



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:38 AM GMT

PDB ID : 3PL9
Title : Crystal structure of spinach minor light-harvesting complex CP29 at 2.80 angstrom resolution
Authors : Pan, X.W.; Li, M.; Wan, T.; Wang, L.F.; Jia, C.J.; Hou, Z.Q.; Zhao, X.L.; Zhang, J.P.; Chang, W.R.
Deposited on : 2010-11-14
Resolution : 2.80 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

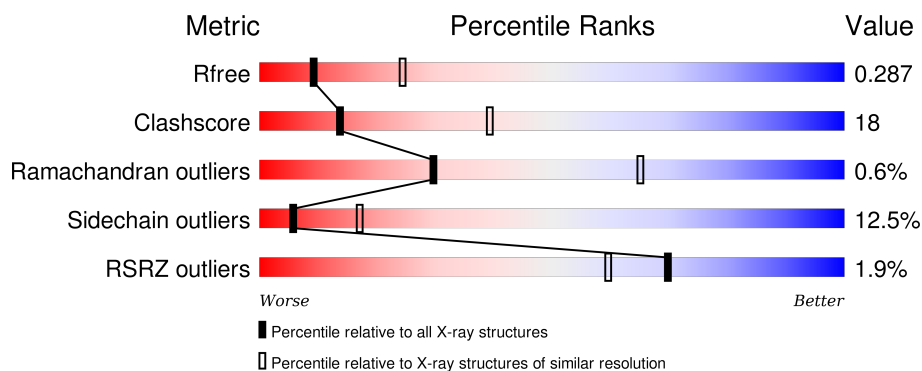
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	243	<div> <div></div> <div>34%</div> <div>25%</div> <div>5%</div> <div>36%</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
2	CLA	A	602	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CLA	A	603	X	-	-	-
2	CLA	A	604	X	-	-	-
2	CLA	A	609	X	-	-	-
2	CLA	A	610	X	-	-	-
2	CLA	A	611	X	-	-	-
2	CLA	A	612	X	-	-	X
2	CLA	A	613	X	-	-	-
2	CLA	A	615	X	-	-	-
3	CHL	A	606	X	-	-	-
3	CHL	A	607	X	-	-	X
3	CHL	A	608	X	-	-	-
3	CHL	A	614	X	-	-	-
5	XAT	A	622	-	-	-	X
6	NEX	A	623	-	-	-	X
8	HTG	A	631	-	-	-	X

2 Entry composition [i](#)

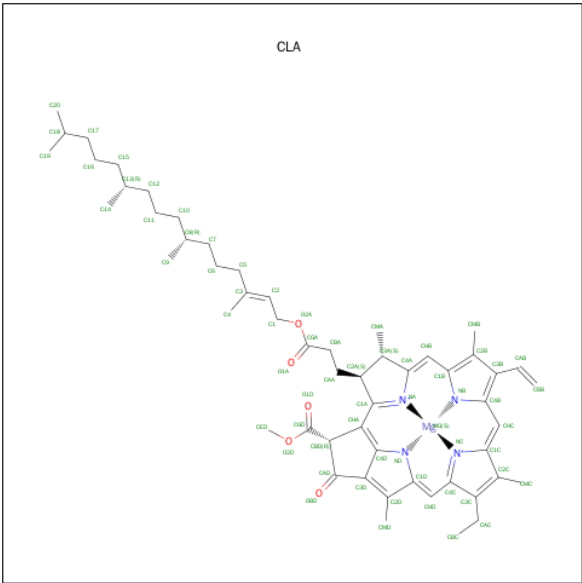
There are 9 unique types of molecules in this entry. The entry contains 2317 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chlorophyll A-B binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1217	790	204	219	4			

- Molecule 2 is CHLOROPHYLL A (three-letter code: CLA) (formula: C₅₅H₇₂MgN₄O₅).



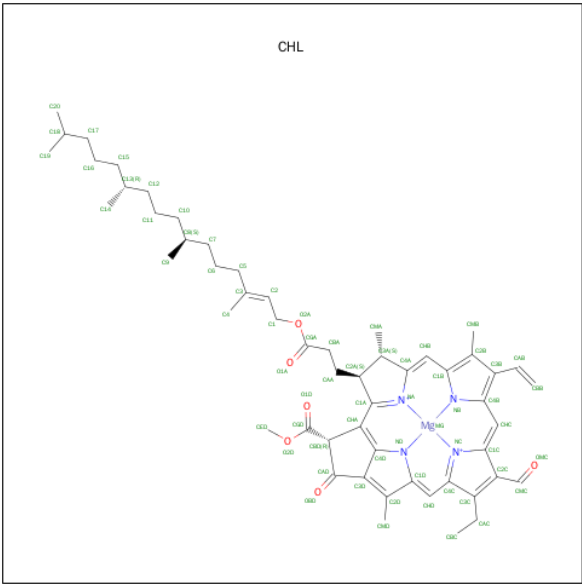
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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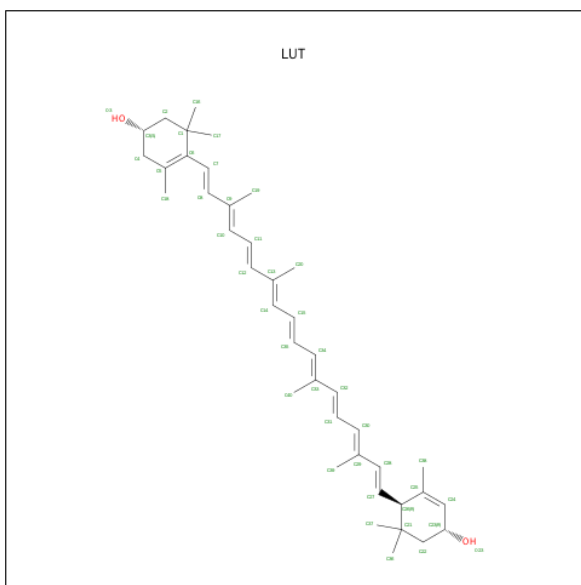
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
2	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 3 is CHLOROPHYLL B (three-letter code: CHL) (formula: C₅₅H₇₀MgN₄O₆).



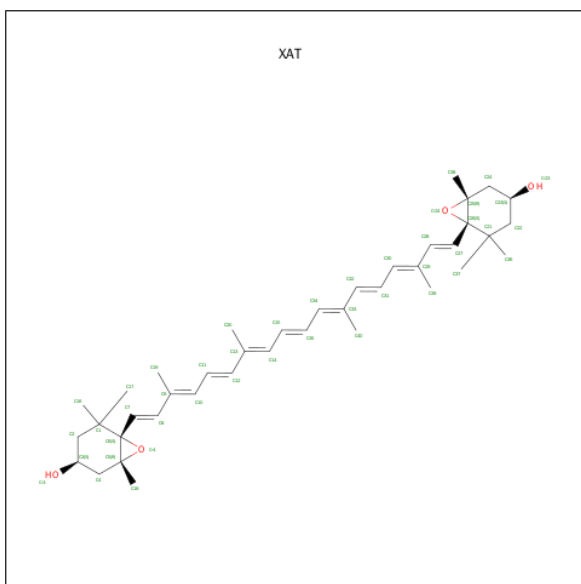
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
3	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
3	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
3	A	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 4 is (3R,3'R,6S)-4,5-DIDEHYDRO-5,6-DIHYDRO-BETA,BETA-CAROTENE-3, 3'-DIOL (three-letter code: LUT) (formula: C₄₀H₅₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			42	40	2		

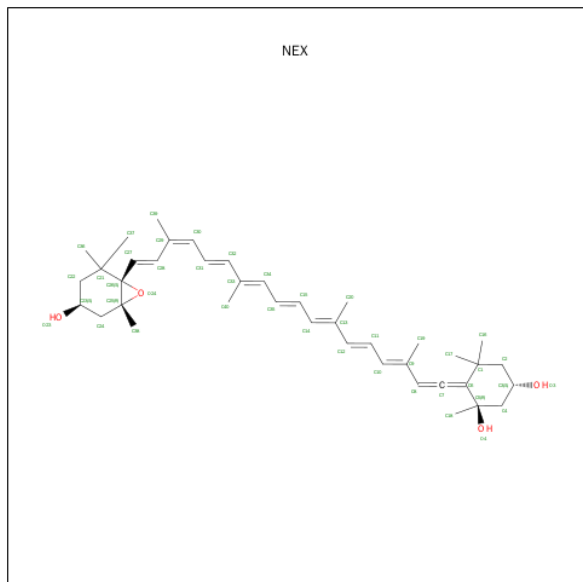
- Molecule 5 is (3S,5R,6S,3'S,5'R,6'S)-5,6,5',6'-DIEPOXY-5,6,5',6'- TETRAHYDRO-BETA, BETA-CAROTENE-3,3'-DIOL (three-letter code: XAT) (formula: $C_{40}H_{56}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			44	40	4		

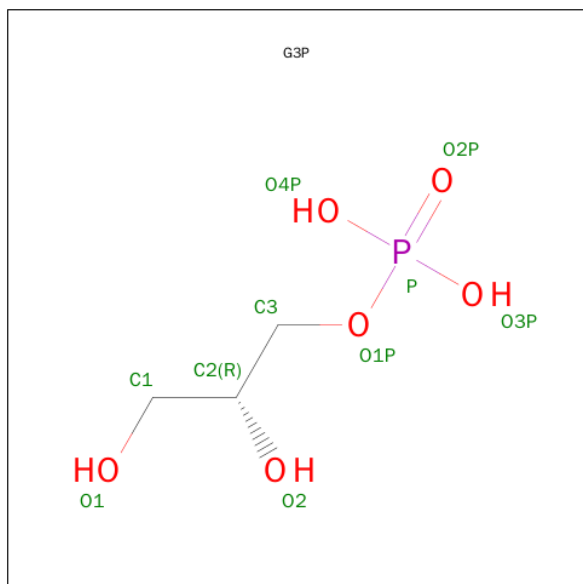
- Molecule 6 is (1R,3R)-6-[(3E,5E,7E,9E,11E,13E,15E,17E)-18-[(1S,4R,6R)-4-HYDROXY-2,6-TRIMETHYL-7-OXABICYCLO[4.1.0]HEPT-1-YL]-3,7,12,16-TETRAMETHYLOCTA

DECA-1,3,5,7,9,11,13,15,17-NONAENYLIDENE}-1,5,5-TRIMETHYLCYCLOHEXANE-1,3-DIOL (three-letter code: NEX) (formula: $C_{40}H_{56}O_4$).



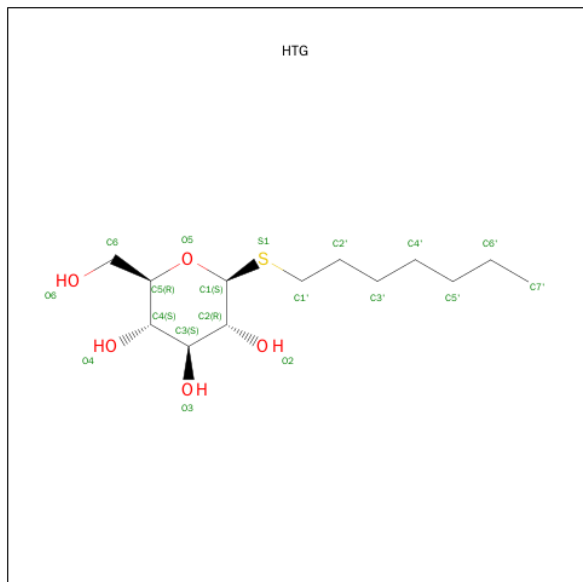
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			44	40	4		

- Molecule 7 is SN-GLYCEROL-3-PHOSPHATE (three-letter code: G3P) (formula: $C_3H_9O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 8 is HEPTYL 1-THIOHEXOPYRANOSIDE (three-letter code: HTG) (formula: $C_{13}H_{26}O_5S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	O	S	0	0
			17	13	3	1		
8	A	1	Total	C	O	S	0	0
			15	9	5	1		

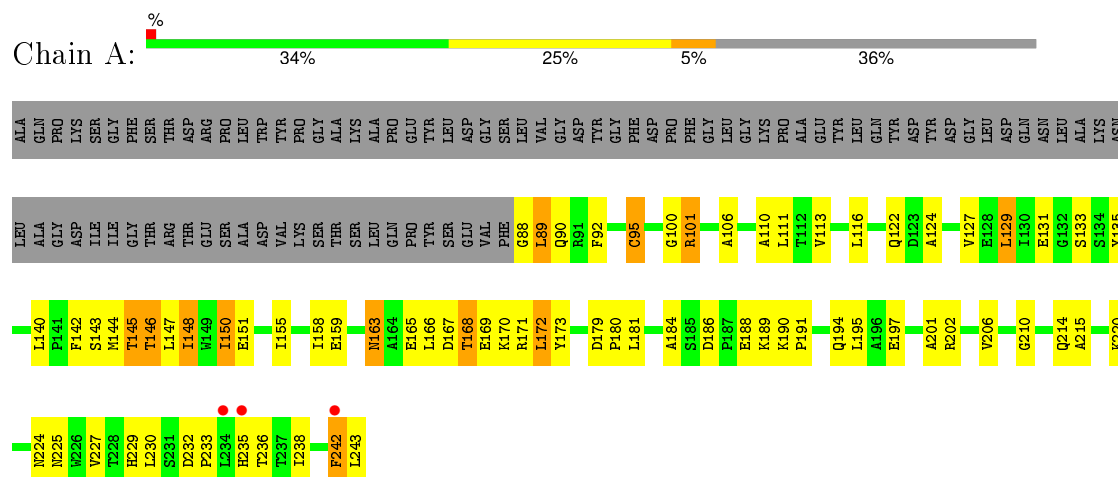
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	79	Total	O	0	0
			79	79		

3 Residue-property plots

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

- Molecule 1: Chlorophyll A-B binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	68.79 Å 68.79 Å 425.78 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.56 – 2.80 48.82 – 2.81	Depositor EDS
% Data completeness (in resolution range)	92.4 (42.56-2.80) 92.5 (48.82-2.81)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.41 (at 2.81 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.282 , 0.293 0.278 , 0.287	Depositor DCC
R_{free} test set	738 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	50.9	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 65.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 14625 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	2317	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.27% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: HTG, G3P, LUT, XAT, CHL, CLA, NEX

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	0.40	0/1246	0.67	0/1694

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1217	0	1233	71	0
2	A	585	0	647	23	0
3	A	264	0	278	9	0
4	A	42	0	56	3	0
5	A	44	0	55	1	0
6	A	44	0	56	3	0
7	A	10	0	7	0	0
8	A	32	0	37	5	0
9	A	79	0	0	5	0
All	All	2317	0	2369	85	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (85) 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)
8:A:632:HTG:O5	8:A:632:HTG:C1	1.64	1.43
1:A:146:THR:O	1:A:150:ILE:HD13	1.78	0.83
1:A:206:VAL:HG11	2:A:615:CLA:H41	1.60	0.82
1:A:151:GLU:HG3	1:A:155:ILE:HD13	1.64	0.80
1:A:220:LYS:HD3	1:A:224:ASN:ND2	1.96	0.79
1:A:242:PHE:HB3	9:A:313:HOH:O	1.84	0.76
1:A:143:SER:O	1:A:147:LEU:HB2	1.88	0.74
1:A:88:GLY:N	9:A:322:HOH:O	2.20	0.73
1:A:166:LEU:H	8:A:632:HTG:H2'1	1.55	0.70
1:A:195:LEU:HD11	2:A:615:CLA:HMD3	1.73	0.70
1:A:155:ILE:HD11	3:A:606:CHL:HMA1	1.72	0.70
8:A:632:HTG:C1	8:A:632:HTG:C5	2.70	0.69
1:A:135:TYR:HD2	2:A:604:CLA:HBA1	1.59	0.68
1:A:158:ILE:HG22	9:A:247:HOH:O	1.92	0.67
1:A:124:ALA:CB	2:A:604:CLA:HED1	2.24	0.67
1:A:131:GLU:HB3	9:A:310:HOH:O	1.95	0.67
2:A:613:CLA:H193	4:A:620:LUT:H193	1.78	0.65
1:A:210:GLY:O	1:A:214:GLN:HG3	1.97	0.64
1:A:158:ILE:HD11	6:A:623:NEX:H34	1.78	0.64
1:A:230:LEU:HD21	3:A:614:CHL:HMC	1.81	0.63
1:A:89:LEU:O	1:A:92:PHE:N	2.31	0.63
1:A:184:ALA:HB3	2:A:610:CLA:HED3	1.81	0.61
1:A:145:THR:HG22	1:A:146:THR:N	2.14	0.61
1:A:142:PHE:HB2	1:A:147:LEU:HD13	1.83	0.60
1:A:173:TYR:CE1	1:A:194:GLN:HG2	2.37	0.60
1:A:195:LEU:CD1	2:A:615:CLA:HMD3	2.32	0.59
1:A:229:HIS:HA	1:A:236:THR:OG1	2.02	0.59
1:A:232:ASP:OD2	1:A:235:HIS:HB2	2.02	0.59
1:A:124:ALA:HB1	2:A:604:CLA:HED1	1.85	0.58
1:A:151:GLU:HG3	1:A:155:ILE:CD1	2.32	0.57
1:A:129:LEU:HB2	1:A:144:MET:HE3	1.87	0.56
1:A:100:GLY:HA3	1:A:201:ALA:HB1	1.86	0.56
1:A:172:LEU:HB3	1:A:173:TYR:CD2	2.42	0.54
1:A:206:VAL:HG11	2:A:615:CLA:H51	1.90	0.54
1:A:147:LEU:HD12	3:A:606:CHL:HED3	1.91	0.52
1:A:238:ILE:HD13	2:A:613:CLA:OBD	2.10	0.52
1:A:101:ARG:NH1	1:A:197:GLU:OE1	2.41	0.52
1:A:202:ARG:O	1:A:206:VAL:HG23	2.10	0.52
1:A:167:ASP:O	1:A:169:GLU:N	2.42	0.51
1:A:151:GLU:CG	1:A:155:ILE:HD13	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:CYS:SG	2:A:603:CLA:HAA2	2.50	0.51
1:A:122:GLN:HE21	1:A:215:ALA:HB1	1.75	0.50
1:A:145:THR:CG2	1:A:146:THR:N	2.74	0.50
1:A:159:GLU:HG3	2:A:609:CLA:C4B	2.42	0.50
1:A:179:ASP:N	1:A:180:PRO:HD3	2.27	0.50
1:A:155:ILE:CD1	3:A:606:CHL:HMA1	2.42	0.49
1:A:225:ASN:HB3	2:A:613:CLA:HED2	1.94	0.49
2:A:615:CLA:HBB1	2:A:615:CLA:HHC	1.95	0.49
1:A:155:ILE:N	1:A:155:ILE:HD12	2.28	0.49
1:A:165:GLU:OE1	3:A:608:CHL:HBC1	2.13	0.49
1:A:159:GLU:HG3	2:A:609:CLA:NB	2.28	0.48
1:A:144:MET:O	1:A:148:ILE:HG23	2.14	0.48
2:A:613:CLA:HHC	2:A:613:CLA:HBB1	1.96	0.47
3:A:606:CHL:HBA2	6:A:623:NEX:H403	1.96	0.47
1:A:166:LEU:N	8:A:632:HTG:H2'1	2.27	0.47
1:A:166:LEU:HA	1:A:171:ARG:HD2	1.95	0.47
1:A:238:ILE:HG13	1:A:238:ILE:O	2.16	0.46
1:A:163:ASN:ND2	1:A:171:ARG:HH12	2.13	0.46
3:A:607:CHL:HBA2	3:A:607:CHL:H93	1.98	0.45
1:A:225:ASN:ND2	1:A:225:ASN:N	2.65	0.45
1:A:225:ASN:HD22	1:A:225:ASN:N	2.14	0.45
3:A:606:CHL:H61	6:A:623:NEX:H402	2.00	0.44
2:A:603:CLA:HHC	2:A:603:CLA:HBB1	1.99	0.44
1:A:233:PRO:HD2	3:A:614:CHL:H151	1.99	0.44
1:A:186:ASP:HB3	1:A:189:LYS:HD2	2.00	0.44
1:A:143:SER:OG	1:A:146:THR:HG23	2.17	0.43
1:A:163:ASN:ND2	1:A:171:ARG:NH1	2.66	0.43
1:A:110:ALA:O	1:A:113:VAL:HG12	2.19	0.43
2:A:609:CLA:HBB1	2:A:609:CLA:HHC	2.01	0.43
2:A:604:CLA:HMA3	9:A:244:HOH:O	2.18	0.42
1:A:179:ASP:HA	4:A:620:LUT:H24	2.00	0.42
1:A:190:LYS:HB2	1:A:191:PRO:HD3	2.01	0.42
2:A:613:CLA:H143	2:A:613:CLA:H91	2.01	0.42
1:A:89:LEU:O	1:A:90:GLN:C	2.57	0.42
2:A:602:CLA:HAB	2:A:602:CLA:HMB1	1.91	0.42
1:A:101:ARG:HD2	2:A:610:CLA:C4C	2.50	0.41
1:A:227:VAL:O	1:A:227:VAL:HG12	2.20	0.41
1:A:181:LEU:HD12	4:A:620:LUT:H222	2.03	0.41
1:A:206:VAL:CG1	2:A:615:CLA:H41	2.41	0.41
1:A:172:LEU:HB3	1:A:173:TYR:CE2	2.56	0.41
1:A:133:SER:HB2	1:A:140:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ALA:HA	5:A:622:XAT:H181	2.03	0.41
1:A:170:LYS:HE2	1:A:170:LYS:HB3	1.86	0.41
1:A:168:THR:HA	1:A:171:ARG:HG3	2.02	0.40
8:A:632:HTG:O5	8:A:632:HTG:C2	2.60	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	154/243 (63%)	141 (92%)	12 (8%)	1 (1%)	30	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	THR

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	128/198 (65%)	112 (88%)	16 (12%)	6	17

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	LEU
1	A	95	CYS
1	A	101	ARG
1	A	111	LEU
1	A	116	LEU
1	A	127	VAL
1	A	129	LEU
1	A	145	THR
1	A	146	THR
1	A	148	ILE
1	A	150	ILE
1	A	163	ASN
1	A	172	LEU
1	A	188	GLU
1	A	242	PHE
1	A	243	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	GLN
1	A	163	ASN
1	A	224	ASN
1	A	225	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

19 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CLA	A	602	1	55,73,73	1.38	6 (10%)	61,113,113	2.16	14 (22%)
2	CLA	A	603	-	55,73,73	1.32	5 (9%)	61,113,113	1.86	14 (22%)
2	CLA	A	604	9	55,73,73	1.31	4 (7%)	61,113,113	2.44	17 (27%)
3	CHL	A	606	9	57,74,74	1.55	8 (14%)	56,114,114	2.09	19 (33%)
3	CHL	A	607	9	57,74,74	1.56	6 (10%)	56,114,114	2.02	20 (35%)
3	CHL	A	608	9	57,74,74	1.77	11 (19%)	56,114,114	2.20	17 (30%)
2	CLA	A	609	1	55,73,73	1.29	8 (14%)	61,113,113	1.73	16 (26%)
2	CLA	A	610	1	55,73,73	1.32	4 (7%)	61,113,113	2.05	17 (27%)
2	CLA	A	611	7	55,73,73	1.39	7 (12%)	61,113,113	1.87	16 (26%)
2	CLA	A	612	-	55,73,73	1.51	7 (12%)	61,113,113	1.76	15 (24%)
2	CLA	A	613	1	55,73,73	1.23	6 (10%)	61,113,113	1.91	13 (21%)
3	CHL	A	614	-	57,74,74	1.50	9 (15%)	56,114,114	2.02	16 (28%)
2	CLA	A	615	7	55,73,73	1.30	7 (12%)	61,113,113	1.69	16 (26%)
4	LUT	A	620	-	41,43,43	1.23	3 (7%)	51,60,60	1.91	11 (21%)
5	XAT	A	622	-	41,47,47	1.01	3 (7%)	48,74,74	1.40	5 (10%)
6	NEX	A	623	-	39,46,46	1.18	3 (7%)	48,70,70	1.36	7 (14%)
7	G3P	A	630	2	9,9,9	0.83	0	10,12,12	1.17	2 (20%)
8	HTG	A	631	-	17,17,19	3.45	9 (52%)	18,20,24	4.10	4 (22%)
8	HTG	A	632	-	15,15,19	4.32	8 (53%)	18,20,24	4.04	3 (16%)

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	CLA	A	602	1	4/4/20/25	0/37/135/135	0/0/9/9
2	CLA	A	603	-	3/3/20/25	0/37/135/135	0/0/9/9
2	CLA	A	604	9	5/5/20/25	0/37/135/135	0/0/9/9
3	CHL	A	606	9	1/1/20/26	0/39/137/137	0/0/9/9

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CHL	A	607	9	1/1/20/26	0/39/137/137	0/0/9/9
3	CHL	A	608	9	1/1/20/26	0/39/137/137	0/0/9/9
2	CLA	A	609	1	5/5/20/25	0/37/135/135	0/0/9/9
2	CLA	A	610	1	4/4/20/25	0/37/135/135	0/0/9/9
2	CLA	A	611	7	4/4/20/25	0/37/135/135	0/0/9/9
2	CLA	A	612	-	5/5/20/25	0/37/135/135	0/0/9/9
2	CLA	A	613	1	5/5/20/25	0/37/135/135	0/0/9/9
3	CHL	A	614	-	1/1/20/26	0/39/137/137	0/0/9/9
2	CLA	A	615	7	4/4/20/25	0/37/135/135	0/0/9/9
4	LUT	A	620	-	-	0/29/67/67	0/2/2/2
5	XAT	A	622	-	-	0/31/93/93	0/2/4/4
6	NEX	A	623	-	-	0/27/83/83	0/2/3/3
7	G3P	A	630	2	-	0/8/8/8	0/0/0/0
8	HTG	A	631	-	-	0/10/23/30	0/1/1/1
8	HTG	A	632	-	-	0/6/26/30	0/1/1/1

All (114) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	607	CHL	C4D-CHA	-4.80	1.39	1.45
3	A	606	CHL	C4D-CHA	-4.33	1.39	1.45
3	A	608	CHL	C4D-CHA	-4.26	1.39	1.45
2	A	604	CLA	O2D-CED	-3.50	1.36	1.45
2	A	611	CLA	O2D-CED	-3.33	1.37	1.45
2	A	610	CLA	O2D-CED	-3.28	1.37	1.45
2	A	612	CLA	C3B-C2B	-3.16	1.36	1.40
2	A	611	CLA	C3B-C2B	-3.13	1.36	1.40
3	A	614	CHL	C4D-CHA	-3.05	1.41	1.45
2	A	603	CLA	C3B-C2B	-2.83	1.36	1.40
3	A	608	CHL	O2D-CED	-2.81	1.38	1.45
2	A	602	CLA	C3B-C2B	-2.81	1.36	1.40
2	A	615	CLA	O2D-CED	-2.80	1.38	1.45
3	A	614	CHL	C3B-C2B	-2.68	1.36	1.40
3	A	606	CHL	O2D-CED	-2.58	1.39	1.45
2	A	609	CLA	C3B-C2B	-2.56	1.36	1.40
2	A	613	CLA	O2D-CED	-2.55	1.39	1.45
3	A	608	CHL	C3B-C2B	-2.53	1.37	1.40
2	A	609	CLA	O2D-CED	-2.50	1.39	1.45
3	A	606	CHL	C3B-C2B	-2.46	1.37	1.40
2	A	613	CLA	C3B-C2B	-2.43	1.37	1.40
2	A	615	CLA	C3B-C2B	-2.27	1.37	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	607	CHL	C3B-C2B	-2.15	1.37	1.40
3	A	614	CHL	O2D-CED	-2.12	1.40	1.45
2	A	602	CLA	CHC-C1C	2.01	1.41	1.35
3	A	614	CHL	C4-C3	2.01	1.55	1.50
2	A	615	CLA	C5-C3	2.02	1.55	1.51
2	A	602	CLA	CMB-C2B	2.06	1.55	1.51
2	A	609	CLA	C4-C3	2.09	1.55	1.50
2	A	609	CLA	CMB-C2B	2.09	1.56	1.51
3	A	608	CHL	CAA-C2A	2.11	1.58	1.54
2	A	609	CLA	C5-C3	2.13	1.56	1.51
3	A	608	CHL	C1A-CHA	2.15	1.42	1.37
3	A	608	CHL	CMB-C2B	2.15	1.56	1.51
2	A	615	CLA	CMB-C2B	2.15	1.56	1.51
3	A	614	CHL	C5-C3	2.17	1.56	1.51
2	A	612	CLA	C4-C3	2.17	1.56	1.50
2	A	611	CLA	C4-C3	2.18	1.56	1.50
2	A	603	CLA	CMB-C2B	2.18	1.56	1.51
2	A	612	CLA	C5-C3	2.19	1.56	1.51
8	A	632	HTG	C1-S1	2.20	1.84	1.80
3	A	606	CHL	C1A-CHA	2.23	1.42	1.37
5	A	622	XAT	C28-C27	2.27	1.36	1.32
4	A	620	LUT	C24-C25	2.31	1.36	1.33
2	A	613	CLA	CMC-C2C	2.33	1.55	1.50
2	A	612	CLA	CMB-C2B	2.38	1.56	1.51
3	A	608	CHL	C4-C3	2.47	1.56	1.50
5	A	622	XAT	C8-C7	2.50	1.37	1.32
6	A	623	NEX	C28-C29	2.59	1.51	1.45
3	A	608	CHL	C5-C3	2.61	1.57	1.51
6	A	623	NEX	C1-C6	2.66	1.59	1.54
3	A	606	CHL	C5-C3	2.84	1.57	1.51
3	A	614	CHL	C1A-CHA	2.84	1.43	1.37
2	A	611	CLA	C5-C3	2.84	1.57	1.51
2	A	615	CLA	C2-C3	2.96	1.38	1.33
3	A	606	CHL	O2D-CGD	2.99	1.40	1.33
2	A	615	CLA	O2D-CGD	3.09	1.41	1.33
3	A	607	CHL	C1A-CHA	3.12	1.44	1.37
8	A	632	HTG	C6-C5	3.13	1.63	1.51
4	A	620	LUT	C1-C6	3.18	1.58	1.53
5	A	622	XAT	O23-C23	3.31	1.53	1.43
8	A	631	HTG	C4-C3	3.34	1.61	1.52
8	A	631	HTG	C6-C5	3.35	1.59	1.50
2	A	613	CLA	C2-C3	3.36	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	610	CLA	O2D-CGD	3.41	1.41	1.33
3	A	607	CHL	C2-C3	3.46	1.39	1.33
2	A	609	CLA	C2-C3	3.49	1.39	1.33
2	A	610	CLA	C2-C3	3.50	1.39	1.33
2	A	603	CLA	C2-C3	3.52	1.39	1.33
2	A	602	CLA	C2-C3	3.57	1.40	1.33
2	A	604	CLA	C2-C3	3.57	1.40	1.33
2	A	613	CLA	O2D-CGD	3.59	1.42	1.33
8	A	631	HTG	C3-C2	3.59	1.57	1.52
2	A	611	CLA	C2-C3	3.65	1.40	1.33
3	A	614	CHL	C2-C3	3.66	1.40	1.33
2	A	612	CLA	C2-C3	3.66	1.40	1.33
2	A	609	CLA	O2A-CGA	3.73	1.44	1.33
3	A	608	CHL	O2D-CGD	3.75	1.42	1.33
8	A	632	HTG	C3-C2	3.81	1.62	1.52
8	A	631	HTG	C1-C2	3.95	1.60	1.53
3	A	606	CHL	C2-C3	3.97	1.40	1.33
3	A	608	CHL	C2-C3	4.02	1.40	1.33
8	A	631	HTG	C1-S1	4.03	1.87	1.80
2	A	604	CLA	O2D-CGD	4.06	1.43	1.33
2	A	611	CLA	O2D-CGD	4.15	1.43	1.33
8	A	632	HTG	C4-C3	4.29	1.63	1.52
2	A	602	CLA	O2A-CGA	4.31	1.46	1.33
8	A	632	HTG	O5-C5	4.34	1.55	1.44
2	A	612	CLA	O2A-CGA	4.35	1.46	1.33
8	A	631	HTG	O2-C2	4.36	1.53	1.43
3	A	614	CHL	O2D-CGD	4.36	1.44	1.33
2	A	611	CLA	O2A-CGA	4.37	1.46	1.33
2	A	613	CLA	O2A-CGA	4.44	1.46	1.33
2	A	609	CLA	O2D-CGD	4.45	1.44	1.33
2	A	615	CLA	O2A-CGA	4.46	1.46	1.33
2	A	603	CLA	O2A-CGA	4.46	1.46	1.33
8	A	632	HTG	C4-C5	4.50	1.62	1.53
2	A	604	CLA	O2A-CGA	4.55	1.47	1.33
6	A	623	NEX	C7-C8	4.62	1.40	1.32
2	A	603	CLA	O2D-CGD	4.82	1.45	1.33
2	A	610	CLA	O2A-CGA	4.86	1.48	1.33
8	A	632	HTG	C1-C2	5.00	1.62	1.53
8	A	631	HTG	C4-C5	5.12	1.64	1.51
4	A	620	LUT	C23-C24	5.12	1.54	1.50
3	A	607	CHL	O2D-CGD	5.19	1.46	1.33
3	A	614	CHL	O2A-CGA	5.26	1.49	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	607	CHL	O2A-CGA	5.31	1.49	1.33
8	A	631	HTG	O5-C5	5.59	1.54	1.44
3	A	606	CHL	O2A-CGA	5.72	1.50	1.33
2	A	602	CLA	O2D-CGD	5.94	1.48	1.33
2	A	612	CLA	O2D-CGD	6.43	1.49	1.33
8	A	631	HTG	O5-C1	7.60	1.55	1.42
3	A	608	CHL	O2A-CGA	7.82	1.56	1.33
8	A	632	HTG	O5-C1	12.78	1.64	1.42

All (242) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	604	CLA	CMB-C2B-C1B	-6.93	116.89	128.36
2	A	602	CLA	O1D-CGD-CBD	-6.55	115.23	124.62
2	A	610	CLA	CMB-C2B-C1B	-5.99	118.45	128.36
2	A	604	CLA	O1D-CGD-CBD	-5.89	116.18	124.62
2	A	603	CLA	O1D-CGD-CBD	-5.84	116.25	124.62
6	A	623	NEX	C4-C3-C2	-4.72	99.98	110.41
2	A	615	CLA	CMB-C2B-C1B	-4.28	121.29	128.36
4	A	620	LUT	C38-C25-C24	-4.16	114.40	123.59
2	A	611	CLA	CAA-C2A-C3A	-4.12	101.38	113.22
3	A	606	CHL	C4-C3-C5	-3.99	109.31	115.41
4	A	620	LUT	C18-C5-C4	-3.87	107.17	114.24
8	A	631	HTG	C4-C3-C2	-3.86	105.75	111.93
2	A	611	CLA	OBD-CAD-CBD	-3.72	120.32	125.94
2	A	602	CLA	CMB-C2B-C1B	-3.68	122.27	128.36
2	A	609	CLA	OBD-CAD-CBD	-3.57	120.55	125.94
2	A	604	CLA	OBD-CAD-CBD	-3.56	120.57	125.94
3	A	608	CHL	O1D-CGD-CBD	-3.49	119.61	124.62
2	A	611	CLA	CMB-C2B-C1B	-3.42	122.70	128.36
2	A	604	CLA	CAA-C2A-C3A	-3.42	103.39	113.22
8	A	632	HTG	O5-C1-C2	-3.37	105.61	110.19
2	A	603	CLA	OBD-CAD-CBD	-3.36	120.87	125.94
8	A	631	HTG	O5-C1-C2	-3.34	105.65	110.19
2	A	615	CLA	OBD-CAD-CBD	-3.34	120.89	125.94
3	A	606	CHL	OBD-CAD-CBD	-3.33	120.91	125.94
2	A	612	CLA	CMB-C2B-C1B	-3.33	122.86	128.36
3	A	607	CHL	OBD-CAD-CBD	-3.32	120.93	125.94
2	A	613	CLA	OBD-CAD-CBD	-3.21	121.09	125.94
2	A	602	CLA	C4-C3-C5	-3.20	110.52	115.41
2	A	613	CLA	C5-C3-C2	-3.20	114.99	121.05
2	A	613	CLA	CMB-C2B-C1B	-3.17	123.12	128.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	614	CHL	OBD-CAD-CBD	-3.17	121.16	125.94
3	A	608	CHL	O1A-CGA-CBA	-3.17	111.06	123.72
3	A	614	CHL	C4-C3-C5	-3.04	110.77	115.41
2	A	612	CLA	CAA-C2A-C3A	-2.90	104.89	113.22
3	A	606	CHL	O1D-CGD-CBD	-2.88	120.49	124.62
2	A	602	CLA	OBD-CAD-CBD	-2.88	121.59	125.94
2	A	609	CLA	CMB-C2B-C1B	-2.86	123.63	128.36
3	A	606	CHL	CAA-C2A-C3A	-2.84	105.05	113.22
6	A	623	NEX	C18-C5-C4	-2.77	107.51	110.97
2	A	603	CLA	CMB-C2B-C1B	-2.74	123.83	128.36
2	A	610	CLA	OBD-CAD-CBD	-2.68	121.89	125.94
3	A	608	CHL	OBD-CAD-CBD	-2.62	121.99	125.94
4	A	620	LUT	C1-C6-C5	-2.58	118.87	122.66
3	A	606	CHL	C3B-CAB-CBB	-2.44	121.33	126.32
4	A	620	LUT	C23-C24-C25	-2.42	122.96	125.22
2	A	611	CLA	O2A-CGA-O1A	-2.33	117.47	123.49
3	A	608	CHL	O2A-CGA-O1A	-2.25	117.68	123.49
3	A	607	CHL	C4-C3-C5	-2.24	111.98	115.41
3	A	614	CHL	O2A-CGA-O1A	-2.24	117.71	123.49
3	A	607	CHL	O1D-CGD-CBD	-2.24	121.42	124.62
2	A	604	CLA	C4-C3-C5	-2.23	112.00	115.41
2	A	615	CLA	O2A-CGA-O1A	-2.16	117.91	123.49
3	A	614	CHL	O1A-CGA-CBA	-2.12	115.23	123.72
2	A	609	CLA	O2D-CGD-CBD	-2.12	108.39	111.30
2	A	602	CLA	O2A-CGA-O1A	-2.08	118.13	123.49
2	A	612	CLA	O2A-CGA-O1A	-2.07	118.14	123.49
2	A	609	CLA	C12-C11-C10	-2.07	102.73	112.99
2	A	615	CLA	C5-C3-C2	-2.07	117.13	121.05
2	A	603	CLA	O2A-CGA-O1A	-2.06	118.16	123.49
2	A	609	CLA	O2A-CGA-O1A	-2.04	118.22	123.49
2	A	610	CLA	O1A-CGA-CBA	-2.03	115.59	123.72
3	A	606	CHL	O2A-CGA-O1A	-2.02	118.28	123.49
2	A	603	CLA	C4-C3-C5	-2.01	112.34	115.41
2	A	611	CLA	C6-C7-C8	2.01	122.14	115.49
3	A	606	CHL	CMD-C2D-C3D	2.01	129.02	125.09
6	A	623	NEX	C37-C21-C36	2.03	110.39	107.35
2	A	609	CLA	C17-C16-C15	2.04	123.11	112.99
2	A	611	CLA	C2A-C1A-CHA	2.04	127.65	123.89
2	A	610	CLA	C14-C13-C15	2.05	118.96	111.08
3	A	607	CHL	CMD-C2D-C3D	2.07	129.13	125.09
5	A	622	XAT	C26-O24-C25	2.07	63.69	61.25
3	A	607	CHL	C16-C17-C18	2.09	126.38	115.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	615	CLA	CBC-CAC-C3C	2.09	118.78	112.39
3	A	607	CHL	O2D-CGD-CBD	2.10	114.18	111.30
2	A	612	CLA	CAC-C3C-C4C	2.10	127.88	124.83
2	A	609	CLA	CMB-C2B-C3B	2.12	129.23	125.09
3	A	607	CHL	C14-C13-C12	2.13	119.27	111.08
2	A	613	CLA	CMB-C2B-C3B	2.14	129.28	125.09
2	A	602	CLA	C2A-C1A-CHA	2.14	127.83	123.89
3	A	607	CHL	C17-C16-C15	2.16	123.70	112.99
3	A	607	CHL	C7-C6-C5	2.17	119.47	113.06
2	A	612	CLA	C1D-CHD-C4C	2.18	125.90	122.60
5	A	622	XAT	C6-O4-C5	2.18	63.82	61.25
2	A	613	CLA	C7-C6-C5	2.18	119.52	113.06
2	A	615	CLA	CED-O2D-CGD	2.18	121.11	115.99
2	A	610	CLA	C2A-C1A-CHA	2.20	127.93	123.89
6	A	623	NEX	C1-C2-C3	2.20	118.57	113.41
7	A	630	G3P	O3P-P-O2P	2.20	117.66	110.58
3	A	606	CHL	CMB-C2B-C3B	2.22	129.43	125.09
3	A	608	CHL	CED-O2D-CGD	2.22	121.20	115.99
3	A	614	CHL	C9-C8-C10	2.23	119.63	111.08
2	A	609	CLA	C2A-C1A-CHA	2.24	128.01	123.89
6	A	623	NEX	C26-O24-C25	2.26	63.91	61.25
2	A	603	CLA	C6-C7-C8	2.28	123.05	115.49
4	A	620	LUT	C26-C25-C24	2.30	125.02	121.21
3	A	607	CHL	C11-C10-C8	2.30	123.13	115.49
2	A	604	CLA	C2A-C1A-CHA	2.30	128.13	123.89
2	A	611	CLA	C7-C6-C5	2.33	119.94	113.06
3	A	607	CHL	CMB-C2B-C3B	2.34	129.66	125.09
3	A	614	CHL	CMB-C2B-C3B	2.35	129.68	125.09
2	A	609	CLA	C11-C12-C13	2.35	123.28	115.49
2	A	602	CLA	CMC-C2C-C1C	2.35	128.66	125.02
2	A	611	CLA	CMB-C2B-C3B	2.35	129.69	125.09
2	A	603	CLA	C6-C5-C3	2.36	117.66	112.48
2	A	612	CLA	C14-C13-C15	2.36	120.15	111.08
3	A	608	CHL	CMB-C2B-C3B	2.37	129.72	125.09
3	A	608	CHL	C14-C13-C12	2.37	120.17	111.08
2	A	612	CLA	CAA-CBA-CGA	2.38	120.28	113.32
8	A	632	HTG	O5-C5-C6	2.38	112.37	106.36
3	A	608	CHL	C9-C8-C7	2.38	120.24	111.08
2	A	610	CLA	C9-C8-C7	2.39	120.26	111.08
2	A	613	CLA	O2A-CGA-CBA	2.39	119.19	111.90
2	A	615	CLA	C14-C13-C15	2.40	120.31	111.08
2	A	603	CLA	CMD-C2D-C3D	2.44	129.87	125.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	613	CLA	C1D-CHD-C4C	2.45	126.31	122.60
7	A	630	G3P	O1P-P-O2P	2.49	113.49	107.14
2	A	602	CLA	CMB-C2B-C3B	2.51	130.00	125.09
2	A	610	CLA	C16-C17-C18	2.53	128.62	115.87
2	A	615	CLA	C11-C10-C8	2.55	123.95	115.49
2	A	612	CLA	CMB-C2B-C3B	2.57	130.10	125.09
3	A	607	CHL	C16-C15-C13	2.59	124.07	115.49
4	A	620	LUT	C1-C2-C3	2.59	119.49	113.41
2	A	611	CLA	C1D-CHD-C4C	2.61	126.55	122.60
2	A	604	CLA	CAA-CBA-CGA	2.63	121.01	113.32
2	A	615	CLA	C4A-NA-C1A	2.64	109.77	106.36
2	A	609	CLA	C16-C15-C13	2.65	124.26	115.49
2	A	612	CLA	C2A-C1A-CHA	2.67	128.79	123.89
2	A	615	CLA	C1D-CHD-C4C	2.67	126.64	122.60
3	A	608	CHL	C11-C10-C8	2.68	124.36	115.49
2	A	603	CLA	C1D-CHD-C4C	2.70	126.69	122.60
3	A	606	CHL	C5-C3-C2	2.71	126.19	121.05
2	A	615	CLA	C11-C12-C13	2.73	124.55	115.49
2	A	604	CLA	C4A-NA-C1A	2.75	109.91	106.36
2	A	611	CLA	CAA-C2A-C1A	2.76	122.20	112.47
2	A	602	CLA	C1D-CHD-C4C	2.76	126.78	122.60
2	A	611	CLA	C4A-NA-C1A	2.77	109.94	106.36
2	A	615	CLA	C6-C5-C3	2.80	118.62	112.48
2	A	604	CLA	C11-C12-C13	2.84	124.89	115.49
2	A	609	CLA	C1D-CHD-C4C	2.84	126.91	122.60
2	A	604	CLA	O2A-CGA-CBA	2.86	120.60	111.90
2	A	610	CLA	C11-C12-C13	2.86	124.97	115.49
2	A	603	CLA	C16-C15-C13	2.87	125.02	115.49
2	A	610	CLA	C4A-NA-C1A	2.89	110.09	106.36
2	A	609	CLA	C4A-NA-C1A	2.90	110.10	106.36
3	A	608	CHL	CAA-CBA-CGA	2.91	121.83	113.32
2	A	602	CLA	C4A-NA-C1A	2.91	110.12	106.36
2	A	610	CLA	C1D-CHD-C4C	2.91	127.01	122.60
6	A	623	NEX	C24-C23-C22	2.93	116.90	110.41
3	A	607	CHL	CAA-C2A-C1A	2.95	122.87	112.47
2	A	604	CLA	C9-C8-C10	2.95	122.43	111.08
2	A	604	CLA	C1D-CHD-C4C	2.96	127.08	122.60
3	A	606	CHL	C4B-CHC-C1C	2.99	127.12	122.60
2	A	603	CLA	C4A-NA-C1A	3.04	110.29	106.36
2	A	613	CLA	C4A-NA-C1A	3.05	110.30	106.36
3	A	614	CHL	CAA-C2A-C1A	3.05	123.24	112.47
3	A	606	CHL	C11-C10-C8	3.07	125.67	115.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	615	CLA	CMB-C2B-C3B	3.10	131.15	125.09
2	A	612	CLA	C4A-NA-C1A	3.13	110.40	106.36
3	A	606	CHL	C11-C12-C13	3.13	125.88	115.49
3	A	608	CHL	C6-C7-C8	3.18	126.05	115.49
6	A	623	NEX	C21-C22-C23	3.20	120.42	115.02
2	A	612	CLA	C16-C15-C13	3.22	126.17	115.49
2	A	615	CLA	C4-C3-C5	3.23	120.34	115.41
2	A	609	CLA	C6-C5-C3	3.26	119.63	112.48
2	A	612	CLA	C6-C5-C3	3.27	119.65	112.48
3	A	607	CHL	CBC-CAC-C3C	3.28	122.41	112.39
4	A	620	LUT	C2-C3-C4	3.30	116.17	110.32
2	A	613	CLA	CED-O2D-CGD	3.32	123.77	115.99
3	A	614	CHL	C4A-NA-C1A	3.32	109.95	106.04
3	A	608	CHL	C4A-NA-C1A	3.34	109.98	106.04
3	A	608	CHL	C4B-CHC-C1C	3.35	127.67	122.60
3	A	607	CHL	C4B-CHC-C1C	3.36	127.69	122.60
3	A	606	CHL	C4A-NA-C1A	3.37	110.01	106.04
2	A	611	CLA	C11-C12-C13	3.37	126.68	115.49
3	A	614	CHL	C4B-CHC-C1C	3.39	127.74	122.60
3	A	614	CHL	C16-C15-C13	3.42	126.84	115.49
5	A	622	XAT	C21-C22-C23	3.50	120.92	115.02
3	A	607	CHL	C4A-NA-C1A	3.50	110.17	106.04
2	A	604	CLA	C11-C10-C8	3.51	127.12	115.49
2	A	611	CLA	CAA-CBA-CGA	3.51	123.60	113.32
3	A	607	CHL	O2A-CGA-CBA	3.60	122.86	111.90
2	A	609	CLA	O2A-CGA-CBA	3.61	122.91	111.90
2	A	615	CLA	C16-C15-C13	3.63	127.51	115.49
2	A	610	CLA	C11-C10-C8	3.63	127.54	115.49
8	A	631	HTG	O5-C5-C6	3.71	111.16	106.62
3	A	606	CHL	O2D-CGD-CBD	3.71	116.39	111.30
2	A	610	CLA	C16-C15-C13	3.79	128.06	115.49
3	A	606	CHL	O2A-CGA-CBA	3.89	123.75	111.90
2	A	602	CLA	O2A-CGA-CBA	3.90	123.77	111.90
2	A	612	CLA	O2A-CGA-CBA	3.92	123.85	111.90
2	A	611	CLA	O2A-CGA-CBA	3.95	123.94	111.90
2	A	603	CLA	O2A-CGA-CBA	3.96	123.96	111.90
4	A	620	LUT	C3-C4-C5	3.97	120.03	111.86
2	A	610	CLA	C7-C6-C5	3.97	124.80	113.06
2	A	612	CLA	CBA-CAA-C2A	4.01	125.06	113.73
3	A	614	CHL	C11-C12-C13	4.02	128.82	115.49
5	A	622	XAT	O23-C23-C22	4.03	118.17	109.91
2	A	615	CLA	O2A-CGA-CBA	4.10	124.41	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	609	CLA	CBA-CAA-C2A	4.12	125.35	113.73
3	A	614	CHL	CED-O2D-CGD	4.15	125.71	115.99
2	A	613	CLA	C6-C7-C8	4.15	129.25	115.49
3	A	614	CHL	CAA-CBA-CGA	4.15	125.47	113.32
3	A	606	CHL	C16-C15-C13	4.15	129.26	115.49
3	A	606	CHL	CBA-CAA-C2A	4.18	125.54	113.73
3	A	614	CHL	C6-C5-C3	4.23	121.77	112.48
2	A	603	CLA	CED-O2D-CGD	4.28	126.03	115.99
3	A	614	CHL	C11-C10-C8	4.36	129.95	115.49
3	A	607	CHL	OMC-CMC-C2C	4.38	136.83	125.58
2	A	610	CLA	CED-O2D-CGD	4.40	126.31	115.99
3	A	608	CHL	O2D-CGD-CBD	4.42	117.37	111.30
4	A	620	LUT	C18-C5-C6	4.42	128.95	124.61
3	A	606	CHL	C7-C6-C5	4.44	126.19	113.06
3	A	607	CHL	CED-O2D-CGD	4.50	126.55	115.99
2	A	610	CLA	O2A-CGA-CBA	4.52	125.66	111.90
3	A	606	CHL	C6-C5-C3	4.58	122.54	112.48
2	A	613	CLA	CAA-CBA-CGA	4.66	126.95	113.32
4	A	620	LUT	C2-C1-C6	4.71	118.01	110.49
2	A	610	CLA	CBA-CAA-C2A	4.77	127.18	113.73
2	A	610	CLA	CMB-C2B-C3B	4.77	134.42	125.09
2	A	611	CLA	CED-O2D-CGD	4.80	127.25	115.99
2	A	612	CLA	CED-O2D-CGD	4.89	127.46	115.99
2	A	611	CLA	C6-C5-C3	4.90	123.23	112.48
3	A	607	CHL	CBA-CAA-C2A	4.95	127.71	113.73
3	A	614	CHL	O2A-CGA-CBA	4.98	127.06	111.90
2	A	602	CLA	CBA-CAA-C2A	4.99	127.81	113.73
2	A	604	CLA	C6-C5-C3	5.13	123.75	112.48
3	A	608	CHL	OMC-CMC-C2C	5.16	138.84	125.58
2	A	613	CLA	CBA-CAA-C2A	5.24	128.51	113.73
2	A	609	CLA	CED-O2D-CGD	5.28	128.37	115.99
5	A	622	XAT	C24-C23-C22	5.43	122.42	110.41
2	A	604	CLA	CMB-C2B-C3B	5.49	135.82	125.09
2	A	603	CLA	O2D-CGD-CBD	5.60	118.98	111.30
2	A	613	CLA	C6-C5-C3	6.02	125.69	112.48
4	A	620	LUT	C38-C25-C26	6.06	120.57	116.04
3	A	608	CHL	CBA-CAA-C2A	6.11	130.98	113.73
2	A	602	CLA	CED-O2D-CGD	6.27	130.71	115.99
3	A	608	CHL	O2A-CGA-CBA	6.34	131.21	111.90
2	A	604	CLA	O2D-CGD-CBD	6.59	120.33	111.30
2	A	602	CLA	O2D-CGD-CBD	6.88	120.73	111.30
2	A	604	CLA	CBA-CAA-C2A	7.09	133.74	113.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	631	HTG	C1'-S1-C1	15.90	122.22	100.30
8	A	632	HTG	C1'-S1-C1	16.25	122.70	100.30

All (43) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	613	CLA	C8
2	A	613	CLA	C13
2	A	613	CLA	NC
2	A	613	CLA	ND
2	A	613	CLA	NA
3	A	606	CHL	C13
3	A	608	CHL	C13
2	A	609	CLA	C8
2	A	609	CLA	C13
2	A	609	CLA	NC
2	A	609	CLA	NA
2	A	609	CLA	ND
2	A	604	CLA	C8
2	A	604	CLA	C13
2	A	604	CLA	NC
2	A	604	CLA	ND
2	A	604	CLA	NA
2	A	612	CLA	C8
2	A	612	CLA	C13
2	A	612	CLA	NC
2	A	612	CLA	ND
2	A	612	CLA	NA
2	A	615	CLA	C13
2	A	615	CLA	NC
2	A	615	CLA	ND
2	A	615	CLA	NA
2	A	611	CLA	C13
2	A	611	CLA	NC
2	A	611	CLA	ND
2	A	611	CLA	NA
3	A	607	CHL	C13
2	A	610	CLA	C13
2	A	610	CLA	NC
2	A	610	CLA	NA
2	A	610	CLA	ND
2	A	602	CLA	C8

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Mol	Chain	Res	Type	Atom
2	A	602	CLA	NC
2	A	602	CLA	ND
2	A	602	CLA	NA
2	A	603	CLA	NC
2	A	603	CLA	ND
2	A	603	CLA	NA
3	A	614	CHL	C13

There are no torsion outliers.

There are no ring outliers.

15 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	CLA	1	0
2	A	603	CLA	2	0
2	A	604	CLA	4	0
3	A	606	CHL	5	0
3	A	607	CHL	1	0
3	A	608	CHL	1	0
2	A	609	CLA	3	0
2	A	610	CLA	2	0
2	A	613	CLA	5	0
3	A	614	CHL	2	0
2	A	615	CLA	6	0
4	A	620	LUT	3	0
5	A	622	XAT	1	0
6	A	623	NEX	3	0
8	A	632	HTG	5	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	156/243 (64%)	-0.15	3 (1%) 70 59	18, 41, 97, 128	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	LEU	4.0
1	A	235	HIS	3.3
1	A	242	PHE	3.1

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(Å ²)	Q<0.9
2	CLA	A	612	65/65	0.86	0.37	4.44	24,54,143,144	0
6	NEX	A	623	44/44	0.85	0.32	4.32	22,49,158,159	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	XAT	A	622	44/44	0.88	0.25	3.90	21,53,122,127	0
3	CHL	A	607	66/66	0.93	0.23	2.40	39,53,154,156	0
8	HTG	A	631	17/19	0.82	0.36	2.11	85,86,88,89	0
3	CHL	A	608	66/66	0.88	0.25	1.62	32,63,90,94	0
2	CLA	A	611	65/65	0.93	0.27	1.32	13,28,162,165	0
3	CHL	A	606	66/66	0.94	0.21	1.03	18,38,127,129	0
4	LUT	A	620	42/42	0.94	0.21	0.85	21,31,37,39	0
2	CLA	A	602	65/65	0.88	0.23	0.73	37,74,125,129	0
2	CLA	A	604	65/65	0.93	0.19	0.66	23,44,99,100	0
2	CLA	A	609	65/65	0.92	0.20	0.57	38,56,119,125	0
2	CLA	A	615	65/65	0.93	0.20	0.44	15,35,141,144	0
8	HTG	A	632	15/19	0.84	0.24	0.35	85,87,89,89	0
3	CHL	A	614	66/66	0.88	0.24	0.09	36,52,133,134	0
2	CLA	A	613	65/65	0.92	0.20	0.05	41,49,109,125	0
2	CLA	A	610	65/65	0.93	0.17	-0.24	29,44,54,67	0
2	CLA	A	603	65/65	0.91	0.27	-	40,61,157,158	0
7	G3P	A	630	10/10	0.94	0.31	-	69,78,82,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.