



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:43 AM UTC

PDB ID : 7Y5O / pdb_00007y5o
Title : Crystal structure of human CAF-1 core complex in spacegroup P21
Authors : Liu, C.P.; Wang, M.Z.; Xu, R.M.
Deposited on : 2022-06-17
Resolution : 3.57 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

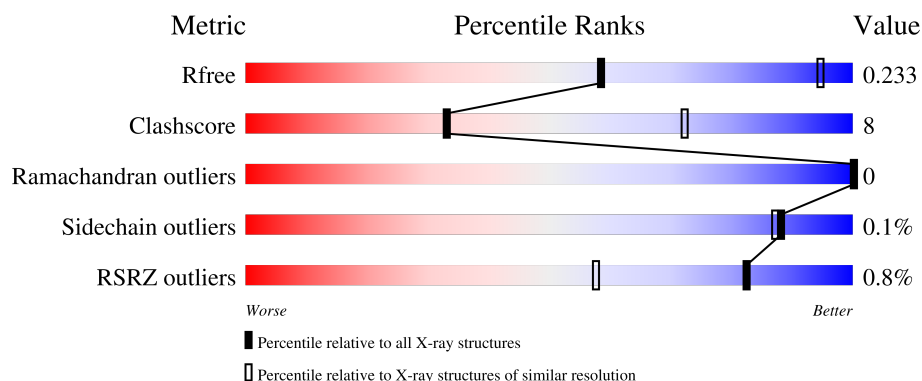
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.57 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	1521 (3.66-3.50)
Clashscore	190562	1595 (3.66-3.50)
Ramachandran outliers	187476	1551 (3.66-3.50)
Sidechain outliers	187428	1551 (3.66-3.50)
RSRZ outliers	180081	1520 (3.66-3.50)

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	273	0.2% 58% 14% 28%
1	D	273	0.2% 59% 13% 28%
2	B	419	71% 20% 9%
2	E	419	2% 69% 21% 9%
3	C	425	77% 18% 5%

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Mol	Chain	Length	Quality of chain
3	F	425	 79%16%5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15561 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 Chromatin assembly factor 1 subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1595	1008	294	285	8			
1	D	197	Total	C	N	O	S	0	0	0
			1595	1008	294	285	8			

- Molecule 2 is a protein called Chromatin assembly factor 1 subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	380	Total	C	N	O	S	0	0	0
			2965	1894	511	544	16			
2	E	380	Total	C	N	O	S	0	0	0
			2965	1894	511	544	16			

- Molecule 3 is a protein called Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	405	Total	C	N	O	S	0	0	0
			3197	2018	543	626	10			
3	F	405	Total	C	N	O	S	0	0	0
			3197	2018	543	626	10			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



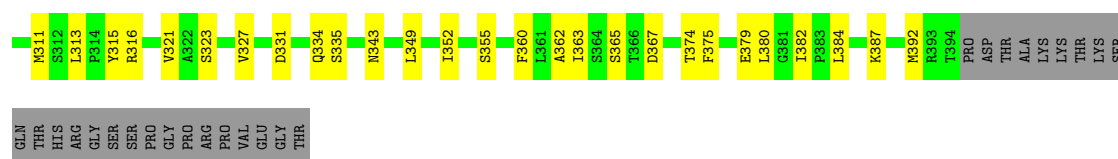
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

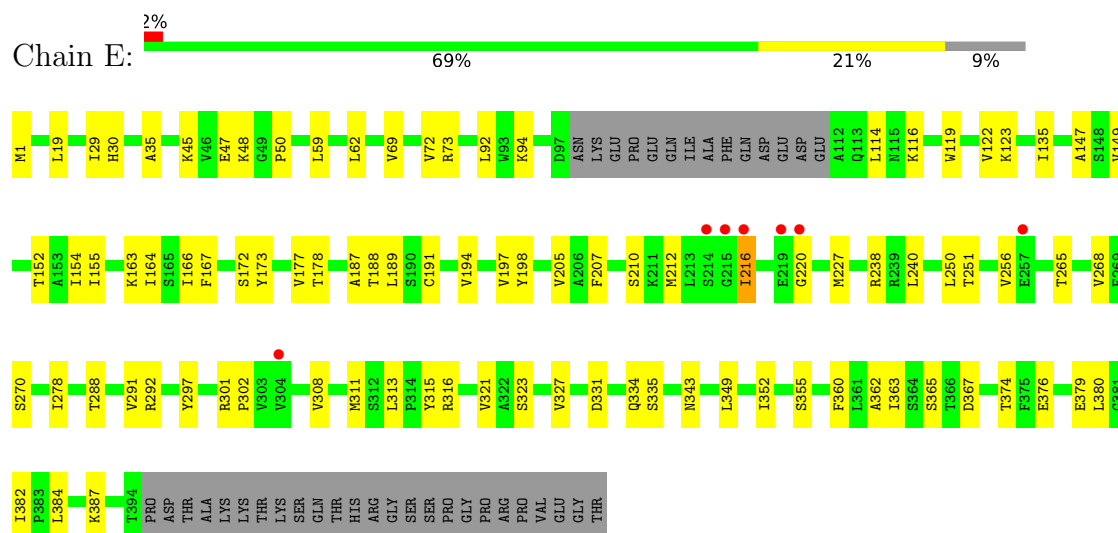
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	B	2	Total	O	0	0
			2	2		
5	C	4	Total	O	0	0
			4	4		
5	D	2	Total	O	0	0
			2	2		
5	E	3	Total	O	0	0
			3	3		
5	F	2	Total	O	0	0
			2	2		

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.

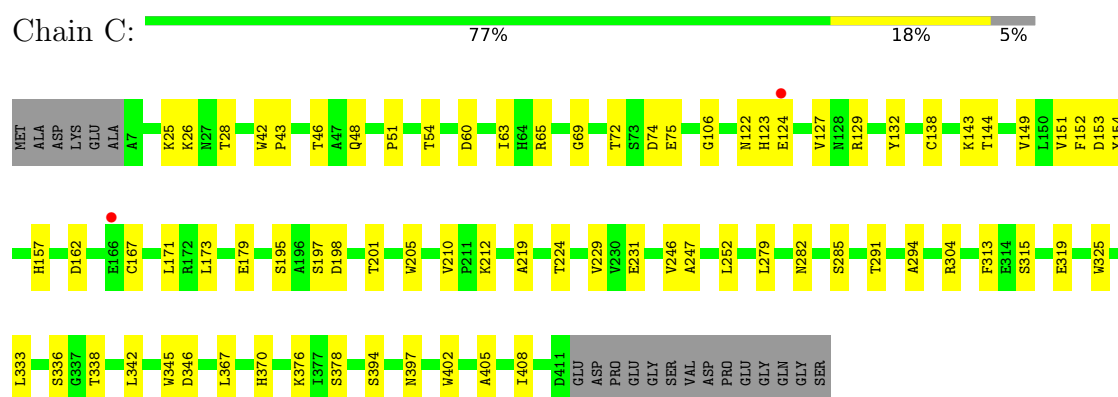
- Chain B:
-
- 71% 20% 9%
- M1 L19 I29 H30 A35 K45 V46 E47 K48 L59 L62 V69 V72 R73 D87 D89 ASN LYS GIU PHO GLU GLN TLE ALA PHE GLN ASP GLU ASP GLU A112 W119 T135 T139 A147 S148 V149 T152 A153 T154 T166 F167 Y172 V177 T178 W179 D180 Q184 A187 T188 L189 V194 V197 Y198 Q201 K202 V205 A206 F207 S210 L213 S214 E219 R223 R238 R239 L240 L250 T251 V256 E257 T265 V268 F269 S270 R271 I278 T288 V291 R292 Y297 Y298



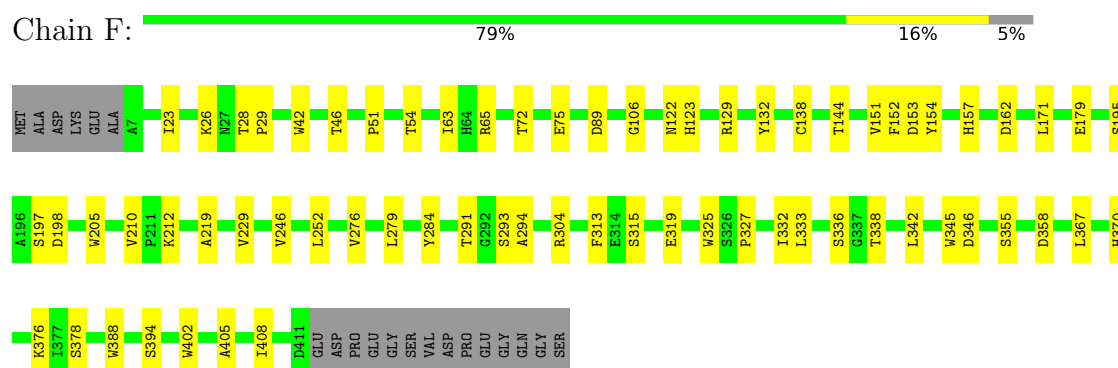
• Molecule 2: Chromatin assembly factor 1 subunit B



• Molecule 3: Histone-binding protein RBBP4



• Molecule 3: Histone-binding protein RBBP4



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	100.61Å 176.09Å 100.91Å 90.00° 115.09° 90.00°	Depositor
Resolution (Å)	26.98 – 3.57 26.98 – 3.57	Depositor EDS
% Data completeness (in resolution range)	76.0 (26.98-3.57) 84.5 (26.98-3.57)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.15 (at 3.57Å)	Xtriage
Refinement program	PHENIX (1.20_4459: ???)	Depositor
R, R_{free}	0.214 , 0.232 0.214 , 0.233	Depositor DCC
R_{free} test set	2012 reflections (5.32%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 11.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.146 for l,-k,h	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	15561	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.08	0/1630	0.24	0/2191
1	D	0.08	0/1630	0.23	0/2191
2	B	0.11	0/3034	0.30	0/4119
2	E	0.11	0/3034	0.32	0/4119
3	C	0.10	0/3287	0.26	0/4483
3	F	0.08	0/3287	0.25	0/4483
All	All	0.10	0/15902	0.27	0/21586

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1595	0	1581	31	0
1	D	1595	0	1581	31	0
2	B	2965	0	2940	53	0
2	E	2965	0	2940	56	0
3	C	3197	0	3009	53	0
3	F	3197	0	3009	47	0
4	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	12	0	16	1	0
4	E	6	0	8	1	0
4	F	6	0	8	0	0
5	A	4	0	0	0	0
5	B	2	0	0	0	0
5	C	4	0	0	0	0
5	D	2	0	0	0	0
5	E	3	0	0	0	0
5	F	2	0	0	0	0
All	All	15561	0	15100	240	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 8.

The worst 5 of 240 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)
2:B:270:SER:HB2	2:B:278:ILE:HD11	1.60	0.81
2:E:270:SER:HB2	2:E:278:ILE:HD11	1.62	0.79
2:E:301:ARG:HG3	2:E:302:PRO:HD2	1.73	0.71
3:F:346:ASP:HB2	3:F:367:LEU:HD12	1.72	0.70
3:C:346:ASP:HB2	3:C:367:LEU:HD12	1.73	0.69

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	193/273 (71%)	189 (98%)	4 (2%)	0	100	100
1	D	193/273 (71%)	188 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	376/419 (90%)	365 (97%)	11 (3%)	0	100	100
2	E	376/419 (90%)	366 (97%)	10 (3%)	0	100	100
3	C	403/425 (95%)	396 (98%)	7 (2%)	0	100	100
3	F	403/425 (95%)	395 (98%)	8 (2%)	0	100	100
All	All	1944/2234 (87%)	1899 (98%)	45 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	168/235 (72%)	168 (100%)	0	100	100
1	D	168/235 (72%)	168 (100%)	0	100	100
2	B	323/363 (89%)	323 (100%)	0	100	100
2	E	323/363 (89%)	322 (100%)	1 (0%)	86	83
3	C	354/375 (94%)	354 (100%)	0	100	100
3	F	354/375 (94%)	353 (100%)	1 (0%)	86	83
All	All	1690/1946 (87%)	1688 (100%)	2 (0%)	88	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	216	ILE
3	F	28	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	347	HIS
3	F	78	HIS

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Mol	Chain	Res	Type
3	F	122	ASN
3	C	122	ASN
3	C	324	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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	$\# Z > 2$
4	GOL	B	501	-	5,5,5	0.94	0	5,5,5	1.07	0
4	GOL	C	501	-	5,5,5	0.92	0	5,5,5	1.09	0
4	GOL	E	501	-	5,5,5	0.93	0	5,5,5	1.09	0
4	GOL	F	501	-	5,5,5	0.89	0	5,5,5	1.14	1 (20%)
4	GOL	C	502	-	5,5,5	0.98	0	5,5,5	1.03	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
4	GOL	B	501	-	-	0/4/4/4	-
4	GOL	C	501	-	-	0/4/4/4	-
4	GOL	E	501	-	-	0/4/4/4	-
4	GOL	F	501	-	-	0/4/4/4	-
4	GOL	C	502	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	501	GOL	C3-C2-C1	-2.00	104.45	111.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	501	GOL	1	0
4	C	502	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 [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	197/273 (72%)	0.27	3 (1%) 72 44	29, 60, 84, 107	0
1	D	197/273 (72%)	0.24	2 (1%) 79 53	38, 64, 93, 115	0
2	B	380/419 (90%)	0.14	2 (0%) 87 66	37, 52, 89, 115	0
2	E	380/419 (90%)	0.14	7 (1%) 67 40	37, 51, 87, 125	0
3	C	405/425 (95%)	0.15	2 (0%) 87 66	30, 47, 77, 107	0
3	F	405/425 (95%)	0.07	0 100 100	37, 59, 83, 125	0
All	All	1964/2234 (87%)	0.15	16 (0%) 82 58	29, 54, 86, 125	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	219	GLU	4.0
2	E	220	GLY	2.7
2	B	257	GLU	2.7
2	E	216	ILE	2.5
3	C	166	GLU	2.5

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

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

6.3 Carbohydrates [i](#)

There are no 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
4	GOL	F	501	6/6	0.61	0.16	58,58,59,59	0
4	GOL	C	502	6/6	0.75	0.21	39,39,39,40	0
4	GOL	C	501	6/6	0.83	0.12	50,50,50,51	0
4	GOL	E	501	6/6	0.90	0.13	49,50,51,51	0
4	GOL	B	501	6/6	0.90	0.13	51,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.