



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 01:39 am BST

PDB ID : 4CFM  
Title : Structure-based design of C8-substituted O6-cyclohexylmethoxyguanine CDK1 and 2 inhibitors.  
Authors : Carbain, B.; Paterson, D.J.; Anscombe, E.; Campbell, A.; Cano, C.; Echaliér, A.; Endicott, J.; Golding, B.T.; Haggerty, K.; Hardcastle, I.R.; Jewsbury, P.; Newell, D.R.; Noble, M.E.M.; Roche, C.; Wang, L.Z.; Griffin, R.  
Deposited on : 2013-11-18  
Resolution : 2.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
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) : 2.11

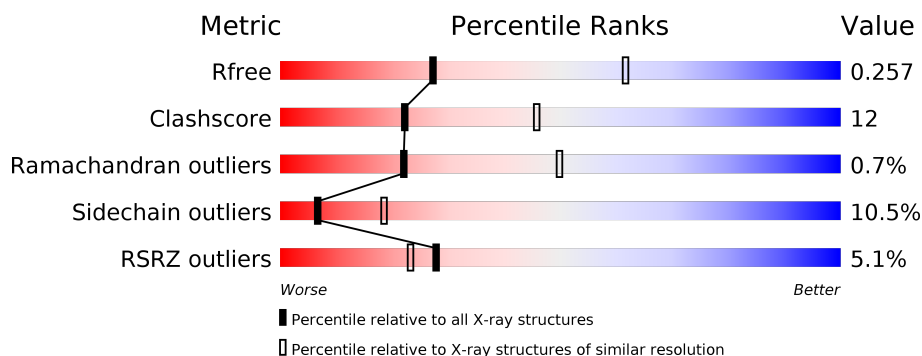
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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  $\leq 5\%$ . 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	303	<div> <div>4%</div> <div> <div></div> <div>66%</div> <div>27%</div> <div>5%</div> </div> </div>
1	C	303	<div> <div>7%</div> <div> <div></div> <div>61%</div> <div>21%</div> <div>5%</div> <div>12%</div> </div> </div>
2	B	258	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>5%</div> </div> </div>
2	D	258	<div> <div>7%</div> <div> <div></div> <div>72%</div> <div>24%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8829 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 CYCLIN-DEPENDENT KINASE 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	P	S	0	5	0
			2425	1573	411	432	1	8			
1	C	267	Total	C	N	O	P	S	0	5	0
			2178	1410	372	388	1	7			

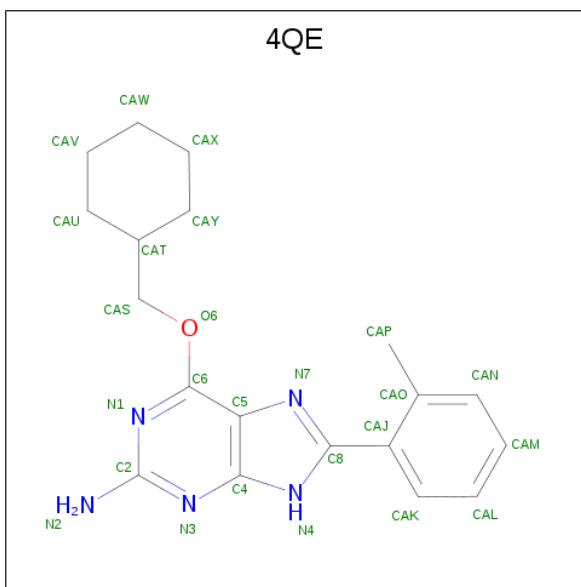
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P24941
A	-3	PRO	-	expression tag	UNP P24941
A	-2	LEU	-	expression tag	UNP P24941
A	-1	GLY	-	expression tag	UNP P24941
A	0	SER	-	expression tag	UNP P24941
C	-4	GLY	-	expression tag	UNP P24941
C	-3	PRO	-	expression tag	UNP P24941
C	-2	LEU	-	expression tag	UNP P24941
C	-1	GLY	-	expression tag	UNP P24941
C	0	SER	-	expression tag	UNP P24941

- Molecule 2 is a protein called CYCLIN-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	0	0
			2083	1350	339	383	11			
2	D	258	Total	C	N	O	S	0	0	0
			2083	1350	339	383	11			

- Molecule 3 is 6-(cyclohexylmethoxy)-8-(2-methylphenyl)-9H-purin-2-amine (three-letter code: 4QE) (formula: C<sub>19</sub>H<sub>23</sub>N<sub>5</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			25	19	5	1		
3	C	1	Total	C	N	O	0	0
			25	19	5	1		

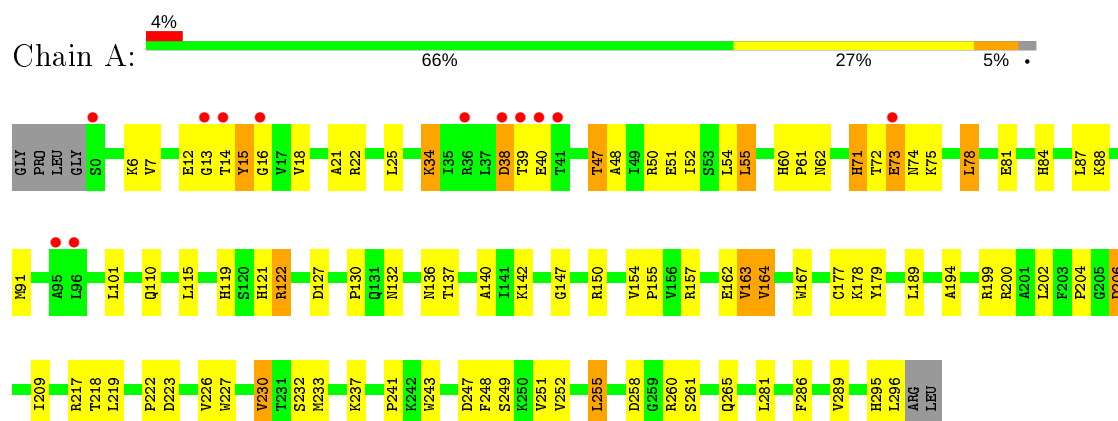
- Molecule 4 is water.

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

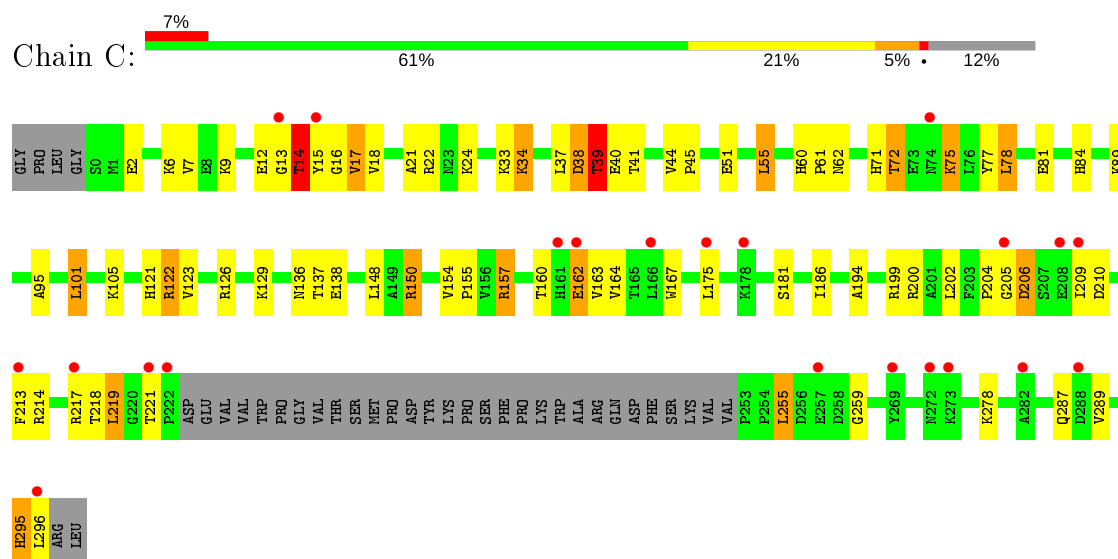
### 3 Residue-property plots [i](#)

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.

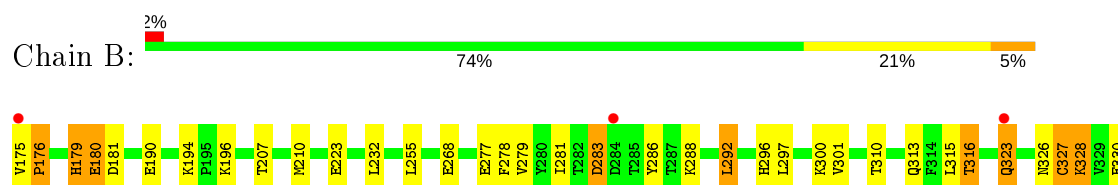
#### • Molecule 1: CYCLIN-DEPENDENT KINASE 2

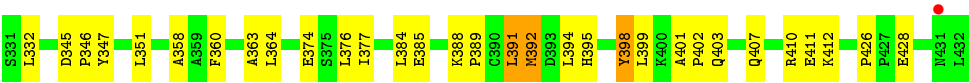


#### • Molecule 1: CYCLIN-DEPENDENT KINASE 2

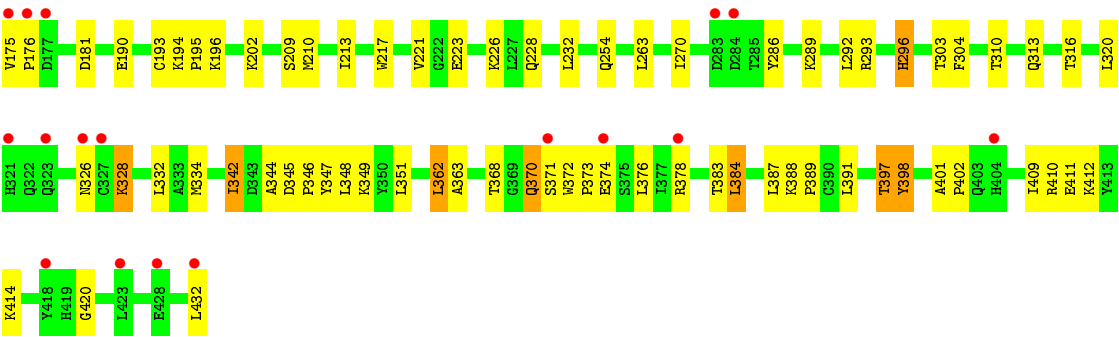


#### • Molecule 2: CYCLIN-A2





● Molecule 2: CYCLIN-A2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.11Å 135.44Å 149.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.34 – 2.85 22.28 – 2.85	Depositor EDS
% Data completeness (in resolution range)	94.0 (22.34-2.85) 94.2 (22.28-2.85)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 2.84Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.217 , 0.258 0.216 , 0.257	Depositor DCC
$R_{free}$ test set	1671 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.7	Xtriage
Anisotropy	0.690	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8829	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 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: TPO, 4QE

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	0.81	0/2477	0.96	3/3361 (0.1%)
1	C	0.65	0/2218	0.88	1/3003 (0.0%)
2	B	0.81	0/2133	0.92	1/2897 (0.0%)
2	D	0.65	0/2133	0.83	0/2897
All	All	0.74	0/8961	0.90	5/12158 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	C	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	ASP	CB-CG-OD1	5.75	123.47	118.30
1	C	101	LEU	CA-CB-CG	5.68	128.38	115.30
1	A	78	LEU	CA-CB-CG	5.58	128.14	115.30
2	B	175	VAL	CB-CA-C	5.15	121.19	111.40
1	A	258	ASP	CB-CG-OD1	5.06	122.85	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	12	GLU	Peptide
1	A	38	ASP	Peptide
1	C	12	GLU	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2425	0	2457	77	0
1	C	2178	0	2220	62	0
2	B	2083	0	2107	43	0
2	D	2083	0	2107	42	0
3	A	25	0	23	4	0
3	C	25	0	23	5	0
4	A	5	0	0	0	0
4	C	5	0	0	1	0
All	All	8829	0	8937	208	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 12.

All (208) 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:84[B]:HIS:CD2	1:C:296:LEU:CD1	2.09	1.36
1:C:84[B]:HIS:HD2	1:C:296:LEU:HD13	0.99	1.14
1:C:84[B]:HIS:CD2	1:C:296:LEU:HD13	1.75	1.09
1:C:84[B]:HIS:CD2	1:C:296:LEU:HD12	1.81	1.09
1:A:84[B]:HIS:HD2	1:A:296:LEU:HD13	1.19	1.04
1:C:84[B]:HIS:HD2	1:C:296:LEU:CD1	1.63	0.96
1:C:71:HIS:HD2	2:D:296:HIS:CE1	1.83	0.96
1:A:71:HIS:CD2	2:B:296:HIS:NE2	2.41	0.88
1:A:60:HIS:CD2	1:A:62:ASN:H	1.95	0.84
1:C:38:ASP:O	1:C:39:THR:HB	1.78	0.83
1:A:84[B]:HIS:HD2	1:A:296:LEU:CD1	1.91	0.83
1:C:71:HIS:CD2	2:D:296:HIS:CE1	2.66	0.83
1:A:71:HIS:CD2	2:B:296:HIS:CE1	2.67	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:GLU:O	3:A:1297:4QE:N2	2.13	0.81
1:A:15[A]:TYR:HD1	1:A:15[A]:TYR:N	1.77	0.80
1:C:95:ALA:O	1:C:199:ARG:NH1	2.14	0.80
1:A:60:HIS:HD2	1:A:62:ASN:H	1.29	0.80
1:A:251:VAL:HG12	1:A:252:VAL:HG23	1.64	0.79
1:A:71:HIS:HD2	2:B:296:HIS:NE2	1.80	0.78
1:A:84[B]:HIS:CD2	1:A:296:LEU:HD13	2.12	0.77
1:A:39:THR:HA	2:B:292:LEU:HD23	1.67	0.76
1:A:154:VAL:O	2:B:316:THR:CG2	2.34	0.75
1:C:84[A]:HIS:CD2	1:C:136:ASN:HA	2.21	0.75
2:B:392:MET:HA	2:B:392:MET:HE2	1.68	0.73
1:A:154:VAL:O	2:B:316:THR:HG22	1.87	0.73
1:C:81:GLU:O	3:C:1297:4QE:N2	2.22	0.73
1:A:249:SER:HA	1:A:260:ARG:HD3	1.71	0.73
1:C:60:HIS:CD2	1:C:62:ASN:H	2.06	0.73
2:D:347:TYR:HH	2:D:397:THR:HG1	1.31	0.73
1:A:15[A]:TYR:CD1	1:A:15[A]:TYR:N	2.50	0.71
1:C:154:VAL:O	2:D:316:THR:HG23	1.91	0.70
1:A:121:HIS:O	1:A:122:ARG:HG3	1.93	0.69
3:C:1297:4QE:H9	4:C:2003:HOH:O	1.92	0.68
1:A:51:GLU:O	1:A:55:LEU:HB2	1.93	0.68
1:C:126:ARG:HD2	1:C:163:VAL:HG11	1.74	0.68
1:C:155:PRO:HG3	2:D:320:LEU:HD21	1.75	0.68
1:A:13[A]:GLY:HA2	3:A:1297:4QE:H3	1.76	0.67
1:C:51:GLU:O	1:C:55:LEU:HB2	1.94	0.67
1:A:16[B]:GLY:HA3	1:A:34:LYS:O	1.95	0.67
1:C:84[A]:HIS:HD2	1:C:136:ASN:HA	1.59	0.66
2:B:347:TYR:OH	2:B:394:LEU:HA	1.95	0.66
1:C:121:HIS:O	1:C:122:ARG:HG3	1.96	0.65
1:A:71:HIS:HD2	2:B:296:HIS:CE1	2.07	0.65
1:A:25:LEU:HD11	2:D:293:ARG:HB3	1.79	0.65
1:C:14[A]:THR:HB	1:C:15[A]:TYR:HD1	1.62	0.65
2:B:392:MET:HA	2:B:392:MET:CE	2.28	0.63
1:A:38:ASP:O	1:A:39:THR:HB	1.98	0.63
1:A:177:CYS:HB2	1:A:233:MET:CE	2.28	0.63
1:C:213:PHE:HB3	1:C:217:ARG:CZ	2.29	0.62
1:C:84[B]:HIS:NE2	1:C:296:LEU:HD12	2.12	0.62
1:A:194:ALA:CB	1:A:202:LEU:HD22	2.29	0.62
2:B:278:PHE:HA	2:B:281:ILE:HD11	1.80	0.61
1:C:13[A]:GLY:HA2	3:C:1297:4QE:H3	1.82	0.61
1:A:84[B]:HIS:CD2	1:A:296:LEU:CD1	2.78	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:190:GLU:HG3	2:B:351:LEU:HD22	1.83	0.61
1:A:227:TRP:O	1:A:230:VAL:HG22	2.00	0.60
1:A:295:HIS:CG	1:A:295:HIS:O	2.51	0.60
1:A:88:LYS:HB2	1:A:130:PRO:HB2	1.84	0.59
1:A:252:VAL:CG1	1:A:255:LEU:HD22	2.31	0.59
1:A:261:SER:O	1:A:265:GLN:HG3	2.03	0.58
2:B:268:GLU:HG3	2:B:268:GLU:O	2.04	0.57
2:D:254:GLN:HG2	2:D:286:TYR:HE2	1.68	0.57
1:A:252:VAL:HG11	1:A:255:LEU:HD22	1.87	0.57
2:D:370:GLN:H	2:D:370:GLN:HE21	1.53	0.57
1:A:177:CYS:HB2	1:A:233:MET:HE2	1.86	0.56
2:D:310:THR:HG23	2:D:313:GLN:HE21	1.70	0.56
1:C:13[A]:GLY:HA2	3:C:1297:4QE:CAV	2.35	0.56
1:A:87:LEU:HG	1:A:91:MET:HE2	1.88	0.55
1:C:295:HIS:O	1:C:295:HIS:CD2	2.59	0.55
1:C:84[A]:HIS:N	1:C:84[A]:HIS:CD2	2.74	0.55
2:B:310:THR:HG23	2:B:313:GLN:HE21	1.72	0.55
1:A:127:ASP:O	1:A:132:ASN:ND2	2.39	0.54
1:A:121:HIS:C	1:A:122:ARG:HG3	2.27	0.54
2:B:176:PRO:HA	2:B:179:HIS:ND1	2.23	0.54
1:A:178:LYS:HE2	1:A:179:TYR:CZ	2.43	0.54
1:C:34:LYS:HG3	1:C:77:TYR:CE1	2.43	0.54
2:B:332:LEU:HD23	2:B:363:ALA:HA	1.90	0.54
1:C:39:THR:CG2	1:C:40:GLU:N	2.71	0.54
2:D:342:ILE:HD11	2:D:409:ILE:CD1	2.38	0.54
2:D:370:GLN:H	2:D:370:GLN:NE2	2.06	0.53
1:C:84[A]:HIS:CD2	1:C:84[A]:HIS:H	2.26	0.53
1:C:15[A]:TYR:CE2	1:C:33:LYS:HE2	2.44	0.52
1:C:71:HIS:CD2	2:D:296:HIS:HE1	2.23	0.52
1:C:60:HIS:HD2	1:C:62:ASN:H	1.51	0.52
1:C:2:GLU:O	1:C:24:LYS:NZ	2.42	0.52
2:D:346:PRO:O	2:D:349:LYS:HG2	2.09	0.52
1:A:14[A]:THR:C	1:A:15[A]:TYR:HD1	2.13	0.52
1:A:87:LEU:HG	1:A:91:MET:CE	2.39	0.52
1:A:155:PRO:HD2	2:B:316:THR:HG23	1.93	0.51
1:C:121:HIS:C	1:C:122:ARG:HG3	2.31	0.51
2:B:327:CYS:HA	2:B:330:GLU:HG3	1.93	0.51
1:C:18:VAL:HG21	3:C:1297:4QE:H1	1.91	0.51
2:D:373:PRO:HD2	2:D:376:LEU:HD12	1.93	0.51
1:A:218:THR:HG22	1:A:219:LEU:HD23	1.92	0.51
2:B:297:LEU:O	2:B:301:VAL:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14[A]:THR:HB	1:C:15[A]:TYR:CD1	2.44	0.50
1:C:16[B]:GLY:HA3	1:C:34:LYS:O	2.12	0.50
1:C:218:THR:HG22	1:C:219:LEU:HD23	1.94	0.50
1:C:72:THR:HB	1:C:75:LYS:H	1.76	0.50
2:D:378:ARG:HB2	2:D:378:ARG:NH1	2.28	0.49
2:D:346:PRO:HB2	2:D:349:LYS:HE2	1.93	0.49
1:A:177:CYS:HB2	1:A:233:MET:HE1	1.95	0.49
2:D:388:LYS:HB3	2:D:389:PRO:HD3	1.95	0.48
1:A:39:THR:CG2	1:A:40:GLU:N	2.76	0.48
2:D:362:LEU:HD21	2:D:398:TYR:HD2	1.78	0.48
1:A:206:ASP:OD1	1:A:206:ASP:N	2.46	0.48
2:B:392:MET:CE	2:B:392:MET:CA	2.92	0.48
2:D:384:LEU:HD11	2:D:432:LEU:HD22	1.94	0.48
1:A:223:ASP:H	1:A:226:VAL:CG1	2.26	0.48
2:B:358:ALA:HB1	2:B:391:LEU:HD13	1.96	0.48
1:C:78:LEU:N	1:C:78:LEU:HD23	2.28	0.48
1:C:162:GLU:OE1	1:C:162:GLU:N	2.47	0.48
1:C:126:ARG:HB3	1:C:163:VAL:CG1	2.44	0.47
1:C:150:ARG:NH2	1:C:160:TPO:O2P	2.47	0.47
1:C:39:THR:HG23	1:C:40:GLU:H	1.78	0.47
1:A:7:VAL:HG23	1:A:21:ALA:HA	1.96	0.47
1:C:194:ALA:HB1	1:C:202:LEU:HD13	1.96	0.47
1:A:255:LEU:O	1:A:260:ARG:NH1	2.48	0.47
2:B:401:ALA:HB3	2:B:402:PRO:HD3	1.96	0.47
1:A:115:LEU:HD11	1:A:119:HIS:CE1	2.50	0.47
1:C:39:THR:HG22	1:C:40:GLU:OE2	2.15	0.47
2:D:223:GLU:OE1	2:D:412:LYS:HE3	2.13	0.47
1:A:137:THR:HG22	1:A:296:LEU:HD12	1.96	0.46
1:C:255:LEU:HG	1:C:259:GLY:HA3	1.96	0.46
2:D:414:LYS:HA	2:D:420:GLY:HA2	1.98	0.46
2:B:326:ASN:OD1	2:B:328:LYS:HB3	2.16	0.46
2:B:384:LEU:HA	2:B:384:LEU:HD12	1.51	0.46
1:C:105:LYS:HG2	1:C:289:VAL:HG23	1.98	0.46
2:D:217:TRP:O	2:D:221:VAL:HG23	2.15	0.46
1:A:48:ALA:O	1:A:52:ILE:HG13	2.16	0.46
1:A:47:THR:HG22	1:A:147:GLY:O	2.16	0.45
1:C:213:PHE:HB3	1:C:217:ARG:NH2	2.30	0.45
1:A:163:VAL:HG13	1:A:164:VAL:HG23	1.97	0.45
1:A:223:ASP:H	1:A:226:VAL:HG12	1.82	0.45
1:A:260:ARG:HG3	1:A:260:ARG:HH11	1.81	0.45
1:A:50:ARG:O	1:A:54:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:407:GLN:O	2:B:411:GLU:HG2	2.16	0.45
2:D:332:LEU:HD23	2:D:363:ALA:HA	1.98	0.45
2:B:279:VAL:HG21	2:B:288:LYS:HA	1.98	0.45
1:C:121:HIS:O	1:C:123:VAL:HG23	2.16	0.45
2:D:345:ASP:HA	2:D:346:PRO:HA	1.75	0.45
1:A:13[A]:GLY:HA2	3:A:1297:4QE:CAV	2.45	0.45
1:C:60:HIS:CG	1:C:61:PRO:HD2	2.51	0.45
2:D:401:ALA:N	2:D:402:PRO:HD2	2.32	0.45
2:B:346:PRO:HD2	2:B:347:TYR:CD2	2.51	0.44
1:C:157:ARG:NH2	2:D:228:GLN:HG3	2.32	0.44
1:A:39:THR:HG22	1:A:40:GLU:N	2.31	0.44
1:C:206:ASP:N	1:C:206:ASP:OD1	2.50	0.44
1:A:61:PRO:O	1:A:142:LYS:HE2	2.18	0.44
1:C:136:ASN:HD21	1:C:138:GLU:HB2	1.83	0.44
1:A:217:ARG:HG2	1:A:243:TRP:CD2	2.53	0.43
2:D:326:ASN:OD1	2:D:328:LYS:HB2	2.18	0.43
1:A:209:ILE:HA	1:A:209:ILE:HD12	1.84	0.43
2:B:180:GLU:OE1	2:B:180:GLU:HA	2.18	0.43
1:C:39:THR:HG21	2:D:289:LYS:NZ	2.34	0.43
2:B:194:LYS:HD3	2:B:351:LEU:HD23	2.00	0.43
2:B:374:GLU:HA	2:B:377:ILE:HD12	2.00	0.43
1:A:136:ASN:ND2	1:A:140:ALA:HB3	2.34	0.43
2:B:207:THR:OG1	2:B:210:MET:HG3	2.19	0.43
1:A:189:LEU:HD23	1:A:189:LEU:HA	1.73	0.43
1:A:72:THR:HG22	1:A:73:GLU:H	1.83	0.43
2:B:345:ASP:HA	2:B:346:PRO:HA	1.84	0.43
1:A:14[A]:THR:C	1:A:15[A]:TYR:CD1	2.90	0.43
2:B:376:LEU:HA	2:B:376:LEU:HD23	1.77	0.43
1:A:249:SER:CA	1:A:260:ARG:HD3	2.47	0.43
2:B:315:LEU:HD23	2:B:315:LEU:HA	1.84	0.43
2:B:395:HIS:CE1	2:B:399:LEU:HD11	2.54	0.43
2:D:344:ALA:HB1	2:D:348:LEU:HD22	2.01	0.43
1:A:167:TRP:CD1	1:A:204:PRO:HA	2.54	0.43
1:A:60:HIS:CD2	1:A:61:PRO:HD2	2.54	0.43
1:A:13[B]:GLY:C	1:A:14[B]:THR:HG23	2.40	0.42
1:A:222:PRO:HA	1:A:226:VAL:HG11	2.00	0.42
2:D:210:MET:O	2:D:213:ILE:HB	2.19	0.42
1:C:9:LYS:HE2	1:C:17:VAL:HG11	2.01	0.42
2:B:223:GLU:CD	2:B:412:LYS:HG3	2.39	0.42
1:A:13[B]:GLY:C	1:A:14[B]:THR:CG2	2.88	0.42
2:D:410:ARG:O	2:D:414:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:303:THR:O	2:D:304:PHE:HB2	2.19	0.42
1:A:39:THR:CG2	1:A:40:GLU:H	2.32	0.42
1:C:205:GLY:HA2	1:C:210:ASP:OD1	2.20	0.41
2:B:360:PHE:CZ	2:B:364:LEU:HD22	2.55	0.41
2:D:175:VAL:HA	2:D:176:PRO:HD3	1.89	0.41
2:D:342:ILE:HD11	2:D:409:ILE:HD11	2.02	0.41
2:B:255:LEU:HB2	2:B:286:TYR:CZ	2.55	0.41
1:C:295:HIS:O	1:C:295:HIS:CG	2.74	0.41
1:A:241:PRO:HG2	1:A:243:TRP:CH2	2.55	0.41
1:A:286:PHE:O	1:A:289:VAL:HG12	2.20	0.41
1:C:167:TRP:CD1	1:C:204:PRO:HA	2.56	0.41
1:C:7:VAL:HG23	1:C:21:ALA:HA	2.03	0.41
2:D:194:LYS:HA	2:D:195:PRO:HD3	1.95	0.41
1:A:87:LEU:HD12	1:A:87:LEU:HA	1.85	0.41
2:D:376:LEU:HD23	2:D:376:LEU:HA	1.94	0.41
2:B:407:GLN:OE1	2:B:410:ARG:HD3	2.21	0.41
2:D:263:LEU:HA	2:D:263:LEU:HD23	1.96	0.41
1:A:18:VAL:HG21	3:A:1297:4QE:H1	2.03	0.41
2:D:190:GLU:O	2:D:194:LYS:HB2	2.21	0.41
2:B:385:GLU:OE1	2:B:385:GLU:HA	2.21	0.41
1:C:71:HIS:CE1	2:D:304:PHE:HE2	2.39	0.41
2:D:372:TRP:CZ3	2:D:376:LEU:HD13	2.55	0.41
2:B:388:LYS:HB3	2:B:389:PRO:HD3	2.02	0.40
2:B:398:TYR:CD2	2:B:426:PRO:HB3	2.56	0.40
2:D:310:THR:HG23	2:D:313:GLN:NE2	2.34	0.40
1:C:202:LEU:HA	1:C:202:LEU:HD12	1.83	0.40
2:D:383:THR:O	2:D:387:LEU:HD12	2.22	0.40
1:A:62:ASN:ND2	1:A:110:GLN:HB3	2.36	0.40
1:A:227:TRP:HB3	1:A:230:VAL:HG22	2.03	0.40
2:B:323:GLN:HA	2:B:323:GLN:OE1	2.21	0.40
1:C:44:VAL:HA	1:C:45:PRO:HD2	1.93	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	299/303 (99%)	278 (93%)	19 (6%)	2 (1%)	22	50
1	C	267/303 (88%)	247 (92%)	15 (6%)	5 (2%)	8	24
2	B	256/258 (99%)	249 (97%)	5 (2%)	2 (1%)	19	46
2	D	256/258 (99%)	248 (97%)	8 (3%)	0	100	100
All	All	1078/1122 (96%)	1022 (95%)	47 (4%)	9 (1%)	22	46

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	283	ASP
1	A	162	GLU
1	A	164	VAL
1	C	164	VAL
1	C	39	THR
2	B	176	PRO
1	C	14[A]	THR
1	C	14[B]	THR
1	C	162	GLU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	264/265 (100%)	238 (90%)	26 (10%)	8	21
1	C	236/265 (89%)	201 (85%)	35 (15%)	3	8
2	B	232/232 (100%)	214 (92%)	18 (8%)	12	32
2	D	232/232 (100%)	208 (90%)	24 (10%)	7	19
All	All	964/994 (97%)	861 (89%)	103 (11%)	7	18

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	15[A]	TYR
1	A	15[B]	TYR
1	A	22	ARG
1	A	34	LYS
1	A	47	THR
1	A	55	LEU
1	A	71	HIS
1	A	73	GLU
1	A	74	ASN
1	A	75	LYS
1	A	78	LEU
1	A	101	LEU
1	A	122	ARG
1	A	150	ARG
1	A	157	ARG
1	A	163	VAL
1	A	199	ARG
1	A	200	ARG
1	A	206	ASP
1	A	230	VAL
1	A	232	SER
1	A	237	LYS
1	A	248	PHE
1	A	255	LEU
1	A	281	LEU
2	B	179	HIS
2	B	180	GLU
2	B	181	ASP
2	B	196	LYS
2	B	232	LEU
2	B	277	GLU
2	B	283	ASP
2	B	292	LEU
2	B	300	LYS
2	B	316	THR
2	B	323	GLN
2	B	327	CYS
2	B	328	LYS
2	B	391	LEU
2	B	392	MET
2	B	398	TYR
2	B	403	GLN

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Mol	Chain	Res	Type
2	B	428	GLU
1	C	6	LYS
1	C	14[A]	THR
1	C	14[B]	THR
1	C	17	VAL
1	C	22	ARG
1	C	34	LYS
1	C	37	LEU
1	C	38	ASP
1	C	39	THR
1	C	41	THR
1	C	55	LEU
1	C	72	THR
1	C	75	LYS
1	C	78	LEU
1	C	89	LYS
1	C	101	LEU
1	C	122	ARG
1	C	129	LYS
1	C	137	THR
1	C	148	LEU
1	C	150	ARG
1	C	157	ARG
1	C	175	LEU
1	C	181	SER
1	C	186	ILE
1	C	200	ARG
1	C	206	ASP
1	C	209	ILE
1	C	214	ARG
1	C	219	LEU
1	C	221	THR
1	C	255	LEU
1	C	278	LYS
1	C	287	GLN
1	C	295	HIS
2	D	181	ASP
2	D	193	CYS
2	D	196	LYS
2	D	202	LYS
2	D	209	SER
2	D	226	LYS

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Mol	Chain	Res	Type
2	D	232	LEU
2	D	270	ILE
2	D	292	LEU
2	D	296	HIS
2	D	328	LYS
2	D	334	MET
2	D	342	ILE
2	D	351	LEU
2	D	362	LEU
2	D	368	THR
2	D	370	GLN
2	D	371	SER
2	D	374	GLU
2	D	384	LEU
2	D	391	LEU
2	D	397	THR
2	D	398	TYR
2	D	411	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	71	HIS
1	A	265	GLN
2	B	313	GLN
2	B	395	HIS
2	B	403	GLN
2	B	425	ASN
1	C	60	HIS
1	C	71	HIS
1	C	295	HIS
2	D	229	ASN
2	D	254	GLN
2	D	296	HIS
2	D	313	GLN
2	D	317	GLN
2	D	370	GLN
2	D	395	HIS
2	D	396	GLN
2	D	403	GLN
2	D	425	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	TPO	A	160	1	8,10,11	1.00	0	10,14,16	1.77	2 (20%)
1	TPO	C	160	1	8,10,11	0.68	0	10,14,16	1.38	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	TPO	A	160	1	-	1/9/11/13	-
1	TPO	C	160	1	-	2/9/11/13	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	TPO	OG1-P-O1P	-3.80	94.73	109.39
1	A	160	TPO	O3P-P-O2P	2.24	116.22	107.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	160	TPO	CB-OG1-P-O1P
1	C	160	TPO	CB-OG1-P-O1P

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Mol	Chain	Res	Type	Atoms
1	C	160	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	160	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 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
3	4QE	A	1297	-	26,28,28	1.99	6 (23%)	30,39,39	2.20	6 (20%)
3	4QE	C	1297	-	26,28,28	2.00	5 (19%)	30,39,39	2.13	7 (23%)

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
3	4QE	A	1297	-	-	2/9/17/17	0/4/4/4
3	4QE	C	1297	-	-	4/9/17/17	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1297	4QE	CAJ-C8	-6.02	1.34	1.48
3	A	1297	4QE	CAJ-C8	-5.46	1.35	1.48
3	A	1297	4QE	CAP-CAO	-5.39	1.40	1.51
3	C	1297	4QE	CAP-CAO	-5.04	1.40	1.51
3	A	1297	4QE	O6-C6	3.48	1.38	1.35
3	C	1297	4QE	O6-C6	3.37	1.37	1.35
3	C	1297	4QE	C8-N4	-2.48	1.32	1.35
3	C	1297	4QE	C5-C4	-2.46	1.34	1.40
3	A	1297	4QE	C8-N4	-2.41	1.32	1.35
3	A	1297	4QE	C5-C4	-2.34	1.34	1.40
3	A	1297	4QE	CAV-CAU	-2.20	1.47	1.53

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1297	4QE	CAS-O6-C6	-7.57	110.27	117.50
3	A	1297	4QE	CAS-O6-C6	-7.38	110.45	117.50
3	C	1297	4QE	N3-C2-N1	-4.97	120.60	127.22
3	A	1297	4QE	N3-C2-N1	-4.69	120.97	127.22
3	A	1297	4QE	C2-N3-C4	4.30	120.27	115.36
3	C	1297	4QE	C2-N3-C4	3.60	119.47	115.36
3	A	1297	4QE	C4-C5-N7	-2.89	106.53	109.47
3	A	1297	4QE	CAY-CAT-CAS	-2.80	104.26	111.28
3	C	1297	4QE	CAY-CAT-CAS	-2.74	104.39	111.28
3	A	1297	4QE	CAJ-C8-N7	2.22	126.50	123.67
3	C	1297	4QE	CAY-CAT-CAU	2.13	114.55	109.33
3	C	1297	4QE	CAJ-C8-N7	2.08	126.33	123.67
3	C	1297	4QE	C2-N1-C6	2.08	119.42	116.08

There are no chirality outliers.

All (6) torsion outliers are listed below:

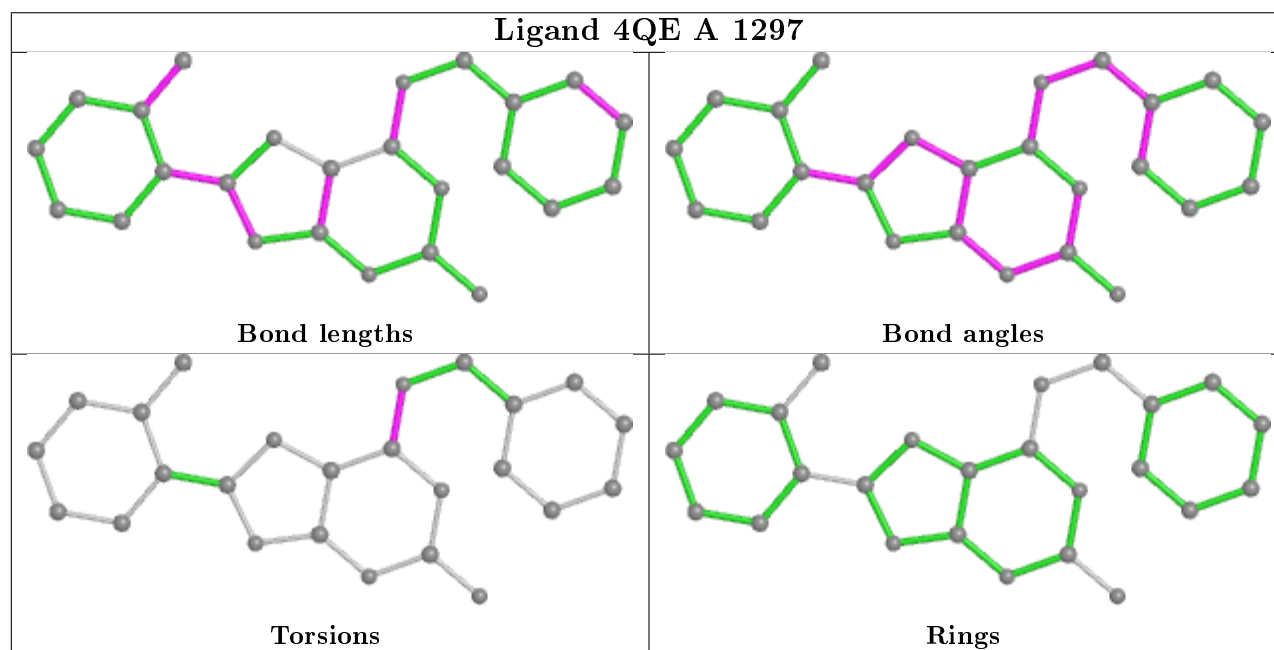
Mol	Chain	Res	Type	Atoms
3	A	1297	4QE	N1-C6-O6-CAS
3	A	1297	4QE	C5-C6-O6-CAS
3	C	1297	4QE	N1-C6-O6-CAS
3	C	1297	4QE	C5-C6-O6-CAS
3	C	1297	4QE	N7-C8-CAJ-CAK
3	C	1297	4QE	N4-C8-CAJ-CAK

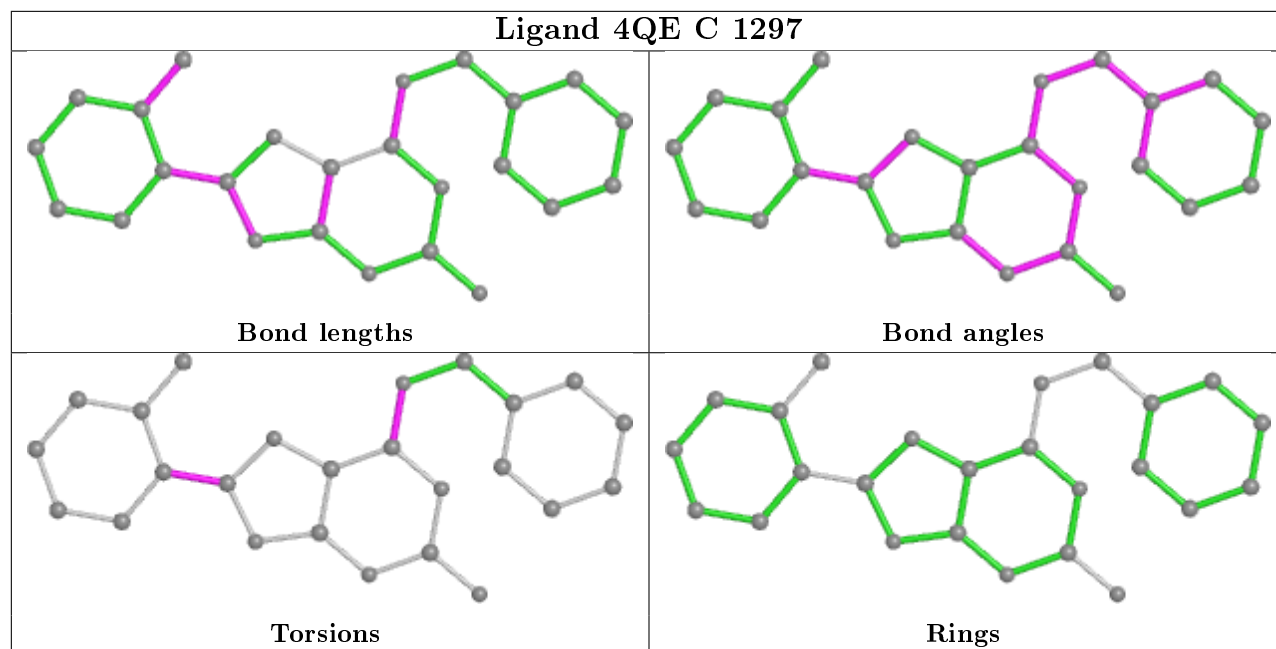
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1297	4QE	4	0
3	C	1297	4QE	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	296/303 (97%)	-0.28	12 (4%) 37 31	25, 36, 60, 80	0
1	C	266/303 (87%)	0.35	22 (8%) 11 8	41, 73, 120, 144	0
2	B	258/258 (100%)	-0.31	4 (1%) 72 70	24, 39, 55, 63	0
2	D	258/258 (100%)	0.30	17 (6%) 18 14	39, 75, 134, 156	0
All	All	1078/1122 (96%)	0.01	55 (5%) 28 23	24, 51, 117, 156	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	222	PRO	5.6
1	A	40	GLU	5.1
2	D	176	PRO	5.1
2	D	428	GLU	5.0
1	C	282	ALA	4.5
2	D	423	LEU	4.5
2	D	175	VAL	4.4
2	B	175	VAL	4.3
1	A	39	THR	4.3
1	C	273	LYS	4.3
2	D	323	GLN	4.1
1	C	208	GLU	3.4
1	C	269	TYR	3.4
1	A	36	ARG	3.4
1	C	209	ILE	3.3
1	C	13[A]	GLY	3.3
2	D	327	CYS	3.2
1	C	296	LEU	3.1
2	B	431	ASN	3.1
1	C	272	ASN	3.1
1	C	213	PHE	3.1

*Continued on next page...*



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Mol	Chain	Res	Type	RSRZ
1	C	288	ASP	3.0
2	D	326	ASN	2.9
1	C	221	THR	2.8
2	D	432	LEU	2.8
2	D	418	TYR	2.8
1	A	14[A]	THR	2.8
1	A	13[A]	GLY	2.8
2	D	284	ASP	2.8
1	C	15[A]	TYR	2.7
1	C	178	LYS	2.7
1	C	166	LEU	2.7
1	A	96	LEU	2.7
1	C	74	ASN	2.6
1	C	257	GLU	2.6
1	A	73	GLU	2.5
1	C	175	LEU	2.5
1	A	41	THR	2.5
2	D	378	ARG	2.4
1	C	205	GLY	2.4
1	A	16[A]	GLY	2.4
1	C	217	ARG	2.4
2	D	404	HIS	2.4
1	C	162	GLU	2.3
2	D	374	GLU	2.3
1	A	95	ALA	2.3
2	D	321	HIS	2.3
2	D	177	ASP	2.2
1	C	161	HIS	2.2
1	A	0	SER	2.2
2	D	371	SER	2.2
1	A	38	ASP	2.1
2	D	283	ASP	2.1
2	B	323	GLN	2.0
2	B	284	ASP	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<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
1	TPO	C	160	11/12	0.90	0.16	72,78,82,84	0
1	TPO	A	160	11/12	0.97	0.12	31,32,34,34	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

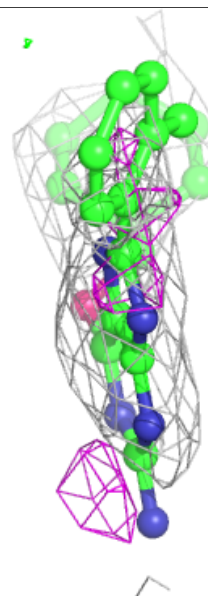
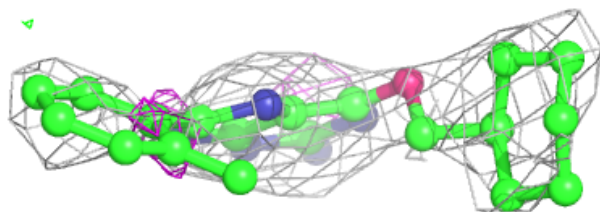
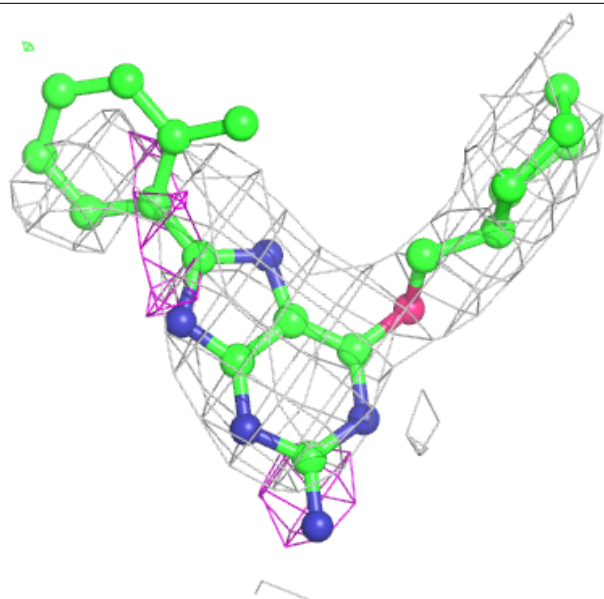
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	4QE	C	1297	25/25	0.84	0.30	80,87,93,94	0
3	4QE	A	1297	25/25	0.85	0.27	73,77,80,80	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

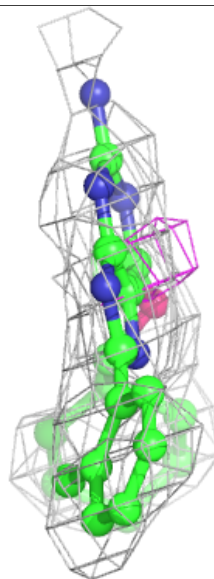
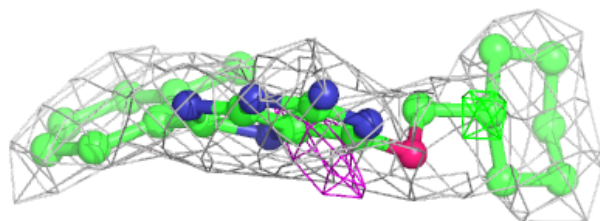
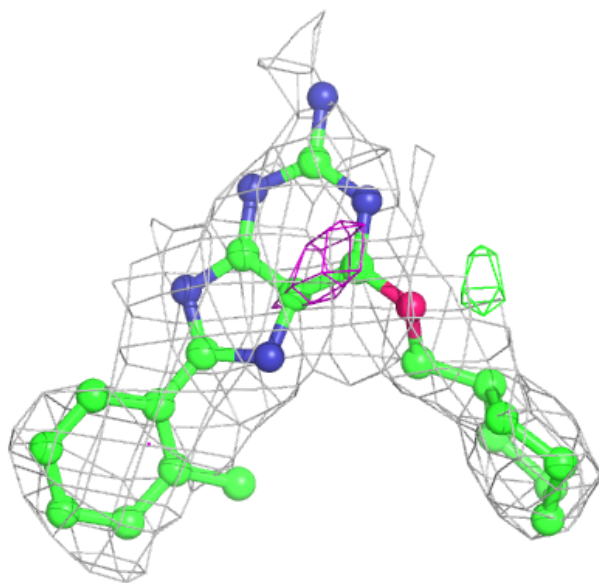
**Electron density around 4QE C 1297:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 4QE A 1297:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers ⓘ

There are no such residues in this entry.