



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:51 PM UTC

PDB ID : 4OYW / pdb_00004oyw
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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

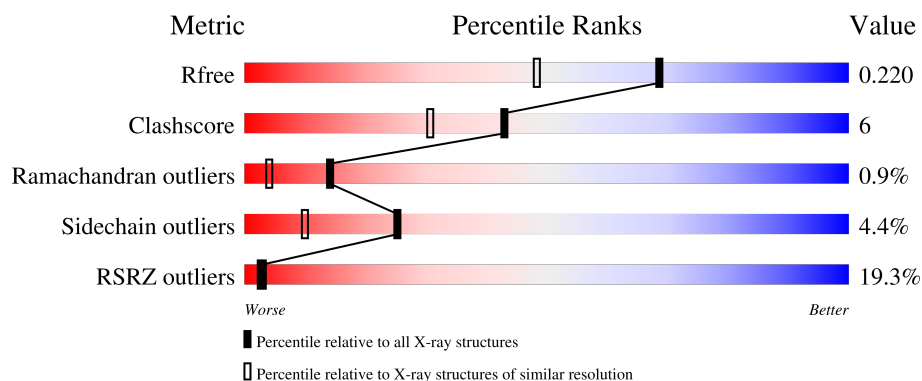
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (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 $\leq 5\%$. 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	470	19% 83% 15%

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.

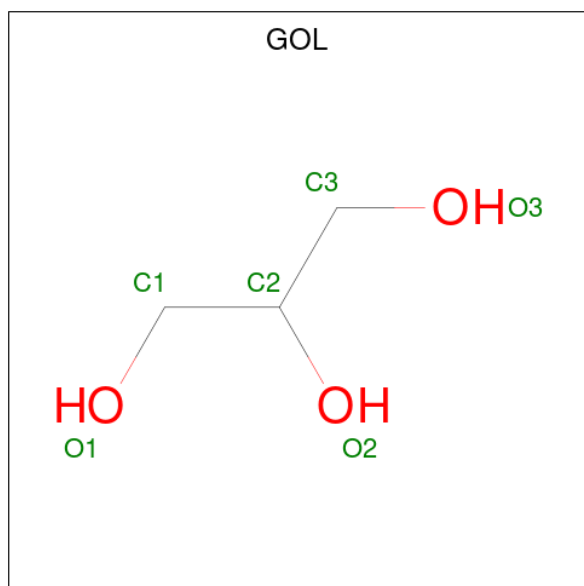
- Molecule 1 is a protein called Adenylate cyclase type 10.

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 (CCD ID: 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 (CCD ID: CL) (formula: Cl).

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

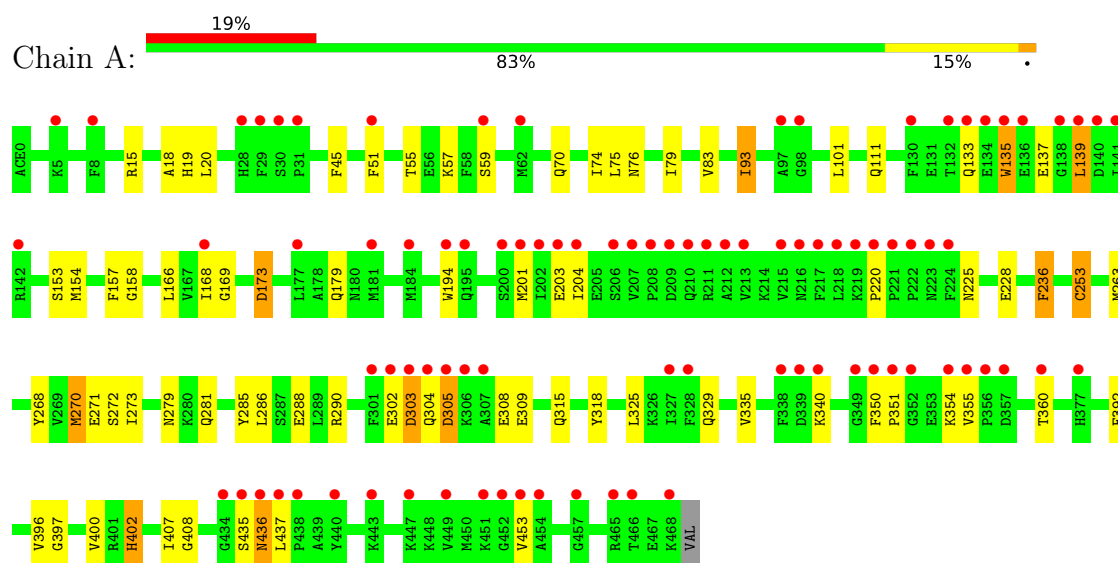
- Molecule 4 is water.

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



4 Data and refinement statistics

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 49.71 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.71-1.70) 99.7 (49.71-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 1.70Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.182 , 0.211 0.197 , 0.220	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)	0.35 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CME, ACE, GOL, 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	0.99	1/3903 (0.0%)	1.12	8/5280 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	TYR	CA-C	6.21	1.61	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	PHE	CA-CB-CG	6.59	120.39	113.80
1	A	303	ASP	CA-C-N	6.28	129.54	120.38
1	A	303	ASP	C-N-CA	6.28	129.54	120.38
1	A	305	ASP	CA-CB-CG	6.03	118.63	112.60
1	A	173	ASP	CA-C-N	5.62	127.81	120.28
1	A	173	ASP	C-N-CA	5.62	127.81	120.28
1	A	236	PHE	CA-CB-CG	-5.46	108.34	113.80
1	A	392	PHE	CA-CB-CG	-5.37	108.44	113.80

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	47	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	47	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 (47) 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:201:MET:HE1	1:A:220:PRO:HB3	1.69	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:288[A]:GLU:CD	1:A:290:ARG:HD2	2.36	0.50
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:308:GLU:H	1:A:308:GLU:CD	2.23	0.47
1:A:173:ASP:CG	1:A:340:LYS:HG2	2.40	0.46
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:19:HIS:HE1	4:A:779:HOH:O	1.99	0.45
1:A:253:CME:HZ3	4:A:1020:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:435:SER:C	1:A:437:LEU:H	2.28	0.42
1:A:273:ILE:HD13	1:A:286:LEU:CD1	2.50	0.42
1:A:270[B]:MET:HE3	1:A:272:SER:OG	2.20	0.41
1:A:19:HIS:HA	1:A:402:HIS:O	2.22	0.40
1:A:263:MET:HE3	1:A:263:MET:HB3	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	16	5

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 ⓘ

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%)	400 (95%)	21 (5%)	22 8

All (21) 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	270[A]	MET
1	A	270[B]	MET
1	A	271[A]	GLU
1	A	271[B]	GLU
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 (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	76	ASN
1	A	78	HIS
1	A	133	GLN

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Mol	Chain	Res	Type
1	A	162	HIS
1	A	179	GLN
1	A	192	ASN
1	A	195	GLN
1	A	225	ASN
1	A	279	ASN
1	A	281	GLN
1	A	315	GLN
1	A	375	GLN
1	A	433	ASN
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	0.41	0	6,9,11	2.27	2 (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
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(°)	Ideal(°)
1	A	253	CME	CZ-CE-SD	-4.22	99.28	113.39
1	A	253	CME	CB-SG-SD	-2.62	97.08	103.86

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 oligosaccharides 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	1.03	1 (20%)

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.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	GOL	C3-C2-C1	2.09	119.45	111.80

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 [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, 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	467/470 (99%)	0.85	90 (19%) 3 3	4, 27, 71, 120	10 (2%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	135	TRP	9.3
1	A	139	LEU	6.8
1	A	141	ILE	6.3
1	A	350	PHE	6.1
1	A	31	PRO	5.8
1	A	454	ALA	5.5
1	A	351	PRO	5.3
1	A	355	VAL	5.2
1	A	51	PHE	4.9
1	A	338	PHE	4.5
1	A	356	PRO	4.4
1	A	132	THR	4.4
1	A	468	LYS	4.4
1	A	303	ASP	4.3
1	A	354	LYS	4.0
1	A	204	ILE	3.9
1	A	217	PHE	3.9
1	A	437	LEU	3.8
1	A	218	LEU	3.8
1	A	340	LYS	3.8
1	A	453	VAL	3.8
1	A	352	GLY	3.8
1	A	222	PRO	3.7
1	A	438	PRO	3.5
1	A	29	PHE	3.5
1	A	357	ASP	3.3
1	A	219	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	140	ASP	3.2
1	A	8	PHE	3.2
1	A	304	GLN	3.2
1	A	305	ASP	3.2
1	A	200	SER	3.1
1	A	457	GLY	3.1
1	A	327	ILE	3.1
1	A	349	GLY	3.1
1	A	202	ILE	3.1
1	A	223	ASN	3.0
1	A	377	HIS	3.0
1	A	207	VAL	3.0
1	A	138	GLY	2.9
1	A	133	GLN	2.9
1	A	220	PRO	2.9
1	A	465	ARG	2.9
1	A	194	TRP	2.9
1	A	307	ALA	2.8
1	A	449	VAL	2.8
1	A	360	THR	2.8
1	A	306	LYS	2.8
1	A	452	GLY	2.8
1	A	221	PRO	2.8
1	A	206	SER	2.7
1	A	28[A]	HIS	2.7
1	A	451	LYS	2.7
1	A	328	PHE	2.7
1	A	213	VAL	2.7
1	A	211	ARG	2.6
1	A	168	ILE	2.6
1	A	212	ALA	2.6
1	A	98	GLY	2.5
1	A	203	GLU	2.5
1	A	216	ASN	2.5
1	A	215	VAL	2.5
1	A	195	GLN	2.4
1	A	436	ASN	2.4
1	A	210	GLN	2.4
1	A	209	ASP	2.4
1	A	134	GLU	2.4
1	A	224	PHE	2.3
1	A	184	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	59	SER	2.3
1	A	435	SER	2.3
1	A	208	PRO	2.3
1	A	30	SER	2.3
1	A	142	ARG	2.3
1	A	181	MET	2.3
1	A	201	MET	2.3
1	A	466	THR	2.2
1	A	97	ALA	2.2
1	A	130	PHE	2.2
1	A	177	LEU	2.1
1	A	136	GLU	2.1
1	A	339	ASP	2.1
1	A	434	GLY	2.1
1	A	62[A]	MET	2.1
1	A	302	GLU	2.0
1	A	5	LYS	2.0
1	A	301	PHE	2.0
1	A	440	TYR	2.0
1	A	443	LYS	2.0
1	A	447	LYS	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	0.94	0.11	6,12,19,22	4

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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	GOL	A	501	6/6	0.67	0.19	49,53,54,55	0
3	CL	A	502	1/1	0.98	0.05	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.