Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 11:48 AM BST

PDB ID	:	1EG1
Title	:	ENDOGLUCANASE I FROM TRICHODERMA REESEI
Authors	:	Kleywegt, G.J.; Zou, J.-Y.; Jones, T.A.
Deposited on	:	1996-11-26
Resolution	:	3.60 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
https://www.wwpdb.org/validation/2017/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:

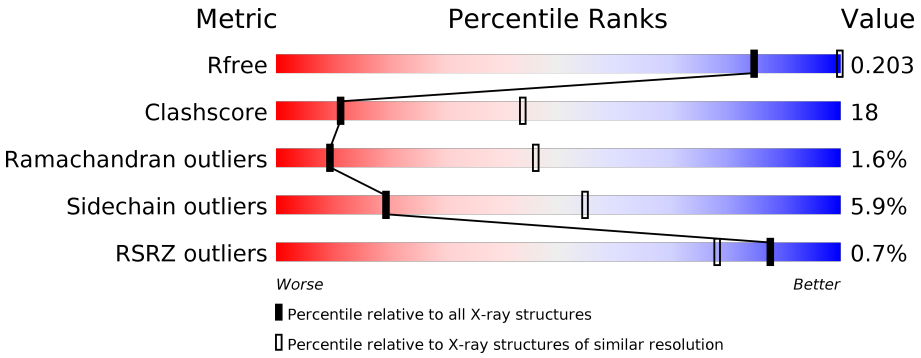
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	371	64% 33%
1	C	371	% 64% 32%

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
1	PCA	A	1	-	-	X	-
1	PCA	C	1	-	-	X	-

2 Entry composition

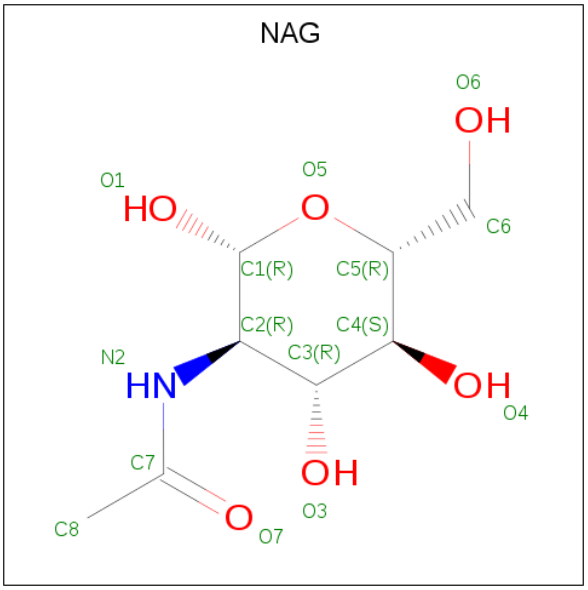
There are 2 unique types of molecules in this entry. The entry contains 5528 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDOGLUCANASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	0	0
			2736	1671	461	579	25			
1	C	371	Total	C	N	O	S	0	0	0
			2736	1671	461	579	25			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



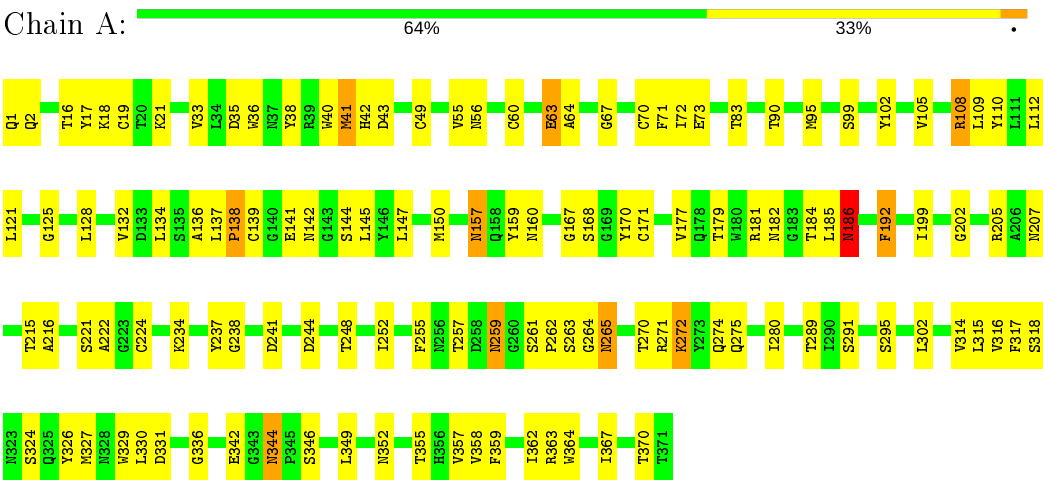
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots (i)

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

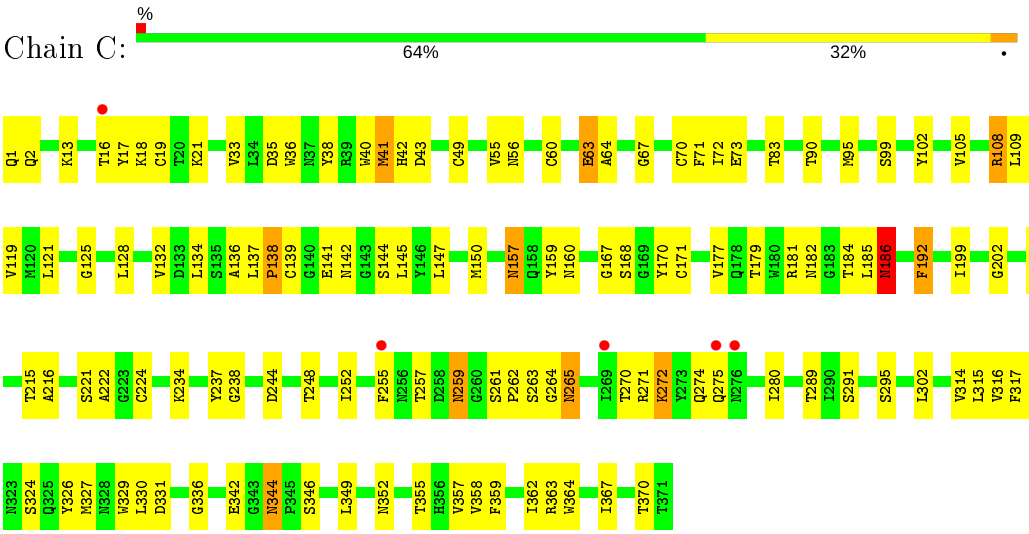
- Molecule 1: ENDOGLUCANASE I

Chain A:



- Molecule 1: ENDOGLUCANASE I

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	101.40Å 101.40Å 199.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 3.60 71.11 – 3.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-3.60) 92.1 (71.11-3.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.04 (at 3.58Å)	Xtriage
Refinement program	X-PLOR 4.0	Depositor
R, R_{free}	0.201 , 0.258 0.196 , 0.203	Depositor DCC
R_{free} test set	945 reflections (8.08%)	wwPDB-VP
Wilson B-factor (Å^2)	70.4	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 125.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	5528	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: PCA, NAG

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	0.32	0/2790	0.66	0/3805
1	C	0.32	0/2790	0.66	0/3805
All	All	0.32	0/5580	0.66	0/7610

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	2736	0	2502	95	4
1	C	2736	0	2502	94	4
2	A	28	0	26	0	0
2	C	28	0	26	0	0
All	All	5528	0	5056	187	4

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 18.

All (187) 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:202:GLY:HA2	1:C:330:LEU:HD21	1.64	0.80
1:A:202:GLY:HA2	1:A:330:LEU:HD21	1.64	0.79
1:C:138:PRO:HD3	1:C:355:THR:HG21	1.68	0.75
1:A:138:PRO:HD3	1:A:355:THR:HG21	1.68	0.73
1:A:95:MET:HG2	1:A:105:VAL:HG21	1.71	0.72
1:C:252:ILE:HB	1:C:272:LYS:HG3	1.71	0.72
1:A:252:ILE:HB	1:A:272:LYS:HG3	1.71	0.72
1:A:41:MET:HB2	1:A:72:ILE:HG22	1.72	0.71
1:C:95:MET:HG2	1:C:105:VAL:HG21	1.71	0.71
1:C:41:MET:HB2	1:C:72:ILE:HG22	1.71	0.71
1:C:41:MET:HG2	1:C:49:CYS:HB2	1.74	0.69
1:A:41:MET:HG2	1:A:49:CYS:HB2	1.74	0.69
1:A:137:LEU:HD21	1:A:357:VAL:HG22	1.77	0.67
1:A:138:PRO:HD3	1:A:355:THR:CG2	2.26	0.66
1:C:137:LEU:HD21	1:C:357:VAL:HG22	1.77	0.66
1:C:138:PRO:HD3	1:C:355:THR:CG2	2.26	0.65
1:A:145:LEU:HD11	1:A:315:LEU:HD11	1.80	0.64
1:C:145:LEU:HD11	1:C:315:LEU:HD11	1.80	0.64
1:A:90:THR:HG23	1:A:358:VAL:HG22	1.81	0.63
1:C:90:THR:HG23	1:C:358:VAL:HG22	1.81	0.63
1:C:157:ASN:HD22	1:C:157:ASN:H	1.49	0.60
1:A:157:ASN:HD22	1:A:157:ASN:H	1.49	0.60
1:A:134:LEU:HD12	1:A:237:TYR:OH	2.02	0.59
1:C:134:LEU:HD12	1:C:237:TYR:OH	2.02	0.59
1:C:181:ARG:HB2	1:C:186:ASN:HB2	1.84	0.58
1:C:108:ARG:HG2	1:C:108:ARG:HH11	1.68	0.58
1:A:181:ARG:HB2	1:A:186:ASN:HB2	1.84	0.57
1:A:108:ARG:HH11	1:A:108:ARG:HG2	1.68	0.57
1:A:270:THR:HA	1:A:289:THR:HG22	1.87	0.57
1:A:109:LEU:HB2	1:A:317:PHE:HB2	1.87	0.57
1:C:109:LEU:HB2	1:C:317:PHE:HB2	1.87	0.57
1:C:33:VAL:O	1:C:109:LEU:HA	2.05	0.56
1:A:33:VAL:O	1:A:109:LEU:HA	2.05	0.56
1:C:270:THR:HA	1:C:289:THR:HG22	1.87	0.56
1:C:40:TRP:CE3	1:C:73:GLU:HG3	2.41	0.55
1:A:40:TRP:CE3	1:A:73:GLU:HG3	2.41	0.55
1:A:324:SER:O	1:C:222:ALA:HB2	2.06	0.55
1:A:128:LEU:HD13	1:A:364:TRP:HB3	1.90	0.54
1:C:95:MET:HG2	1:C:105:VAL:CG2	2.38	0.54
1:C:128:LEU:HD13	1:C:364:TRP:HB3	1.89	0.53
1:A:17:TYR:HB2	1:A:363:ARG:HB3	1.90	0.53
1:A:147:LEU:HD11	1:A:199:ILE:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:TYR:HB2	1:C:363:ARG:HB3	1.90	0.53
1:C:147:LEU:HD11	1:C:199:ILE:HD11	1.91	0.53
1:C:261:SER:HB2	1:C:262:PRO:HD2	1.92	0.52
1:A:95:MET:HG2	1:A:105:VAL:CG2	2.38	0.52
1:A:132:VAL:HG12	1:A:359:PHE:CD1	2.44	0.52
1:A:139:CYS:SG	1:A:205:ARG:HG3	2.50	0.52
1:A:261:SER:HB2	1:A:262:PRO:HD2	1.91	0.52
1:A:102:TYR:HB2	1:A:349:LEU:HD11	1.92	0.52
1:C:139:CYS:SG	1:C:205:ARG:HG3	2.50	0.51
1:C:132:VAL:HG12	1:C:359:PHE:CD1	2.45	0.51
1:A:274:GLN:HA	1:A:280:ILE:HG12	1.92	0.51
1:C:274:GLN:HA	1:C:280:ILE:HG12	1.92	0.51
1:C:138:PRO:CD	1:C:355:THR:HG21	2.40	0.51
1:C:259:ASN:HD22	1:C:259:ASN:N	2.09	0.51
1:C:102:TYR:HB2	1:C:349:LEU:HD11	1.92	0.51
1:A:2:GLN:O	1:A:71:PHE:HA	2.11	0.50
1:A:222:ALA:HB2	1:C:324:SER:O	2.12	0.50
1:A:327:MET:HG3	1:A:330:LEU:HB3	1.94	0.50
1:A:215:THR:HG22	1:A:216:ALA:H	1.77	0.50
1:C:215:THR:HG22	1:C:216:ALA:H	1.77	0.50
1:A:259:ASN:N	1:A:259:ASN:HD22	2.09	0.49
1:C:327:MET:HG3	1:C:330:LEU:HB3	1.94	0.49
1:C:259:ASN:HD22	1:C:259:ASN:H	1.61	0.49
1:A:138:PRO:CD	1:A:355:THR:HG21	2.40	0.49
1:C:2:GLN:O	1:C:71:PHE:HA	2.11	0.49
1:C:19:CYS:SG	1:C:370:THR:HA	2.53	0.49
1:A:157:ASN:ND2	1:A:160:ASN:H	2.11	0.48
1:A:170:TYR:CG	1:A:171:CYS:N	2.82	0.48
1:A:19:CYS:SG	1:A:370:THR:HA	2.53	0.48
1:A:150:MET:SD	1:A:170:TYR:HA	2.54	0.48
1:C:150:MET:SD	1:C:170:TYR:HA	2.54	0.48
1:A:142:ASN:O	1:A:319:ILE:HA	2.14	0.48
1:A:142:ASN:HB2	1:A:327:MET:CE	2.44	0.48
1:C:157:ASN:ND2	1:C:160:ASN:H	2.11	0.48
1:C:170:TYR:CG	1:C:171:CYS:N	2.82	0.47
1:A:259:ASN:H	1:A:259:ASN:HD22	1.61	0.47
1:A:110:TYR:CD1	1:A:316:VAL:HG22	2.49	0.47
1:C:110:TYR:CD1	1:C:316:VAL:HG22	2.49	0.47
1:C:142:ASN:HB2	1:C:327:MET:CE	2.44	0.47
1:C:42:HIS:HD2	1:C:43:ASP:O	1.98	0.47
1:A:42:HIS:HD2	1:A:43:ASP:O	1.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:ASN:O	1:C:319:ILE:HA	2.14	0.47
1:A:125:GLY:HA2	1:A:255:PHE:O	2.15	0.47
1:C:36:TRP:CE3	1:C:168:SER:HB2	2.51	0.46
1:A:326:TYR:CD1	1:A:344:ASN:HA	2.50	0.46
1:A:344:ASN:ND2	1:A:346:SER:H	2.13	0.46
1:C:344:ASN:ND2	1:C:346:SER:H	2.13	0.46
1:A:132:VAL:HG12	1:A:359:PHE:HD1	1.80	0.46
1:A:36:TRP:CE3	1:A:168:SER:HB2	2.51	0.46
1:A:1:PCA:HG2	1:A:36:TRP:HH2	1.81	0.46
1:C:215:THR:HG22	1:C:216:ALA:N	2.30	0.46
1:C:137:LEU:HD11	1:C:357:VAL:HG22	1.97	0.46
1:C:125:GLY:HA2	1:C:255:PHE:O	2.15	0.46
1:C:1:PCA:HG2	1:C:36:TRP:HH2	1.81	0.46
1:C:326:TYR:CD1	1:C:344:ASN:HA	2.51	0.46
1:A:108:ARG:HG2	1:A:108:ARG:NH1	2.31	0.46
1:C:108:ARG:HG2	1:C:108:ARG:NH1	2.31	0.46
1:A:137:LEU:HD11	1:A:357:VAL:HG22	1.97	0.46
1:A:215:THR:HG22	1:A:216:ALA:N	2.30	0.45
1:A:248:THR:O	1:A:275:GLN:HG3	2.16	0.45
1:C:110:TYR:CE1	1:C:316:VAL:HG22	2.51	0.45
1:A:110:TYR:CE1	1:A:316:VAL:HG22	2.51	0.45
1:C:132:VAL:HG12	1:C:359:PHE:HD1	1.80	0.45
1:A:16:THR:HG22	1:A:362:ILE:HB	1.99	0.45
1:A:63:GLU:HG2	1:A:184:THR:CG2	2.47	0.45
1:A:119:VAL:HG12	1:A:121:LEU:HD23	1.99	0.45
1:C:248:THR:O	1:C:275:GLN:HG3	2.17	0.45
1:A:257:THR:HA	1:A:265:ASN:O	2.17	0.44
1:A:134:LEU:HD12	1:A:237:TYR:HH	1.80	0.44
1:C:291:SER:O	1:C:302:LEU:HD11	2.18	0.44
1:A:291:SER:O	1:A:302:LEU:HD11	2.18	0.44
1:C:63:GLU:HG2	1:C:184:THR:CG2	2.47	0.44
1:A:1:PCA:N	1:A:67:GLY:HA2	2.33	0.44
1:C:119:VAL:HG12	1:C:121:LEU:HD23	1.99	0.44
1:A:157:ASN:HD22	1:A:157:ASN:N	2.11	0.44
1:A:1:PCA:HA	1:A:70:CYS:O	2.18	0.44
1:A:55:VAL:HG13	1:A:179:THR:HG21	2.00	0.44
1:C:55:VAL:HG13	1:C:179:THR:HG21	2.00	0.44
1:C:1:PCA:HA	1:C:70:CYS:O	2.18	0.44
1:A:21:LYS:HE3	1:A:367:ILE:O	2.18	0.44
1:C:179:THR:O	1:C:185:LEU:HD12	2.18	0.44
1:C:33:VAL:HG23	1:C:112:LEU:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:PCA:N	1:C:67:GLY:HA2	2.33	0.43
1:A:33:VAL:HG23	1:A:112:LEU:HB2	2.00	0.43
1:C:238:GLY:O	1:C:244:ASP:HA	2.18	0.43
1:A:238:GLY:O	1:A:244:ASP:HA	2.18	0.43
1:A:35:ASP:HB3	1:A:38:TYR:CE1	2.53	0.43
1:C:157:ASN:ND2	1:C:157:ASN:H	2.16	0.43
1:C:322:ASP:HB3	1:C:327:MET:N	2.34	0.43
1:A:357:VAL:HG11	1:A:359:PHE:CZ	2.54	0.43
1:A:1:PCA:HG2	1:A:36:TRP:CH2	2.54	0.43
1:C:16:THR:HG22	1:C:362:ILE:HB	1.99	0.43
1:A:331:ASP:O	1:A:336:GLY:HA3	2.19	0.43
1:C:35:ASP:HB3	1:C:38:TYR:CE1	2.53	0.43
1:C:212:HIS:CE1	1:C:221:SER:O	2.72	0.43
1:A:212:HIS:CE1	1:A:221:SER:O	2.72	0.43
1:A:259:ASN:H	1:A:259:ASN:ND2	2.16	0.43
1:C:157:ASN:HD22	1:C:157:ASN:N	2.11	0.43
1:C:257:THR:HA	1:C:265:ASN:O	2.18	0.43
1:C:357:VAL:HG11	1:C:359:PHE:CZ	2.54	0.43
1:C:21:LYS:HE3	1:C:367:ILE:O	2.18	0.42
1:A:182:ASN:HB2	1:A:192:PHE:CE2	2.55	0.42
1:A:179:THR:O	1:A:185:LEU:HD12	2.18	0.42
1:A:18:LYS:HA	1:A:364:TRP:O	2.18	0.42
1:A:322:ASP:HB3	1:A:327:MET:N	2.34	0.42
1:C:259:ASN:ND2	1:C:259:ASN:H	2.16	0.42
1:A:224:CYS:SG	1:A:224:CYS:O	2.77	0.42
1:C:144:SER:N	1:C:318:SER:O	2.52	0.42
1:A:257:THR:HB	1:A:264:GLY:O	2.20	0.42
1:A:64:ALA:HA	1:A:159:TYR:CD1	2.55	0.42
1:C:182:ASN:HB2	1:C:192:PHE:CE2	2.55	0.42
1:C:1:PCA:HG2	1:C:36:TRP:CH2	2.54	0.42
1:C:331:ASP:O	1:C:336:GLY:HA3	2.19	0.42
1:C:136:ALA:O	1:C:355:THR:HG22	2.20	0.42
1:C:118:TYR:OH	1:C:167:GLY:HA2	2.20	0.42
1:C:257:THR:HB	1:C:264:GLY:O	2.20	0.42
1:C:55:VAL:HG13	1:C:179:THR:CG2	2.50	0.42
1:C:118:TYR:HB3	1:C:314:VAL:HG13	2.01	0.42
1:C:18:LYS:HA	1:C:364:TRP:O	2.18	0.42
1:A:329:TRP:CZ3	1:A:330:LEU:HB2	2.55	0.42
1:C:224:CYS:O	1:C:224:CYS:SG	2.77	0.42
1:A:144:SER:N	1:A:318:SER:O	2.52	0.42
1:A:118:TYR:HB3	1:A:314:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:THR:HA	1:A:211:PRO:HD3	1.83	0.41
1:A:55:VAL:HG13	1:A:179:THR:CG2	2.50	0.41
1:C:329:TRP:CZ3	1:C:330:LEU:HB2	2.55	0.41
1:A:118:TYR:OH	1:A:167:GLY:HA2	2.20	0.41
1:A:56:ASN:O	1:A:60:CYS:N	2.51	0.41
1:C:134:LEU:HD12	1:C:237:TYR:HH	1.85	0.41
1:A:321:ASN:ND2	1:A:321:ASN:H	2.19	0.41
1:C:64:ALA:HA	1:C:159:TYR:CD1	2.55	0.41
1:A:136:ALA:O	1:A:355:THR:HG22	2.20	0.41
1:C:321:ASN:ND2	1:C:321:ASN:H	2.19	0.41
1:A:319:ILE:HD12	1:A:357:VAL:HG23	2.03	0.41
1:A:157:ASN:ND2	1:A:157:ASN:H	2.17	0.41
1:A:157:ASN:ND2	1:A:160:ASN:N	2.68	0.41
1:C:317:PHE:HE1	1:C:362:ILE:HD11	1.86	0.41
1:C:157:ASN:ND2	1:C:160:ASN:N	2.68	0.41
1:C:319:ILE:HD12	1:C:357:VAL:HG23	2.03	0.41
1:A:331:ASP:C	1:A:336:GLY:HA3	2.42	0.40
1:A:344:ASN:HD22	1:A:346:SER:N	2.20	0.40
1:C:72:ILE:O	1:C:72:ILE:HG13	2.21	0.40
1:A:138:PRO:HD2	1:A:141:GLU:CG	2.52	0.40
1:C:56:ASN:O	1:C:60:CYS:N	2.51	0.40
1:C:138:PRO:HD2	1:C:141:GLU:CG	2.52	0.40

All (4) 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:A:241:ASP:OD1	1:C:13:LYS:NZ[3_645]	1.42	0.78
1:A:241:ASP:CG	1:C:13:LYS:NZ[3_645]	1.82	0.38
1:A:241:ASP:OD2	1:C:13:LYS:NZ[3_645]	1.86	0.34
1:A:241:ASP:OD1	1:C:13:LYS:CE[3_645]	1.99	0.21

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	369/371 (100%)	328 (89%)	35 (10%)	6 (2%)	9	46
1	C	369/371 (100%)	329 (89%)	34 (9%)	6 (2%)	9	46
All	All	738/742 (100%)	657 (89%)	69 (9%)	12 (2%)	9	46

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	SER
1	C	99	SER
1	A	186	ASN
1	A	342	GLU
1	C	186	ASN
1	C	342	GLU
1	A	234	LYS
1	A	265	ASN
1	C	234	LYS
1	C	265	ASN
1	A	138	PRO
1	C	138	PRO

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	305/305 (100%)	287 (94%)	18 (6%)	19	55
1	C	305/305 (100%)	287 (94%)	18 (6%)	19	55
All	All	610/610 (100%)	574 (94%)	36 (6%)	19	55

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	MET

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Mol	Chain	Res	Type
1	A	63	GLU
1	A	83	THR
1	A	108	ARG
1	A	157	ASN
1	A	177	VAL
1	A	186	ASN
1	A	192	PHE
1	A	207	ASN
1	A	259	ASN
1	A	263	SER
1	A	271	ARG
1	A	272	LYS
1	A	295	SER
1	A	319	ILE
1	A	321	ASN
1	A	344	ASN
1	A	352	ASN
1	C	41	MET
1	C	63	GLU
1	C	83	THR
1	C	108	ARG
1	C	157	ASN
1	C	177	VAL
1	C	186	ASN
1	C	192	PHE
1	C	207	ASN
1	C	259	ASN
1	C	263	SER
1	C	271	ARG
1	C	272	LYS
1	C	295	SER
1	C	319	ILE
1	C	321	ASN
1	C	344	ASN
1	C	352	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	HIS
1	A	93	GLN
1	A	142	ASN

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Mol	Chain	Res	Type
1	A	157	ASN
1	A	212	HIS
1	A	321	ASN
1	A	344	ASN
1	A	347	ASN
1	A	351	ASN
1	A	352	ASN
1	A	361	ASN
1	C	42	HIS
1	C	93	GLN
1	C	142	ASN
1	C	157	ASN
1	C	212	HIS
1	C	321	ASN
1	C	344	ASN
1	C	347	ASN
1	C	351	ASN
1	C	352	ASN
1	C	361	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PCA	A	1	1	7,8,9	0.94	0	9,10,12	1.12	0
1	PCA	C	1	1	7,8,9	0.94	0	9,10,12	1.12	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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1
1	PCA	C	1	1	-	0/0/11/13	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	PCA	4	0
1	C	1	PCA	4	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	NAG	A	402	1	14,14,15	0.57	0	17,19,21	0.96	1 (5%)
2	NAG	A	401	1	14,14,15	0.44	0	17,19,21	0.79	0
2	NAG	C	401	1	14,14,15	0.44	0	17,19,21	0.79	0
2	NAG	C	402	1	14,14,15	0.57	0	17,19,21	0.96	1 (5%)

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	NAG	A	402	1	-	2/6/23/26	0/1/1/1
2	NAG	A	401	1	-	2/6/23/26	0/1/1/1
2	NAG	C	401	1	-	2/6/23/26	0/1/1/1
2	NAG	C	402	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	402	NAG	C1-O5-C5	2.17	115.13	112.19
2	A	402	NAG	C1-O5-C5	2.14	115.10	112.19

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	NAG	O5-C5-C6-O6
2	C	402	NAG	O5-C5-C6-O6
2	A	402	NAG	C4-C5-C6-O6
2	C	402	NAG	C4-C5-C6-O6
2	A	401	NAG	O5-C5-C6-O6
2	C	401	NAG	O5-C5-C6-O6
2	A	401	NAG	C4-C5-C6-O6
2	C	401	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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^{th} 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	370/371 (99%)	-0.16	0 100 100	2, 37, 96, 164	0
1	C	370/371 (99%)	-0.01	5 (1%) 75 61	2, 37, 96, 164	0
All	All	740/742 (99%)	-0.08	5 (0%) 87 78	2, 37, 99, 164	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	276	ASN	2.6
1	C	255	PHE	2.4
1	C	269	ILE	2.3
1	C	16	THR	2.3
1	C	275	GLN	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	PCA	C	1	8/9	0.95	0.23	13,13,53,53	0
1	PCA	A	1	8/9	0.98	0.41	13,13,53,53	0

6.3 Carbohydrates

There are no monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	A	401	14/15	0.81	0.35	93,93,93,93	0
2	NAG	C	401	14/15	0.81	0.34	93,93,93,93	0
2	NAG	C	402	14/15	0.88	0.26	56,56,56,56	0
2	NAG	A	402	14/15	0.93	0.19	56,56,56,56	0

6.5 Other polymers

There are no such residues in this entry.