Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 03:23 AM EDT

PDB ID	:	1B74
Title	:	GLUTAMATE RACEMASE FROM AQUIFEX PYROPHILUS
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Deposited on	:	1999-01-27
Resolution	:	2.30 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:

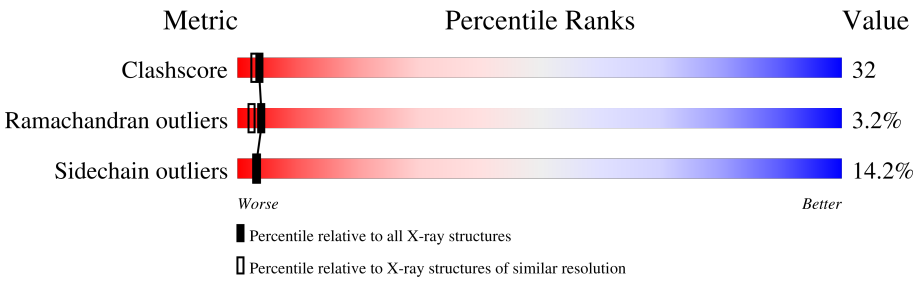
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	254	46% 42% 11% •

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	DGN	A	538	-	-	X	-

2 Entry composition (i)

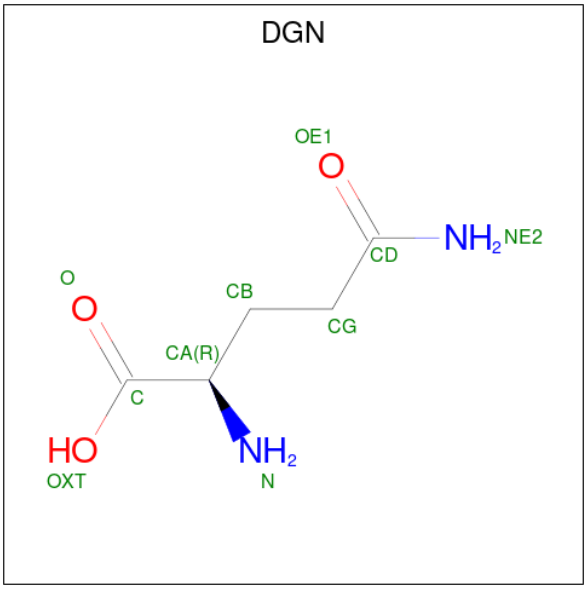
There are 3 unique types of molecules in this entry. The entry contains 2066 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLUTAMATE RACEMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	1952	1264	326	357	5	0	0	0

- Molecule 2 is D-GLUTAMINE (three-letter code: DGN) (formula: $C_5H_{10}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	10	5	2	3	0	0

- Molecule 3 is water.

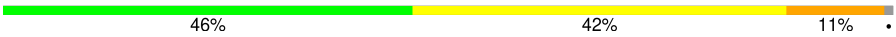
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	104	104	104	0	0

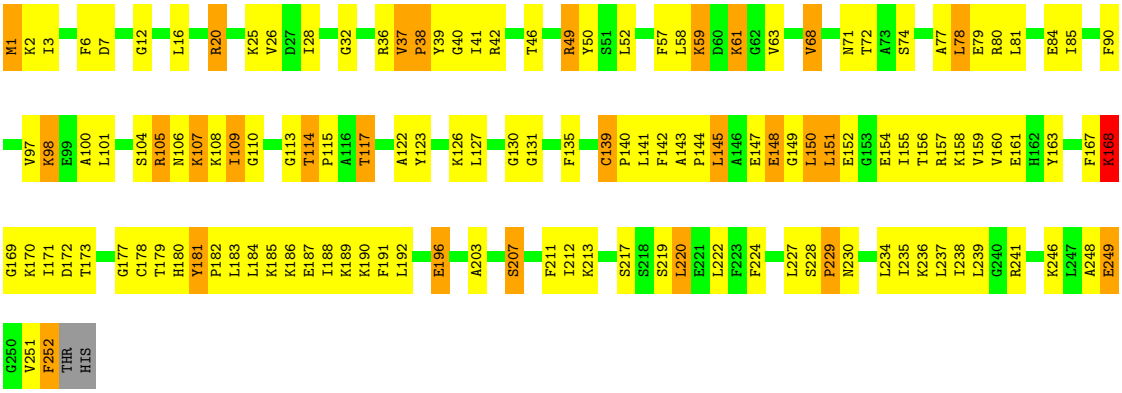
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

- Molecule 1: GLUTAMATE RACEMASE

Chain A: 



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	72.17Å 72.17Å 184.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	88.7 (8.00-2.30)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.09	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.221 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2066	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

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: DGN

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	0.67	0/1984	0.90	1/2670 (0.0%)

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	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	213	LYS	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	TYR	Sidechain

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	1952	0	2052	126	0
2	A	10	0	9	9	0
3	A	104	0	0	5	0
All	All	2066	0	2061	127	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 32.

All (127) 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:3:ILE:HD11	1:A:212:ILE:HD11	1.45	0.98
1:A:100:ALA:HB1	1:A:109:ILE:HD13	1.47	0.94
1:A:71:ASN:H	2:A:538:DGN:H	1.18	0.90
1:A:177:GLY:O	1:A:178:CYS:SG	2.31	0.88
1:A:105:ARG:HA	1:A:105:ARG:HE	1.41	0.86
1:A:159:VAL:HG11	1:A:182:PRO:HG2	1.60	0.84
1:A:20:ARG:HG2	1:A:28:ILE:HD12	1.61	0.83
1:A:71:ASN:H	2:A:538:DGN:H2	1.28	0.81
1:A:100:ALA:HB1	1:A:109:ILE:CD1	2.09	0.80
1:A:150:LEU:H	1:A:150:LEU:HD22	1.47	0.80
1:A:3:ILE:HD11	1:A:212:ILE:CD1	2.14	0.77
1:A:186:LYS:O	1:A:190:LYS:HG2	1.81	0.77
1:A:177:GLY:C	1:A:178:CYS:SG	2.63	0.76
1:A:71:ASN:N	2:A:538:DGN:N	2.26	0.76
1:A:177:GLY:C	1:A:178:CYS:HG	1.90	0.74
1:A:178:CYS:SG	2:A:538:DGN:C	2.79	0.71
1:A:168:LYS:HG3	1:A:169:GLY:H	1.56	0.70
1:A:37:VAL:HG13	1:A:38:PRO:HD3	1.72	0.70
1:A:148:GLU:HG3	1:A:181:TYR:CD2	2.26	0.70
1:A:178:CYS:SG	3:A:599:HOH:O	2.51	0.69
1:A:71:ASN:HB2	2:A:538:DGN:H	1.57	0.68
1:A:72:THR:OG1	1:A:117:THR:HG22	1.94	0.68
1:A:235:ILE:HG23	1:A:239:LEU:HD12	1.76	0.67
1:A:236:LYS:HA	1:A:241:ARG:O	1.95	0.67
1:A:20:ARG:HG2	1:A:28:ILE:CD1	2.25	0.66
1:A:3:ILE:CD1	1:A:212:ILE:HD11	2.23	0.66
1:A:115:PRO:HG3	1:A:141:LEU:HD11	1.77	0.66
1:A:156:THR:HG23	1:A:182:PRO:HB3	1.79	0.65
1:A:156:THR:HG23	1:A:182:PRO:CB	2.27	0.65
1:A:71:ASN:N	2:A:538:DGN:H	1.91	0.63
1:A:140:PRO:HB3	1:A:163:TYR:CE2	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ARG:HH11	1:A:187:GLU:HA	1.64	0.62
1:A:110:GLY:HA2	1:A:135:PHE:O	1.99	0.62
1:A:156:THR:O	1:A:159:VAL:HG12	1.99	0.62
1:A:154:GLU:O	1:A:158:LYS:HG3	1.99	0.62
1:A:108:LYS:HZ2	1:A:170:LYS:HB3	1.63	0.61
1:A:150:LEU:H	1:A:150:LEU:CD2	2.13	0.61
1:A:6:PHE:HB3	1:A:58:LEU:HD11	1.83	0.61
1:A:228:SER:HB3	1:A:229:PRO:HD2	1.82	0.60
1:A:234:LEU:O	1:A:238:ILE:HG13	2.00	0.60
1:A:57:PHE:CE2	1:A:252:PHE:HE1	2.19	0.60
1:A:114:THR:HB	1:A:117:THR:HG23	1.84	0.60
1:A:104:SER:HB3	1:A:107:LYS:HE3	1.83	0.60
1:A:59:LYS:HG3	1:A:85:ILE:HG23	1.83	0.59
1:A:77:ALA:O	1:A:81:LEU:HG	2.03	0.59
1:A:142:PHE:HE2	1:A:159:VAL:HG21	1.68	0.58
1:A:101:LEU:HD13	1:A:130:GLY:HA3	1.85	0.58
1:A:59:LYS:HG3	1:A:85:ILE:CG2	2.34	0.58
1:A:140:PRO:HG3	1:A:183:LEU:HD22	1.87	0.57
1:A:16:LEU:HD23	1:A:16:LEU:O	2.05	0.57
1:A:101:LEU:CD1	1:A:130:GLY:HA3	2.35	0.56
1:A:122:ALA:O	1:A:126:LYS:HG3	2.05	0.56
1:A:107:LYS:HG2	1:A:131:GLY:O	2.07	0.55
1:A:41:ILE:HG13	1:A:42:ARG:N	2.21	0.55
1:A:98:LYS:HE3	1:A:98:LYS:HA	1.88	0.55
1:A:151:LEU:HD22	1:A:151:LEU:H	1.72	0.55
1:A:41:ILE:HG13	1:A:42:ARG:H	1.72	0.54
1:A:68:VAL:HG22	1:A:68:VAL:O	2.07	0.54
1:A:168:LYS:HG3	1:A:169:GLY:N	2.22	0.54
1:A:71:ASN:ND2	1:A:123:TYR:HE2	2.06	0.54
1:A:161:GLU:HG3	1:A:191:PHE:CE1	2.42	0.54
1:A:114:THR:HG22	1:A:117:THR:H	1.73	0.53
1:A:147:GLU:O	1:A:151:LEU:HD23	2.09	0.53
1:A:80:ARG:NH1	1:A:80:ARG:HB3	2.24	0.53
1:A:248:ALA:O	1:A:249:GLU:HB2	2.09	0.52
1:A:156:THR:O	1:A:160:VAL:HG23	2.11	0.51
1:A:117:THR:HG21	3:A:599:HOH:O	2.11	0.51
1:A:237:LEU:HD21	3:A:617:HOH:O	2.10	0.51
1:A:220:LEU:HD13	1:A:222:LEU:HD21	1.93	0.51
1:A:151:LEU:HD13	1:A:155:ILE:CD1	2.41	0.50
1:A:61:LYS:NZ	3:A:560:HOH:O	2.45	0.50
1:A:36:ARG:HD2	1:A:50:TYR:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ILE:HD11	1:A:192:LEU:HD13	1.94	0.50
1:A:39:TYR:O	1:A:41:ILE:N	2.45	0.50
1:A:71:ASN:HB2	2:A:538:DGN:N	2.25	0.49
1:A:90:PHE:HZ	1:A:211:PHE:CD1	2.31	0.49
2:A:538:DGN:HG2	3:A:540:HOH:O	2.12	0.49
1:A:113:GLY:O	1:A:139:CYS:N	2.45	0.49
1:A:123:TYR:O	1:A:127:LEU:HG	2.13	0.49
1:A:114:THR:CB	1:A:117:THR:HG23	2.44	0.48
1:A:143:ALA:N	1:A:144:PRO:HD2	2.29	0.48
1:A:246:LYS:N	1:A:246:LYS:HD3	2.28	0.48
1:A:46:THR:HA	1:A:49:ARG:HG2	1.95	0.48
1:A:68:VAL:HG22	1:A:74:SER:OG	2.14	0.48
1:A:80:ARG:O	1:A:84:GLU:HG3	2.14	0.47
1:A:184:LEU:HB2	1:A:187:GLU:HG2	1.96	0.47
1:A:142:PHE:CE2	1:A:159:VAL:HG21	2.49	0.47
1:A:185:LYS:O	1:A:189:LYS:HG3	2.15	0.47
1:A:156:THR:HG23	1:A:182:PRO:HB2	1.95	0.47
1:A:147:GLU:C	1:A:149:GLY:H	2.17	0.47
1:A:52:LEU:HD23	1:A:81:LEU:HD23	1.97	0.46
1:A:71:ASN:N	2:A:538:DGN:H2	2.05	0.46
1:A:203:ALA:O	1:A:207:SER:HB3	2.16	0.46
1:A:105:ARG:HA	1:A:105:ARG:NE	2.19	0.46
1:A:106:ASN:HD22	1:A:108:LYS:HB2	1.81	0.45
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.60	0.45
1:A:114:THR:HG22	1:A:117:THR:HG23	1.99	0.45
1:A:185:LYS:HE3	1:A:186:LYS:HZ1	1.81	0.45
1:A:108:LYS:HZ2	1:A:170:LYS:CB	2.29	0.45
1:A:32:GLY:O	1:A:224:PHE:HA	2.17	0.44
1:A:78:LEU:HD12	1:A:78:LEU:HA	1.78	0.44
1:A:139:CYS:SG	1:A:178:CYS:HB2	2.58	0.44
1:A:173:THR:HA	1:A:196:GLU:O	2.18	0.44
1:A:167:PHE:N	1:A:167:PHE:CD1	2.86	0.44
1:A:108:LYS:HD3	1:A:170:LYS:O	2.18	0.44
1:A:7:ASP:OD2	1:A:12:GLY:N	2.51	0.43
1:A:16:LEU:HD23	1:A:16:LEU:C	2.38	0.43
1:A:150:LEU:HD22	1:A:150:LEU:N	2.24	0.43
1:A:150:LEU:O	1:A:152:GLU:N	2.48	0.43
1:A:68:VAL:O	1:A:68:VAL:CG2	2.66	0.43
1:A:167:PHE:N	1:A:167:PHE:HD1	2.17	0.43
1:A:2:LYS:HG2	1:A:63:VAL:HG12	2.01	0.43
1:A:80:ARG:HB3	1:A:80:ARG:HH11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:N	1:A:190:LYS:HD3	2.35	0.42
1:A:20:ARG:NH2	1:A:219:SER:O	2.47	0.42
1:A:114:THR:CG2	1:A:117:THR:HG23	2.50	0.42
1:A:109:ILE:HD12	1:A:173:THR:HG22	2.01	0.41
1:A:184:LEU:O	1:A:188:ILE:HG12	2.19	0.41
1:A:74:SER:HA	1:A:78:LEU:HD13	2.03	0.41
1:A:1:MET:HE2	1:A:1:MET:HB2	1.83	0.41
1:A:222:LEU:H	1:A:246:LYS:NZ	2.19	0.41
1:A:79:GLU:H	1:A:79:GLU:HG2	1.71	0.41
1:A:25:LYS:HA	1:A:25:LYS:HD3	1.90	0.41
1:A:97:VAL:HG13	1:A:127:LEU:HD23	2.02	0.41
1:A:159:VAL:HG13	1:A:160:VAL:N	2.35	0.41
1:A:71:ASN:HD21	1:A:123:TYR:HE2	1.68	0.40
1:A:234:LEU:HA	1:A:234:LEU:HD23	1.87	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	250/254 (98%)	225 (90%)	17 (7%)	8 (3%)	4 2

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	GLY
1	A	168	LYS
1	A	151	LEU
1	A	229	PRO
1	A	249	GLU
1	A	37	VAL
1	A	145	LEU

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Mol	Chain	Res	Type
1	A	38	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	211/213 (99%)	181 (86%)	30 (14%)	3 3

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	20	ARG
1	A	26	VAL
1	A	49	ARG
1	A	59	LYS
1	A	61	LYS
1	A	68	VAL
1	A	78	LEU
1	A	98	LYS
1	A	105	ARG
1	A	107	LYS
1	A	109	ILE
1	A	114	THR
1	A	117	THR
1	A	139	CYS
1	A	145	LEU
1	A	148	GLU
1	A	150	LEU
1	A	168	LYS
1	A	172	ASP
1	A	179	THR
1	A	180	HIS
1	A	196	GLU
1	A	207	SER
1	A	217	SER

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Mol	Chain	Res	Type
1	A	220	LEU
1	A	227	LEU
1	A	230	ASN
1	A	251	VAL
1	A	252	PHE

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

Mol	Chain	Res	Type
1	A	210	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	$\#\|Z\| > 2$
2	DGN	A	538	-	8,9,9	1.50	1 (12%)	8,11,11	1.33	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
2	DGN	A	538	-	-	1/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	538	DGN	CB-CA	-2.47	1.47	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	538	DGN	O-C-CA-N

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	538	DGN	9	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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.