



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:14 PM GMT

PDB ID : 1SPU
Title : STRUCTURE OF OXIDOREDUCTASE
Authors : Wilmot, C.M.; Phillips, S.E.V.
Deposited on : 1996-11-13
Resolution : 2.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

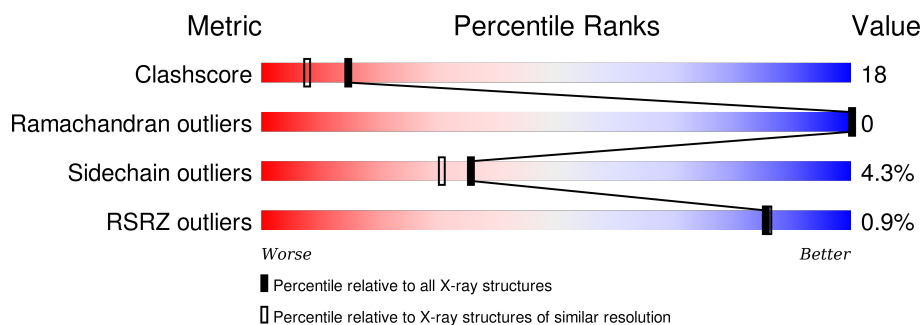
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	727	
1	B	727	

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
1	PAQ	A	466	X	-	-	-
1	PAQ	B	466	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12431 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 COPPER AMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	718	Total	C	N	O	S	0	0	0
			5671	3607	967	1075	22			
1	B	720	Total	C	N	O	S	0	0	0
			5690	3619	972	1077	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	466	PAQ	TYR	MODIFIED RESIDUE	UNP P46883
B	466	PAQ	TYR	MODIFIED RESIDUE	UNP P46883

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cu	0	0
			1	1		
2	A	1	Total	Cu	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	539	Total	O	0	0
			539	539		

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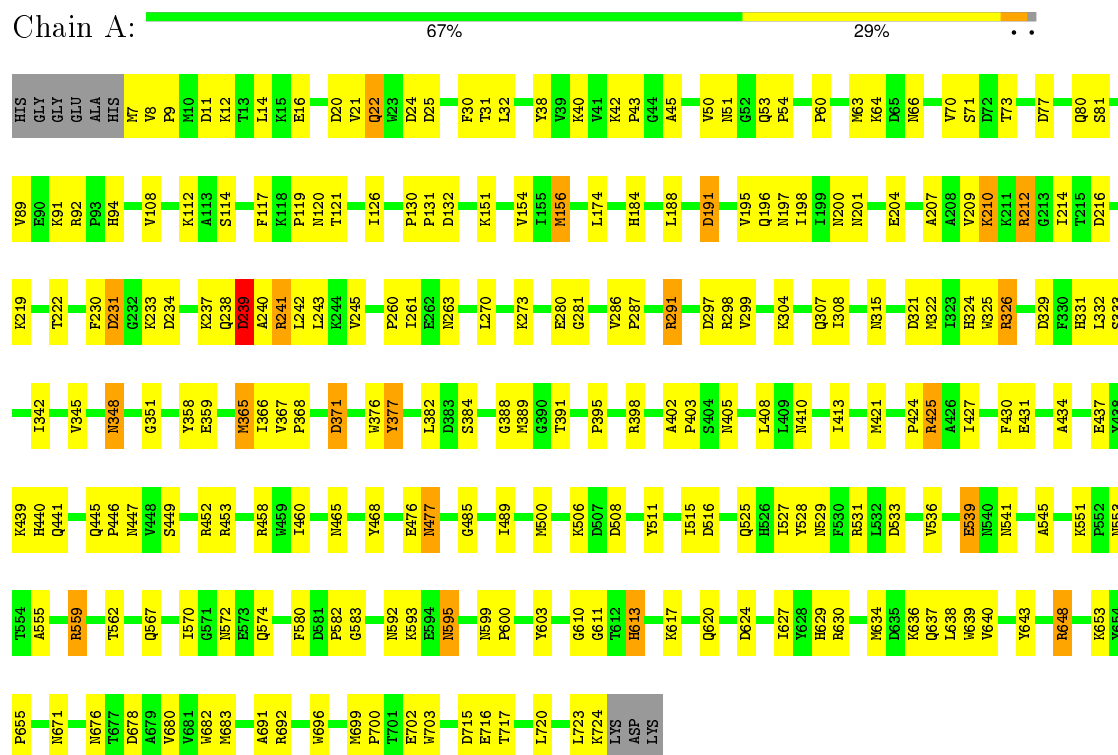
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	525	Total	O	0	0
			525	525		

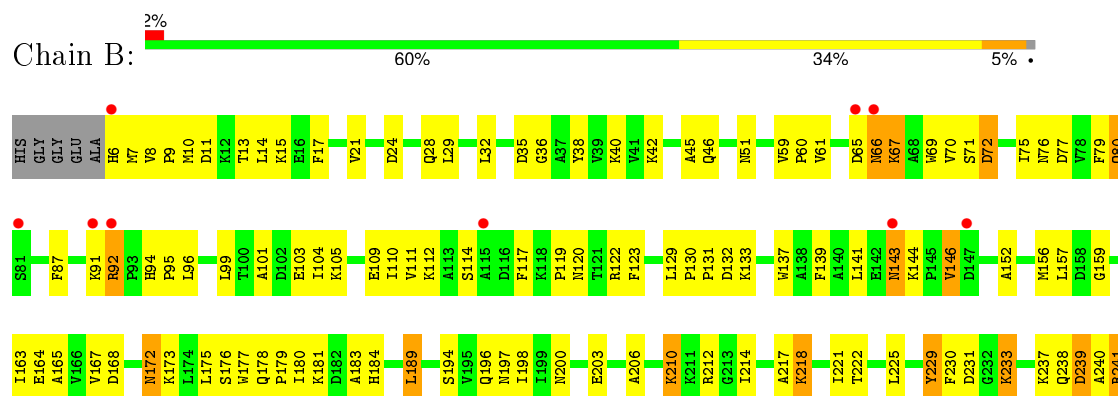
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: COPPER AMINE OXIDASE



• Molecule 1: COPPER AMINE OXIDASE



G665	Q578	Y466	P340	L242
K669	R579	D467	T346	L243
D670	F580	Y468	E359	I246
N671	D581	I469	I366	L249
E672	T584	E476	V367	D250
N676	L585	M477	P368	D253
A679	L587	A484	Y369	H259
M682	L588	K496	I374	P260
M683	M595	E503	R377	L261
R692	R596	R510	A380	E262
A693	H597	D516	Y381	N263
E694	G598	I519	L382	D269
P697	M605	Q525	D383	L270
I698	G610	H526	Y387	E271
M699	H613	R531	T391	Q272
P700	F614	L532	R398	K273
N712	Y615	D533	G399	K274
A616	A619	V536	K400	L275
T717	Q620	D537	L408	V276
L720	F621	G538	M410	V286
A722	D624	H539	E411	P287
L723	E625	N540	T412	M288
K724	M626	N541	I413	T289
K725	I627	A545	Y416	A290
ASP	Y628	M546	V419	R291
LYS	H629	D547	P420	P292
	R630	F548	M421	R296
	L631	K551	P424	D297
	M634	P552	R425	R298
	D635	N553	R432	V299
	K636	T554	E437	A300
	D637	A555	H440	P301
	L638	F558	Q445	A302
	M639	R559	P446	V303
	R642	M563	R452	K304
	Y643	N566	R453	Q307
	H644	Q567	M458	I308
	E647	Y568	W459	K314
	R648	M569	R572	N315
	F649	I570	E573	I318
	K653	G571	Q574	M322
	M656	R572		R326
	D661	E573		F330
		Q574		R337
				V338
				G339

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.46 Å 166.07 Å 79.41 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 18.59 – 1.99	Depositor EDS
% Data completeness (in resolution range)	83.7 (20.00-2.00) 80.3 (18.59-1.99)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.60 (at 1.99 Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.206 , (Not available) 0.181 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.665	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 97.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 100528 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12431	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PAQ, CA, CU

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	0.80	0/5793	1.57	51/7886 (0.6%)
1	B	0.79	0/5813	1.62	51/7912 (0.6%)
All	All	0.79	0/11606	1.60	102/15798 (0.6%)

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	1	1
1	B	1	0
All	All	2	1

There are no bond length outliers.

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	291	ARG	NE-CZ-NH1	22.14	131.37	120.30
1	B	630	ARG	NE-CZ-NH1	15.28	127.94	120.30
1	B	291	ARG	CD-NE-CZ	14.99	144.59	123.60
1	B	291	ARG	NE-CZ-NH2	-13.27	113.67	120.30
1	A	648	ARG	NE-CZ-NH2	-12.95	113.82	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	466	PAQ	CG
1	B	466	PAQ	CG

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	648	ARG	Sidechain

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	5671	0	5545	188	0
1	B	5690	0	5563	242	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	539	0	0	17	0
4	B	525	0	0	20	0
All	All	12431	0	11108	400	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 18.

The worst 5 of 400 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:B:210:LYS:HE3	1:B:217:ALA:HB2	1.24	1.14
1:B:368:PRO:HB2	1:B:621:PHE:HZ	1.09	1.12
1:B:92:ARG:HB2	1:B:92:ARG:HH11	1.24	1.00
1:B:368:PRO:HB2	1:B:621:PHE:CZ	1.97	0.98
1:A:297:ASP:HB2	1:B:725:LYS:HE3	1.46	0.98

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	715/727 (98%)	684 (96%)	31 (4%)	0	100	100
1	B	717/727 (99%)	691 (96%)	26 (4%)	0	100	100
All	All	1432/1454 (98%)	1375 (96%)	57 (4%)	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	609/615 (99%)	591 (97%)	18 (3%)	48	47
1	B	611/615 (99%)	576 (94%)	35 (6%)	25	19
All	All	1220/1230 (99%)	1167 (96%)	53 (4%)	35	30

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	132	ASP
1	B	173	LYS
1	B	635	ASP
1	B	137	TRP
1	B	144	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	46	GLN
1	B	178	GLN
1	B	629	HIS
1	B	51	ASN
1	B	76	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	PAQ	A	466	1	17,22,23	2.03	4 (23%)	11,29,31	1.54	2 (18%)
1	PAQ	B	466	1	17,22,23	2.09	5 (29%)	11,29,31	1.26	1 (9%)

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	PAQ	A	466	1	1/1/5/10	0/7/27/29	0/2/2/2
1	PAQ	B	466	1	1/1/5/10	0/7/27/29	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	466	PAQ	CG-CD2	-4.63	1.40	1.50
1	B	466	PAQ	CG-CD2	-4.53	1.40	1.50
1	B	466	PAQ	C3-C2	-3.99	1.30	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	466	PAQ	C3-C2	-3.74	1.31	1.38
1	B	466	PAQ	OH-CZ	-3.13	1.25	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	466	PAQ	O2-CD1-CE1	-3.24	116.22	121.62
1	B	466	PAQ	O-C-CA	-2.86	118.05	125.49
1	A	466	PAQ	CB-CA-N	2.86	117.02	109.91

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	466	PAQ	CG
1	A	466	PAQ	CG

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	466	PAQ	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	717/727 (98%)	-0.54	0 100 100	8, 21, 53, 82	0
1	B	719/727 (98%)	-0.43	13 (1%) 71 72	11, 24, 60, 99	0
All	All	1436/1454 (98%)	-0.48	13 (0%) 85 86	8, 23, 58, 99	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	301	PRO	5.2
1	B	65	ASP	4.8
1	B	302	ALA	4.5
1	B	6	HIS	3.8
1	B	143	ASN	2.8

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	PAQ	B	466	21/22	0.97	0.08	-	10,29,33,35	0
1	PAQ	A	466	21/22	0.96	0.09	-	9,23,34,38	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	CA	B	802	1/1	0.61	0.19	0.87	71,71,71,71	0
3	CA	A	802	1/1	0.92	0.10	-0.27	56,56,56,56	0
3	CA	A	801	1/1	0.99	0.05	-2.25	19,19,19,19	0
3	CA	B	801	1/1	1.00	0.04	-2.40	20,20,20,20	0
2	CU	B	800	1/1	1.00	0.03	-	20,20,20,20	0
2	CU	A	800	1/1	0.99	0.03	-	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.