 (0.4%)	1.15	16/4342 (0.4%)
1	B	1.25	6/3201 (0.2%)	1.05	10/4369 (0.2%)
1	C	1.01	0/3196	0.88	2/4362 (0.0%)
All	All	1.19	18/9578 (0.2%)	1.03	28/13073 (0.2%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	159	CYS	CB-SG	7.55	1.95	1.82
1	A	309	PHE	CE1-CZ	6.50	1.49	1.37
1	B	289	ARG	CB-CG	-6.29	1.35	1.52
1	A	69	PHE	CE1-CZ	6.26	1.49	1.37
1	A	303	VAL	CB-CG1	-6.11	1.40	1.52
1	A	377	TRP	CE3-CZ3	5.89	1.48	1.38
1	A	154	TYR	CD2-CE2	5.77	1.48	1.39
1	B	329	TYR	CE1-CZ	5.76	1.46	1.38
1	B	269	TYR	CD1-CE1	5.68	1.47	1.39
1	A	109	SER	CA-CB	5.67	1.61	1.52
1	B	285	VAL	CB-CG2	5.33	1.64	1.52
1	A	339	VAL	CB-CG1	5.27	1.64	1.52
1	A	368	GLU	CG-CD	5.24	1.59	1.51
1	A	295	SER	CB-OG	5.22	1.49	1.42
1	A	375	PHE	CE1-CZ	5.11	1.47	1.37
1	A	342	GLU	CG-CD	5.11	1.59	1.51
1	B	294	TYR	CD2-CE2	5.03	1.46	1.39
1	A	163	GLU	CB-CG	5.01	1.61	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	MET	CG-SD-CE	-7.42	88.33	100.20
1	A	131	ASP	CB-CG-OD1	7.16	124.74	118.30
1	A	83	LYS	CD-CE-NZ	6.82	127.39	111.70
1	A	400	ASP	CB-CG-OD1	6.71	124.34	118.30
1	B	84	ARG	NE-CZ-NH2	-6.51	117.04	120.30
1	A	102	ARG	NE-CZ-NH1	6.51	123.56	120.30
1	A	81	LEU	CB-CG-CD2	6.48	122.02	111.00
1	A	393	ASP	CB-CG-OD2	6.18	123.86	118.30
1	A	153	ASP	CB-CG-OD1	6.00	123.70	118.30
1	A	197	ASP	CB-CG-OD1	5.98	123.68	118.30
1	A	186	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	B	277	LEU	CB-CG-CD1	-5.93	100.91	111.00
1	B	289	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	A	102	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	A	364	ASP	CB-CG-OD1	5.78	123.50	118.30
1	B	400	ASP	CB-CG-OD1	5.63	123.37	118.30
1	A	251	VAL	CG1-CB-CG2	5.60	119.87	110.90
1	B	145	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	B	334	LEU	CB-CG-CD1	-5.57	101.53	111.00
1	A	186	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	405	LEU	CB-CG-CD2	-5.55	101.56	111.00
1	A	317	ASP	CB-CG-OD1	5.51	123.25	118.30
1	A	127	LEU	CB-CG-CD1	-5.35	101.91	111.00
1	B	289	ARG	CG-CD-NE	-5.33	100.60	111.80
1	C	84	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	197	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	409	MET	CB-CA-C	5.08	120.56	110.40
1	C	153	ASP	CB-CG-OD2	-5.02	113.78	118.30

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	3070	0	2910	33	0
1	B	3089	0	2919	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3085	0	2919	40	0
2	A	45	0	42	0	0
2	B	45	0	42	2	0
2	C	45	0	42	0	0
3	A	5	0	0	0	0
3	C	20	0	0	3	0
4	A	190	0	0	7	1
4	B	160	0	0	0	0
4	C	130	0	0	5	1
All	All	9884	0	8874	104	1

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 6.

All (104) 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:266:LYS:H	1:C:266:LYS:HD2	0.91	1.04
1:C:266:LYS:N	1:C:266:LYS:HD2	1.74	0.97
1:B:62[A]:HIS:ND1	1:B:372:CYS:SG	2.41	0.94
1:C:266:LYS:H	1:C:266:LYS:CD	1.77	0.93
1:A:367:ILE:HD13	4:A:650:HOH:O	1.67	0.92
1:C:238:LYS:HE2	4:C:580:HOH:O	1.70	0.90
1:A:67:ASN:HD21	1:A:102:ARG:HH11	1.23	0.86
1:C:67:ASN:HD21	1:C:102:ARG:HH11	1.21	0.84
1:A:361:LYS:HD2	4:A:632:HOH:O	1.81	0.80
1:C:34:GLN:HB2	4:C:559:HOH:O	1.89	0.72
1:A:289:ARG:HG3	1:A:289:ARG:HH11	1.55	0.72
1:C:67:ASN:ND2	1:C:102:ARG:HH11	1.89	0.70
1:B:67:ASN:HD21	1:B:102:ARG:HH11	1.37	0.70
1:A:86:TRP:HD1	1:A:124:ASN:HD22	1.42	0.68
1:A:67:ASN:ND2	1:A:102:ARG:HH11	1.91	0.68
1:A:106:CYS:HG	1:A:159:CYS:HG	0.69	0.68
1:C:62:HIS:HE1	3:C:462:PO4:O4	1.77	0.67
1:B:62[A]:HIS:CE1	1:B:372:CYS:SG	2.89	0.66
1:C:102:ARG:HH22	1:C:200:ASN:HD22	1.42	0.65
1:B:86:TRP:H	1:B:124:ASN:ND2	1.97	0.61
1:C:76:HIS:HE1	1:C:159:CYS:SG	2.23	0.61
1:A:86:TRP:H	1:A:124:ASN:HD21	1.46	0.61
1:B:86:TRP:H	1:B:124:ASN:HD21	1.49	0.60
1:C:110:VAL:HA	1:C:133:LEU:HD13	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ARG:HH22	1:A:200:ASN:HD22	1.51	0.58
1:A:160:THR:CG2	1:B:169[B]:GLU:HG3	2.35	0.57
1:A:316:PRO:HG3	1:A:357:ILE:CG2	2.35	0.57
1:B:67:ASN:ND2	1:B:102:ARG:HH11	2.02	0.56
1:B:102:ARG:HH22	1:B:200:ASN:HD22	1.52	0.55
1:A:160:THR:HG23	1:B:169[B]:GLU:HG3	1.87	0.55
1:A:76:HIS:HE1	1:A:159:CYS:SG	2.29	0.55
1:A:393:ASP:OD1	1:A:396:THR:HG23	2.06	0.55
1:B:131:ASP:H	1:B:134:GLN:HE21	1.54	0.55
1:A:108:GLU:HG3	4:A:571:HOH:O	2.07	0.55
1:A:372:CYS:SG	4:A:636:HOH:O	2.57	0.54
1:A:253:GLY:O	1:A:274:GLY:HA2	2.07	0.54
1:B:62[A]:HIS:CG	1:B:372:CYS:HG	2.25	0.54
3:C:460:PO4:O2	3:C:461:PO4:O4	2.26	0.53
1:B:67:ASN:HD21	1:B:102:ARG:HD3	1.73	0.52
1:C:128:ARG:HD2	4:C:644:HOH:O	2.08	0.51
1:A:220:TRP:CE2	1:A:230:ASN:HB3	2.46	0.51
1:B:51:ILE:HG12	1:B:58:GLU:HG2	1.93	0.51
1:C:291:LYS:HA	1:C:291:LYS:HE2	1.93	0.50
1:C:137:GLU:OE2	1:C:186:ARG:HD3	2.11	0.50
1:B:153:ASP:HA	1:B:197:ASP:HB3	1.92	0.50
1:C:178:ASN:O	1:C:182:GLU:HG3	2.11	0.50
1:A:86:TRP:H	1:A:124:ASN:ND2	2.09	0.50
1:C:108:GLU:HG3	4:C:561:HOH:O	2.11	0.50
1:A:198:LEU:HD21	1:A:249:ILE:HG23	1.94	0.49
1:A:160:THR:OG1	1:A:161:HIS:HD2	1.95	0.49
1:B:86:TRP:HD1	1:B:124:ASN:HD22	1.59	0.49
1:C:85:ASN:HA	1:C:124:ASN:HD21	1.78	0.48
1:C:44:ARG:NH2	1:C:58[A]:GLU:OE2	2.47	0.48
1:B:166:TRP:CZ2	1:B:232:ALA:HB2	2.49	0.48
1:A:289:ARG:HG3	1:A:289:ARG:NH1	2.27	0.48
1:A:346:LYS:NZ	4:A:637:HOH:O	2.32	0.48
1:B:260:LYS:HE2	1:B:260:LYS:HB2	1.48	0.48
1:B:86:TRP:N	1:B:124:ASN:HD21	2.11	0.48
1:C:311:PRO:HD3	4:C:476:HOH:O	2.14	0.48
1:C:62:HIS:CE1	3:C:462:PO4:O4	2.63	0.47
1:C:86:TRP:H	1:C:124:ASN:HD21	1.61	0.47
1:B:131:ASP:H	1:B:134:GLN:NE2	2.13	0.47
1:B:102:ARG:HH22	1:B:200:ASN:ND2	2.12	0.47
1:C:358:TRP:CE3	1:C:359:GLN:HG2	2.50	0.47
1:C:67:ASN:HD21	1:C:102:ARG:HD3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ASP:HB3	1:B:385:ASP:O	2.15	0.46
1:A:102:ARG:HH22	1:A:200:ASN:ND2	2.13	0.46
1:A:76:HIS:CE1	1:A:159:CYS:SG	3.08	0.46
1:A:372:CYS:HA	4:A:594:HOH:O	2.15	0.45
1:A:108:GLU:CG	4:A:571:HOH:O	2.63	0.45
1:C:267:TRP:CZ3	1:C:307:PRO:HB2	2.51	0.45
1:B:62[A]:HIS:CG	1:B:372:CYS:SG	3.09	0.45
1:C:86:TRP:HD1	1:C:124:ASN:HD22	1.64	0.44
1:B:96:LEU:O	1:B:409:MET:HE1	2.18	0.44
1:C:50:MET:HE2	1:C:61:ILE:HG21	1.99	0.44
1:A:57:GLU:HG3	1:A:58:GLU:N	2.31	0.44
1:A:166:TRP:CZ2	1:A:232:ALA:HB2	2.53	0.44
1:C:316:PRO:HG3	1:C:357:ILE:HG21	2.00	0.43
1:C:102:ARG:HH22	1:C:200:ASN:ND2	2.11	0.43
1:C:220:TRP:CE2	1:C:230:ASN:HB3	2.54	0.42
1:B:130:LEU:HA	1:B:134:GLN:NE2	2.35	0.42
1:C:86:TRP:H	1:C:124:ASN:ND2	2.16	0.42
1:C:391:GLN:HG2	1:C:398:TRP:CE2	2.55	0.42
1:A:184:ALA:HA	1:A:247:TRP:CH2	2.55	0.42
1:B:201:GLU:OE1	2:B:2739:CTT:H1D	2.19	0.42
1:C:35:THR:HB	1:C:246:HIS:HB3	2.02	0.42
1:B:253:GLY:O	1:B:274:GLY:HA2	2.20	0.41
1:C:252:GLU:HG2	1:C:295:SER:O	2.20	0.41
1:C:155:HIS:HA	1:C:200:ASN:HB3	2.02	0.41
1:B:162:ILE:HD11	2:B:2739:CTT:H2D	2.01	0.41
1:C:34:GLN:HE21	1:C:34:GLN:HA	1.86	0.41
1:C:380:ASN:HB3	1:C:382:ASP:OD1	2.20	0.41
1:C:155:HIS:HA	1:C:200:ASN:CB	2.51	0.41
1:C:208:PRO:HD3	1:C:256:PHE:CZ	2.55	0.41
1:B:155:HIS:HA	1:B:200:ASN:CB	2.51	0.41
1:B:220:TRP:CE2	1:B:230:ASN:HB3	2.55	0.41
1:C:34:GLN:NE2	1:C:34:GLN:HA	2.35	0.41
1:A:200:ASN:ND2	1:A:297:HIS:HE1	2.19	0.41
1:B:278:MET:HE3	1:B:278:MET:HB2	2.00	0.41
1:B:85:ASN:HA	1:B:124:ASN:HD21	1.86	0.41
1:A:380:ASN:O	1:A:388:GLY:HA3	2.21	0.40
1:B:380:ASN:HB3	1:B:382:ASP:OD1	2.21	0.40
1:C:308:TYR:CG	1:C:322:ILE:HD13	2.56	0.40
1:A:252:GLU:HG2	1:A:295:SER:O	2.21	0.40

All (1) 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)
4:A:609:HOH:O	4:C:481:HOH:O[4_545]	1.59	0.61

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	375/458 (82%)	366 (98%)	9 (2%)	0	100	100
1	B	377/458 (82%)	368 (98%)	9 (2%)	0	100	100
1	C	377/458 (82%)	363 (96%)	14 (4%)	0	100	100
All	All	1129/1374 (82%)	1097 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	324/396 (82%)	316 (98%)	8 (2%)	53	25
1	B	326/396 (82%)	320 (98%)	6 (2%)	64	40
1	C	326/396 (82%)	320 (98%)	6 (2%)	64	40
All	All	976/1188 (82%)	956 (98%)	20 (2%)	59	36

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	35	THR
1	A	115	GLN
1	A	154	TYR
1	A	286	ASN
1	A	320	PRO
1	A	372	CYS
1	A	406	LYS
1	B	94	LYS
1	B	136	MET
1	B	153	ASP
1	B	154	TYR
1	B	289	ARG
1	B	399	GLU
1	C	47	THR
1	C	154	TYR
1	C	207	SER
1	C	264	SER
1	C	266	LYS
1	C	370	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	HIS
1	A	67	ASN
1	A	76	HIS
1	A	124	ASN
1	A	161	HIS
1	A	178	ASN
1	A	200	ASN
1	A	359	GLN
1	B	67	ASN
1	B	124	ASN
1	B	134	GLN
1	B	200	ASN
1	B	359	GLN
1	C	34	GLN
1	C	62	HIS
1	C	67	ASN
1	C	76	HIS
1	C	124	ASN
1	C	161	HIS

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Mol	Chain	Res	Type
1	C	200	ASN
1	C	359	GLN

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 ⓘ

8 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	CTT	A	2739	-	48,48,48	1.47	7 (14%)	71,71,71	1.94	20 (28%)
3	PO4	A	459	-	4,4,4	0.54	0	6,6,6	0.94	1 (16%)
2	CTT	B	2739	-	48,48,48	1.33	6 (12%)	71,71,71	1.92	21 (29%)
2	CTT	C	2739	-	48,48,48	1.17	3 (6%)	71,71,71	1.87	22 (30%)
3	PO4	C	459	-	4,4,4	0.97	0	6,6,6	1.06	0
3	PO4	C	460	-	4,4,4	0.64	0	6,6,6	1.22	0
3	PO4	C	461	-	4,4,4	0.47	0	6,6,6	1.23	1 (16%)
3	PO4	C	462	-	4,4,4	1.10	1 (25%)	6,6,6	1.01	0

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	CTT	A	2739	-	-	0/20/100/100	0/4/4/4
3	PO4	A	459	-	-	0/0/0/0	0/0/0/0
2	CTT	B	2739	-	-	0/20/100/100	0/4/4/4
2	CTT	C	2739	-	-	0/20/100/100	0/4/4/4
3	PO4	C	459	-	-	0/0/0/0	0/0/0/0
3	PO4	C	460	-	-	0/0/0/0	0/0/0/0
3	PO4	C	461	-	-	0/0/0/0	0/0/0/0
3	PO4	C	462	-	-	0/0/0/0	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2739	CTT	O5B-C1B	-3.39	1.37	1.43
2	B	2739	CTT	O4D-C4D	-3.15	1.36	1.43
2	B	2739	CTT	C4D-C5D	-2.27	1.46	1.52
2	B	2739	CTT	O3E-C3E	2.06	1.47	1.43
3	C	462	PO4	P-O1	2.10	1.55	1.50
2	A	2739	CTT	O5E-C5E	2.20	1.49	1.44
2	B	2739	CTT	O3D-C3D	2.29	1.48	1.43
2	C	2739	CTT	O4B-C4B	2.36	1.49	1.43
2	C	2739	CTT	O3D-C3D	2.46	1.48	1.43
2	A	2739	CTT	C6B-C5B	2.50	1.60	1.51
2	A	2739	CTT	C1B-C2B	2.51	1.57	1.52
2	A	2739	CTT	C3B-C4B	2.59	1.59	1.52
2	A	2739	CTT	O3C-C3C	3.10	1.50	1.43
2	A	2739	CTT	O4C-C1D	3.15	1.50	1.41
2	B	2739	CTT	O4C-C1D	3.52	1.51	1.41
2	C	2739	CTT	O4C-C1D	4.08	1.52	1.41
2	A	2739	CTT	O3D-C3D	4.92	1.54	1.43

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2739	CTT	O5C-C1C-C2C	-5.50	99.69	110.30
2	A	2739	CTT	O5B-C1B-C2B	-4.55	102.49	110.04
2	C	2739	CTT	C3D-C4D-C5D	-4.11	102.15	110.88
2	A	2739	CTT	O5D-C5D-C6D	-4.04	96.73	106.41
2	A	2739	CTT	C3D-C4D-C5D	-3.97	102.46	110.88
2	B	2739	CTT	O4D-C1E-O5E	-3.95	101.11	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2739	CTT	C3C-C4C-C5C	-3.91	102.58	110.88
2	B	2739	CTT	O4D-C4D-C5D	-3.70	100.25	109.34
2	A	2739	CTT	O4D-C4D-C5D	-3.53	100.67	109.34
2	A	2739	CTT	O2C-C2C-C3C	-3.46	102.83	110.36
2	A	2739	CTT	O4B-C4B-C5B	-3.45	100.87	109.34
2	B	2739	CTT	C6E-C5E-C4E	-3.41	105.03	113.00
2	C	2739	CTT	O4D-C4D-C5D	-3.27	101.31	109.34
2	C	2739	CTT	O5D-C5D-C6D	-3.26	98.59	106.41
2	A	2739	CTT	O5C-C1C-C2C	-3.25	104.02	110.30
2	A	2739	CTT	O4D-C1E-O5E	-2.89	103.69	110.70
2	A	2739	CTT	O4C-C4C-C3C	-2.86	100.31	107.19
2	C	2739	CTT	O4C-C1D-C2D	-2.75	101.90	108.11
2	C	2739	CTT	O5C-C1C-C2C	-2.66	105.17	110.30
2	B	2739	CTT	C4E-C3E-C2E	-2.63	106.20	110.84
2	B	2739	CTT	O6B-C6B-C5B	-2.60	102.58	111.34
2	B	2739	CTT	C1E-O4D-C4D	-2.59	111.68	118.00
2	B	2739	CTT	O3D-C3D-C2D	-2.59	104.72	110.36
2	A	2739	CTT	C6C-C5C-C4C	-2.49	106.44	113.24
2	B	2739	CTT	O2C-C2C-C1C	-2.48	104.84	110.03
2	B	2739	CTT	C3D-C4D-C5D	-2.45	105.68	110.88
2	A	2739	CTT	O5B-C5B-C4B	-2.37	104.90	109.75
2	B	2739	CTT	O5B-C1B-C2B	-2.32	106.19	110.04
2	C	2739	CTT	O4B-C1C-O5C	-2.19	105.38	110.70
2	A	2739	CTT	C3C-C4C-C5C	-2.17	106.27	110.88
2	B	2739	CTT	O1B-C1B-O5B	-2.16	103.82	110.20
2	C	2739	CTT	O6B-C6B-C5B	-2.13	104.17	111.34
2	B	2739	CTT	C3C-C4C-C5C	-2.12	106.38	110.88
2	C	2739	CTT	O3B-C3B-C2B	-2.08	105.84	110.36
2	C	2739	CTT	C1D-C2D-C3D	2.02	113.72	109.98
3	A	459	PO4	O3-P-O2	2.10	115.62	107.90
2	A	2739	CTT	C1D-C2D-C3D	2.10	113.89	109.98
2	B	2739	CTT	O4D-C1E-C2E	2.13	112.91	108.11
2	B	2739	CTT	O5E-C5E-C6E	2.15	111.56	106.41
3	C	461	PO4	O4-P-O2	2.21	116.03	107.90
2	B	2739	CTT	O3E-C3E-C2E	2.24	115.23	110.36
2	A	2739	CTT	O5D-C1D-C2D	2.25	114.64	110.30
2	C	2739	CTT	O2D-C2D-C1D	2.26	114.75	110.03
2	A	2739	CTT	C1D-O4C-C4C	2.31	123.61	118.00
2	C	2739	CTT	O5E-C5E-C6E	2.34	112.02	106.41
2	C	2739	CTT	C2B-C3B-C4B	2.40	114.58	109.61
2	C	2739	CTT	O5E-C5E-C4E	2.47	114.20	109.66
2	C	2739	CTT	O5B-C5B-C4B	2.67	115.22	109.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2739	CTT	O4C-C4C-C5C	2.73	116.06	109.34
2	B	2739	CTT	C2B-C3B-C4B	2.80	115.41	109.61
2	B	2739	CTT	O4B-C4B-C3B	2.88	114.12	107.19
2	C	2739	CTT	O5C-C5C-C4C	2.93	115.74	109.75
2	B	2739	CTT	O3D-C3D-C4D	2.95	116.59	109.87
2	C	2739	CTT	O4B-C4B-C3B	3.18	114.85	107.19
2	C	2739	CTT	O4D-C4D-C3D	3.20	114.90	107.19
2	A	2739	CTT	O4D-C4D-C3D	3.24	114.98	107.19
2	A	2739	CTT	O3D-C3D-C4D	3.31	117.41	109.87
2	C	2739	CTT	O4B-C1C-C2C	3.40	115.77	108.11
2	C	2739	CTT	O5D-C5D-C4D	3.48	116.87	109.75
2	C	2739	CTT	O4C-C4C-C5C	3.94	119.04	109.34
2	B	2739	CTT	O4C-C4C-C5C	4.08	119.37	109.34
2	A	2739	CTT	O4B-C4B-C3B	4.13	117.14	107.19
2	C	2739	CTT	O5D-C1D-C2D	4.29	118.58	110.30
2	A	2739	CTT	C1D-O5D-C5D	4.45	122.10	113.72
2	B	2739	CTT	C1D-O5D-C5D	5.09	123.31	113.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2739	CTT	2	0
3	C	460	PO4	1	0
3	C	461	PO4	1	0
3	C	462	PO4	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	377/458 (82%)	-0.02	11 (2%) 52 54	9, 21, 38, 48	8 (2%)
1	B	377/458 (82%)	-0.07	11 (2%) 52 54	9, 21, 36, 45	9 (2%)
1	C	377/458 (82%)	0.26	23 (6%) 22 20	13, 29, 45, 56	10 (2%)
All	All	1131/1374 (82%)	0.06	45 (3%) 39 40	9, 24, 41, 56	27 (2%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	88	ASP	5.4
1	C	136	MET	5.4
1	B	286	ASN	4.8
1	A	136	MET	4.7
1	B	136	MET	3.9
1	B	122	SER	3.8
1	C	310	GLY	3.8
1	C	312	ALA	3.7
1	C	353	PRO	3.6
1	C	315	PHE	3.4
1	A	169	GLU	3.4
1	A	311	PRO	3.2
1	B	234	GLU	3.2
1	C	205	VAL	3.1
1	A	161	HIS	2.8
1	C	170	ASP	2.8
1	C	286	ASN	2.7
1	A	208	PRO	2.7
1	A	310	GLY	2.6
1	C	311	PRO	2.6
1	B	313	LYS	2.5
1	C	309	PHE	2.5
1	A	170	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	311	PRO	2.5
1	C	34	GLN	2.5
1	B	368	GLU	2.4
1	C	305	ASN	2.4
1	C	161	HIS	2.4
1	A	269	TYR	2.4
1	A	312	ALA	2.4
1	A	209	PRO	2.3
1	B	174	GLU	2.3
1	C	267	TRP	2.3
1	C	159	CYS	2.3
1	A	210	ALA	2.3
1	C	324	TYR	2.2
1	C	368	GLU	2.2
1	B	207	SER	2.2
1	C	313	LYS	2.2
1	C	307	PRO	2.1
1	C	143	ALA	2.1
1	C	314	GLY	2.1
1	B	159	CYS	2.1
1	B	128	ARG	2.1
1	C	148	ILE	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	PO4	C	462	5/5	0.93	0.14	1.58	34,39,41,45	0
3	PO4	A	459	5/5	0.98	0.10	1.08	33,39,40,43	0
2	CTT	B	2739	45/45	0.92	0.09	0.72	20,28,33,38	0
2	CTT	C	2739	45/45	0.91	0.11	0.39	29,38,44,52	0
2	CTT	A	2739	45/45	0.94	0.08	-0.33	21,28,34,45	0
3	PO4	C	459	5/5	0.96	0.09	-0.40	32,38,44,46	0
3	PO4	C	461	5/5	0.99	0.04	-1.49	24,25,26,30	0
3	PO4	C	460	5/5	0.99	0.04	-2.34	19,23,27,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.