Full wwPDB X-ray Structure Validation Report (i)

Jun 19, 2024 – 02:40 AM EDT

PDB ID	:	4CLF
Title	:	Crystal structure of human soluble Adenylyl Cyclase (Apo form)
Authors	:	Kleinboelting, S.; Moniot, S.; Weyand, M.; Steegborn, C.
Deposited on	:	2014-01-14
Resolution	:	1.70 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

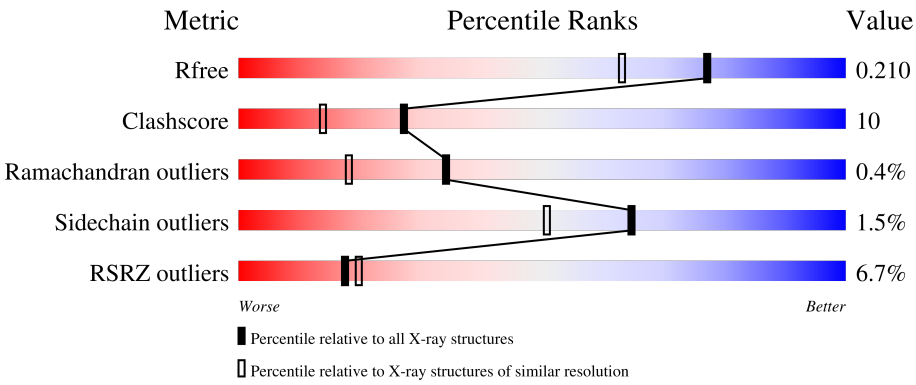
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

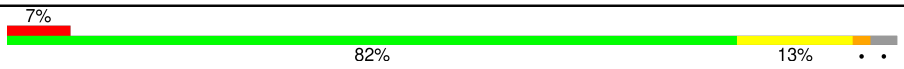
The reported resolution of this entry is 1.70 Å.

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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 of 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	475	

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	ACT	A	1469	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	1470	-	X	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4036 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.

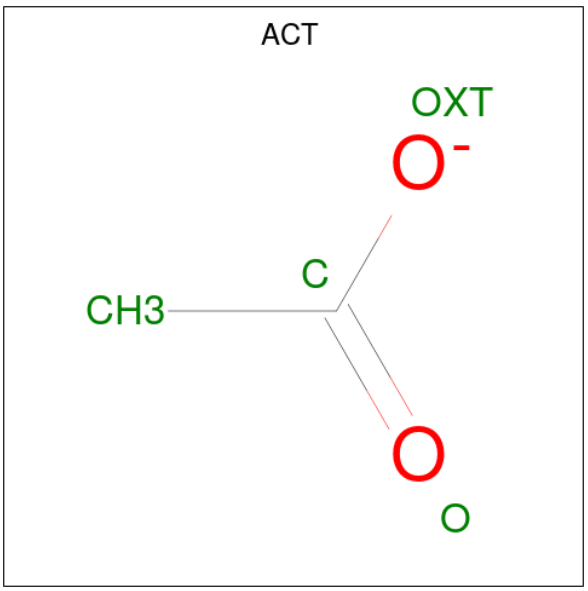
- Molecule 1 is a protein called ADENYLATE CYCLASE TYPE 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3740	2432	599	671	38	0	18	0

There are 6 discrepancies between the modelled and reference sequences:

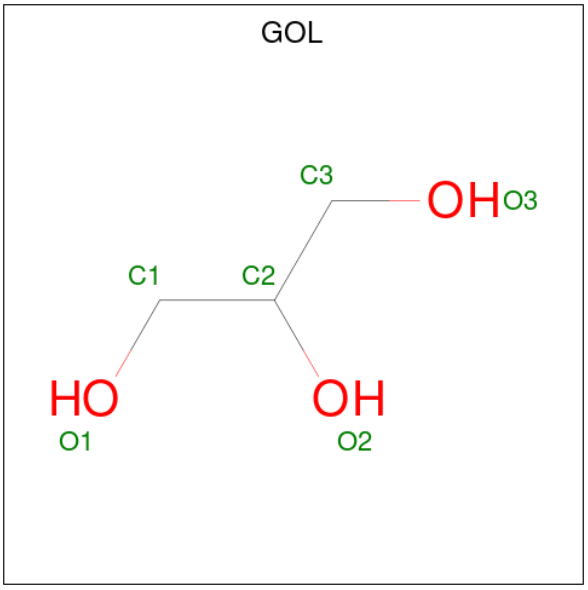
Chain	Residue	Modelled	Actual	Comment	Reference
A	470	HIS	-	expression tag	UNP Q96PN6
A	471	HIS	-	expression tag	UNP Q96PN6
A	472	HIS	-	expression tag	UNP Q96PN6
A	473	HIS	-	expression tag	UNP Q96PN6
A	474	HIS	-	expression tag	UNP Q96PN6
A	475	HIS	-	expression tag	UNP Q96PN6

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

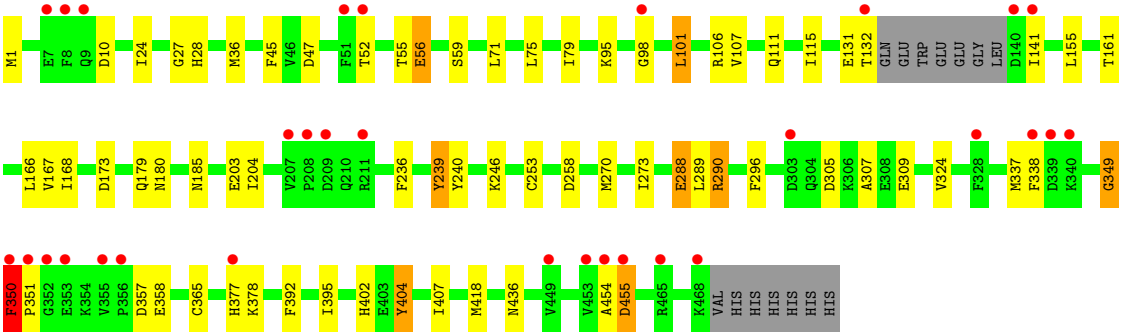
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	286	286	286	0	0

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: ADENYLATE CYCLASE TYPE 10

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	99.66Å 99.66Å 97.93Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.83 – 1.70 44.41 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.83-1.70) 100.0 (44.41-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.20 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.165 , 0.205 0.175 , 0.210	Depositor DCC
R_{free} test set	3081 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	20.4	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 48.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4036	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CME, GOL, ACT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	1.04	6/3872 (0.2%)	1.03	11/5237 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	56	GLU	CD-OE2	8.69	1.35	1.25
1	A	404	TYR	CZ-OH	5.88	1.47	1.37
1	A	239	TYR	CE1-CZ	-5.79	1.31	1.38
1	A	1	MET	N-CA	5.55	1.57	1.46
1	A	288[A]	GLU	CD-OE1	5.50	1.31	1.25
1	A	288[B]	GLU	CD-OE1	5.50	1.31	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	10	ASP	CB-CG-OD2	-7.76	111.31	118.30
1	A	350	PHE	N-CA-C	6.40	128.27	111.00
1	A	101	LEU	CA-CB-CG	6.00	129.09	115.30
1	A	106	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	10	ASP	CB-CG-OD1	5.63	123.36	118.30
1	A	258	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	418	MET	CG-SD-CE	-5.45	91.47	100.20
1	A	240	TYR	CB-CG-CD2	5.26	124.16	121.00
1	A	290	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	349	GLY	CA-C-N	5.12	128.47	117.20
1	A	404	TYR	CB-CG-CD2	-5.02	117.99	121.00

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	3740	0	3755	76	0
2	A	4	0	3	5	0
3	A	6	0	7	1	0
4	A	286	0	0	12	0
All	All	4036	0	3765	76	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 10.

All (76) 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:A:36[B]:MET:HG2	1:A:155[B]:LEU:CD2	1.78	1.13
1:A:36[B]:MET:HG2	1:A:155[B]:LEU:HD23	1.15	1.10
1:A:36[B]:MET:CG	1:A:155[B]:LEU:HD23	1.82	1.09
1:A:36[B]:MET:CG	1:A:155[B]:LEU:CD2	2.33	1.06
1:A:36[B]:MET:SD	1:A:155[B]:LEU:HD21	2.04	0.98
1:A:239:TYR:CZ	4:A:2022:HOH:O	2.09	0.98
1:A:203:GLU:HB2	4:A:2148:HOH:O	1.67	0.94
1:A:141:ILE:HG21	4:A:2046:HOH:O	1.70	0.92
1:A:239:TYR:CE2	4:A:2022:HOH:O	2.21	0.92
1:A:350:PHE:CD1	1:A:351:PRO:HD2	2.05	0.91
1:A:289:LEU:HD21	1:A:392[B]:PHE:CE2	2.06	0.91
1:A:141:ILE:HD12	1:A:141:ILE:O	1.70	0.90
1:A:166:LEU:HA	2:A:1469:ACT:O	1.71	0.90
1:A:324:VAL:HG12	1:A:365[B]:CYS:SG	2.11	0.90
1:A:289:LEU:HD21	1:A:392[B]:PHE:CZ	2.07	0.89
1:A:52:THR:HG21	1:A:98:GLY:O	1.74	0.86
1:A:289:LEU:HD21	1:A:392[B]:PHE:CD2	2.14	0.82
1:A:309:GLU:OE1	1:A:378:LYS:NZ	2.13	0.81
1:A:71:LEU:HD23	1:A:392[B]:PHE:CD2	2.16	0.81
1:A:56:GLU:O	1:A:59:SER:OG	1.97	0.80
1:A:289:LEU:HD21	1:A:392[B]:PHE:CE1	2.16	0.80
1:A:36[B]:MET:CG	1:A:155[B]:LEU:HD21	2.06	0.80
1:A:324:VAL:CG1	1:A:365[B]:CYS:SG	2.72	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:GLU:O	1:A:132:THR:OG1	2.03	0.76
1:A:289:LEU:HD21	1:A:392[B]:PHE:CG	2.27	0.70
1:A:289:LEU:HD21	1:A:392[B]:PHE:CD1	2.27	0.68
1:A:141:ILE:CG2	4:A:2046:HOH:O	2.34	0.65
1:A:75[A]:LEU:HG	1:A:79:ILE:HD12	1.77	0.65
1:A:107:VAL:HG11	1:A:115:ILE:HG13	1.79	0.64
1:A:52:THR:CG2	1:A:98:GLY:O	2.47	0.62
1:A:166:LEU:CA	2:A:1469:ACT:O	2.45	0.62
1:A:47:ASP:HB2	1:A:179:GLN:HE21	1.67	0.60
1:A:36[B]:MET:SD	1:A:307:ALA:O	2.60	0.59
1:A:36[B]:MET:HG3	1:A:155[B]:LEU:HD23	1.83	0.59
1:A:155[B]:LEU:HD12	1:A:168:ILE:CD1	2.34	0.57
1:A:155[B]:LEU:HD12	1:A:168:ILE:HD11	1.87	0.57
1:A:289:LEU:CD2	1:A:392[B]:PHE:CD2	2.88	0.56
1:A:36[B]:MET:HG3	1:A:155[B]:LEU:CD2	2.31	0.56
1:A:71:LEU:CD2	1:A:392[B]:PHE:CD2	2.88	0.55
1:A:377:HIS:O	1:A:378:LYS:HB2	2.05	0.55
1:A:167:VAL:N	2:A:1469:ACT:O	2.38	0.55
1:A:337:MET:H	2:A:1469:ACT:H3	1.73	0.54
1:A:24:ILE:O	3:A:1470:GOL:H31	2.07	0.53
1:A:377:HIS:HB2	4:A:2248:HOH:O	2.08	0.52
1:A:55:THR:HG21	1:A:407:ILE:HG22	1.91	0.52
1:A:239:TYR:OH	4:A:2022:HOH:O	1.73	0.51
1:A:180:ASN:HB2	4:A:2138:HOH:O	2.12	0.49
1:A:27:GLY:O	1:A:28:HIS:C	2.49	0.49
1:A:290:ARG:NE	1:A:349:GLY:O	2.37	0.49
1:A:204:ILE:C	1:A:204:ILE:HD12	2.33	0.49
1:A:324:VAL:HG11	1:A:365[B]:CYS:SG	2.53	0.48
1:A:289:LEU:CD2	1:A:392[B]:PHE:CG	2.94	0.47
1:A:28:HIS:O	1:A:28:HIS:ND1	2.47	0.47
1:A:161:THR:HG23	4:A:2117:HOH:O	2.15	0.47
1:A:246:LYS:HE2	4:A:2167:HOH:O	2.15	0.47
1:A:289:LEU:CD2	1:A:392[B]:PHE:CE2	2.91	0.47
1:A:36[B]:MET:SD	1:A:307:ALA:HB1	2.55	0.47
1:A:45:PHE:HD1	1:A:179:GLN:HG3	1.80	0.46
1:A:273:ILE:CD1	1:A:395:ILE:HD11	2.46	0.45
1:A:185[C]:ASN:ND2	4:A:2104:HOH:O	2.49	0.45
1:A:350:PHE:CE2	1:A:404:TYR:HE2	2.34	0.44
1:A:55:THR:O	1:A:392[B]:PHE:CE1	2.71	0.44
1:A:45:PHE:CD1	1:A:179:GLN:HG3	2.53	0.44
1:A:95:LYS:HZ2	2:A:1469:ACT:C	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:ASP:O	1:A:358:GLU:C	2.54	0.43
1:A:75[A]:LEU:HG	1:A:79:ILE:CD1	2.48	0.42
1:A:155[B]:LEU:HD23	1:A:155[B]:LEU:HA	1.81	0.42
1:A:111:GLN:HG3	1:A:236:PHE:CG	2.54	0.42
1:A:173:ASP:OD2	1:A:305:ASP:OD1	2.38	0.42
1:A:270[A]:MET:HG2	4:A:2195:HOH:O	2.20	0.42
1:A:289:LEU:HD11	1:A:392[B]:PHE:CE2	2.55	0.42
1:A:454:ALA:O	1:A:455:ASP:C	2.57	0.42
1:A:273:ILE:HD13	1:A:395:ILE:HD11	2.01	0.41
1:A:288[A]:GLU:CD	1:A:290:ARG:HD2	2.40	0.41
1:A:289:LEU:CD2	1:A:392[B]:PHE:CD1	3.01	0.41
1:A:111:GLN:HG3	1:A:236:PHE:CD2	2.54	0.41

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	474/475 (100%)	462 (98%)	10 (2%)	2 (0%)	34 18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	455	ASP
1	A	350	PHE

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	417/418 (100%)	411 (99%)	6 (1%)	67 53

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LEU
1	A	296	PHE
1	A	338	PHE
1	A	350	PHE
1	A	402	HIS
1	A	436	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	GLN
1	A	238	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CME	A	253	1	8,9,10	0.90	0	6,9,11	1.24	1 (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
1	CME	A	253	1	-	0/5/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	253	CME	OH-CZ-CE	2.18	119.34	110.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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	GOL	A	1470	-	5,5,5	0.89	0	5,5,5	2.41	2 (40%)
2	ACT	A	1469	-	3,3,3	1.10	0	3,3,3	1.65	1 (33%)

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	GOL	A	1470	-	-	4/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1470	GOL	O3-C3-C2	4.21	129.31	110.38
3	A	1470	GOL	O1-C1-C2	-2.89	97.36	110.38
2	A	1469	ACT	OXT-C-CH3	2.31	124.74	115.05

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1470	GOL	O1-C1-C2-O2
3	A	1470	GOL	O1-C1-C2-C3
3	A	1470	GOL	C1-C2-C3-O3
3	A	1470	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1470	GOL	1	0
2	A	1469	ACT	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	460/475 (96%)	-0.01	31 (6%) 17 20	11, 25, 58, 83	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	GLY	6.8
1	A	453	VAL	6.2
1	A	51	PHE	6.0
1	A	351	PRO	5.6
1	A	356	PRO	5.3
1	A	454	ALA	5.1
1	A	355	VAL	4.5
1	A	338	PHE	4.2
1	A	449	VAL	3.8
1	A	8	PHE	3.7
1	A	140	ASP	3.6
1	A	208	PRO	3.5
1	A	340	LYS	3.4
1	A	7	GLU	3.3
1	A	350	PHE	3.2
1	A	455	ASP	3.0
1	A	377	HIS	2.7
1	A	468	LYS	2.7
1	A	339	ASP	2.6
1	A	132	THR	2.5
1	A	209	ASP	2.4
1	A	353	GLU	2.3
1	A	98	GLY	2.2
1	A	328	PHE	2.2
1	A	9	GLN	2.2
1	A	141	ILE	2.2
1	A	211	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	207	VAL	2.1
1	A	465	ARG	2.0
1	A	303	ASP	2.0
1	A	52	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 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	B-factors(Å^2)	Q<0.9
1	CME	A	253	10/11	0.98	0.06	14,19,25,26	0

6.3 Carbohydrates (i)

There are no monosaccharides 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, 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	B-factors(Å^2)	Q<0.9
2	ACT	A	1469	4/4	0.89	0.15	30,39,42,53	0
3	GOL	A	1470	6/6	0.90	0.16	23,29,29,34	6

6.5 Other polymers (i)

There are no such residues in this entry.