Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 11:05 AM EST

PDB ID	:	4OYW
Title	:	Crystal Structure of Human Soluble Adenylate Cyclase
Authors	:	Vinkovic, M.
Deposited on	:	2014-02-13
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 (1)) were used in the production of this report:

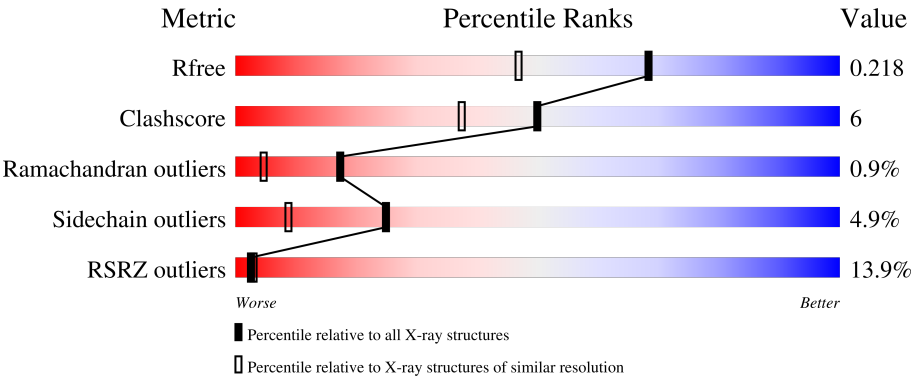
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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	470	14% 84% 14% ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4213 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.

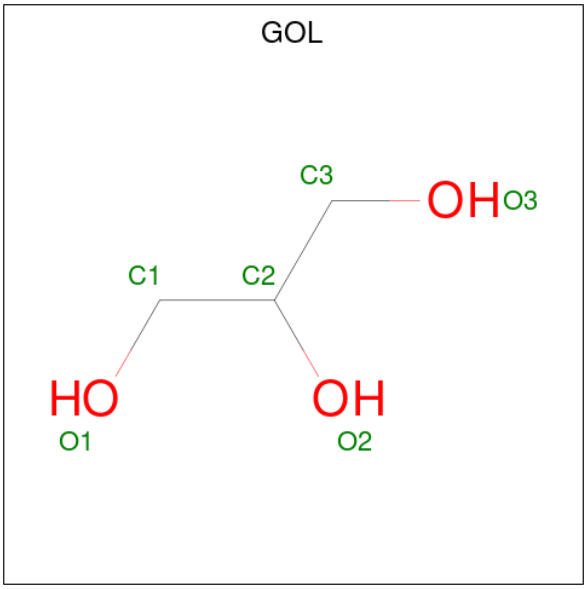
- Molecule 1 is a protein called Adenylate cyclase type 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	469	3786	2452	611	688	35	0	10	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP Q96PN6

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is water.

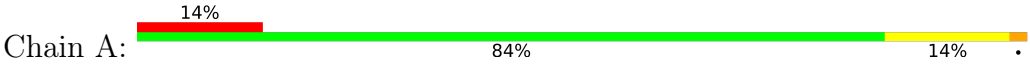
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	420	Total O 420 420	0	0

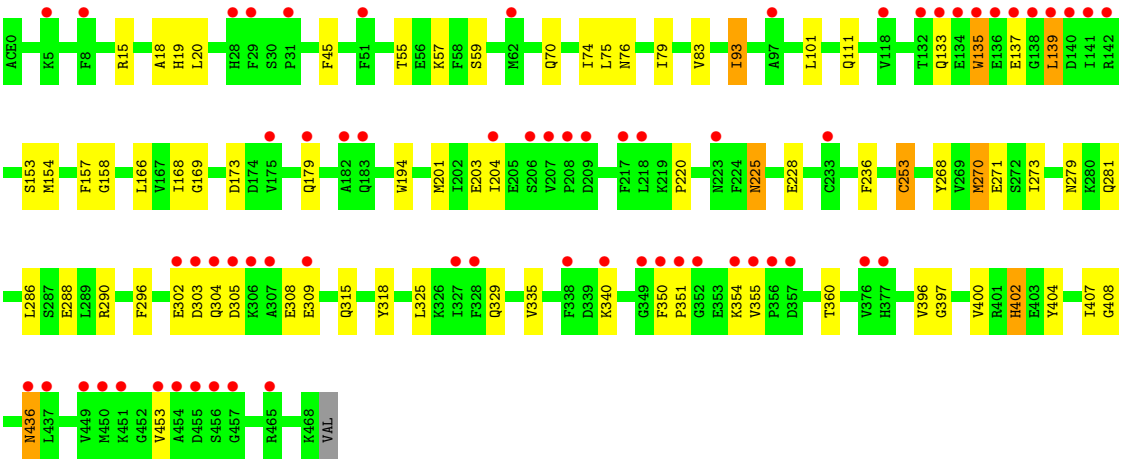
3 Residue-property plots (i)

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	99.42Å 99.42Å 97.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.71 – 1.70 44.28 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.71-1.70) 99.7 (44.28-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 1.70Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.182 , 0.211 0.195 , 0.218	Depositor DCC
R_{free} test set	3025 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	19.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 56.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.041 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4213	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.64	0/3903	0.69	0/5280

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3786	0	3775	44	0
2	A	6	0	8	1	0
3	A	1	0	0	0	0
4	A	420	0	0	6	0
All	All	4213	0	3783	44	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 6.

All (44) 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:158:GLY:H	1:A:315:GLN:HE22	1.32	0.76
1:A:93[A]:ILE:HD13	1:A:101:LEU:HD21	1.68	0.74
1:A:55[A]:THR:HG21	1:A:408:GLY:HA2	1.71	0.73
1:A:76:ASN:HD21	1:A:396:VAL:HA	1.60	0.66
1:A:76:ASN:ND2	1:A:397:GLY:H	1.98	0.62
1:A:304:GLN:HB3	1:A:340:LYS:HB3	1.82	0.61
1:A:15:ARG:HH22	1:A:279:ASN:HD21	1.50	0.60
1:A:18:ALA:HB2	1:A:253:CME:HZ2	1.82	0.60
1:A:303:ASP:OD1	1:A:309:GLU:HB2	2.00	0.60
1:A:225:ASN:HD22	1:A:228:GLU:H	1.50	0.59
1:A:74:ILE:HD11	1:A:135:TRP:HZ2	1.68	0.59
1:A:135:TRP:HA	1:A:135:TRP:CE3	2.38	0.58
1:A:15:ARG:HH22	1:A:279:ASN:ND2	2.04	0.56
1:A:166:LEU:HD21	1:A:335:VAL:HG12	1.89	0.55
1:A:304:GLN:HB3	1:A:340:LYS:CB	2.37	0.55
1:A:139:LEU:HD13	1:A:139:LEU:H	1.75	0.52
1:A:55[B]:THR:HG21	1:A:407:ILE:HG22	1.92	0.51
1:A:75:LEU:HG	1:A:79:ILE:HD12	1.94	0.49
1:A:169:GLY:HA2	1:A:305:ASP:HB2	1.93	0.49
1:A:19:HIS:HD2	4:A:773:HOH:O	1.96	0.49
1:A:45:PHE:HD2	1:A:179:GLN:HG3	1.78	0.49
1:A:201:MET:CE	1:A:220:PRO:HB3	2.43	0.48
1:A:253:CME:HE3	4:A:1020:HOH:O	2.15	0.46
1:A:83:VAL:HG13	1:A:93[B]:ILE:HD13	1.97	0.46
1:A:270[B]:MET:HE1	1:A:404:TYR:CE2	2.50	0.46
1:A:19:HIS:HE1	4:A:779:HOH:O	1.99	0.45
1:A:288[A]:GLU:CD	1:A:290:ARG:HD2	2.36	0.45
1:A:253:CME:HZ3	4:A:1020:HOH:O	2.17	0.44
1:A:281:GLN:HG3	4:A:749:HOH:O	2.17	0.44
1:A:20:LEU:HD21	1:A:268:TYR:CB	2.47	0.44
1:A:351:PRO:HG2	4:A:891:HOH:O	2.16	0.44
1:A:135:TRP:HA	1:A:135:TRP:HE3	1.82	0.44
1:A:253:CME:HE2	1:A:400:VAL:HB	1.99	0.44
1:A:157:PHE:HB2	1:A:315:GLN:NE2	2.33	0.43
1:A:153:SER:HB2	1:A:168:ILE:HB	2.00	0.43
1:A:325:LEU:HB2	2:A:501:GOL:H2	2.00	0.43
1:A:111:GLN:HG3	1:A:236:PHE:CG	2.53	0.43
1:A:158:GLY:HA2	1:A:318:TYR:CE2	2.55	0.42
1:A:288[A]:GLU:HG3	1:A:290:ARG:HB2	2.01	0.42
1:A:194:TRP:CH2	1:A:204:ILE:HG12	2.55	0.42
1:A:308:GLU:H	1:A:308:GLU:CD	2.23	0.42
1:A:273:ILE:HD13	1:A:286:LEU:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:ASP:CG	1:A:340:LYS:HG2	2.40	0.41
1:A:19:HIS:HA	1:A:402:HIS:O	2.22	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	476/470 (101%)	457 (96%)	15 (3%)	4 (1%)	19 6

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	LYS
1	A	355	VAL
1	A	436	ASN
1	A	137	GLU

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	421/412 (102%)	398 (94%)	23 (6%)	21 7

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LYS
1	A	59	SER
1	A	70	GLN
1	A	93[A]	ILE
1	A	93[B]	ILE
1	A	133	GLN
1	A	135	TRP
1	A	139	LEU
1	A	154	MET
1	A	203	GLU
1	A	225	ASN
1	A	270[A]	MET
1	A	270[B]	MET
1	A	271[A]	GLU
1	A	271[B]	GLU
1	A	296	PHE
1	A	302	GLU
1	A	329	GLN
1	A	350	PHE
1	A	360	THR
1	A	402	HIS
1	A	436	ASN
1	A	453	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	76	ASN
1	A	162	HIS
1	A	192	ASN
1	A	195	GLN
1	A	225	ASN
1	A	245	HIS
1	A	276	GLN
1	A	279	ASN
1	A	298	ASN
1	A	315	GLN
1	A	461	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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	0.40	0	5,9,11	2.35	2 (40%)

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	-	2/5/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	253	CME	CZ-CE-SD	-4.06	99.28	113.37
1	A	253	CME	CB-SG-SD	-2.60	97.08	103.82

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	253	CME	SD-CE-CZ-OH
1	A	253	CME	CZ-CE-SD-SG

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	253	CME	4	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	GOL	A	501	-	5,5,5	0.13	0	5,5,5	0.99	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	501	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
2	A	501	GOL	C1-C2-C3-O3
2	A	501	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GOL	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	467/470 (99%)	1.01	65 (13%)	2	3	4, 27, 71, 120	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	139	LEU	18.4
1	A	135	TRP	13.1
1	A	351	PRO	9.4
1	A	352	GLY	8.2
1	A	303	ASP	8.1
1	A	356	PRO	8.1
1	A	454	ALA	7.9
1	A	132	THR	7.8
1	A	137	GLU	7.7
1	A	350	PHE	7.4
1	A	136	GLU	7.2
1	A	140	ASP	7.0
1	A	138	GLY	6.8
1	A	141	ILE	5.8
1	A	451	LYS	5.8
1	A	208	PRO	5.6
1	A	304	GLN	5.1
1	A	449	VAL	5.0
1	A	8	PHE	4.8
1	A	206	SER	4.7
1	A	453	VAL	4.6
1	A	207	VAL	4.6
1	A	355	VAL	4.4
1	A	133	GLN	4.4
1	A	338	PHE	4.4
1	A	377	HIS	4.1
1	A	340	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	209	ASP	3.8
1	A	5	LYS	3.8
1	A	354	LYS	3.8
1	A	31	PRO	3.5
1	A	302	GLU	3.5
1	A	457	GLY	3.5
1	A	223	ASN	3.4
1	A	134	GLU	3.4
1	A	182	ALA	3.3
1	A	437	LEU	3.3
1	A	436	ASN	3.1
1	A	306	LYS	3.1
1	A	51	PHE	3.1
1	A	183	GLN	3.1
1	A	327	ILE	2.9
1	A	376	VAL	2.8
1	A	455	ASP	2.8
1	A	357	ASP	2.7
1	A	309	GLU	2.6
1	A	465	ARG	2.6
1	A	307	ALA	2.6
1	A	29	PHE	2.5
1	A	328	PHE	2.5
1	A	305	ASP	2.5
1	A	456	SER	2.4
1	A	450	MET	2.4
1	A	349	GLY	2.4
1	A	62[A]	MET	2.3
1	A	142	ARG	2.3
1	A	217	PHE	2.2
1	A	97	ALA	2.2
1	A	28[A]	HIS	2.2
1	A	233	CYS	2.2
1	A	118	VAL	2.2
1	A	175	VAL	2.2
1	A	204	ILE	2.2
1	A	179	GLN	2.1
1	A	218	LEU	2.1

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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CME	A	253	10/11	0.91	0.13	6,12,19,22	4

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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GOL	A	501	6/6	0.52	0.40	49,53,54,55	0
3	CL	A	502	1/1	0.97	0.11	27,27,27,27	0

6.5 Other polymers (i)

There are no such residues in this entry.