



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 08:02 AM GMT

PDB ID : 2P1C  
Title : T. Brucei Farnesyl Diphosphate Synthase Complexed with Bisphosphonate BPH-210  
Authors : Cao, R.; Gao, Y.; Oldfield, E.  
Deposited on : 2007-03-04  
Resolution : 2.45 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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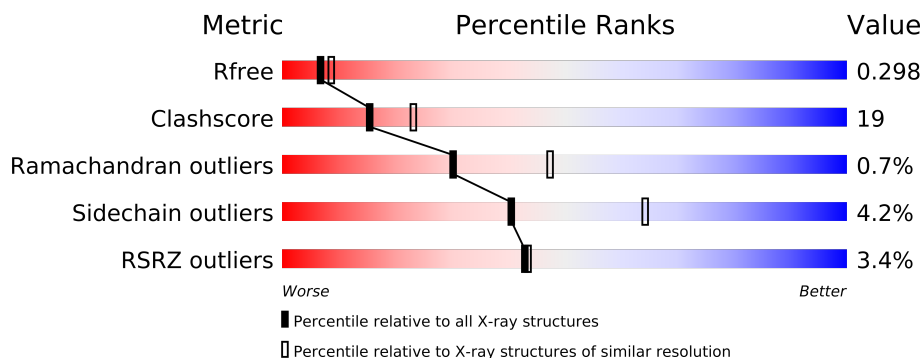
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.45 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))
$R_{free}$	66092	3566 (2.50-2.42)
Clashscore	79885	4471 (2.50-2.42)
Ramachandran outliers	78287	4383 (2.50-2.42)
Sidechain outliers	78261	4385 (2.50-2.42)
RSRZ outliers	66119	3568 (2.50-2.42)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	390	
1	B	390	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	MG	A	3002	-	X
2	MG	A	3003	-	X
2	MG	A	3004	-	X
2	MG	B	4001	-	X
2	MG	B	4002	-	X
2	MG	B	4003	-	X
3	ACT	B	8002	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6080 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2854	1819	469	538	28			
1	B	357	Total	C	N	O	S	0	0	0
			2850	1817	468	537	28			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	EXPRESSION TAG	UNP Q86C09
A	-21	GLY	-	EXPRESSION TAG	UNP Q86C09
A	-20	SER	-	EXPRESSION TAG	UNP Q86C09
A	-19	SER	-	EXPRESSION TAG	UNP Q86C09
A	-18	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-17	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-16	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-15	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-14	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-13	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-12	SER	-	EXPRESSION TAG	UNP Q86C09
A	-11	SER	-	EXPRESSION TAG	UNP Q86C09
A	-10	GLY	-	EXPRESSION TAG	UNP Q86C09
A	-9	LEU	-	EXPRESSION TAG	UNP Q86C09
A	-8	VAL	-	EXPRESSION TAG	UNP Q86C09
A	-7	PRO	-	EXPRESSION TAG	UNP Q86C09
A	-6	ARG	-	EXPRESSION TAG	UNP Q86C09
A	-5	GLY	-	EXPRESSION TAG	UNP Q86C09
A	-4	SER	-	EXPRESSION TAG	UNP Q86C09
A	-3	HIS	-	EXPRESSION TAG	UNP Q86C09
A	-2	MET	-	EXPRESSION TAG	UNP Q86C09
A	-1	ALA	-	EXPRESSION TAG	UNP Q86C09
A	0	SER	-	EXPRESSION TAG	UNP Q86C09
B	-22	MET	-	EXPRESSION TAG	UNP Q86C09
B	-21	GLY	-	EXPRESSION TAG	UNP Q86C09

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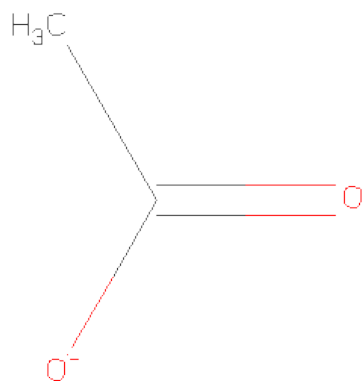
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	SER	-	EXPRESSION TAG	UNP Q86C09
B	-19	SER	-	EXPRESSION TAG	UNP Q86C09
B	-18	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-17	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-16	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-15	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-14	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-13	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-12	SER	-	EXPRESSION TAG	UNP Q86C09
B	-11	SER	-	EXPRESSION TAG	UNP Q86C09
B	-10	GLY	-	EXPRESSION TAG	UNP Q86C09
B	-9	LEU	-	EXPRESSION TAG	UNP Q86C09
B	-8	VAL	-	EXPRESSION TAG	UNP Q86C09
B	-7	PRO	-	EXPRESSION TAG	UNP Q86C09
B	-6	ARG	-	EXPRESSION TAG	UNP Q86C09
B	-5	GLY	-	EXPRESSION TAG	UNP Q86C09
B	-4	SER	-	EXPRESSION TAG	UNP Q86C09
B	-3	HIS	-	EXPRESSION TAG	UNP Q86C09
B	-2	MET	-	EXPRESSION TAG	UNP Q86C09
B	-1	ALA	-	EXPRESSION TAG	UNP Q86C09
B	0	SER	-	EXPRESSION TAG	UNP Q86C09

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

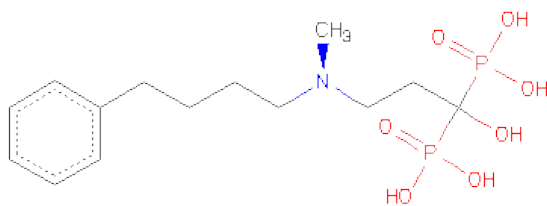
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	3	Total Mg 3 3	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



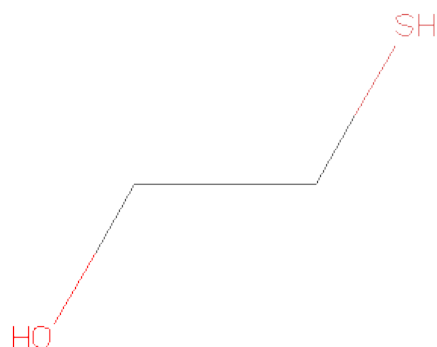
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is {1-HYDROXY-3-[METHYL(4-PHENYLBUTYL)AMINO]PROPANE-1,1-DIYL}BIS(PHOSPHONICACID) (three-letter code: GG3) (formula: C<sub>14</sub>H<sub>25</sub>NO<sub>7</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			24	14	1	7	2		
4	B	1	Total	C	N	O	P	0	0
			24	14	1	7	2		

- Molecule 5 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula:  $C_2H_6OS$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 6 is water.

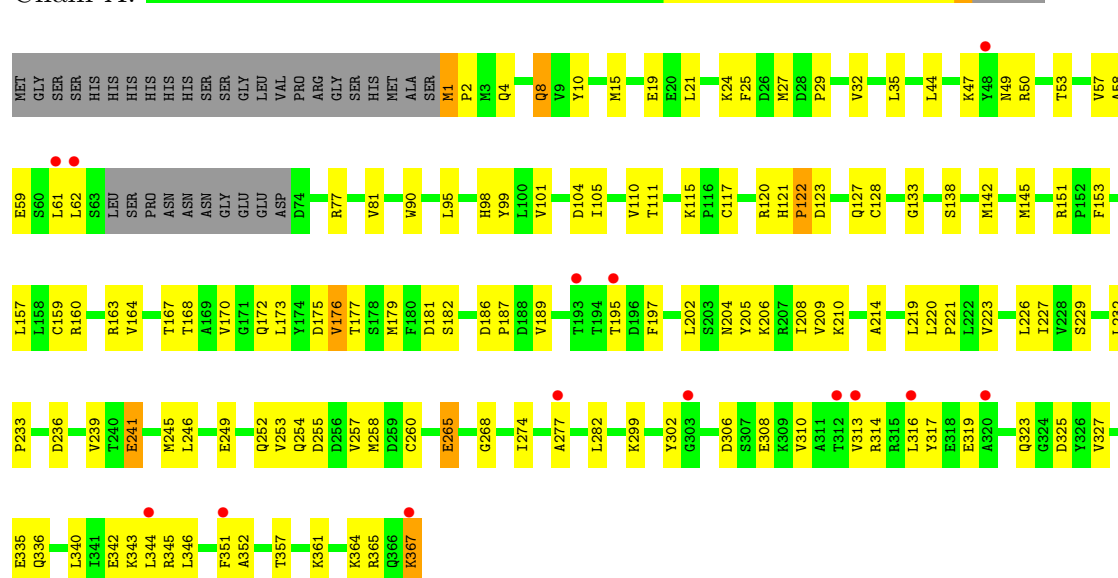
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	151	Total	O	0	0
			151	151		
6	B	155	Total	O	0	0
			155	155		

### 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.

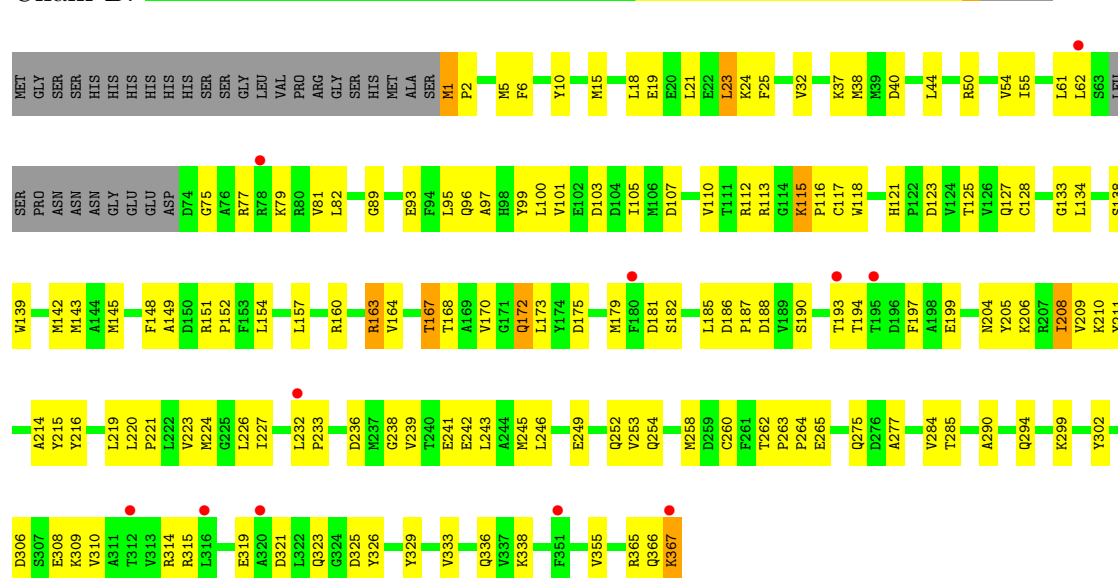
#### • Molecule 1: Farnesyl pyrophosphate synthase

Chain A:



#### • Molecule 1: Farnesyl pyrophosphate synthase

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.12Å 92.12Å 177.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.69 – 2.45 47.57 – 2.37	Depositor EDS
% Data completeness (in resolution range)	87.4 (29.69-2.45) 84.2 (47.57-2.37)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 2.37Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.266 , 0.299 0.268 , 0.298	Depositor DCC
$R_{free}$ test set	859 reflections (2.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.6	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 51.5	EDS
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 34569 reflections (0.012%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6080	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	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 92.33 % 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 9.7474e-09. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ACT, GG3, BME

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	0.34	0/2913	0.56	0/3939
1	B	0.34	0/2909	0.55	0/3934
All	All	0.34	0/5822	0.55	0/7873

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2854	0	2808	104	0
1	B	2850	0	2802	121	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	8	0	6	2	0
3	B	4	0	3	1	0
4	A	24	0	21	5	0
4	B	24	0	21	1	0
5	B	4	0	5	1	0
6	A	151	0	0	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	155	0	0	11	0
All	All	6080	0	5666	214	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

All (214) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:47:LYS:HB2	3:A:8003:ACT:H3	1.41	1.02
1:A:365:ARG:HD2	1:A:367:LYS:HG2	1.46	0.95
1:A:367:LYS:HE3	1:A:367:LYS:HA	1.50	0.93
1:B:365:ARG:HH11	1:B:367:LYS:HE2	1.40	0.87
1:B:172:GLN:HA	1:B:172:GLN:HE21	1.43	0.82
1:B:209:VAL:HG22	1:B:252:GLN:HG2	1.61	0.81
1:A:163:ARG:O	1:A:167:THR:HG23	1.83	0.79
1:A:122:PRO:O	1:B:190:SER:HB3	1.82	0.79
1:B:365:ARG:HD2	1:B:367:LYS:HE2	1.67	0.77
1:A:367:LYS:CE	1:A:367:LYS:HA	2.16	0.75
1:B:97:ALA:O	1:B:101:VAL:HG23	1.87	0.75
1:A:145:MET:HG3	6:A:8128:HOH:O	1.88	0.74
1:B:133:GLY:HA3	6:B:9050:HOH:O	1.88	0.74
1:B:23:LEU:HD12	1:B:24:LYS:HG3	1.70	0.72
1:A:365:ARG:HD2	1:A:367:LYS:CG	2.21	0.71
1:A:15:MET:HG3	6:A:8090:HOH:O	1.90	0.70
1:B:101:VAL:HB	6:B:9050:HOH:O	1.90	0.70
1:B:367:LYS:HA	1:B:367:LYS:HZ2	1.56	0.70
1:B:204:ASN:O	1:B:208:ILE:HG22	1.93	0.69
1:B:113:ARG:HE	3:B:8002:ACT:H3	1.56	0.69
1:A:254:GLN:O	1:A:258:MET:HG3	1.93	0.68
1:B:148:PHE:O	1:B:154:LEU:HD22	1.94	0.68
1:A:209:VAL:HG11	1:A:249:GLU:HA	1.76	0.67
1:A:357:THR:O	1:A:361:LYS:HG3	1.94	0.67
1:A:220:LEU:HB3	1:A:221:PRO:HD3	1.75	0.67
1:A:50:ARG:HH11	1:A:50:ARG:HG3	1.59	0.67
1:A:99:TYR:HB3	4:A:3001:GG3:H261	1.77	0.67
1:B:306:ASP:OD2	1:B:308:GLU:HG2	1.95	0.67
1:B:160:ARG:HD2	1:B:227:ILE:HD11	1.76	0.67
1:B:175:ASP:HA	1:B:208:ILE:HD12	1.76	0.66
1:A:206:LYS:HE2	6:A:8061:HOH:O	1.94	0.65
1:B:365:ARG:HH11	1:B:367:LYS:CE	2.09	0.65
1:B:315:ARG:O	1:B:319:GLU:HG3	1.98	0.64
1:B:220:LEU:HB3	1:B:221:PRO:HD3	1.80	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:209:VAL:HG11	1:B:249:GLU:HA	1.81	0.63
1:A:206:LYS:HG2	1:A:249:GLU:OE2	1.99	0.62
1:A:4:GLN:HE22	1:A:8:GLN:HE22	1.45	0.62
1:B:209:VAL:HG22	1:B:252:GLN:CG	2.29	0.62
1:A:209:VAL:CG1	1:A:249:GLU:HA	2.30	0.62
1:A:21:LEU:HD13	1:A:35:LEU:HD12	1.81	0.62
1:B:209:VAL:CG1	1:B:249:GLU:HA	2.30	0.61
1:A:209:VAL:HG22	1:A:252:GLN:HG2	1.82	0.61
1:B:216:TYR:OH	4:B:8004:GG3:H213	2.01	0.61
1:A:59:GLU:HG2	6:A:8092:HOH:O	2.00	0.60
1:A:172:GLN:HG3	4:A:3001:GG3:C28	2.31	0.60
1:A:364:LYS:HA	6:A:8071:HOH:O	2.00	0.60
1:A:138:SER:O	1:A:142:MET:HG2	2.02	0.59
1:A:58:ALA:HA	1:A:229:SER:OG	2.03	0.59
1:B:61:LEU:HD13	1:B:226:LEU:HD23	1.84	0.59
1:B:96:GLN:O	1:B:100:LEU:HG	2.03	0.59
1:B:366:GLN:O	1:B:367:LYS:HB2	2.02	0.58
1:B:206:LYS:HG2	1:B:249:GLU:OE2	2.02	0.58
1:A:204:ASN:O	1:A:208:ILE:HG13	2.04	0.58
1:B:219:LEU:O	1:B:223:VAL:HG23	2.04	0.57
1:B:325:ASP:HB3	6:B:9053:HOH:O	2.04	0.57
1:A:306:ASP:O	1:A:310:VAL:HG23	2.04	0.57
1:A:197:PHE:CD2	1:A:299:LYS:HG2	2.40	0.57
1:B:306:ASP:HB3	1:B:309:LYS:HD2	1.87	0.56
1:B:367:LYS:NZ	1:B:367:LYS:HA	2.20	0.56
1:A:151:ARG:HG2	1:A:153:PHE:CZ	2.41	0.56
1:B:172:GLN:HA	1:B:172:GLN:NE2	2.17	0.56
1:B:40:ASP:O	1:B:44:LEU:HB2	2.05	0.56
1:B:50:ARG:HG3	1:B:50:ARG:HH11	1.71	0.56
1:B:164:VAL:HG13	1:B:215:TYR:HB3	1.88	0.55
1:A:25:PHE:HE1	1:B:167:THR:HB	1.71	0.55
1:B:125:THR:HB	1:B:127:GLN:OE1	2.07	0.55
1:B:62:LEU:O	1:B:62:LEU:HD12	2.07	0.55
1:A:255:ASP:HA	1:A:258:MET:HE2	1.89	0.55
1:B:181:ASP:HB2	6:B:9134:HOH:O	2.06	0.55
1:B:205:TYR:O	1:B:208:ILE:HG23	2.07	0.55
1:A:15:MET:O	1:A:19:GLU:HB2	2.07	0.54
1:B:246:LEU:HD21	1:B:336:GLN:HB3	1.89	0.54
1:B:238:GLY:O	1:B:242:GLU:HG3	2.07	0.54
1:B:5:MET:HE1	1:B:82:LEU:HD12	1.89	0.54
1:A:104:ASP:HA	6:A:8135:HOH:O	2.06	0.54
1:A:50:ARG:HG3	1:A:50:ARG:NH1	2.23	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:61:LEU:CD1	1:B:226:LEU:HD23	2.38	0.54
4:A:3001:GG3:H31	1:B:134:LEU:HD13	1.90	0.54
1:A:265:GLU:H	1:A:265:GLU:CD	2.12	0.54
1:B:241:GLU:O	1:B:245:MET:HG2	2.08	0.54
1:A:257:VAL:HG22	1:A:282:LEU:HD21	1.89	0.54
1:A:10:TYR:HB2	1:A:90:TRP:CZ2	2.42	0.54
1:B:21:LEU:HA	1:B:25:PHE:HB2	1.90	0.53
1:B:243:LEU:HD13	1:B:355:VAL:HG11	1.91	0.53
1:B:306:ASP:O	1:B:310:VAL:HG23	2.09	0.53
1:A:357:THR:HG22	1:A:361:LYS:HE3	1.90	0.53
1:B:1:MET:HB3	1:B:2:PRO:HD3	1.91	0.53
1:B:62:LEU:HD12	6:B:9054:HOH:O	2.09	0.53
1:A:49:ASN:HD22	3:A:8003:ACT:H1	1.74	0.52
1:B:264:PRO:HD3	6:B:9118:HOH:O	2.08	0.52
1:A:236:ASP:OD2	1:A:239:VAL:HG23	2.09	0.52
1:B:164:VAL:HG21	1:B:220:LEU:HD13	1.92	0.52
1:A:163:ARG:NH1	1:B:142:MET:HE3	2.25	0.52
1:A:111:THR:HG23	1:A:115:LYS:O	2.09	0.51
1:A:101:VAL:O	1:A:105:ILE:HG13	2.10	0.51
1:B:193:THR:O	1:B:194:THR:C	2.49	0.51
1:B:50:ARG:HG3	6:B:9003:HOH:O	2.09	0.51
1:A:115:LYS:HG3	6:A:8127:HOH:O	2.09	0.51
1:A:205:TYR:CZ	1:A:209:VAL:HG21	2.46	0.51
1:A:160:ARG:O	1:A:164:VAL:HG23	2.11	0.51
1:B:145:MET:O	1:B:149:ALA:HB2	2.10	0.51
1:A:327:VAL:HG13	6:A:8029:HOH:O	2.10	0.51
1:A:340:LEU:HD23	1:A:343:LYS:HE2	1.93	0.50
1:A:170:VAL:O	1:A:173:LEU:HB3	2.12	0.50
1:A:223:VAL:O	1:A:227:ILE:HG13	2.12	0.50
1:B:77:ARG:O	1:B:81:VAL:HG23	2.10	0.50
1:B:275:GLN:OE1	1:B:275:GLN:N	2.42	0.50
1:A:232:LEU:N	1:A:233:PRO:HD2	2.27	0.50
1:A:246:LEU:HD21	1:A:336:GLN:HB3	1.93	0.50
1:B:323:GLN:HG3	6:B:9104:HOH:O	2.12	0.49
1:A:367:LYS:HD3	6:A:8019:HOH:O	2.12	0.49
1:A:111:THR:HG22	1:A:268:GLY:O	2.12	0.49
1:A:219:LEU:HD13	1:A:219:LEU:C	2.33	0.49
1:B:367:LYS:N	1:B:367:LYS:HZ3	2.10	0.49
1:A:306:ASP:OD1	1:A:308:GLU:HG2	2.13	0.48
1:B:101:VAL:O	1:B:105:ILE:HG13	2.13	0.48
1:B:164:VAL:HA	1:B:167:THR:HG23	1.94	0.48
1:A:344:LEU:HD21	1:A:351:PHE:CD2	2.49	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:187:PRO:HD2	1:B:37:LYS:HD2	1.95	0.48
1:A:168:THR:HG22	4:A:3001:GG3:H33	1.95	0.48
1:A:98:HIS:ND1	1:A:133:GLY:O	2.38	0.48
1:A:123:ASP:CB	1:B:186:ASP:O	2.62	0.48
1:A:53:THR:O	1:A:57:VAL:HG23	2.14	0.48
1:A:176:VAL:HG12	1:A:177:THR:HG23	1.94	0.48
1:B:163:ARG:O	1:B:167:THR:HG22	2.14	0.48
1:B:89:GLY:O	1:B:93:GLU:HG2	2.14	0.48
1:A:342:GLU:O	1:A:346:LEU:HD13	2.13	0.48
1:B:205:TYR:CZ	1:B:209:VAL:HG21	2.49	0.48
1:A:167:THR:HG22	1:B:25:PHE:HE1	1.78	0.47
1:A:29:PRO:HG3	6:A:8032:HOH:O	2.13	0.47
1:A:219:LEU:O	1:A:219:LEU:HD13	2.14	0.47
1:B:38:MET:HA	1:B:118:TRP:CH2	2.49	0.47
1:A:189:VAL:O	1:B:123:ASP:CB	2.62	0.47
1:B:139:TRP:O	1:B:143:MET:HG2	2.14	0.47
1:B:127:GLN:HG2	1:B:128:CYS:N	2.29	0.47
1:A:95:LEU:HG	1:A:99:TYR:CE2	2.50	0.47
1:B:163:ARG:HG3	5:B:9001:BME:S2	2.54	0.47
1:A:27:MET:HG2	1:A:32:VAL:HG23	1.96	0.47
1:A:122:PRO:HB2	1:B:188:ASP:O	2.14	0.47
1:B:329:TYR:O	1:B:333:VAL:HG23	2.15	0.47
1:B:366:GLN:O	1:B:367:LYS:CB	2.63	0.47
4:A:3001:GG3:H31	1:B:134:LEU:CD1	2.45	0.47
1:B:290:ALA:HB1	1:B:294:GLN:HB2	1.97	0.46
1:A:306:ASP:OD1	1:A:308:GLU:CG	2.63	0.46
1:A:61:LEU:HD13	1:A:226:LEU:HD23	1.96	0.46
1:B:321:ASP:HA	6:B:9104:HOH:O	2.15	0.46
1:B:117:CYS:O	1:B:121:HIS:HD2	1.98	0.46
1:B:157:LEU:HD21	1:B:224:MET:HE2	1.98	0.46
1:B:160:ARG:O	1:B:164:VAL:HG23	2.16	0.45
1:B:79:LYS:HA	1:B:82:LEU:HB2	1.98	0.45
1:A:10:TYR:CE2	1:A:44:LEU:HD11	2.51	0.45
1:A:186:ASP:O	1:B:123:ASP:CB	2.65	0.45
1:A:210:LYS:O	1:A:214:ALA:HB3	2.16	0.45
1:B:6:PHE:CD1	1:B:55:ILE:HD11	2.52	0.45
1:B:18:LEU:HD22	1:B:32:VAL:HG13	1.99	0.45
1:B:232:LEU:N	1:B:233:PRO:HD2	2.31	0.45
1:A:127:GLN:HG2	1:A:128:CYS:N	2.30	0.45
1:B:265:GLU:HB2	6:B:9125:HOH:O	2.17	0.45
1:B:284:VAL:HG23	1:B:285:THR:N	2.32	0.45
1:A:24:LYS:NZ	6:A:8105:HOH:O	2.47	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:249:GLU:O	1:B:253:VAL:HG23	2.17	0.45
1:A:202:LEU:HD13	6:A:8114:HOH:O	2.16	0.45
1:A:316:LEU:HD23	1:A:319:GLU:OE1	2.17	0.45
1:A:167:THR:HG22	1:B:25:PHE:CE1	2.52	0.44
1:B:168:THR:HA	1:B:211:TYR:O	2.17	0.44
1:A:117:CYS:O	1:A:121:HIS:HD2	2.00	0.44
1:B:254:GLN:O	1:B:258:MET:HG3	2.17	0.44
1:A:249:GLU:O	1:A:253:VAL:HG23	2.17	0.44
1:B:315:ARG:HD3	1:B:319:GLU:OE2	2.18	0.44
1:B:145:MET:HB2	6:B:9049:HOH:O	2.17	0.44
1:B:236:ASP:CG	1:B:239:VAL:HG23	2.38	0.44
1:B:115:LYS:HB2	1:B:116:PRO:HD2	1.99	0.44
1:A:345:ARG:HA	1:A:352:ALA:HB2	2.00	0.44
1:B:10:TYR:CE2	1:B:44:LEU:HD11	2.53	0.44
1:B:182:SER:OG	1:B:199:GLU:OE1	2.26	0.44
1:A:274:ILE:HD13	1:A:313:VAL:HB	2.00	0.44
1:B:277:ALA:HA	1:B:302:TYR:CE2	2.53	0.43
1:A:335:GLU:HB2	6:A:8056:HOH:O	2.18	0.43
1:B:138:SER:O	1:B:142:MET:HG2	2.17	0.43
1:B:160:ARG:CD	1:B:227:ILE:HD11	2.46	0.43
1:B:95:LEU:HG	1:B:99:TYR:CE2	2.54	0.43
1:B:50:ARG:NH1	1:B:50:ARG:HG3	2.33	0.43
1:A:314:ARG:O	1:A:317:TYR:HB2	2.19	0.43
1:A:365:ARG:NH1	1:A:367:LYS:HG3	2.34	0.43
1:A:163:ARG:NH1	1:B:142:MET:CE	2.82	0.43
1:A:241:GLU:O	1:A:245:MET:HG2	2.19	0.43
1:B:23:LEU:H	1:B:23:LEU:HG	1.67	0.42
1:A:257:VAL:HA	1:A:282:LEU:HD11	2.01	0.42
1:A:172:GLN:O	1:A:176:VAL:HB	2.19	0.42
1:B:112:ARG:O	1:B:115:LYS:HD2	2.19	0.42
1:B:50:ARG:O	1:B:54:VAL:HG23	2.18	0.42
1:B:103:ASP:OD1	1:B:107:ASP:OD2	2.36	0.42
1:B:5:MET:SD	1:B:82:LEU:HD12	2.59	0.42
1:B:197:PHE:CD2	1:B:299:LYS:HG2	2.55	0.42
1:A:260:CYS:SG	1:A:314:ARG:HG3	2.60	0.42
1:B:260:CYS:O	1:B:314:ARG:NH1	2.53	0.42
1:A:21:LEU:HD13	1:A:35:LEU:CD1	2.46	0.42
1:B:118:TRP:HA	1:B:121:HIS:CD2	2.54	0.42
1:A:255:ASP:HA	1:A:258:MET:CE	2.49	0.41
1:B:367:LYS:NZ	1:B:367:LYS:CA	2.83	0.41
1:B:170:VAL:O	1:B:173:LEU:HB3	2.20	0.41
1:A:367:LYS:HE3	1:A:367:LYS:CA	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:110:VAL:HG13	1:A:120:ARG:NH1	2.35	0.41
1:A:197:PHE:CE2	1:A:299:LYS:HG2	2.55	0.41
1:B:254:GLN:HG2	1:B:326:TYR:OH	2.20	0.41
1:A:120:ARG:HA	1:A:120:ARG:HD3	1.91	0.41
1:A:277:ALA:HA	1:A:302:TYR:CE2	2.56	0.41
1:B:15:MET:O	1:B:19:GLU:HG3	2.21	0.41
1:A:77:ARG:O	1:A:81:VAL:HG23	2.21	0.41
1:B:262:THR:HA	1:B:263:PRO:HD3	1.88	0.41
1:A:1:MET:N	1:A:2:PRO:CD	2.84	0.41
1:B:151:ARG:HA	1:B:152:PRO:HD3	1.83	0.40
1:A:336:GLN:HG2	6:A:8139:HOH:O	2.22	0.40
1:B:210:LYS:O	1:B:214:ALA:HB3	2.21	0.40

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	353/390 (90%)	337 (96%)	13 (4%)	3 (1%)	27	43
1	B	353/390 (90%)	334 (95%)	17 (5%)	2 (1%)	33	52
All	All	706/780 (90%)	671 (95%)	30 (4%)	5 (1%)	30	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	75	GLY
1	A	182	SER
1	A	181	ASP
1	B	187	PRO
1	A	122	PRO

### 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	310/340 (91%)	296 (96%)	14 (4%)	38	61
1	B	309/340 (91%)	297 (96%)	12 (4%)	43	68
All	All	619/680 (91%)	593 (96%)	26 (4%)	40	64

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	8	GLN
1	A	62	LEU
1	A	157	LEU
1	A	159	CYS
1	A	175	ASP
1	A	176	VAL
1	A	179	MET
1	A	195	THR
1	A	241	GLU
1	A	265	GLU
1	A	323	GLN
1	A	325	ASP
1	A	367	LYS
1	B	1	MET
1	B	23	LEU
1	B	110	VAL
1	B	115	LYS
1	B	163	ARG
1	B	167	THR
1	B	172	GLN
1	B	179	MET
1	B	185	LEU
1	B	208	ILE
1	B	338	LYS
1	B	367	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	8	GLN
1	A	49	ASN
1	A	121	HIS
1	A	146	HIS
1	A	323	GLN
1	B	121	HIS
1	B	146	HIS
1	B	172	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	GG3	A	3001	-	24,24,24	1.64	2 (8%)	35,35,35	1.43	7 (20%)
3	ACT	A	8001	-	1,3,3	2.01	1 (100%)	0,3,3	0.00	-
3	ACT	A	8003	-	1,3,3	1.70	0	0,3,3	0.00	-
3	ACT	B	8002	-	1,3,3	1.90	0	0,3,3	0.00	-
4	GG3	B	8004	-	24,24,24	1.63	5 (20%)	35,35,35	1.37	6 (17%)
5	BME	B	9001	-	3,3,3	2.26	1 (33%)	2,2,2	0.12	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	GG3	A	3001	-	-	0/31/31/31	0/1/1/1
3	ACT	A	8001	-	-	0/0/0/0	0/0/0/0
3	ACT	A	8003	-	-	0/0/0/0	0/0/0/0
3	ACT	B	8002	-	-	0/0/0/0	0/0/0/0
4	GG3	B	8004	-	-	0/31/31/31	0/1/1/1
5	BME	B	9001	-	-	0/1/1/1	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3001	GG3	P14-C8	-4.99	1.81	1.85
5	B	9001	BME	O1-C1	-3.82	1.21	1.42
4	B	8004	GG3	P14-C8	-3.47	1.82	1.85
4	B	8004	GG3	C7-C2	3.42	1.58	1.53
4	B	8004	GG3	C29-C28	2.55	1.44	1.38
4	A	3001	GG3	C29-C28	2.41	1.44	1.38
4	B	8004	GG3	P9-O10	2.37	1.54	1.50
4	B	8004	GG3	C7-C8	2.16	1.56	1.54
3	A	8001	ACT	CH3-C	2.01	1.51	1.48

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	8004	GG3	O11-P9-O12	3.26	117.23	107.93
4	A	3001	GG3	O11-P9-O12	3.15	116.91	107.93
4	B	8004	GG3	O16-P14-C8	2.75	112.44	105.98
4	A	3001	GG3	O16-P14-C8	2.73	112.40	105.98
4	A	3001	GG3	P14-C8-O13	-2.71	102.86	107.98
4	B	8004	GG3	C2-C7-C8	-2.57	107.46	114.47
4	A	3001	GG3	C2-C7-C8	-2.50	107.66	114.47
4	B	8004	GG3	O17-P14-C8	-2.44	103.63	110.04
4	A	3001	GG3	O17-P14-C8	-2.29	104.01	110.04
4	A	3001	GG3	O11-P9-O10	-2.27	108.06	113.14
4	B	8004	GG3	P14-C8-O13	-2.14	103.94	107.98
4	B	8004	GG3	O11-P9-O10	-2.06	108.53	113.14
4	A	3001	GG3	P9-C8-O13	2.05	111.86	107.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	357/390 (91%)	0.06	14 (3%) 37 38	34, 53, 73, 87	0
1	B	357/390 (91%)	0.06	11 (3%) 47 47	32, 52, 73, 84	0
All	All	714/780 (91%)	0.06	25 (3%) 43 42	32, 52, 73, 87	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	316	LEU	4.7
1	A	62	LEU	4.4
1	B	193	THR	4.3
1	A	195	THR	4.3
1	A	313	VAL	3.8
1	A	312	THR	3.5
1	B	180	PHE	3.4
1	B	78	ARG	2.9
1	B	195	THR	2.9
1	B	351	PHE	2.9
1	A	367	LYS	2.8
1	A	351	PHE	2.7
1	A	61	LEU	2.6
1	B	62	LEU	2.5
1	B	367	LYS	2.5
1	B	312	THR	2.5
1	B	316	LEU	2.4
1	A	303	GLY	2.4
1	A	320	ALA	2.4
1	A	193	THR	2.3
1	A	344	LEU	2.3
1	A	277	ALA	2.2
1	B	232	LEU	2.1
1	A	48	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	320	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MG	A	3003	1/1	0.27	13.03	45,45,45,45	0
2	MG	B	4002	1/1	0.20	10.85	45,45,45,45	0
2	MG	A	3004	1/1	0.28	8.33	38,38,38,38	0
3	ACT	B	8002	4/4	0.25	4.58	28,29,31,33	0
2	MG	B	4001	1/1	0.25	3.03	49,49,49,49	0
2	MG	B	4003	1/1	0.25	2.86	49,49,49,49	0
2	MG	A	3002	1/1	0.23	2.68	52,52,52,52	0
3	ACT	A	8001	4/4	0.17	1.06	28,31,34,39	0
5	BME	B	9001	4/4	0.17	1.06	64,68,68,69	0
4	GG3	A	3001	24/24	0.15	0.92	36,42,50,61	0
4	GG3	B	8004	24/24	0.16	0.75	24,45,60,71	0
3	ACT	A	8003	4/4	0.19	-0.17	45,45,49,50	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.