



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2017 – 03:00 AM EDT

PDB ID : 3MOF
Title : The structure of rat cytosolic PEPCK mutant A467G in complex with oxalate and GTP
Authors : Johnson, T.A.; Holyoak, T.
Deposited on : unknown
Resolution : 1.75 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

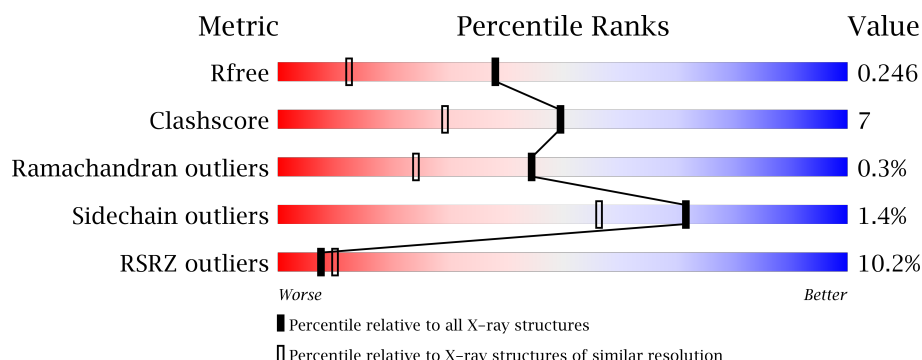
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	100719	1762 (1.76-1.76)
Clashscore	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)
RSRZ outliers	101464	1770 (1.76-1.76)

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	624	<div> <div>10%</div> <div>89%</div> <div>10%</div> </div>
1	B	624	<div> <div>11%</div> <div>89%</div> <div>10%</div> </div>

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
2	GTP	A	900[A]	-	-	-	X
2	GTP	A	900[B]	-	-	X	X
3	MN	A	700[A]	-	-	-	X
3	MN	A	700[B]	-	-	-	X
3	MN	A	800	-	-	-	X
3	MN	B	701	-	-	-	X
6	1PE	A	1201	-	-	-	X
7	EDO	A	3001	-	-	-	X
7	EDO	B	3000	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11021 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.

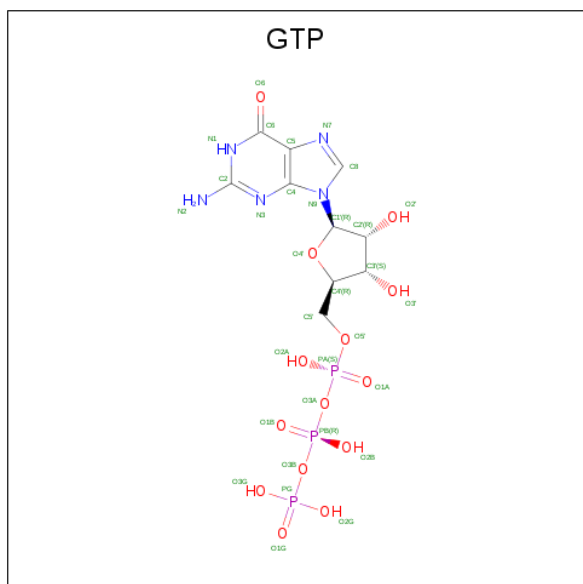
- Molecule 1 is a protein called Phosphoenolpyruvate carboxykinase, cytosolic [GTP].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	624	Total	C	N	O	S	0	21	0
			5009	3215	847	912	35			
1	B	616	Total	C	N	O	S	0	14	0
			4920	3155	836	895	34			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P07379
A	0	SER	-	EXPRESSION TAG	UNP P07379
A	467	GLY	ALA	ENGINEERED	UNP P07379
B	-1	GLY	-	EXPRESSION TAG	UNP P07379
B	0	SER	-	EXPRESSION TAG	UNP P07379
B	467	GLY	ALA	ENGINEERED	UNP P07379

- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

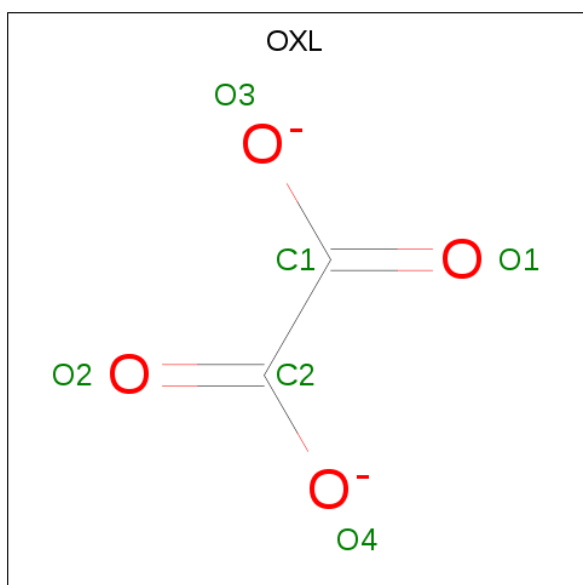


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
2	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mn	0	0
			2	2		
3	A	2	Total	Mn	0	1
			3	3		

- Molecule 4 is OXALATE ION (three-letter code: OXL) (formula: C₂O₄).



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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

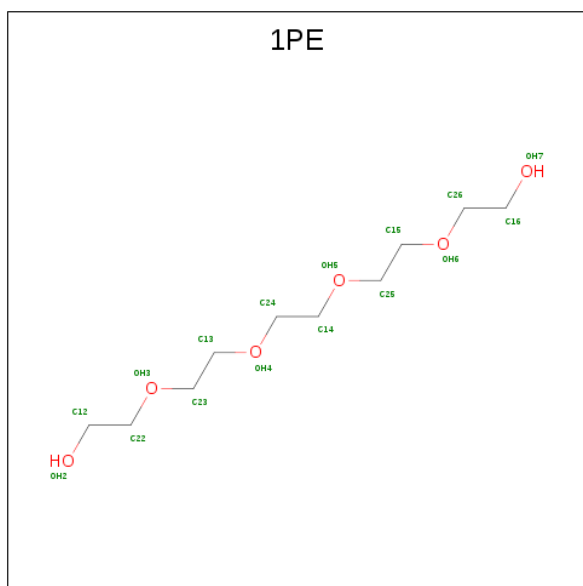
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		

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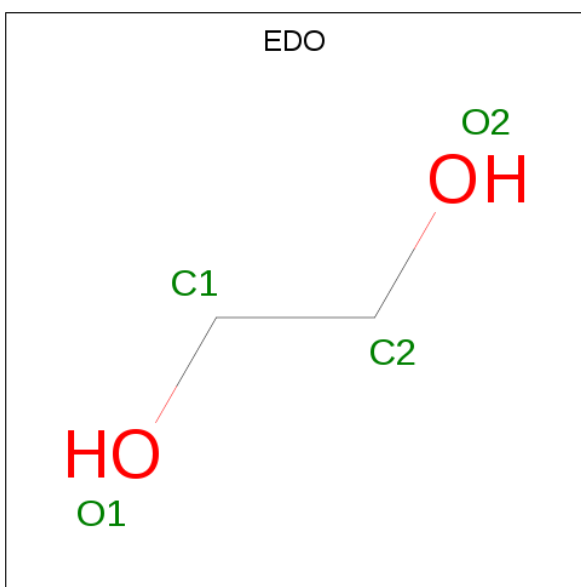
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		

- Molecule 6 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	5	3		
6	A	1	Total	C	O	0	0
			16	10	6		
6	B	1	Total	C	O	0	0
			16	10	6		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0

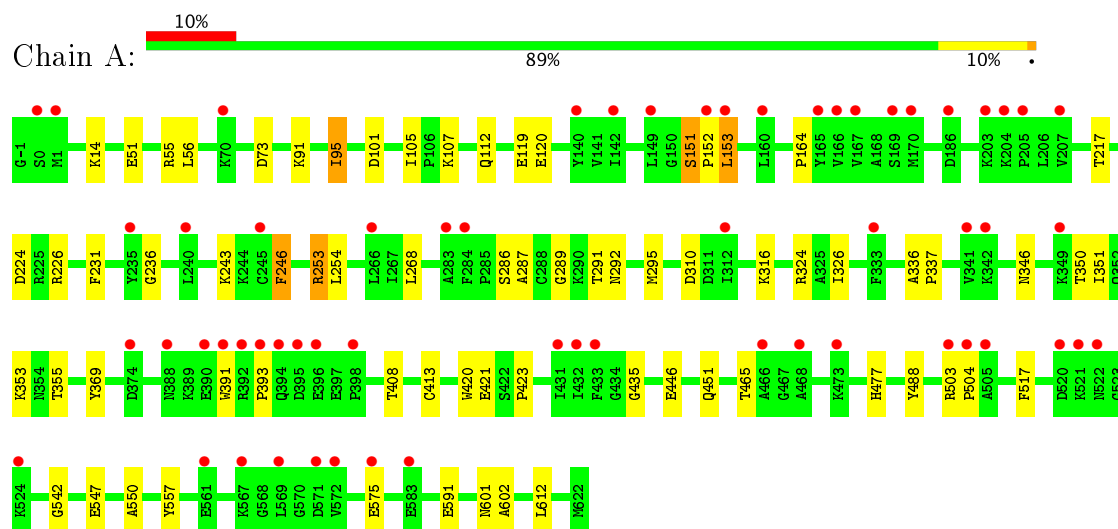
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	457	Total O 457 457	0	0
8	B	456	Total O 456 456	0	0

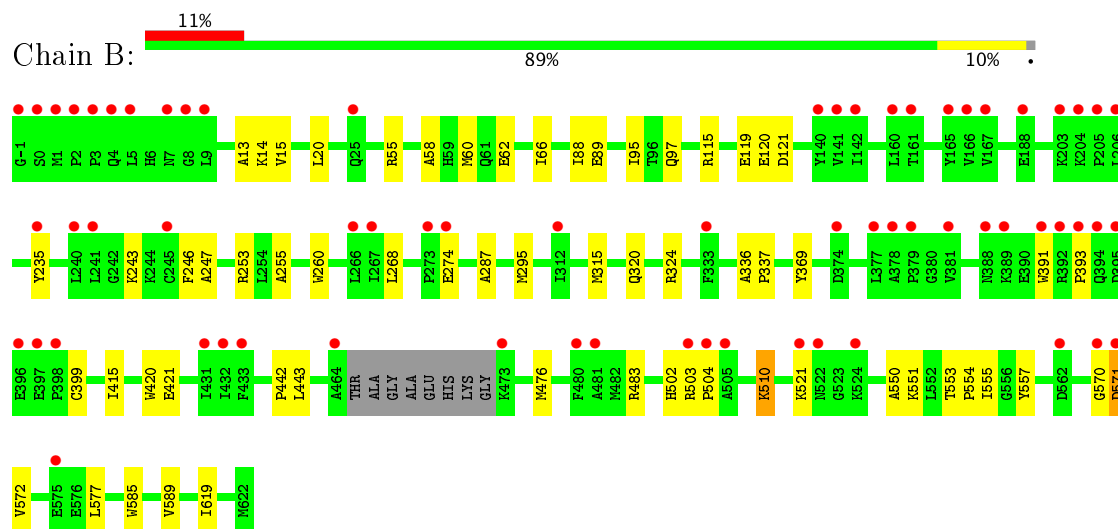
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Phosphoenolpyruvate carboxykinase, cytosolic [GTP]



- Molecule 1: Phosphoenolpyruvate carboxykinase, cytosolic [GTP]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.98 Å 119.60 Å 87.07 Å 90.00° 106.87° 90.00°	Depositor
Resolution (Å)	33.24 – 1.75 33.24 – 1.75	Depositor EDS
% Data completeness (in resolution range)	96.6 (33.24-1.75) 96.6 (33.24-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 1.75 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.179 , 0.228 0.201 , 0.246	Depositor DCC
R_{free} test set	5913 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	19.3	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11021	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 70.48 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.0993e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GTP, NA, MN, EDO, 1PE, OXL

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	0.74	0/5205	0.74	2/7048 (0.0%)
1	B	0.73	0/5091	0.72	0/6888
All	All	0.74	0/10296	0.73	2/13936 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	612	LEU	CB-CG-CD2	-5.80	101.14	111.00
1	A	95	ILE	CG1-CB-CG2	-5.18	100.00	111.40

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	5009	0	5005	77	1
1	B	4920	0	4911	55	0
2	A	64	0	24	13	0
2	B	32	0	12	1	0
3	A	3	0	0	1	0
3	B	2	0	0	0	0
4	A	6	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	24	0	30	5	0
6	B	16	0	22	2	0
7	A	12	0	18	0	0
7	B	12	0	18	1	0
8	A	457	0	0	13	0
8	B	456	0	0	13	1
All	All	11021	0	10040	135	1

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 7.

All (135) 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:A:900[B]:GTP:H1'	8:A:965:HOH:O	1.54	1.07
1:A:351:ILE:HG22	1:A:408[B]:THR:HG21	1.29	1.05
1:A:350[B]:THR:HG22	1:A:413:CYS:HA	1.50	0.91
1:A:152:PRO:HB2	1:A:153:LEU:HD13	1.50	0.90
1:A:153:LEU:HD23	1:A:326:ILE:HG21	1.54	0.90
1:A:151:SER:OG	1:A:153:LEU:HD22	1.76	0.84
1:A:292[A]:ASN:OD1	2:A:900[A]:GTP:C8	2.31	0.83
1:A:112:GLN:NE2	8:A:857:HOH:O	2.11	0.82
1:A:292[A]:ASN:OD1	2:A:900[A]:GTP:H8	1.62	0.82
1:B:589[A]:VAL:HG11	1:B:619[A]:ILE:HD12	1.62	0.80
1:A:153:LEU:HG	6:A:1200:1PE:OH3	1.82	0.79
1:B:55:ARG:HG2	1:B:55:ARG:HH11	1.47	0.79
1:B:89:GLU:OE1	1:B:483:ARG:NH1	2.15	0.79
3:A:700[B]:MN:MN	8:A:794:HOH:O	1.42	0.75
1:A:287:ALA:HA	2:A:900[B]:GTP:O3A	1.87	0.74
1:A:153:LEU:HD23	1:A:326:ILE:CG2	2.19	0.73
1:B:585:TRP:HB3	1:B:619[A]:ILE:HD13	1.72	0.72
1:B:503:ARG:HG2	1:B:504:PRO:HD2	1.72	0.71
1:A:56:LEU:HD11	1:A:164:PRO:HB3	1.71	0.71
1:A:224:ASP:HB3	8:A:909:HOH:O	1.90	0.70
1:B:89:GLU:CD	1:B:483:ARG:HH12	1.95	0.70
1:A:355:THR:OG1	1:A:408[B]:THR:HG22	1.93	0.69
1:B:476[A]:MET:CE	8:B:999:HOH:O	2.40	0.68
1:B:89:GLU:HG2	1:B:115[A]:ARG:HH11	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:510[B]:LYS:HE2	8:B:911:HOH:O	1.94	0.67
1:B:13:ALA:HB3	6:B:1300:1PE:H131	1.76	0.67
1:A:55:ARG:HH11	1:A:55:ARG:HG2	1.61	0.66
1:A:346:ASN:O	1:A:350[B]:THR:HG23	1.97	0.65
1:A:153:LEU:HB3	6:A:1200:1PE:H131	1.80	0.64
1:A:503:ARG:HB2	1:A:504:PRO:CD	2.28	0.63
1:A:351:ILE:HG22	1:A:408[B]:THR:CG2	2.18	0.63
1:B:570:GLY:O	1:B:572:VAL:N	2.29	0.63
1:A:503:ARG:HB2	1:A:504:PRO:HD3	1.79	0.62
1:B:89:GLU:HG2	1:B:115[A]:ARG:NH1	2.15	0.62
1:A:105:ILE:O	1:A:601[B]:ASN:ND2	2.31	0.62
1:A:14:LYS:HZ2	6:A:1201:1PE:H232	1.62	0.62
1:B:510[B]:LYS:HG2	8:B:911:HOH:O	2.00	0.62
1:A:153:LEU:N	1:A:153:LEU:HD13	2.15	0.61
1:A:503:ARG:NH2	8:A:874:HOH:O	2.34	0.61
1:B:476[A]:MET:HE3	8:B:999:HOH:O	1.99	0.60
1:A:95:ILE:CG2	1:A:119[A]:GLU:HG3	2.31	0.60
1:A:287:ALA:HA	2:A:900[B]:GTP:PA	2.42	0.60
1:B:571:ASP:N	1:B:571:ASP:OD1	2.33	0.59
1:B:420:TRP:CE2	1:B:421:GLU:HG3	2.39	0.58
1:A:152:PRO:HA	8:A:1054:HOH:O	2.04	0.57
1:B:557:TYR:CZ	7:B:3001:EDO:H11	2.40	0.57
1:A:152:PRO:HB2	1:A:153:LEU:CD1	2.32	0.55
1:B:60:MET:HB3	1:B:66:ILE:HG12	1.86	0.55
1:A:292[A]:ASN:OD1	2:A:900[A]:GTP:H2'	2.06	0.55
1:B:476[A]:MET:HE2	8:B:999:HOH:O	2.05	0.54
1:B:589[A]:VAL:CG1	1:B:619[A]:ILE:HD12	2.36	0.53
1:B:570:GLY:O	1:B:572:VAL:HG22	2.08	0.53
1:A:391:TRP:CH2	1:A:393:PRO:HA	2.44	0.53
1:A:153:LEU:HG	6:A:1200:1PE:C22	2.38	0.52
1:B:55:ARG:HG2	1:B:55:ARG:NH1	2.22	0.52
1:B:589[A]:VAL:HG23	8:B:1028:HOH:O	2.10	0.52
1:A:153:LEU:CG	6:A:1200:1PE:OH3	2.58	0.51
1:A:550:ALA:HB1	1:A:557:TYR:HB3	1.91	0.51
1:A:287:ALA:HA	2:A:900[B]:GTP:O2A	2.10	0.51
1:A:575:GLU:OE2	1:A:575:GLU:HA	2.10	0.50
1:A:55:ARG:NH2	8:A:632:HOH:O	2.44	0.50
2:A:900[B]:GTP:O1G	8:A:794:HOH:O	2.20	0.50
1:A:152:PRO:HD2	1:A:423:PRO:O	2.12	0.49
1:A:101:ASP:OD2	8:A:625:HOH:O	2.20	0.49
1:A:151:SER:OG	1:A:153:LEU:CD2	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:ALA:HB3	1:A:337:PRO:HD3	1.95	0.49
1:A:95:ILE:HG21	1:A:119[A]:GLU:HG3	1.94	0.48
1:A:316:LYS:HD3	8:A:812:HOH:O	2.12	0.48
1:A:286[B]:SER:HG	4:A:1000:OXL:C2	2.26	0.48
1:B:243:LYS:O	1:B:247:ALA:HB3	2.13	0.48
1:B:589[A]:VAL:CG2	8:B:1028:HOH:O	2.61	0.48
1:A:217:THR:HA	1:A:231:PHE:O	2.15	0.47
1:B:62[B]:GLU:HA	1:B:62[B]:GLU:OE1	2.14	0.47
1:A:289:GLY:HA2	2:A:900[A]:GTP:C8	2.50	0.47
1:A:542:GLY:O	1:A:547:GLU:HB2	2.15	0.46
1:A:355:THR:HG23	1:A:408[B]:THR:CG2	2.46	0.46
1:B:336:ALA:HB3	1:B:337:PRO:HD3	1.98	0.46
1:B:391:TRP:CH2	1:B:393:PRO:HA	2.50	0.46
1:B:97[B]:GLN:NE2	8:B:844:HOH:O	1.57	0.46
1:B:502:HIS:CD2	8:B:839:HOH:O	2.69	0.46
1:A:355:THR:CG2	1:A:408[B]:THR:HG22	2.45	0.46
1:B:89:GLU:HG3	8:B:698:HOH:O	2.16	0.46
1:A:435:GLY:CA	8:A:809:HOH:O	2.65	0.45
1:B:120:GLU:HG2	1:B:121:ASP:N	2.30	0.45
1:A:226:ARG:HD3	8:A:881:HOH:O	2.16	0.45
1:B:14:LYS:HZ2	6:B:1300:1PE:H142	1.82	0.45
1:A:73:ASP:O	1:A:353:LYS:HA	2.17	0.45
1:B:95:ILE:CG2	1:B:119:GLU:HG2	2.47	0.45
1:B:255:ALA:HB1	1:B:260:TRP:O	2.17	0.45
1:B:115[A]:ARG:NH2	8:B:940:HOH:O	2.50	0.44
1:A:268:LEU:C	1:A:268:LEU:HD12	2.38	0.44
1:B:315:MET:HA	1:B:324:ARG:O	2.18	0.44
1:B:287:ALA:HA	2:B:1000:GTP:O1A	2.17	0.44
1:A:291:THR:O	1:A:295:MET:HG2	2.18	0.44
1:A:291:THR:OG1	1:A:310:ASP:OD2	2.35	0.44
1:A:446:GLU:HB3	1:A:557:TYR:HB2	2.00	0.44
1:B:553:THR:HB	1:B:554:PRO:HD2	2.00	0.44
1:B:585:TRP:O	1:B:589[A]:VAL:HG13	2.18	0.43
1:B:391:TRP:CE2	1:B:399:CYS:HB3	2.53	0.43
1:B:521:LYS:HG2	8:B:765:HOH:O	2.17	0.43
1:B:585:TRP:HB3	1:B:619[A]:ILE:CD1	2.46	0.43
1:A:350[B]:THR:CG2	1:A:413:CYS:HA	2.35	0.43
1:A:517:PHE:CE1	2:A:900[B]:GTP:N3	2.87	0.43
1:A:107:LYS:HE3	1:A:601[A]:ASN:OD1	2.19	0.43
1:B:550:ALA:HB1	1:B:557:TYR:HB3	1.99	0.43
1:A:420:TRP:CE2	1:A:421:GLU:HG3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:442:PRO:HG2	1:B:555:ILE:HD11	2.00	0.42
1:A:287:ALA:HB3	1:A:465:THR:CB	2.49	0.42
1:A:153:LEU:CD1	1:A:153:LEU:N	2.83	0.42
1:A:287:ALA:N	2:A:900[B]:GTP:O3B	2.46	0.42
1:B:58:ALA:O	1:B:62[A]:GLU:HG3	2.19	0.42
1:A:91:LYS:HD3	1:A:217:THR:O	2.20	0.42
1:B:268:LEU:HD12	1:B:268:LEU:C	2.40	0.42
1:A:253:ARG:HG2	1:A:488:TYR:HB3	2.02	0.42
1:A:287:ALA:HB3	1:A:465:THR:HB	2.01	0.41
1:B:295:MET:HA	1:B:415:ILE:HD11	2.01	0.41
1:A:601[B]:ASN:OD1	1:A:602:ALA:N	2.44	0.41
1:B:62[B]:GLU:HG3	8:B:1066:HOH:O	2.20	0.41
1:A:151:SER:C	1:A:153:LEU:N	2.74	0.41
1:A:517:PHE:CE1	2:A:900[B]:GTP:C4	3.08	0.41
1:A:451[A]:GLN:CD	1:A:451[A]:GLN:H	2.23	0.41
1:B:255:ALA:HB1	1:B:260:TRP:C	2.40	0.41
1:B:443:LEU:HB2	1:B:577:LEU:HG	2.03	0.41
1:A:355:THR:CG2	1:A:408[B]:THR:CG2	2.99	0.41
1:A:477:HIS:NE2	1:A:591:GLU:OE2	2.52	0.41
1:B:15:VAL:HG21	1:B:20:LEU:HG	2.03	0.41
1:A:152:PRO:C	1:A:153:LEU:HD13	2.42	0.41
1:A:287:ALA:CA	2:A:900[B]:GTP:O3A	2.63	0.41
1:A:226:ARG:HH21	1:A:254:LEU:CD2	2.35	0.40
1:A:601[A]:ASN:HB3	8:A:808:HOH:O	2.20	0.40
1:B:589[A]:VAL:CG1	1:B:619[A]:ILE:CD1	3.00	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:ARG:NH2	8:B:624:HOH:O[1_656]	1.97	0.23

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	643/624 (103%)	620 (96%)	20 (3%)	3 (0%)	32	13
1	B	626/624 (100%)	606 (97%)	19 (3%)	1 (0%)	51	31
All	All	1269/1248 (102%)	1226 (97%)	39 (3%)	4 (0%)	44	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	571	ASP
1	A	236	GLY
1	A	243	LYS
1	A	151	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	541/520 (104%)	534 (99%)	7 (1%)	73	58
1	B	530/520 (102%)	521 (98%)	9 (2%)	66	47
All	All	1071/1040 (103%)	1055 (98%)	16 (2%)	71	53

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	GLU
1	A	120	GLU
1	A	153	LEU
1	A	246[A]	PHE
1	A	246[B]	PHE
1	A	253	ARG
1	A	369	TYR
1	B	88	ILE
1	B	246	PHE

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Mol	Chain	Res	Type
1	B	253	ARG
1	B	274	GLU
1	B	320	GLN
1	B	369	TYR
1	B	510[A]	LYS
1	B	510[B]	LYS
1	B	551	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	297	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 7 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	$\# Z > 2$
4	OXL	A	1000	3	0,5,5	0.00	-	0,6,6	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	1PE	A	1200	-	7,7,15	0.54	0	6,6,14	0.33	0
6	1PE	A	1201	-	15,15,15	0.46	0	14,14,14	0.41	0
7	EDO	A	3001	-	3,3,3	0.62	0	2,2,2	0.27	0
7	EDO	A	3002	-	3,3,3	0.38	0	2,2,2	0.65	0
7	EDO	A	3003	-	3,3,3	0.45	0	2,2,2	0.33	0
2	GTP	A	900[A]	3	27,34,34	1.06	2 (7%)	27,54,54	1.90	5 (18%)
2	GTP	A	900[B]	3	27,34,34	0.92	2 (7%)	27,54,54	1.48	4 (14%)
2	GTP	B	1000	3	27,34,34	1.12	3 (11%)	27,54,54	1.90	7 (25%)
4	OXL	B	1200	3	0,5,5	0.00	-	0,6,6	0.00	-
6	1PE	B	1300	-	15,15,15	0.58	0	14,14,14	0.33	0
7	EDO	B	3000	-	3,3,3	0.91	0	2,2,2	0.42	0
7	EDO	B	3001	-	3,3,3	0.42	0	2,2,2	0.15	0
7	EDO	B	3002	-	3,3,3	0.53	0	2,2,2	0.34	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	OXL	A	1000	3	-	0/0/4/4	0/0/0/0
6	1PE	A	1200	-	-	0/5/5/13	0/0/0/0
6	1PE	A	1201	-	-	0/13/13/13	0/0/0/0
7	EDO	A	3001	-	-	0/1/1/1	0/0/0/0
7	EDO	A	3002	-	-	0/1/1/1	0/0/0/0
7	EDO	A	3003	-	-	0/1/1/1	0/0/0/0
2	GTP	A	900[A]	3	-	0/18/38/38	0/3/3/3
2	GTP	A	900[B]	3	-	0/18/38/38	0/3/3/3
2	GTP	B	1000	3	-	0/18/38/38	0/3/3/3
4	OXL	B	1200	3	-	0/0/4/4	0/0/0/0
6	1PE	B	1300	-	-	0/13/13/13	0/0/0/0
7	EDO	B	3000	-	-	0/1/1/1	0/0/0/0
7	EDO	B	3001	-	-	0/1/1/1	0/0/0/0
7	EDO	B	3002	-	-	0/1/1/1	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900[B]	GTP	C2-N1	2.02	1.39	1.35
2	B	1000	GTP	C2-N1	2.33	1.39	1.35
2	A	900[B]	GTP	C6-N1	2.45	1.37	1.33
2	B	1000	GTP	PG-O3B	2.53	1.64	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900[A]	GTP	PG-O3B	2.81	1.64	1.60
2	A	900[A]	GTP	C6-N1	2.99	1.38	1.33
2	B	1000	GTP	C6-N1	3.05	1.38	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900[A]	GTP	N3-C2-N1	-5.43	119.53	127.46
2	B	1000	GTP	N3-C2-N1	-5.08	120.04	127.46
2	A	900[B]	GTP	N3-C2-N1	-4.35	121.11	127.46
2	B	1000	GTP	C5-C6-N1	-3.77	118.12	123.48
2	B	1000	GTP	C4-C5-N7	-3.03	106.48	109.41
2	A	900[B]	GTP	C5-C6-N1	-2.86	119.41	123.48
2	A	900[A]	GTP	C5-C6-N1	-2.83	119.46	123.48
2	B	1000	GTP	O3G-PG-O2G	2.13	116.21	107.61
2	A	900[A]	GTP	N2-C2-N3	2.31	122.01	117.75
2	A	900[B]	GTP	C6-N1-C2	2.38	119.48	116.06
2	B	1000	GTP	N2-C2-N1	2.57	121.35	117.24
2	A	900[B]	GTP	C2-N3-C4	2.98	118.64	115.16
2	B	1000	GTP	C2-N3-C4	3.13	118.81	115.16
2	A	900[A]	GTP	C6-N1-C2	3.46	121.04	116.06
2	B	1000	GTP	C6-N1-C2	4.00	121.81	116.06
2	A	900[A]	GTP	C2-N3-C4	4.43	120.34	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1000	OXL	1	0
6	A	1200	1PE	4	0
6	A	1201	1PE	1	0
2	A	900[A]	GTP	4	0
2	A	900[B]	GTP	9	0
2	B	1000	GTP	1	0
6	B	1300	1PE	2	0
7	B	3001	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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	624/624 (100%)	0.51	60 (9%)  	3, 8, 21, 29	14 (2%)
1	B	616/624 (98%)	0.56	66 (10%)  	2, 8, 21, 35	1 (0%)
All	All	1240/1248 (99%)	0.54	126 (10%)  	2, 8, 21, 35	15 (1%)

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	10.0
1	B	3	PRO	8.5
1	B	0	SER	7.7
1	A	394	GLN	7.1
1	B	-1	GLY	7.0
1	A	393	PRO	6.9
1	B	504	PRO	6.6
1	B	394	GLN	6.6
1	B	396	GLU	6.5
1	A	504	PRO	6.4
1	B	393	PRO	5.7
1	B	392	ARG	5.7
1	A	152	PRO	5.5
1	B	205	PRO	5.5
1	A	396	GLU	5.4
1	A	392	ARG	5.4
1	B	395	ASP	5.3
1	B	2	PRO	5.3
1	A	205	PRO	5.0
1	A	153	LEU	5.0
1	A	149	LEU	4.9
1	B	9	LEU	4.8
1	B	8	GLY	4.8
1	B	570	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	505	ALA	4.5
1	A	521	LYS	4.5
1	B	7	ASN	4.5
1	A	473	LYS	4.5
1	A	341	VAL	4.1
1	B	391	TRP	4.1
1	A	571	ASP	4.0
1	B	166	VAL	3.9
1	A	391	TRP	3.7
1	A	522	ASN	3.6
1	A	235[A]	TYR	3.6
1	B	522	ASN	3.6
1	B	203	LYS	3.5
1	B	505	ALA	3.5
1	A	390	GLU	3.5
1	B	235[A]	TYR	3.5
1	A	374	ASP	3.5
1	A	395	ASP	3.5
1	B	575	GLU	3.4
1	A	166	VAL	3.4
1	B	521	LYS	3.4
1	B	240	LEU	3.4
1	B	377	LEU	3.3
1	A	0	SER	3.2
1	A	70	LYS	3.1
1	A	575	GLU	3.1
1	B	397	GLU	3.1
1	B	165	TYR	3.0
1	B	524	LYS	3.0
1	A	266	LEU	3.0
1	A	333	PHE	3.0
1	B	381	VAL	3.0
1	A	342	LYS	3.0
1	B	204	LYS	2.9
1	B	241	LEU	2.9
1	B	4	GLN	2.9
1	B	312	ILE	2.9
1	B	379	PRO	2.9
1	A	524	LYS	2.8
1	A	468	ALA	2.8
1	A	203	LYS	2.8
1	A	432	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	389	LYS	2.6
1	A	431	ILE	2.5
1	A	204	LYS	2.5
1	A	1	MET	2.5
1	B	167	VAL	2.5
1	A	312[A]	ILE	2.5
1	A	388	ASN	2.4
1	A	165	TYR	2.4
1	B	273	PRO	2.4
1	B	473	LYS	2.4
1	B	267	ILE	2.4
1	B	432	ILE	2.4
1	B	503	ARG	2.4
1	B	333	PHE	2.3
1	B	388	ASN	2.3
1	B	481	ALA	2.3
1	A	142	ILE	2.3
1	B	140	TYR	2.3
1	A	160	LEU	2.3
1	A	283	ALA	2.3
1	A	433	PHE	2.3
1	A	466	ALA	2.3
1	A	207	VAL	2.3
1	B	25	GLN	2.3
1	B	245	CYS	2.3
1	A	569	LEU	2.2
1	B	266	LEU	2.2
1	A	140	TYR	2.2
1	A	240	LEU	2.2
1	B	206	LEU	2.2
1	A	572	VAL	2.2
1	B	571	ASP	2.2
1	B	274	GLU	2.2
1	B	378	ALA	2.2
1	A	520	ASP	2.2
1	B	374	ASP	2.2
1	B	431	ILE	2.2
1	B	433	PHE	2.1
1	A	167	VAL	2.1
1	A	567	LYS	2.1
1	B	161	THR	2.1
1	A	561	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	398	PRO	2.1
1	A	284	PHE	2.1
1	A	503	ARG	2.1
1	A	186	ASP	2.1
1	A	583	GLU	2.1
1	B	142	ILE	2.1
1	B	188	GLU	2.1
1	A	170	MET	2.1
1	A	349	LYS	2.1
1	A	398	PRO	2.1
1	B	141	VAL	2.1
1	B	160	LEU	2.1
1	A	245	CYS	2.1
1	B	5	LEU	2.0
1	B	464	ALA	2.0
1	A	169	SER	2.0
1	B	480	PHE	2.0
1	B	562	ASP	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 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
7	EDO	B	3000	4/4	0.81	0.28	8.46	20,25,28,31	0
7	EDO	A	3001	4/4	0.93	0.23	5.55	18,20,22,30	0
3	MN	B	701	1/1	0.99	0.25	3.49	13,13,13,13	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MN	A	800	1/1	1.00	0.22	2.41	14,14,14,14	0
3	MN	A	700[A]	1/1	0.98	0.21	2.38	16,16,16,16	1
6	1PE	A	1201	16/16	0.90	0.20	2.37	43,44,48,51	0
2	GTP	A	900[B]	32/32	0.96	0.19	2.32	9,12,18,20	32
3	MN	A	700[B]	1/1	0.98	0.21	2.29	18,18,18,18	1
2	GTP	A	900[A]	32/32	0.96	0.19	2.05	9,19,23,23	32
4	OXL	A	1000	6/6	0.93	0.22	1.72	11,16,19,19	0
5	NA	B	1100	1/1	0.98	0.17	1.30	24,24,24,24	0
7	EDO	A	3003	4/4	0.74	0.21	1.20	47,48,50,50	0
2	GTP	B	1000	32/32	0.97	0.15	0.81	13,19,23,25	0
6	1PE	A	1200	8/16	0.83	0.21	0.63	48,49,50,50	0
7	EDO	B	3001	4/4	0.89	0.14	0.63	39,40,40,41	0
6	1PE	B	1300	16/16	0.67	0.21	0.57	55,57,58,59	0
5	NA	A	1100	1/1	0.99	0.12	0.35	30,30,30,30	0
4	OXL	B	1200	6/6	0.91	0.15	-0.24	12,20,22,22	0
3	MN	B	700	1/1	1.00	0.22	-	14,14,14,14	0
7	EDO	B	3002	4/4	0.78	0.29	-	41,45,45,47	0
7	EDO	A	3002	4/4	0.89	0.25	-	44,44,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.