Full wwPDB X-ray Structure Validation Report (i)

Feb 21, 2024 – 08:31 AM EST

PDB ID	:	4NSD
Title	:	Crystal Structure of CBARA1 in the Ca2+ Binding Form
Authors	:	Wang, L.; Yang, X.; Li, S.; Shen, Y.
Deposited on	:	2013-11-28
Resolution	:	2.70 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:

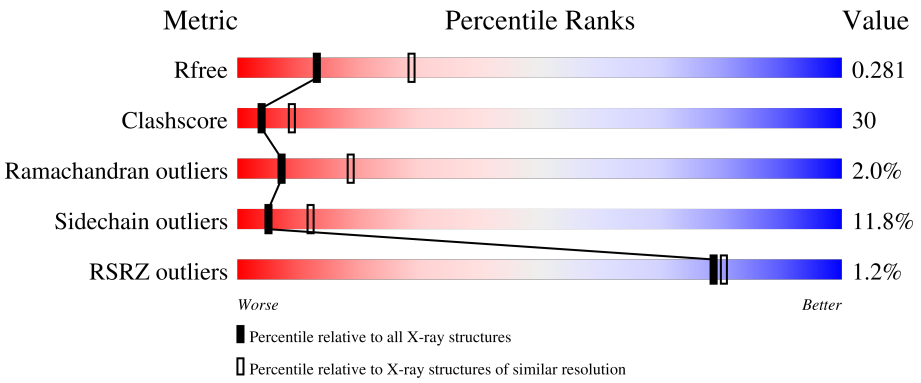
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	351	.% 48% 28% 6% 17%
1	B	351	.% 43% 31% 6% 19%

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
4	MPD	B	505	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4591 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 Calcium uptake protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	290	2302	1477	378	436	11	0	0	0
1	B	283	2229	1432	363	423	11	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	GLY	-	expression tag	UNP Q9BPX6
A	95	SER	-	expression tag	UNP Q9BPX6
A	96	MET	-	expression tag	UNP Q9BPX6
B	94	GLY	-	expression tag	UNP Q9BPX6
B	95	SER	-	expression tag	UNP Q9BPX6
B	96	MET	-	expression tag	UNP Q9BPX6

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

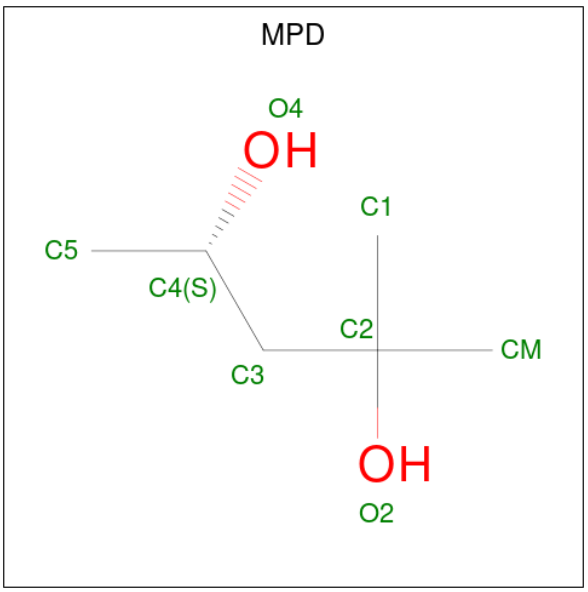
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	2	2	2	0	0
2	B	2	2	2	0	0

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

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

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:

$C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	B	1	8	6	2	0	0
			Total	C	O		
4	B	1	8	6	2	0	0
			Total	C	O		
4	B	1	8	6	2	0	0

- Molecule 5 is water.

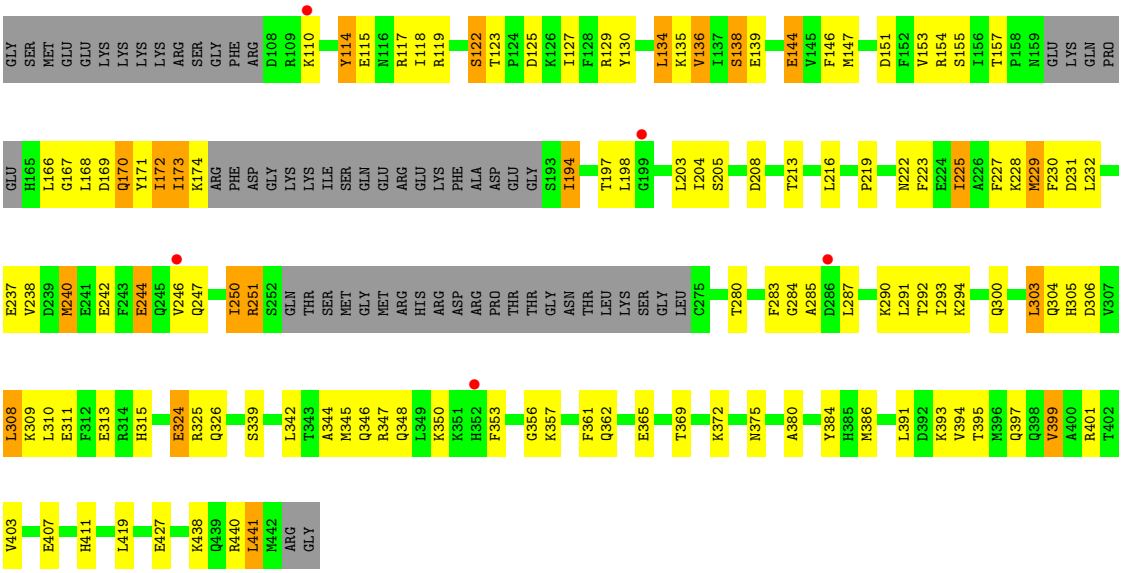
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	15	15	15	0	0
			Total	O		
5	B	15	15	15	0	0

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.

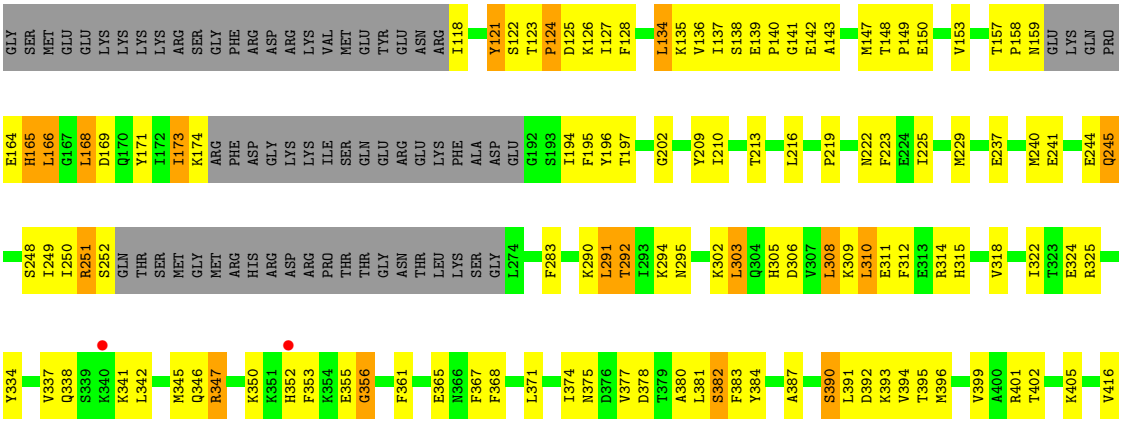
• Molecule 1: Calcium uptake protein 1, mitochondrial

Chain A:



• Molecule 1: Calcium uptake protein 1, mitochondrial

Chain B:



D421
C422
G426
E427
L428
E432
F433
I436
M437
R440
L441
M442
ARG
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	99.28Å 105.80Å 156.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.38 – 2.70 32.38 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.2 (32.38-2.70) 95.7 (32.38-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.46 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.212 , 0.282 0.211 , 0.281	Depositor DCC
R_{free} test set	1167 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	54.0	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 62.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4591	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: MPD, CL, CA

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	0.40	0/2344	0.56	0/3156
1	B	0.40	0/2270	0.56	0/3058
All	All	0.40	0/4614	0.56	0/6214

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	121	TYR	Peptide

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	2302	0	2221	118	0
1	B	2229	0	2147	152	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	24	0	42	10	0
5	A	15	0	0	2	0
5	B	15	0	0	0	0
All	All	4591	0	4410	272	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 30.

All (272) 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:315:HIS:HB3	1:A:326:GLN:OE1	1.57	1.05
1:B:292:THR:HG22	1:B:295:ASN:H	1.19	1.03
1:B:240:MET:HE3	1:B:244:GLU:HG3	1.41	1.02
1:B:402:THR:HG21	4:B:505:MPD:HM3	1.47	0.97
1:B:402:THR:CG2	4:B:505:MPD:HM3	1.99	0.93
1:B:219:PRO:HG2	1:B:222:ASN:OD1	1.69	0.93
1:A:308:LEU:HD12	1:A:361:PHE:CE1	2.05	0.91
1:A:134:LEU:HD11	1:A:168:LEU:HD11	1.50	0.91
1:A:138:SER:HA	1:A:172:ILE:HG22	1.50	0.91
1:A:440:ARG:C	1:A:441:LEU:HD23	1.91	0.90
1:B:142:GLU:HG2	1:B:143:ALA:H	1.34	0.90
1:A:135:LYS:O	1:A:169:ASP:HB2	1.74	0.87
1:B:292:THR:CG2	1:B:295:ASN:H	1.89	0.86
1:B:137:ILE:HB	1:B:171:TYR:HB2	1.56	0.86
1:B:402:THR:CB	4:B:505:MPD:HM3	2.05	0.85
1:A:308:LEU:HD13	1:A:308:LEU:O	1.78	0.83
1:B:194:ILE:O	1:B:197:THR:HG22	1.78	0.83
1:B:194:ILE:HD12	1:B:195:PHE:H	1.44	0.82
1:A:280:THR:HG22	1:A:285:ALA:HA	1.61	0.82
1:B:325:ARG:HB2	1:B:350:LYS:HE2	1.63	0.81
1:A:237:GLU:OE1	1:A:290:LYS:HD2	1.81	0.81
1:B:240:MET:CE	1:B:244:GLU:HG3	2.11	0.80
1:B:248:SER:O	1:B:251:ARG:HG2	1.81	0.80
1:A:401:ARG:HD3	1:A:407:GLU:OE1	1.81	0.80
1:B:142:GLU:HG2	1:B:143:ALA:N	1.96	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:THR:HG21	4:B:505:MPD:CM	2.13	0.78
1:A:119:ARG:NH1	1:A:154:ARG:O	2.16	0.78
1:A:292:THR:HG22	1:A:294:LYS:H	1.49	0.78
1:B:325:ARG:HH22	1:B:347:ARG:HG2	1.49	0.78
1:B:171:TYR:HE2	1:B:173:ILE:HD12	1.48	0.78
1:A:173:ILE:O	1:A:174:LYS:CB	2.32	0.77
1:B:194:ILE:HD12	1:B:195:PHE:N	1.99	0.77
1:B:134:LEU:HD13	1:B:168:LEU:HD13	1.68	0.76
1:A:225:ILE:O	1:A:228:LYS:HB2	1.86	0.75
1:A:144:GLU:HG3	1:A:146:PHE:CE2	2.22	0.75
1:B:392:ASP:OD2	1:B:394:VAL:HG12	1.88	0.74
1:B:325:ARG:HD2	1:B:350:LYS:HE2	1.69	0.74
1:A:308:LEU:HD12	1:A:361:PHE:HE1	1.52	0.74
1:B:134:LEU:CD1	1:B:168:LEU:HD13	2.18	0.73
1:A:232:LEU:HD12	1:A:242:GLU:HG2	1.69	0.73
1:B:251:ARG:HG3	1:B:251:ARG:O	1.89	0.72
1:B:148:THR:OG1	1:B:150:GLU:HG2	1.90	0.72
1:A:223:PHE:HE2	1:A:293:ILE:HA	1.54	0.71
1:A:216:LEU:CD2	1:A:303:LEU:HD13	2.21	0.71
1:A:219:PRO:HB2	1:A:222:ASN:OD1	1.90	0.71
1:A:134:LEU:HD11	1:A:168:LEU:CD1	2.21	0.71
1:B:342:LEU:HA	1:B:345:MET:HB2	1.71	0.71
1:A:250:ILE:HG22	1:A:251:ARG:N	2.06	0.70
1:B:166:LEU:HD12	1:B:166:LEU:N	2.06	0.70
1:B:402:THR:HB	4:B:505:MPD:HM3	1.73	0.70
1:B:334:TYR:O	1:B:440:ARG:HG2	1.89	0.70
1:A:118:ILE:O	1:A:122:SER:HB2	1.91	0.70
1:A:194:ILE:HD11	1:A:303:LEU:HD23	1.72	0.69
1:A:309:LYS:O	1:A:313:GLU:HG2	1.93	0.69
1:B:168:LEU:HD12	1:B:168:LEU:N	2.08	0.69
1:B:237:GLU:OE1	1:B:290:LYS:HD2	1.93	0.69
1:B:216:LEU:HD21	1:B:303:LEU:HD13	1.74	0.69
1:A:325:ARG:HD3	1:A:350:LYS:HD3	1.74	0.68
1:B:245:GLN:O	1:B:249:ILE:HG13	1.93	0.68
1:A:441:LEU:HD23	1:A:441:LEU:N	2.09	0.68
1:B:440:ARG:HD2	1:B:440:ARG:O	1.93	0.68
1:A:247:GLN:O	1:A:250:ILE:HB	1.94	0.68
1:B:324:GLU:HG2	1:B:353:PHE:CG	2.29	0.68
1:B:164:GLU:O	1:B:165:HIS:CB	2.42	0.67
1:B:390:SER:HB3	1:B:427:GLU:OE1	1.95	0.67
1:B:292:THR:HG22	1:B:295:ASN:N	2.01	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:TYR:HB2	1:A:386:MET:CE	2.25	0.66
1:A:345:MET:HG2	1:A:419:LEU:O	1.95	0.66
1:A:380:ALA:O	1:A:384:TYR:HD2	1.80	0.65
1:A:384:TYR:HB2	1:A:386:MET:HE2	1.78	0.64
1:A:170:GLN:N	1:A:170:GLN:CD	2.51	0.64
1:A:325:ARG:HB2	1:A:350:LYS:HD2	1.80	0.63
1:B:165:HIS:C	1:B:166:LEU:HD12	2.18	0.63
1:B:168:LEU:HD12	1:B:168:LEU:H	1.63	0.63
1:B:153:VAL:HG21	1:B:310:LEU:HB3	1.81	0.63
1:A:216:LEU:HD21	1:A:303:LEU:HD13	1.81	0.63
1:A:223:PHE:CE2	1:A:293:ILE:HA	2.34	0.63
1:B:342:LEU:HA	1:B:345:MET:CB	2.29	0.62
1:B:342:LEU:HD21	1:B:422:CYS:SG	2.39	0.62
1:B:440:ARG:C	1:B:442:MET:H	2.03	0.62
1:B:171:TYR:CE2	1:B:173:ILE:HD12	2.31	0.62
1:B:381:LEU:C	1:B:383:PHE:H	2.02	0.62
1:B:194:ILE:HG23	1:B:302:LYS:HG3	1.81	0.61
1:B:216:LEU:CD2	1:B:303:LEU:HD13	2.31	0.60
1:A:395:THR:O	1:A:399:VAL:HG22	2.00	0.60
1:A:244:GLU:OE1	1:A:244:GLU:HA	2.01	0.60
1:A:280:THR:HA	1:A:284:GLY:O	2.01	0.60
1:B:325:ARG:CB	1:B:350:LYS:HE2	2.30	0.60
1:A:198:LEU:CD1	1:A:204:ILE:HG12	2.32	0.60
1:B:157:THR:HB	1:B:314:ARG:HH12	1.67	0.60
1:A:144:GLU:HG3	1:A:146:PHE:HE2	1.66	0.60
1:B:248:SER:HB2	1:B:251:ARG:HE	1.66	0.59
1:A:440:ARG:O	1:A:441:LEU:HD23	2.01	0.58
1:B:341:LYS:O	1:B:345:MET:HB2	2.03	0.58
1:A:123:THR:HB	1:A:125:ASP:OD1	2.03	0.58
1:B:216:LEU:HG	1:B:303:LEU:CD1	2.33	0.58
1:B:283:PHE:HE1	1:B:291:LEU:HB2	1.68	0.58
1:B:325:ARG:NH2	1:B:347:ARG:HG2	2.16	0.58
1:B:428:LEU:HD13	1:B:433:PHE:HB2	1.85	0.58
1:A:308:LEU:HD13	1:A:308:LEU:C	2.24	0.58
1:A:198:LEU:HD11	1:A:204:ILE:HG12	1.87	0.57
1:B:394:VAL:HG13	1:B:395:THR:N	2.17	0.57
1:A:153:VAL:HG21	1:A:310:LEU:HB3	1.87	0.57
1:A:311:GLU:O	1:A:315:HIS:HD2	1.88	0.57
1:B:338:GLN:OE1	1:B:338:GLN:HA	2.04	0.57
1:B:342:LEU:CD2	1:B:422:CYS:SG	2.92	0.57
1:B:432:GLU:O	1:B:436:ILE:HD12	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LEU:HG	1:B:303:LEU:HD11	1.87	0.56
1:B:325:ARG:HD2	1:B:350:LYS:CE	2.35	0.56
1:A:216:LEU:HG	1:A:303:LEU:CD1	2.35	0.56
1:A:136:VAL:HG13	1:A:144:GLU:HG2	1.86	0.56
1:A:344:ALA:O	1:A:348:GLN:HG3	2.06	0.56
1:A:194:ILE:HG13	1:A:306:ASP:OD1	2.05	0.56
1:B:308:LEU:HD13	1:B:361:PHE:CE1	2.40	0.56
1:A:134:LEU:CD1	1:A:168:LEU:CD1	2.84	0.56
1:B:123:THR:HG22	1:B:126:LYS:H	1.70	0.56
1:A:325:ARG:CD	1:A:350:LYS:HD3	2.37	0.55
1:B:124:PRO:CB	1:B:210:ILE:HD11	2.37	0.55
1:A:170:GLN:N	1:A:170:GLN:OE1	2.40	0.55
1:B:194:ILE:HG12	1:B:303:LEU:HA	1.88	0.55
1:B:305:HIS:HD2	1:B:365:GLU:OE2	1.89	0.55
1:A:305:HIS:HD2	1:A:365:GLU:OE2	1.91	0.54
1:B:134:LEU:CD1	1:B:168:LEU:HB2	2.36	0.54
1:B:394:VAL:CG1	1:B:395:THR:N	2.69	0.54
1:A:123:THR:O	1:A:127:ILE:HG13	2.08	0.54
1:A:194:ILE:CD1	1:A:303:LEU:HD23	2.38	0.53
1:B:440:ARG:HD2	1:B:440:ARG:C	2.28	0.53
1:A:114:TYR:CD1	1:A:114:TYR:C	2.81	0.53
1:B:122:SER:O	1:B:127:ILE:HG13	2.07	0.53
1:B:241:GLU:OE1	1:B:241:GLU:N	2.33	0.53
1:B:391:LEU:HD13	1:B:396:MET:HG3	1.91	0.53
1:A:313:GLU:C	1:A:315:HIS:H	2.12	0.52
1:B:165:HIS:CA	1:B:166:LEU:HD12	2.39	0.52
1:A:440:ARG:O	1:A:440:ARG:HD2	2.08	0.52
1:B:136:VAL:HG13	1:B:136:VAL:O	2.09	0.52
1:A:216:LEU:HG	1:A:303:LEU:HD13	1.92	0.52
1:B:194:ILE:HG13	1:B:306:ASP:OD1	2.10	0.52
1:B:311:GLU:O	1:B:315:HIS:HD2	1.92	0.52
1:A:393:LYS:O	1:A:397:GLN:HG3	2.09	0.52
1:B:374:ILE:O	1:B:374:ILE:HG13	2.09	0.52
1:B:240:MET:CE	1:B:244:GLU:CG	2.84	0.52
1:B:118:ILE:CB	1:B:121:TYR:HB2	2.39	0.52
1:B:283:PHE:CE1	1:B:291:LEU:HB2	2.45	0.52
1:A:305:HIS:CD2	1:A:365:GLU:OE2	2.63	0.51
1:B:194:ILE:HG23	1:B:302:LYS:CG	2.40	0.51
1:B:158:PRO:O	1:B:159:ASN:C	2.49	0.50
1:B:173:ILE:O	1:B:174:LYS:CB	2.59	0.50
1:B:347:ARG:HB3	1:B:347:ARG:CZ	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLY:HA3	5:A:610:HOH:O	2.10	0.50
1:B:342:LEU:O	1:B:345:MET:HB3	2.12	0.50
1:A:250:ILE:CG2	1:A:251:ARG:N	2.74	0.49
1:A:114:TYR:HA	1:A:117:ARG:HD2	1.95	0.49
1:A:237:GLU:CD	1:A:290:LYS:HD2	2.31	0.49
1:B:325:ARG:NH2	1:B:347:ARG:HA	2.27	0.49
1:B:122:SER:O	1:B:123:THR:C	2.51	0.49
1:B:399:VAL:HG12	4:B:505:MPD:HM1	1.93	0.49
1:A:138:SER:CA	1:A:172:ILE:HG22	2.35	0.49
1:B:137:ILE:HG22	1:B:139:GLU:H	1.77	0.49
1:B:303:LEU:O	1:B:303:LEU:HD22	2.12	0.49
1:A:242:GLU:O	1:A:246:VAL:HG23	2.12	0.49
1:A:391:LEU:O	1:A:427:GLU:HB2	2.11	0.49
1:A:225:ILE:H	1:A:225:ILE:HG12	1.43	0.49
1:B:375:ASN:OD1	1:B:441:LEU:HD12	2.12	0.49
1:B:312:PHE:CE2	1:B:322:ILE:HG23	2.48	0.48
1:A:134:LEU:CD1	1:A:168:LEU:HD11	2.33	0.48
1:A:324:GLU:OE1	1:A:411:HIS:NE2	2.46	0.48
1:A:375:ASN:HD22	1:A:438:LYS:HG3	1.78	0.48
1:A:114:TYR:HD1	1:A:114:TYR:O	1.97	0.48
1:A:324:GLU:HG3	1:A:353:PHE:HB2	1.95	0.48
1:A:136:VAL:CG1	1:A:146:PHE:CE2	2.97	0.48
1:B:380:ALA:O	1:B:384:TYR:HD2	1.96	0.48
1:A:325:ARG:HE	1:A:347:ARG:HA	1.78	0.48
1:B:291:LEU:HD22	1:B:292:THR:H	1.78	0.48
1:A:244:GLU:OE1	1:A:244:GLU:CA	2.61	0.47
1:B:128:PHE:CE1	1:B:147:MET:HG3	2.50	0.47
1:B:194:ILE:CD1	1:B:195:PHE:N	2.75	0.47
1:B:341:LYS:O	1:B:341:LYS:HD2	2.13	0.47
1:A:136:VAL:CG1	1:A:146:PHE:HE2	2.28	0.47
1:A:147:MET:HG2	1:A:151:ASP:HB3	1.97	0.47
1:B:311:GLU:O	1:B:315:HIS:CD2	2.68	0.47
1:B:312:PHE:CZ	1:B:322:ILE:HG23	2.50	0.47
1:A:308:LEU:C	1:A:308:LEU:CD1	2.82	0.47
1:B:139:GLU:HA	1:B:140:PRO:C	2.35	0.47
1:A:308:LEU:CD1	1:A:361:PHE:CE1	2.88	0.47
1:A:324:GLU:H	1:A:324:GLU:HG2	1.35	0.47
1:A:216:LEU:CG	1:A:303:LEU:HD13	2.45	0.47
1:A:240:MET:O	1:A:244:GLU:HB2	2.15	0.47
1:A:283:PHE:O	1:A:287:LEU:HA	2.14	0.47
1:B:157:THR:CG2	1:B:314:ARG:HH12	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PRO:HB3	1:B:210:ILE:HD11	1.97	0.46
1:A:401:ARG:CD	1:A:407:GLU:OE1	2.59	0.46
1:B:123:THR:O	1:B:125:ASP:N	2.49	0.46
1:B:302:LYS:HE2	1:B:306:ASP:OD1	2.16	0.46
1:B:399:VAL:HG12	4:B:505:MPD:O4	2.16	0.46
1:A:362:GLN:NE2	1:A:362:GLN:HA	2.29	0.46
1:B:250:ILE:C	1:B:252:SER:H	2.19	0.45
1:B:308:LEU:HD13	1:B:361:PHE:HE1	1.81	0.45
1:A:375:ASN:ND2	1:A:438:LYS:CG	2.80	0.45
1:A:300:GLN:O	1:A:304:GLN:HG3	2.17	0.45
1:A:308:LEU:CD1	1:A:361:PHE:HE1	2.26	0.45
1:B:292:THR:HG23	1:B:294:LYS:H	1.81	0.45
1:B:440:ARG:C	1:B:442:MET:N	2.68	0.45
1:B:157:THR:CB	1:B:314:ARG:HH12	2.29	0.45
1:A:240:MET:HG2	1:A:287:LEU:HB3	1.99	0.44
1:A:172:ILE:O	1:A:172:ILE:CG2	2.65	0.44
1:B:291:LEU:HD22	1:B:292:THR:N	2.32	0.44
1:A:153:VAL:CG2	1:A:310:LEU:HD23	2.48	0.44
1:A:324:GLU:OE1	1:A:411:HIS:CE1	2.71	0.44
1:B:134:LEU:HD12	1:B:134:LEU:HA	1.77	0.44
1:B:153:VAL:HG21	1:B:310:LEU:CB	2.48	0.44
1:B:368:PHE:HA	1:B:371:LEU:HD12	1.98	0.44
1:B:380:ALA:O	1:B:384:TYR:CD2	2.69	0.44
1:A:172:ILE:HG23	1:A:173:ILE:O	2.17	0.44
1:B:123:THR:C	1:B:125:ASP:N	2.71	0.44
1:B:374:ILE:HD12	1:B:377:VAL:HG21	1.99	0.44
1:A:114:TYR:C	1:A:114:TYR:HD1	2.21	0.44
1:B:134:LEU:HD11	1:B:168:LEU:HB2	1.99	0.44
1:B:337:VAL:CG1	1:B:338:GLN:N	2.81	0.43
1:B:168:LEU:N	1:B:168:LEU:CD1	2.79	0.43
1:A:225:ILE:O	1:A:228:LYS:N	2.52	0.43
1:A:167:GLY:CA	5:A:610:HOH:O	2.67	0.43
1:B:149:PRO:HD3	1:B:202:GLY:O	2.19	0.43
1:A:325:ARG:CB	1:A:350:LYS:HD2	2.47	0.43
1:B:305:HIS:CD2	1:B:365:GLU:OE2	2.71	0.43
1:B:324:GLU:HG2	1:B:353:PHE:CD2	2.54	0.43
1:A:115:GLU:HG2	1:A:130:TYR:OH	2.19	0.43
1:B:209:TYR:O	1:B:213:THR:HG23	2.19	0.43
1:B:310:LEU:HD12	1:B:310:LEU:HA	1.83	0.43
1:B:342:LEU:HD23	1:B:422:CYS:SG	2.59	0.43
1:B:345:MET:HA	1:B:345:MET:HE2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:421:ASP:OD2	1:B:426:GLY:N	2.50	0.43
1:A:227:PHE:CZ	1:A:238:VAL:HG23	2.54	0.43
1:B:374:ILE:HG21	1:B:437:MET:HB3	2.00	0.43
1:A:203:LEU:HD23	1:A:203:LEU:HA	1.83	0.42
1:A:303:LEU:O	1:A:303:LEU:HD22	2.18	0.42
4:B:504:MPD:H4	4:B:504:MPD:H12	1.68	0.42
1:A:153:VAL:HG21	1:A:310:LEU:HD23	2.00	0.42
1:A:304:GLN:HE22	1:A:372:LYS:HE3	1.84	0.42
1:A:369:THR:O	1:A:372:LYS:HB3	2.19	0.42
1:B:165:HIS:HA	1:B:166:LEU:HD12	2.01	0.42
1:B:134:LEU:HD11	1:B:168:LEU:HD13	1.96	0.42
1:B:381:LEU:C	1:B:383:PHE:N	2.70	0.42
1:A:303:LEU:HD23	1:A:303:LEU:HA	1.86	0.42
1:B:382:SER:OG	1:B:387:ALA:HA	2.20	0.42
1:A:119:ARG:HH11	1:A:119:ARG:HD3	1.70	0.41
1:A:205:SER:O	1:A:208:ASP:HB2	2.20	0.41
1:B:121:TYR:O	1:B:122:SER:C	2.57	0.41
1:B:223:PHE:CE1	4:B:503:MPD:H31	2.55	0.41
1:A:136:VAL:HG13	1:A:144:GLU:CG	2.50	0.41
1:A:395:THR:O	1:A:399:VAL:CG2	2.67	0.41
1:A:375:ASN:ND2	1:A:438:LYS:HG3	2.35	0.41
1:B:367:PHE:CZ	1:B:416:VAL:HG21	2.55	0.41
1:B:401:ARG:O	1:B:405:LYS:HA	2.19	0.41
1:B:122:SER:O	1:B:123:THR:O	2.39	0.41
1:B:135:LYS:HE2	1:B:135:LYS:HB2	1.57	0.41
1:B:166:LEU:N	1:B:166:LEU:CD1	2.77	0.41
1:B:384:TYR:CD2	1:B:384:TYR:N	2.87	0.41
1:B:292:THR:HG23	1:B:294:LYS:N	2.36	0.41
1:B:441:LEU:O	1:B:442:MET:C	2.58	0.41
1:A:229:MET:HG3	1:A:230:PHE:N	2.36	0.41
1:B:250:ILE:O	1:B:252:SER:N	2.47	0.40
1:B:355:GLU:O	1:B:356:GLY:O	2.39	0.40
1:A:342:LEU:HA	1:A:345:MET:HB2	2.03	0.40
1:B:137:ILE:CG2	1:B:139:GLU:HG3	2.51	0.40
1:B:171:TYR:HE2	1:B:173:ILE:CD1	2.28	0.40
1:A:313:GLU:C	1:A:315:HIS:N	2.74	0.40
1:B:210:ILE:HD13	1:B:210:ILE:HA	1.91	0.40
1:B:138:SER:O	1:B:139:GLU:C	2.58	0.40
1:B:352:HIS:HD2	1:B:353:PHE:CE2	2.39	0.40
1:B:382:SER:HA	1:B:387:ALA:HB2	2.02	0.40
4:B:503:MPD:H12	4:B:503:MPD:H4	1.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:SER:O	1:A:139:GLU:C	2.60	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	282/351 (80%)	253 (90%)	25 (9%)	4 (1%)	11 28
1	B	275/351 (78%)	242 (88%)	26 (10%)	7 (2%)	5 14
All	All	557/702 (79%)	495 (89%)	51 (9%)	11 (2%)	7 19

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	165	HIS
1	A	356	GLY
1	B	356	GLY
1	B	382	SER
1	A	231	ASP
1	B	141	GLY
1	B	441	LEU
1	B	251	ARG
1	A	251	ARG
1	A	194	ILE
1	B	124	PRO

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	245/311 (79%)	212 (86%)	33 (14%)	4 9
1	B	237/311 (76%)	213 (90%)	24 (10%)	7 17
All	All	482/622 (78%)	425 (88%)	57 (12%)	5 12

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	LYS
1	A	114	TYR
1	A	122	SER
1	A	129	ARG
1	A	134	LEU
1	A	136	VAL
1	A	138	SER
1	A	144	GLU
1	A	155	SER
1	A	157	THR
1	A	166	LEU
1	A	170	GLN
1	A	171	TYR
1	A	172	ILE
1	A	173	ILE
1	A	197	THR
1	A	213	THR
1	A	225	ILE
1	A	229	MET
1	A	240	MET
1	A	244	GLU
1	A	250	ILE
1	A	291	LEU
1	A	303	LEU
1	A	308	LEU
1	A	324	GLU
1	A	339	SER
1	A	346	GLN
1	A	357	LYS
1	A	394	VAL
1	A	399	VAL
1	A	403	VAL
1	A	441	LEU

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Mol	Chain	Res	Type
1	B	134	LEU
1	B	166	LEU
1	B	168	LEU
1	B	169	ASP
1	B	173	ILE
1	B	196	TYR
1	B	225	ILE
1	B	229	MET
1	B	245	GLN
1	B	291	LEU
1	B	292	THR
1	B	303	LEU
1	B	308	LEU
1	B	309	LYS
1	B	310	LEU
1	B	318	VAL
1	B	346	GLN
1	B	347	ARG
1	B	378	ASP
1	B	390	SER
1	B	393	LYS
1	B	432	GLU
1	B	437	MET
1	B	440	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	A	220	GLN
1	A	300	GLN
1	A	305	HIS
1	A	315	HIS
1	A	326	GLN
1	A	346	GLN
1	A	362	GLN
1	A	375	ASN
1	A	398	GLN
1	B	220	GLN
1	B	245	GLN
1	B	305	HIS
1	B	315	HIS

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Mol	Chain	Res	Type
1	B	326	GLN
1	B	352	HIS
1	B	411	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)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
4	MPD	B	503	-	7,7,7	0.34	0	9,10,10	0.34	0
4	MPD	B	505	-	7,7,7	0.27	0	9,10,10	0.33	0
4	MPD	B	504	-	7,7,7	0.36	0	9,10,10	0.45	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	MPD	B	503	-	-	4/5/5/5	-
4	MPD	B	505	-	-	3/5/5/5	-
4	MPD	B	504	-	-	5/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	503	MPD	C1-C2-C3-C4
4	B	505	MPD	O2-C2-C3-C4
4	B	504	MPD	O2-C2-C3-C4
4	B	503	MPD	CM-C2-C3-C4
4	B	504	MPD	C1-C2-C3-C4
4	B	504	MPD	CM-C2-C3-C4
4	B	505	MPD	C1-C2-C3-C4
4	B	505	MPD	CM-C2-C3-C4
4	B	503	MPD	O2-C2-C3-C4
4	B	503	MPD	C2-C3-C4-C5
4	B	504	MPD	C2-C3-C4-C5
4	B	504	MPD	C2-C3-C4-O4

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	MPD	2	0
4	B	505	MPD	7	0
4	B	504	MPD	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	290/351 (82%)	-0.30	5 (1%)	70	72	31, 58, 106, 123	0
1	B	283/351 (80%)	-0.29	2 (0%)	87	89	26, 58, 111, 155	0
All	All	573/702 (81%)	-0.30	7 (1%)	79	80	26, 58, 108, 155	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	HIS	2.8
1	B	352	HIS	2.5
1	A	110	LYS	2.4
1	A	199	GLY	2.3
1	B	340	LYS	2.3
1	A	286	ASP	2.0
1	A	246	VAL	2.0

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 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
3	CL	A	503	1/1	0.83	1.18	138,138,138,138	1
4	MPD	B	503	8/8	0.92	0.20	52,69,80,87	0
4	MPD	B	505	8/8	0.93	0.40	72,84,89,91	0
4	MPD	B	504	8/8	0.94	0.31	58,68,80,82	0
3	CL	B	506	1/1	0.95	0.17	68,68,68,68	0
2	CA	A	502	1/1	0.98	0.10	52,52,52,52	0
2	CA	B	501	1/1	0.98	0.22	58,58,58,58	0
2	CA	B	502	1/1	0.98	0.10	66,66,66,66	0
2	CA	A	501	1/1	0.98	0.15	59,59,59,59	0

6.5 Other polymers (i)

There are no such residues in this entry.