



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:28 AM GMT

PDB ID : 3M2R
Title : Structural Insight into Methyl-Coenzyme M Reductase Chemistry using Coenzyme B Analogues
Authors : Cedervall, P.E.; Dey, M.; Ragsdale, S.W.; Wilmot, C.M.
Deposited on : 2010-03-08
Resolution : 1.30 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

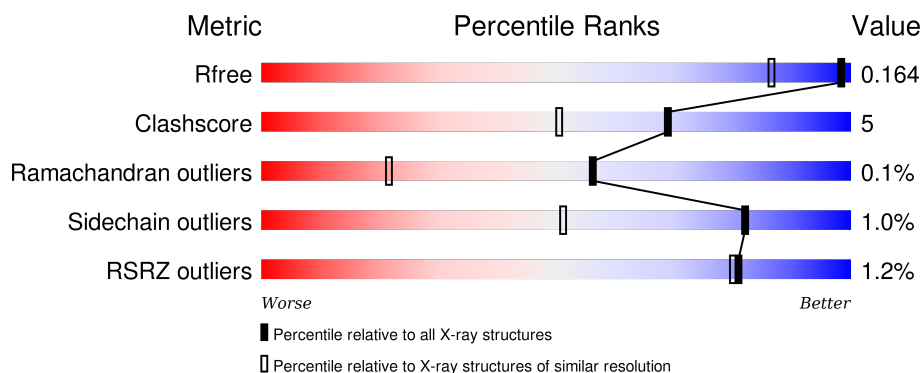
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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}	91344	1475 (1.34-1.26)
Clashscore	102246	1031 (1.32-1.28)
Ramachandran outliers	100387	1504 (1.34-1.26)
Sidechain outliers	100360	1503 (1.34-1.26)
RSRZ outliers	91569	1476 (1.34-1.26)

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	549	<div> <div></div> <div>85%13%.</div> </div>
1	D	549	<div> <div>%</div> <div>83%15%.</div> </div>
2	B	442	<div> <div></div> <div>83%15%.</div> </div>
2	E	442	<div> <div>%</div> <div>83%16%.</div> </div>
3	C	248	<div> <div>4%</div> <div>71%27%..</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	248	

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	MG	C	250	-	-	-	X
4	MG	F	250	-	-	-	X
5	F43	A	1	X	-	-	-
5	F43	D	552	X	-	-	-
6	TP7	A	554[A]	X	-	-	-
6	TP7	D	553[A]	X	-	-	-
9	EDO	F	251	-	-	-	X

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 22783 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 Methyl-coenzyme M reductase I subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	29	0
			4438	2809	731	878	20			
1	D	548	Total	C	N	O	S	0	30	0
			4426	2813	730	863	20			

- Molecule 2 is a protein called Methyl-coenzyme M reductase I subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	442	Total	C	N	O	S	0	24	0
			3456	2205	559	670	22			
2	E	442	Total	C	N	O	S	0	31	0
			3509	2240	569	677	23			

- Molecule 3 is a protein called Methyl-coenzyme M reductase I subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	246	Total	C	N	O	S	0	20	0
			2135	1320	375	426	14			
3	F	246	Total	C	N	O	S	0	22	0
			2121	1316	371	419	15			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

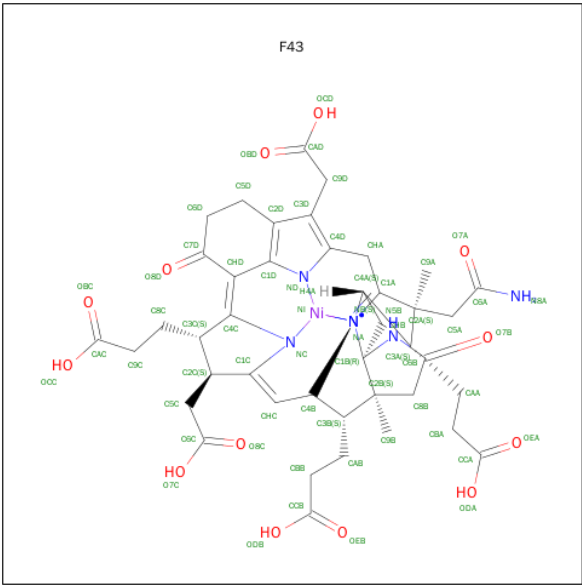
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	2	Total	Mg	0	0
			2	2		
4	E	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		

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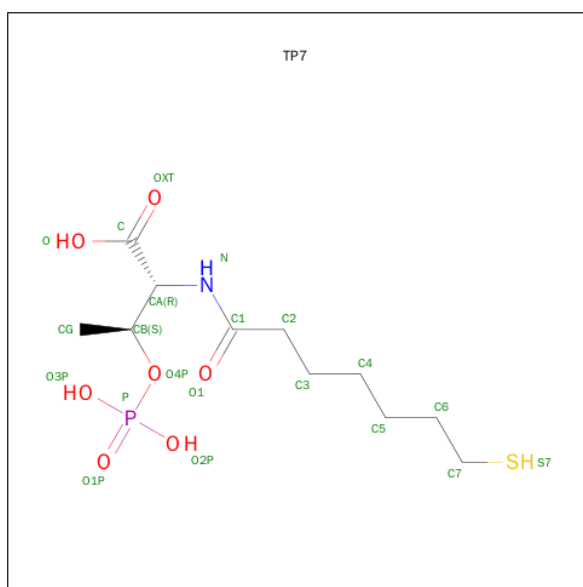
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Mg	0	2
			3	3		
4	F	1	Total	Mg	0	0
			1	1		

- Molecule 5 is FACTOR 430 (three-letter code: F43) (formula: C₄₂H₄₉N₆NiO₁₃).



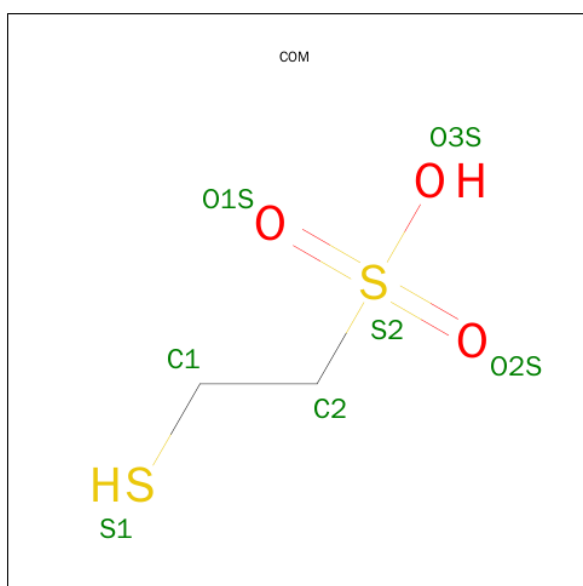
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	Ni	O	0	0
			62	42	6	1	13		
5	D	1	Total	C	N	Ni	O	0	0
			62	42	6	1	13		

- Molecule 6 is COENZYME B (three-letter code: TP7) (formula: C₁₁H₂₂NO₇PS).



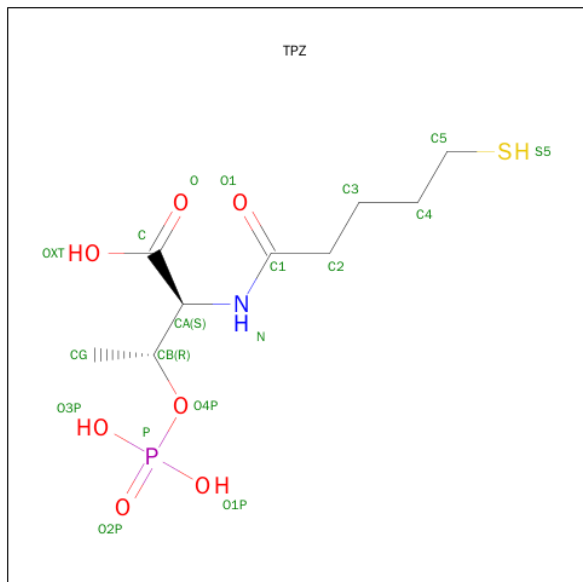
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	S	0	1
			21	11	1	7	1	1		
6	D	1	Total	C	N	O	P	S	0	1
			21	11	1	7	1	1		

- Molecule 7 is 1-THIOETHANESULFONIC ACID (three-letter code: COM) (formula: $C_2H_6O_3S_2$).



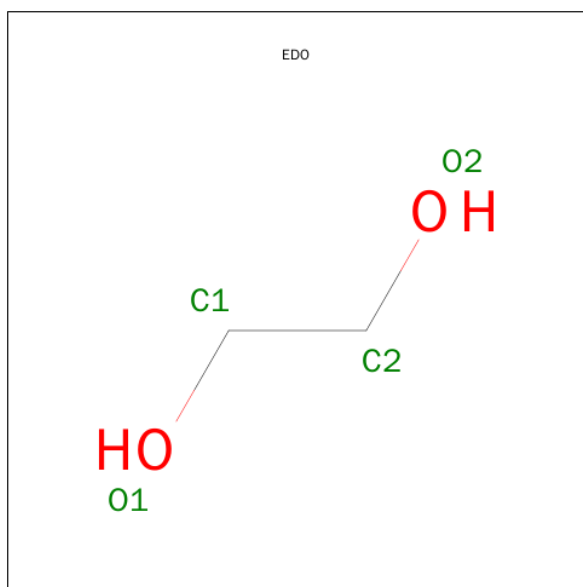
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	S	0	0
			7	2	3	2		
7	D	1	Total	C	O	S	0	0
			7	2	3	2		

- Molecule 8 is O-PHOSPHONO-N-(5-SULFANYLPENTANOYL)-L-THREONINE (three-letter code: TPZ) (formula: $C_9H_{18}NO_7PS$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	A	1	Total	C	N	O	P	S	0	1
			19	9	1	7	1	1		
8	D	1	Total	C	N	O	P	S	0	1
			19	9	1	7	1	1		

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

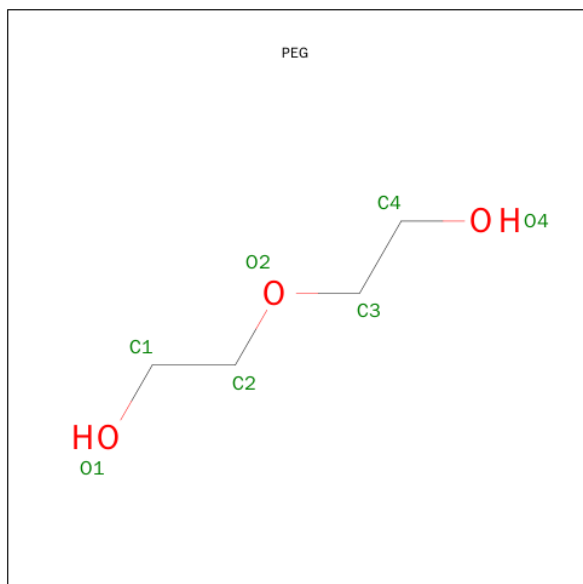


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	2	2		
9	C	1	Total	C	O	0	0
			4	2	2		
9	D	1	Total	C	O	0	0
			4	2	2		
9	F	1	Total	C	O	0	0
			4	2	2		
9	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Zn	0	0
			1	1		

- Molecule 11 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).

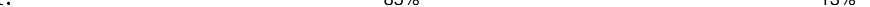


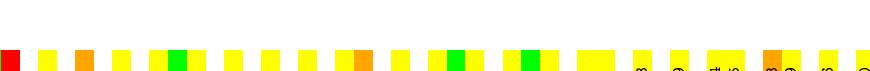
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	C	1	Total	C	O	0	0
			7	4	3		


- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	513	Total 520	O 520	0	18
12	B	451	Total 461	O 461	0	17
12	C	256	Total 259	O 259	0	5
12	D	520	Total 526	O 526	0	15
12	E	418	Total 423	O 423	0	16
12	F	250	Total 254	O 254	0	8

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.

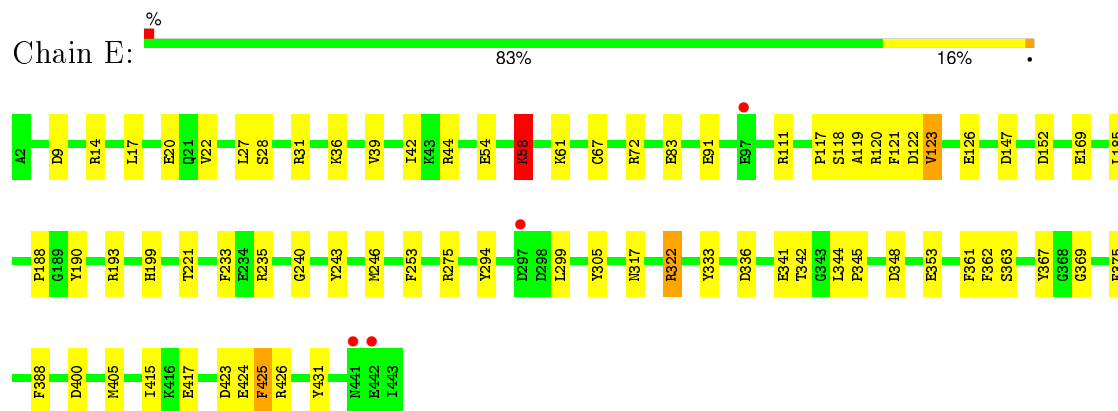
- Chain A: 



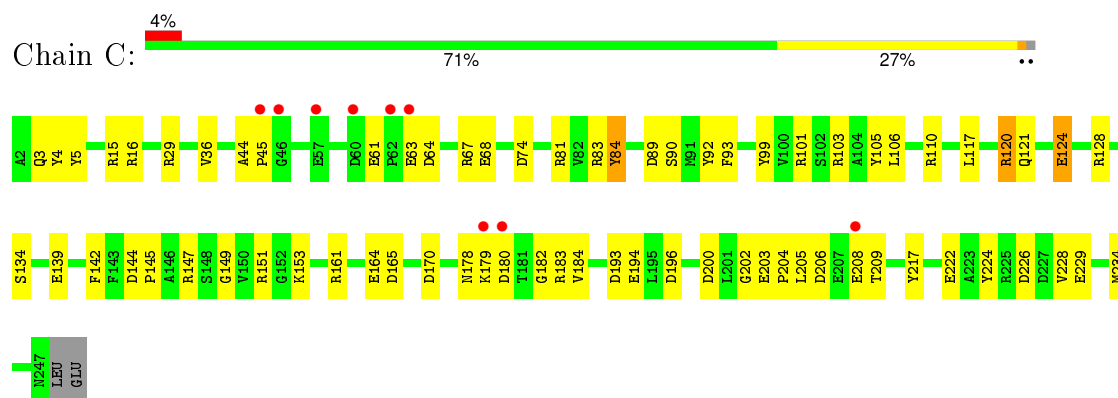
- Chain D: 

- Chain B:
-
- 83% 15%
- | Label | Category |
|-------|----------|
| A2 | Green |
| K3 | Orange |
| V8 | Yellow |
| D12 | Yellow |
| D13 | Green |
| R14 | Yellow |
| G15 | Yellow |
| L27 | Yellow |
| R31 | Yellow |
| K36 | Yellow |
| S37 | Green |
| I38 | Green |
| V39 | Yellow |
| R44 | Yellow |
| E54 | Yellow |
| K68 | Red |
| K61 | Yellow |
| G67 | Yellow |
| R72 | Orange |
| D75 | Yellow |
| L76 | Green |
| D77 | Yellow |
| E97 | Yellow |
| D98 | Green |
| D99 | Yellow |
| R111 | Yellow |
| A112 | Green |
| L113 | Yellow |
| A119 | Yellow |
| R120 | Yellow |
| F121 | Green |
| D122 | Green |
| V123 | Yellow |
| D147 | Yellow |
| D152 | Yellow |
| D180 | Yellow |
| L185 | Yellow |
| P188 | Yellow |
| P192 | Yellow |
| M196 | Yellow |
| H199 | Yellow |
| T221 | Yellow |
| E234 | Yellow |
| G240 | Yellow |
| Y243 | Yellow |
| K246 | Yellow |
| K257 | Yellow |
| K261 | Orange |
| E262 | Yellow |
| E274 | Yellow |
| E278 | Yellow |
| K283 | Yellow |
| K286 | Yellow |
| E287 | Green |
| L288 | Yellow |
| T289 | Green |
| D290 | Yellow |
| Y291 | Yellow |
| D297 | Orange |
| D298 | Green |
| L299 | Yellow |
| Y305 | Yellow |
| R322 | Orange |
| Y333 | Red |
| E339 | Yellow |
| T342 | Yellow |
| G343 | Green |
| L344 | Yellow |
| F345 | Green |
| S346 | Yellow |
| E353 | Yellow |
| F359 | Yellow |
| F362 | Yellow |
| G369 | Yellow |
| M395 | Yellow |

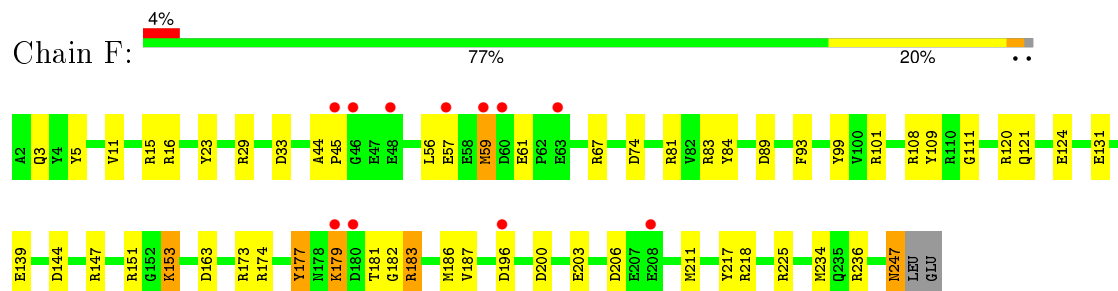
- Molecule 2: Methyl-coenzyme M reductase I subunit beta



- Molecule 3: Methyl-coenzyme M reductase I subunit gamma



- Molecule 3: Methyl-coenzyme M reductase I subunit gamma



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.02Å 118.26Å 122.39Å 90.00° 91.84° 90.00°	Depositor
Resolution (Å)	20.49 – 1.30 20.15 – 1.30	Depositor EDS
% Data completeness (in resolution range)	97.1 (20.49-1.30) 97.1 (20.15-1.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 1.30Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.143 , 0.166 0.142 , 0.164	Depositor DCC
R_{free} test set	27777 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	10.4	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.7	EDS
Estimated twinning fraction	0.000 for -h,l,k 0.006 for -h,-l,-k 0.012 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 553593 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	22783	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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: ZN, PEG, COM, MG, F43, MGN, TP7, AGM, EDO, GL3, SMC, MHS, TPZ

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	1.51	20/4536 (0.4%)	1.46	52/6160 (0.8%)
1	D	1.58	36/4544 (0.8%)	1.47	55/6168 (0.9%)
2	B	1.53	15/3573 (0.4%)	1.44	39/4834 (0.8%)
2	E	1.54	24/3632 (0.7%)	1.41	37/4910 (0.8%)
3	C	1.70	23/2194 (1.0%)	1.64	36/2952 (1.2%)
3	F	1.73	16/2203 (0.7%)	1.69	41/2962 (1.4%)
All	All	1.58	134/20682 (0.6%)	1.49	260/27986 (0.9%)

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	3
1	D	1	1
2	B	0	2
2	E	0	2
All	All	2	8

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	259	GLU	CG-CD	10.02	1.67	1.51
3	F	139	GLU	CD-OE2	9.89	1.36	1.25
1	D	355[A]	GLU	CB-CG	-9.43	1.34	1.52
1	D	355[B]	GLU	CB-CG	-9.43	1.34	1.52
2	E	353	GLU	CG-CD	9.28	1.65	1.51

The worst 5 of 260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	44	ARG	NE-CZ-NH1	18.56	129.58	120.30
3	C	147	ARG	NE-CZ-NH1	14.70	127.65	120.30
3	F	147	ARG	NE-CZ-NH1	13.38	126.99	120.30
3	F	206	ASP	CB-CG-OD1	12.76	129.78	118.30
3	C	120	ARG	NE-CZ-NH1	12.10	126.35	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	450	ASP	CA
1	D	450	ASP	CA

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	480	MET	Peptide
1	A	499	ARG	Sidechain
1	A	51	ARG	Sidechain
2	B	333	TYR	Sidechain
2	B	72	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	4438	0	4236	43	0
1	D	4426	0	4281	34	0
2	B	3456	0	3501	36	0
2	E	3509	0	3569	33	0
3	C	2135	0	2060	35	0
3	F	2121	0	2081	34	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	2	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	62	0	43	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	62	0	43	1	0
6	A	21	0	19	1	0
6	D	21	0	19	1	0
7	A	7	0	4	0	0
7	D	7	0	5	0	0
8	A	19	0	15	0	0
8	D	19	0	15	0	0
9	A	4	0	6	0	0
9	C	4	0	6	0	0
9	D	4	0	6	0	0
9	F	8	0	12	1	0
10	A	1	0	0	0	0
11	C	7	0	10	0	0
12	A	520	0	0	14	0
12	B	461	0	0	5	0
12	C	259	0	0	9	0
12	D	526	0	0	7	0
12	E	423	0	0	14	0
12	F	254	0	0	5	0
All	All	22783	0	19931	185	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 5.

The worst 5 of 185 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)
3:F:181[A]:THR:HB	3:F:183[A]:ARG:CD	1.70	1.20
2:E:91[B]:GLU:HG2	12:E:3974:HOH:O	1.43	1.17
3:F:181[A]:THR:HB	3:F:183[A]:ARG:CG	1.85	1.05
3:F:181[A]:THR:CB	3:F:183[A]:ARG:HG3	1.92	0.99
1:D:24[A]:THR:HG23	12:F:1497:HOH:O	1.65	0.96

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	570/549 (104%)	550 (96%)	19 (3%)	1 (0%)	52	20
1	D	571/549 (104%)	556 (97%)	14 (2%)	1 (0%)	52	20
2	B	465/442 (105%)	456 (98%)	9 (2%)	0	100	100
2	E	472/442 (107%)	461 (98%)	11 (2%)	0	100	100
3	C	264/248 (106%)	256 (97%)	8 (3%)	0	100	100
3	F	266/248 (107%)	261 (98%)	5 (2%)	0	100	100
All	All	2608/2478 (105%)	2540 (97%)	66 (2%)	2 (0%)	56	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	325	SER
1	D	325	SER

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	462/434 (106%)	456 (99%)	6 (1%)	76	38
1	D	462/434 (106%)	456 (99%)	6 (1%)	76	38
2	B	366/341 (107%)	364 (100%)	2 (0%)	92	72
2	E	372/341 (109%)	371 (100%)	1 (0%)	94	79
3	C	233/216 (108%)	231 (99%)	2 (1%)	84	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	235/216 (109%)	229 (97%)	6 (3%)	54	12
All	All	2130/1982 (108%)	2107 (99%)	23 (1%)	82	47

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	36[A]	ARG
1	D	352[A]	GLU
3	F	186	MET
1	D	36[B]	ARG
1	D	352[B]	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	111	HIS
3	F	247	ASN
2	E	318	GLN
1	A	241	GLN
3	F	121	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

10 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	MHS	A	257	1	8,11,12	1.69	1 (12%)	7,14,16	3.63	4 (57%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	AGM	A	271	1	7,11,12	0.70	0	5,13,15	1.61	2 (40%)
1	MGN	A	400	1	6,9,10	0.98	0	6,12,14	0.69	0
1	GL3	A	445	1	3,3,4	2.02	1 (33%)	2,2,4	0.48	0
1	SMC	A	452	1	5,6,7	0.89	0	2,6,8	1.84	1 (50%)
1	MHS	D	257	1	8,11,12	1.36	1 (12%)	7,14,16	4.09	4 (57%)
1	AGM	D	271	1	7,11,12	1.30	1 (14%)	5,13,15	1.48	1 (20%)
1	MGN	D	400	1	6,9,10	1.69	1 (16%)	6,12,14	0.67	0
1	GL3	D	445	1	3,3,4	2.11	1 (33%)	2,2,4	1.28	0
1	SMC	D	452	1	5,6,7	1.10	0	2,6,8	2.20	1 (50%)

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	MHS	A	257	1	-	0/4/6/8	0/1/1/1
1	AGM	A	271	1	-	0/7/11/13	0/0/0/0
1	MGN	A	400	1	-	0/6/9/12	0/0/0/0
1	GL3	A	445	1	-	0/1/1/2	0/0/0/0
1	SMC	A	452	1	-	0/3/5/7	0/0/0/0
1	MHS	D	257	1	-	0/4/6/8	0/1/1/1
1	AGM	D	271	1	-	0/7/11/13	0/0/0/0
1	MGN	D	400	1	-	0/6/9/12	0/0/0/0
1	GL3	D	445	1	-	0/1/1/2	0/0/0/0
1	SMC	D	452	1	-	0/3/5/7	0/0/0/0

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	445	GL3	C-S	-3.51	1.68	1.80
1	D	400	MGN	CB1-CA	-3.29	1.51	1.55
1	A	445	GL3	C-S	-3.21	1.69	1.80
1	D	257	MHS	CB-CG	2.48	1.54	1.50
1	D	271	AGM	CB-CA	2.52	1.56	1.53

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	257	MHS	NE2-CE1-ND1	-7.98	101.48	112.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	MHS	NE2-CE1-ND1	-7.56	102.05	112.28
1	A	257	MHS	O-C-CA	-3.93	115.26	125.49
1	D	452	SMC	O-C-CA	-2.82	118.14	125.49
1	D	257	MHS	O-C-CA	-2.67	118.55	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	271	AGM	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 10 are monoatomic - leaving 14 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	$\# Z > 2$
5	F43	A	1	1,7	42,71,71	3.32	10 (23%)	35,118,118	2.03	8 (22%)
6	TP7	A	554[A]	-	16,20,20	0.69	0	16,26,26	1.50	2 (12%)
7	COM	A	555	5	5,6,6	0.91	0	5,8,8	2.54	3 (60%)
8	TPZ	A	556[B]	-	14,18,18	1.01	0	14,24,24	1.35	2 (14%)
9	EDO	A	557	-	3,3,3	0.53	0	2,2,2	0.41	0
11	PEG	C	1	-	6,6,6	0.54	0	5,5,5	1.26	1 (20%)
9	EDO	C	251	-	3,3,3	0.62	0	2,2,2	1.01	0
5	F43	D	552	1,7	42,71,71	3.25	15 (35%)	35,118,118	2.02	8 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	TP7	D	553[A]	-	16,20,20	0.62	0	16,26,26	1.23	2 (12%)
7	COM	D	554	5	5,6,6	1.47	1 (20%)	5,8,8	2.38	3 (60%)
8	TPZ	D	555[B]	-	14,18,18	1.09	2 (14%)	14,24,24	1.36	2 (14%)
9	EDO	D	556	-	3,3,3	0.56	0	2,2,2	0.59	0
9	EDO	F	251	-	3,3,3	0.67	0	2,2,2	0.46	0
9	EDO	F	252	-	3,3,3	0.67	0	2,2,2	0.28	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
5	F43	A	1	1,7	1/1/25/27	0/18/165/165	0/0/10/10
6	TP7	A	554[A]	-	1/1/5/6	0/20/24/24	0/0/0/0
7	COM	A	555	5	-	0/4/4/4	0/0/0/0
8	TPZ	A	556[B]	-	-	0/18/22/22	0/0/0/0
9	EDO	A	557	-	-	0/1/1/1	0/0/0/0
11	PEG	C	1	-	-	0/4/4/4	0/0/0/0
9	EDO	C	251	-	-	0/1/1/1	0/0/0/0
5	F43	D	552	1,7	1/1/25/27	0/18/165/165	0/0/10/10
6	TP7	D	553[A]	-	1/1/5/6	0/20/24/24	0/0/0/0
7	COM	D	554	5	-	0/4/4/4	0/0/0/0
8	TPZ	D	555[B]	-	-	0/18/22/22	0/0/0/0
9	EDO	D	556	-	-	0/1/1/1	0/0/0/0
9	EDO	F	251	-	-	0/1/1/1	0/0/0/0
9	EDO	F	252	-	-	0/1/1/1	0/0/0/0

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1	F43	C4B-NB	-13.74	1.28	1.49
5	D	552	F43	C4B-NB	-9.40	1.35	1.49
5	D	552	F43	C1D-ND	-6.85	1.23	1.36
5	A	1	F43	C1D-ND	-3.29	1.30	1.36
5	D	552	F43	C6D-C7D	-3.21	1.46	1.50

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1	F43	C9D-C3D-C4D	-8.51	112.68	127.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	552	F43	C9D-C3D-C4D	-7.98	113.57	127.01
5	D	552	F43	C3C-C4C-CHD	-3.51	118.38	124.26
5	A	1	F43	C4A-NA-C1A	-3.43	104.78	108.21
7	A	555	COM	O3S-S2-O2S	-3.37	103.77	111.61

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	554[A]	TP7	C1
5	D	552	F43	C4B
6	D	553[A]	TP7	C1
5	A	1	F43	C4B

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1	F43	1	0
6	A	554[A]	TP7	1	0
5	D	552	F43	1	0
6	D	553[A]	TP7	1	0
9	F	251	EDO	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	543/549 (98%)	-0.47	1 (0%) 95 93	6, 9, 20, 34	0
1	D	543/549 (98%)	-0.46	4 (0%) 89 87	6, 9, 19, 37	0
2	B	442/442 (100%)	-0.49	1 (0%) 95 93	7, 11, 20, 37	0
2	E	442/442 (100%)	-0.41	4 (0%) 85 85	7, 11, 22, 38	0
3	C	246/248 (99%)	-0.21	9 (3%) 45 41	8, 14, 27, 42	0
3	F	246/248 (99%)	-0.14	11 (4%) 37 33	8, 14, 30, 51	0
All	All	2462/2478 (99%)	-0.40	30 (1%) 81 80	6, 11, 22, 51	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	60	ASP	6.9
1	D	549	ALA	6.3
3	F	45	PRO	5.0
3	C	60	ASP	4.7
2	E	441	ASN	4.5

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	MHS	D	257	11/12	0.97	0.05	-	8,9,11,13	0
1	SMC	D	452	7/8	0.99	0.06	-	6,7,8,9	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	SMC	A	452	7/8	0.99	0.05	-	6,7,8,9	0
1	GL3	A	445	4/5	0.99	0.06	-	6,7,7,7	0
1	AGM	A	271	12/13	0.98	0.05	-	5,6,6,7	0
1	MHS	A	257	11/12	0.97	0.05	-	8,9,12,15	0
1	MGN	D	400	10/11	0.98	0.05	-	6,7,7,8	0
1	AGM	D	271	12/13	0.97	0.07	-	5,6,7,8	0
1	MGN	A	400	10/11	0.98	0.05	-	6,7,9,9	0
1	GL3	D	445	4/5	1.00	0.05	-	5,6,6,7	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
9	EDO	F	251	4/4	0.87	0.19	25.25	32,32,34,35	0
4	MG	C	250	1/1	0.98	0.09	3.34	17,17,17,17	0
4	MG	F	250	1/1	0.98	0.10	3.01	15,15,15,15	0
4	MG	A	551	1/1	0.96	0.11	0.45	15,15,15,15	1
6	TP7	A	554[A]	21/21	0.98	0.06	0.04	4,7,10,21	21
5	F43	A	1	62/62	0.99	0.05	-0.08	5,7,9,11	0
6	TP7	D	553[A]	21/21	0.98	0.06	-0.44	5,7,9,23	21
8	TPZ	A	556[B]	19/19	0.98	0.05	-0.59	6,7,11,12	19
5	F43	D	552	62/62	0.99	0.05	-0.73	6,8,9,12	0
7	COM	A	555	7/7	0.99	0.05	-1.01	9,11,11,12	0
8	TPZ	D	555[B]	19/19	0.99	0.04	-1.46	6,7,11,12	19
7	COM	D	554	7/7	0.99	0.04	-1.60	7,9,11,11	0
10	ZN	A	558	1/1	0.99	0.03	-3.30	10,10,10,10	1
4	MG	D	551	1/1	0.99	0.18	-	19,19,19,19	0
4	MG	B	444	1/1	0.96	0.14	-	21,21,21,21	0
9	EDO	D	556	4/4	0.84	0.09	-	28,32,39,40	0
9	EDO	A	557	4/4	0.82	0.09	-	27,33,39,40	0
4	MG	D	1	1/1	0.98	0.08	-	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	EDO	C	251	4/4	0.86	0.15	-	34,35,36,40	0
4	MG	E	444	1/1	0.99	0.23	-	24,24,24,24	0
4	MG	A	552[A]	1/1	0.99	0.22	-	17,17,17,17	1
4	MG	A	553[B]	1/1	0.98	0.12	-	13,13,13,13	1
11	PEG	C	1	7/7	0.84	0.12	-	35,37,43,43	0
9	EDO	F	252	4/4	0.62	0.18	-	41,44,44,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.