



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:49 PM UTC

PDB ID : 1TTI / pdb_00001tti
Title : THREE NEW CRYSTAL STRUCTURES OF POINT MUTATION VARIANTS OF MONOTIM: CONFORMATIONAL FLEXIBILITY OF LOOP-1, LOOP-4 AND LOOP-8
Authors : Radha Kishan, K.V.; Wierenga, R.K.
Deposited on : 1995-04-19
Resolution : 2.40 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

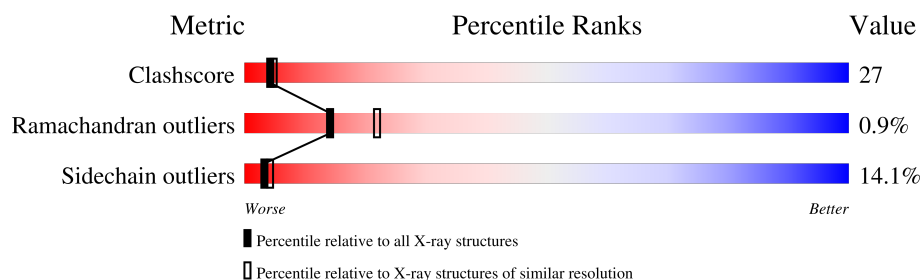
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	243	 45% 39% 12% ..

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	PGA	A	600	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1815 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.

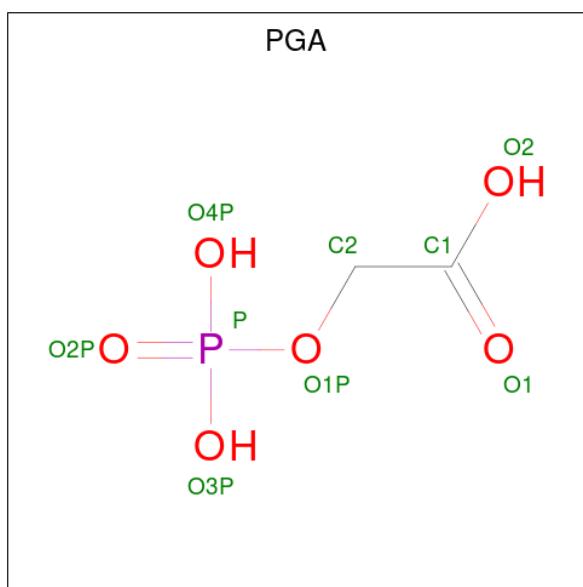
- Molecule 1 is a protein called TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	0	0
			1794	1142	316	332	4			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	GLY	ILE	engineered mutation	UNP P04789
A	69	ASN	ALA	engineered mutation	UNP P04789
A	70	ALA	LYS	engineered mutation	UNP P04789
A	71	ASP	SER	engineered mutation	UNP P04789
A	?	-	GLY	deletion	UNP P04789
A	?	-	ALA	deletion	UNP P04789
A	?	-	PHE	deletion	UNP P04789
A	?	-	THR	deletion	UNP P04789
A	?	-	GLY	deletion	UNP P04789
A	?	-	GLU	deletion	UNP P04789
A	?	-	VAL	deletion	UNP P04789
A	?	-	SER	deletion	UNP P04789
A	81	ALA	PRO	engineered mutation	UNP P04789
A	82	SER	ILE	conflict	UNP P04789
A	100	TRP	ALA	engineered mutation	UNP P04789

- Molecule 2 is 2-PHOSPHOGLYCOLIC ACID (CCD ID: PGA) (formula: C₂H₅O₆P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			9	2	6	1		

- Molecule 3 is water.

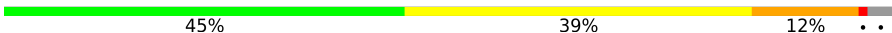
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		

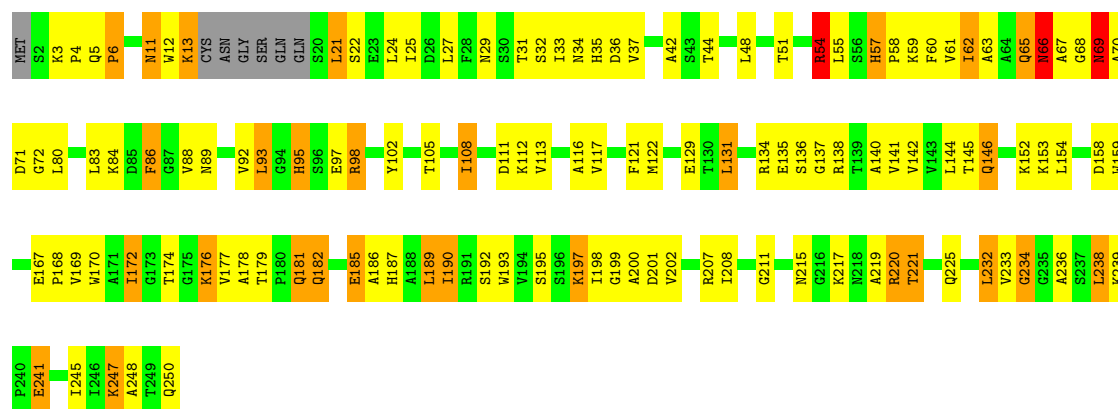
3 Residue-property plots

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: TRIOSEPHOSPHATE ISOMERASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	78.78Å 46.76Å 70.39Å 90.00° 113.99° 90.00°	Depositor
Resolution (Å)	32.00 – 2.40	Depositor
% Data completeness (in resolution range)	75.0 (32.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT, X-PLOR	Depositor
R, R_{free}	0.178 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1815	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGA

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	1.57	9/1827 (0.5%)	1.67	19/2477 (0.8%)

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

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	65	GLN	CD-OE1	6.14	1.35	1.23
1	A	11	ASN	CG-OD1	5.66	1.34	1.23
1	A	225	GLN	CA-C	-5.65	1.45	1.52
1	A	245	ILE	N-CA	-5.37	1.40	1.46
1	A	207	ARG	NE-CZ	5.37	1.39	1.33
1	A	57	HIS	CB-CG	-5.18	1.42	1.50
1	A	220	ARG	NE-CZ	5.16	1.38	1.33
1	A	4	PRO	N-CA	-5.10	1.41	1.47
1	A	95	HIS	ND1-CE1	5.02	1.37	1.32

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	GLY	CA-C-N	7.67	128.46	119.94
1	A	234	GLY	C-N-CA	7.67	128.46	119.94
1	A	66	ASN	N-CA-CB	6.20	120.97	110.49
1	A	21	LEU	N-CA-C	-5.92	104.90	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	ASN	O-C-N	5.87	130.40	122.59
1	A	232	LEU	CB-CA-C	5.61	118.81	110.62
1	A	54	ARG	N-CA-C	5.47	116.93	111.07
1	A	98	ARG	CA-C-N	5.37	128.47	120.31
1	A	98	ARG	C-N-CA	5.37	128.47	120.31
1	A	86	PHE	N-CA-C	-5.26	106.70	113.01
1	A	200	ALA	N-CA-C	-5.25	107.00	113.41
1	A	190	ILE	N-CA-CB	5.18	116.27	110.62
1	A	233	VAL	N-CA-C	5.12	115.23	107.75
1	A	122	MET	N-CA-C	-5.10	101.39	109.96
1	A	172	ILE	N-CA-C	5.09	114.59	107.37
1	A	146	GLN	N-CA-CB	5.08	117.50	109.94
1	A	6	PRO	N-CA-CB	5.04	108.67	103.38
1	A	219	ALA	N-CA-C	5.02	117.13	111.11
1	A	22	SER	N-CA-CB	5.01	118.05	110.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	GLU	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	1794	0	1818	98	0
2	A	9	0	2	4	0
3	A	12	0	0	2	0
All	All	1815	0	1820	98	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 27.

All (98) 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:220:ARG:HH21	1:A:221:THR:HG23	1.33	0.92
1:A:152:LYS:HE2	1:A:153:LYS:HE3	1.52	0.90
1:A:66:ASN:HB2	1:A:98:ARG:NE	1.95	0.82
1:A:144:LEU:HD21	1:A:189:LEU:HD12	1.60	0.81
1:A:220:ARG:NH2	1:A:221:THR:HG23	1.98	0.78
1:A:179:THR:H	1:A:182:GLN:HE21	1.32	0.77
1:A:197:LYS:NZ	1:A:197:LYS:HB3	2.00	0.76
1:A:66:ASN:HB3	1:A:112:LYS:NZ	2.02	0.75
1:A:66:ASN:HB2	1:A:98:ARG:CZ	2.19	0.73
1:A:144:LEU:HD21	1:A:189:LEU:CD1	2.20	0.72
1:A:98:ARG:O	1:A:102:TYR:HB2	1.91	0.70
1:A:179:THR:H	1:A:182:GLN:NE2	1.90	0.70
1:A:195:SER:HA	1:A:199:GLY:O	1.91	0.70
1:A:234:GLY:N	2:A:600:PGA:H22	2.07	0.70
1:A:154:LEU:HD12	1:A:159:TRP:CZ2	2.28	0.69
1:A:178:ALA:HA	1:A:182:GLN:NE2	2.08	0.69
1:A:95:HIS:O	1:A:98:ARG:HB2	1.94	0.68
1:A:179:THR:N	1:A:182:GLN:HE21	1.91	0.67
1:A:35:HIS:CD2	1:A:250:GLN:HB3	2.31	0.65
1:A:65:GLN:O	1:A:67:ALA:N	2.27	0.64
1:A:35:HIS:O	1:A:59:LYS:HE3	1.96	0.64
1:A:84:LYS:HE3	1:A:89:ASN:ND2	2.15	0.62
1:A:138:ARG:O	1:A:142:VAL:HG23	2.00	0.62
1:A:68:GLY:O	1:A:69:ASN:HB2	1.99	0.61
1:A:198:ILE:HD13	1:A:198:ILE:N	2.16	0.60
1:A:83:LEU:O	1:A:88:VAL:N	2.35	0.59
1:A:197:LYS:HB3	1:A:197:LYS:HZ3	1.67	0.59
1:A:220:ARG:O	1:A:220:ARG:HG2	2.03	0.57
1:A:178:ALA:CA	1:A:182:GLN:HE21	2.18	0.57
1:A:11:ASN:ND2	1:A:13:LYS:HD2	2.20	0.56
1:A:11:ASN:HB2	1:A:232:LEU:HD11	1.88	0.56
1:A:236:ALA:HA	1:A:239:LYS:HE3	1.87	0.56
1:A:42:ALA:HA	1:A:63:ALA:O	2.06	0.55
1:A:54:ARG:HH11	1:A:54:ARG:HB3	1.71	0.55
1:A:21:LEU:O	1:A:24:LEU:HB2	2.07	0.54
1:A:178:ALA:HA	1:A:182:GLN:HE21	1.70	0.53
1:A:234:GLY:CA	2:A:600:PGA:H22	2.38	0.53
1:A:25:ILE:O	1:A:29:ASN:HB2	2.09	0.53
1:A:179:THR:OG1	1:A:182:GLN:HG3	2.08	0.53
1:A:129:GLU:OE2	1:A:134:ARG:HB2	2.09	0.53
1:A:197:LYS:C	1:A:198:ILE:HD13	2.34	0.52
1:A:186:ALA:O	1:A:190:ILE:HG13	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:ASN:O	1:A:80:LEU:HG	2.09	0.52
1:A:105:THR:OG1	1:A:108:ILE:HG13	2.09	0.52
1:A:220:ARG:HH21	1:A:221:THR:CG2	2.17	0.52
1:A:92:VAL:O	1:A:93:LEU:HD13	2.11	0.51
1:A:187:HIS:CE1	1:A:208:ILE:HG22	2.45	0.51
1:A:197:LYS:HB3	1:A:197:LYS:HZ2	1.74	0.51
1:A:215:ASN:OD1	1:A:217:LYS:HB3	2.10	0.51
1:A:236:ALA:HB1	1:A:241:GLU:OE2	2.11	0.50
1:A:113:VAL:O	1:A:117:VAL:HG23	2.13	0.49
1:A:33:ILE:HG21	1:A:59:LYS:HD3	1.95	0.48
1:A:51:THR:HG22	1:A:62:ILE:HG21	1.95	0.48
1:A:33:ILE:CG2	1:A:59:LYS:HD3	2.44	0.47
1:A:168:PRO:HB2	1:A:170:TRP:CE2	2.50	0.47
1:A:140:ALA:O	1:A:144:LEU:HG	2.14	0.47
1:A:55:LEU:HD21	1:A:60:PHE:HB3	1.96	0.47
1:A:66:ASN:HB3	1:A:112:LYS:HZ1	1.79	0.47
1:A:66:ASN:HB2	1:A:98:ARG:CD	2.45	0.47
1:A:247:LYS:O	1:A:250:GLN:HG2	2.14	0.47
1:A:117:VAL:HG11	1:A:158:ASP:HB3	1.97	0.46
1:A:215:ASN:OD1	1:A:217:LYS:N	2.44	0.46
1:A:66:ASN:HB3	1:A:112:LYS:HZ2	1.78	0.46
1:A:234:GLY:H	2:A:600:PGA:H22	1.78	0.46
1:A:12:TRP:CE3	1:A:21:LEU:HD13	2.51	0.46
1:A:248:ALA:C	1:A:250:GLN:H	2.24	0.46
1:A:5:GLN:HG3	1:A:36:ASP:OD2	2.17	0.45
1:A:34:ASN:OD1	1:A:247:LYS:NZ	2.50	0.45
1:A:234:GLY:HA3	2:A:600:PGA:H22	1.99	0.45
1:A:116:ALA:HB1	1:A:121:PHE:HB2	1.98	0.44
1:A:69:ASN:ND2	1:A:70:ALA:H	2.16	0.44
1:A:201:ASP:OD1	1:A:202:VAL:N	2.50	0.44
1:A:169:VAL:HA	1:A:172:ILE:HD12	1.99	0.44
1:A:84:LYS:CE	1:A:89:ASN:ND2	2.80	0.44
1:A:86:PHE:HD2	1:A:88:VAL:HG23	1.83	0.43
1:A:181:GLN:O	1:A:185:GLU:HB3	2.19	0.43
1:A:57:HIS:ND1	1:A:58:PRO:HD2	2.33	0.43
1:A:135:GLU:C	1:A:137:GLY:H	2.27	0.43
1:A:142:VAL:O	1:A:145:THR:HB	2.19	0.43
1:A:83:LEU:HD23	1:A:83:LEU:HA	1.74	0.43
1:A:84:LYS:HE3	1:A:89:ASN:HD21	1.81	0.43
1:A:6:PRO:HG3	3:A:602:HOH:O	2.19	0.42
1:A:131:LEU:HB2	1:A:170:TRP:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:HA	1:A:211:GLY:O	2.19	0.42
1:A:69:ASN:HB3	1:A:72:GLY:H	1.84	0.42
1:A:174:THR:OG1	1:A:176:LYS:HB2	2.18	0.42
1:A:3:LYS:HB2	3:A:604:HOH:O	2.19	0.42
1:A:31:THR:HG22	1:A:32:SER:N	2.34	0.42
1:A:66:ASN:CG	1:A:98:ARG:HG3	2.44	0.42
1:A:238:LEU:HD12	1:A:238:LEU:HA	1.87	0.41
1:A:37:VAL:O	1:A:37:VAL:HG13	2.19	0.41
1:A:98:ARG:HA	1:A:98:ARG:HD3	1.81	0.41
1:A:141:VAL:O	1:A:145:THR:OG1	2.31	0.41
1:A:192:SER:OG	1:A:193:TRP:N	2.54	0.41
1:A:144:LEU:HD23	1:A:144:LEU:HA	1.86	0.41
1:A:215:ASN:O	1:A:217:LYS:N	2.53	0.41
1:A:154:LEU:HA	1:A:154:LEU:HD23	1.77	0.41
1:A:215:ASN:C	1:A:217:LYS:H	2.29	0.41

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	232/243 (96%)	214 (92%)	16 (7%)	2 (1%)	14 22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	66	ASN

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	185/191 (97%)	159 (86%)	26 (14%)	3 4

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

Mol	Chain	Res	Type
1	A	13	LYS
1	A	27	LEU
1	A	44	THR
1	A	48	LEU
1	A	54	ARG
1	A	61	VAL
1	A	62	ILE
1	A	69	ASN
1	A	71	ASP
1	A	93	LEU
1	A	97	GLU
1	A	108	ILE
1	A	111	ASP
1	A	131	LEU
1	A	136	SER
1	A	146	GLN
1	A	176	LYS
1	A	177	VAL
1	A	181	GLN
1	A	182	GLN
1	A	185	GLU
1	A	189	LEU
1	A	197	LYS
1	A	221	THR
1	A	238	LEU
1	A	247	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	89	ASN
1	A	106	ASN
1	A	132	GLN
1	A	181	GLN
1	A	182	GLN
1	A	250	GLN

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 oligosaccharides 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	PGA	A	600	-	8,8,8	1.54	2 (25%)	10,11,11	1.19	1 (10%)

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	PGA	A	600	-	-	5/6/6/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	PGA	O2-C1	-2.89	1.21	1.30
2	A	600	PGA	O1-C1	2.44	1.30	1.22

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	PGA	O1P-C2-C1	2.47	114.26	110.54

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	600	PGA	C2-O1P-P-O2P
2	A	600	PGA	C2-O1P-P-O3P
2	A	600	PGA	C2-O1P-P-O4P
2	A	600	PGA	O1-C1-C2-O1P
2	A	600	PGA	O2-C1-C2-O1P

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	PGA	4	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.