



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:42 PM UTC

PDB ID : 1M7P / pdb_00001m7p
Title : Plasmodium Falciparum Triosephosphate isomerase (PfTIM) compled to substrate analog glycerol-3-phosphate (G3P).
Authors : Parthasarathy, S.; Balaram, H.; Balaram, P.; Murthy, M.R.N.
Deposited on : 2002-07-22
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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

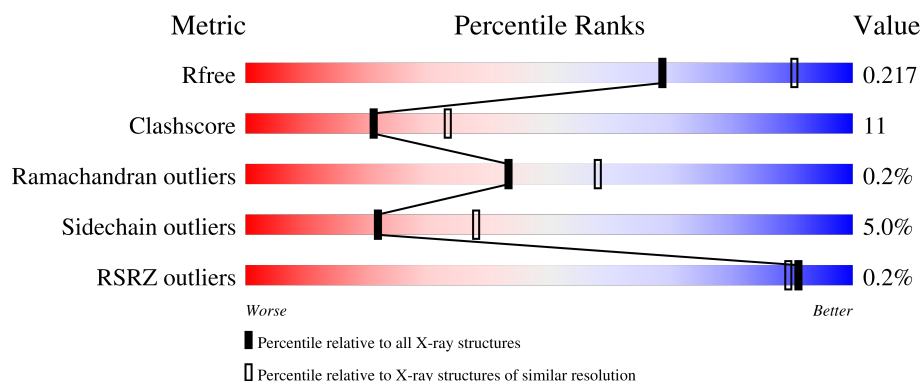
1 Overall quality at a glance

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))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (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 $\leq 5\%$. 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	248	 71% 26% ..
1	B	248	 70% 23% 5% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4067 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.

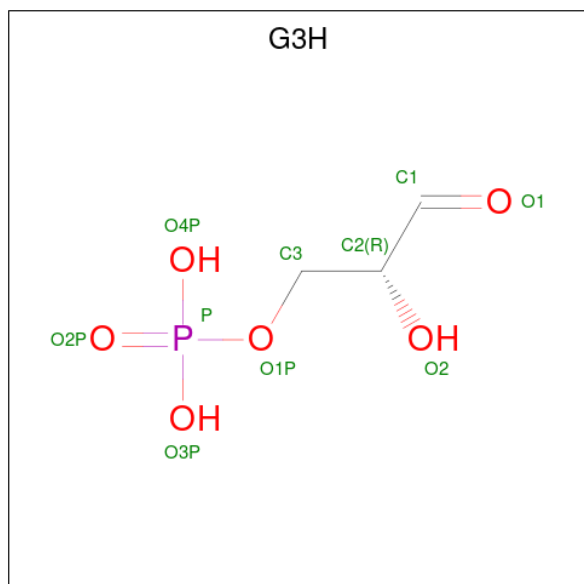
- Molecule 1 is a protein called Triosephosphate Isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	0	0
			1956	1239	333	379	5			
1	B	246	Total	C	N	O	S	0	0	0
			1956	1239	333	379	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	163	VAL	ALA	conflict	UNP Q07412
B	163	VAL	ALA	conflict	UNP Q07412

- Molecule 2 is GLYCERALDEHYDE-3-PHOSPHATE (CCD ID: G3H) (formula: $C_3H_7O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			10	3	6	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	O	P	0	0
			10	3	6	1		

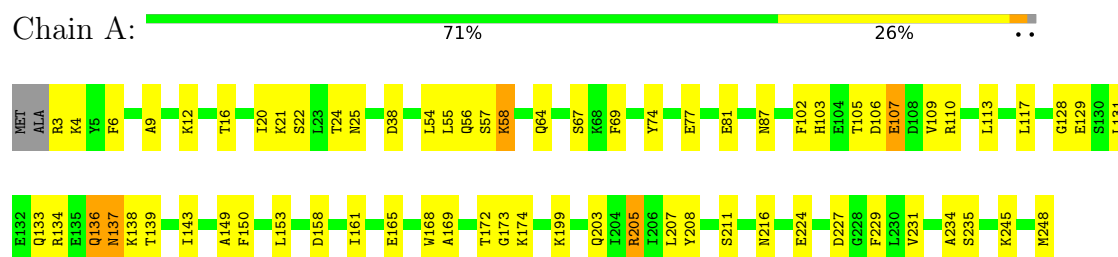
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total	O	0	0
			57	57		
3	B	78	Total	O	0	0
			78	78		

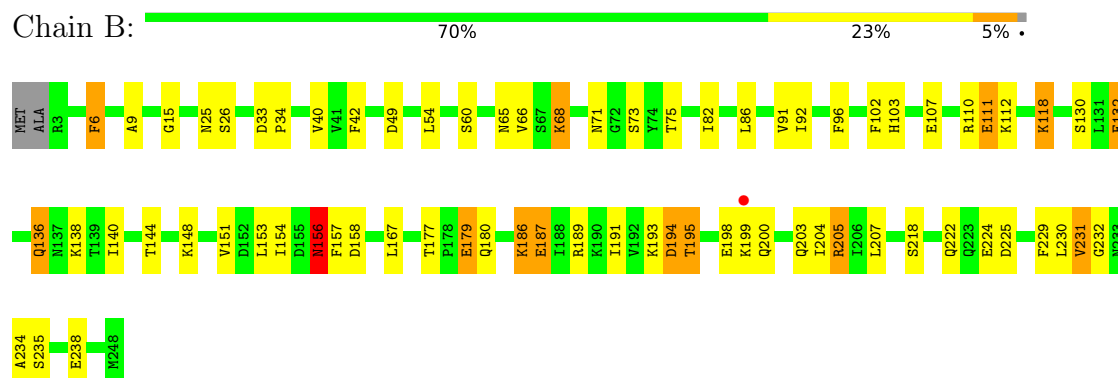
3 Residue-property plots

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 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: Triosephosphate Isomerase



• Molecule 1: Triosephosphate Isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.12Å 51.08Å 89.55Å 90.00° 91.39° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.1 (20.00-2.40) 92.3 (20.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.71 (at 2.41Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.179 , 0.216 0.180 , 0.217	Depositor DCC
R_{free} test set	1755 reflections (9.80%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4067	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G3H

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	0.47	0/1988	1.06	14/2682 (0.5%)
1	B	0.62	1/1988 (0.1%)	1.08	17/2682 (0.6%)
All	All	0.55	1/3976 (0.0%)	1.07	31/5364 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	132	GLU	C-O	5.91	1.31	1.24

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ASN	CA-C-N	-9.24	107.87	122.29
1	A	137	ASN	C-N-CA	-9.24	107.87	122.29
1	B	230	LEU	N-CA-C	-7.81	92.36	107.44
1	A	102	PHE	N-CA-C	7.76	123.89	112.94
1	B	68	LYS	N-CA-C	-7.59	104.02	113.28
1	B	6	PHE	CA-C-N	-7.28	113.42	123.10
1	B	6	PHE	C-N-CA	-7.28	113.42	123.10
1	B	103	HIS	CA-C-N	-6.86	111.93	122.09
1	B	103	HIS	C-N-CA	-6.86	111.93	122.09
1	A	137	ASN	CB-CA-C	-6.70	101.91	111.95
1	B	157	PHE	N-CA-C	6.63	122.53	113.37
1	A	103	HIS	N-CA-C	6.44	120.44	111.74
1	B	158	ASP	N-CA-C	-5.94	106.19	113.50
1	A	58	LYS	N-CA-C	-5.94	104.81	111.28
1	B	102	PHE	N-CA-C	5.88	119.71	111.30
1	B	229	PHE	N-CA-C	5.76	116.98	108.86
1	B	194	ASP	N-CA-C	5.65	119.70	113.21
1	A	16	THR	N-CA-C	-5.56	100.96	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	SER	N-CA-C	-5.54	106.58	113.55
1	B	229	PHE	CA-C-N	-5.50	114.22	122.47
1	B	229	PHE	C-N-CA	-5.50	114.22	122.47
1	A	173	GLY	N-CA-C	-5.39	107.78	115.64
1	A	136	GLN	CB-CA-C	-5.34	102.79	111.06
1	A	158	ASP	N-CA-C	-5.29	107.20	113.97
1	A	107	GLU	N-CA-CB	-5.28	102.35	110.16
1	A	224	GLU	N-CA-C	5.20	119.10	112.34
1	B	156	ASN	N-CA-CB	-5.15	103.01	110.84
1	B	15	GLY	N-CA-C	5.09	118.00	112.29
1	A	208	TYR	N-CA-C	-5.08	101.02	109.46
1	B	231	VAL	N-CA-C	5.08	115.59	108.89
1	B	224	GLU	N-CA-C	5.06	117.18	111.11

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	1956	0	1953	40	0
1	B	1956	0	1953	48	0
2	A	10	0	2	0	0
2	B	10	0	2	1	0
3	A	57	0	0	2	0
3	B	78	0	0	3	0
All	All	4067	0	3910	86	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 11.

All (86) 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:B:66:VAL:HG11	1:B:91:VAL:HG11	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:GLN:N	1:B:200:GLN:OE1	2.21	0.73
1:A:131:LEU:HD11	1:A:174:LYS:HE3	1.73	0.70
1:B:186:LYS:NZ	1:B:186:LYS:HB3	2.08	0.68
1:A:56:GLN:OE1	1:A:58:LYS:HE3	1.95	0.67
1:B:118:LYS:HB2	1:B:118:LYS:NZ	2.10	0.66
1:B:6:PHE:CD1	1:B:207:LEU:HD11	2.31	0.65
1:A:38:ASP:OD2	1:A:205:ARG:NH2	2.31	0.64
1:A:9:ALA:HB1	1:A:235:SER:HB2	1.79	0.64
1:B:9:ALA:HB1	1:B:235:SER:HB2	1.79	0.63
1:B:191:ILE:O	1:B:195:THR:OG1	2.17	0.62
1:B:140:ILE:HD12	1:B:187:GLU:HG3	1.83	0.61
1:A:110:ARG:HD2	1:A:149:ALA:O	2.00	0.61
1:B:65:ASN:HD21	1:B:112:LYS:NZ	1.98	0.61
1:B:218:SER:O	1:B:222:GLN:HG2	2.04	0.58
1:A:12:LYS:HD3	1:B:73:SER:HA	1.86	0.57
1:B:130:SER:HA	1:B:167:LEU:HB2	1.87	0.57
1:B:6:PHE:HB3	1:B:207:LEU:HD21	1.87	0.56
1:A:105:THR:OG1	1:A:107:GLU:HB2	2.06	0.56
1:B:186:LYS:HB3	1:B:186:LYS:HZ3	1.68	0.55
1:B:179:GLU:H	1:B:179:GLU:CD	2.13	0.55
1:B:140:ILE:CD1	1:B:187:GLU:HG3	2.37	0.54
1:A:139:THR:O	1:A:143:ILE:HG12	2.07	0.53
1:A:131:LEU:CD1	1:A:174:LYS:HE3	2.37	0.53
1:B:40:VAL:HG22	1:B:60:SER:HB2	1.90	0.53
1:B:151:VAL:HG23	1:B:154:ILE:HD12	1.90	0.53
1:A:12:LYS:HD2	3:A:630:HOH:O	2.08	0.52
1:A:20:ILE:O	1:A:24:THR:HG23	2.09	0.52
1:B:232:GLY:HA3	2:B:6401:G3H:O3P	2.10	0.52
1:A:133:GLN:O	1:A:138:LYS:HB2	2.09	0.52
1:A:205:ARG:HD3	3:A:529:HOH:O	2.10	0.51
1:B:132:GLU:O	1:B:136:GLN:HG3	2.09	0.51
1:B:205:ARG:NH2	3:B:538:HOH:O	2.44	0.50
1:B:66:VAL:CG1	1:B:91:VAL:HG11	2.37	0.50
1:A:110:ARG:HG3	1:A:153:LEU:HD11	1.94	0.50
1:B:136:GLN:HB2	1:B:138:LYS:HE2	1.94	0.50
1:A:168:TRP:O	1:A:172:THR:HG21	2.11	0.50
1:A:4:LYS:HE2	1:A:38:ASP:CG	2.37	0.49
1:A:3:ARG:HD2	1:A:227:ASP:CG	2.37	0.49
1:B:205:ARG:NE	3:B:538:HOH:O	2.46	0.49
1:A:216:ASN:C	1:A:216:ASN:OD1	2.56	0.48
1:B:189:ARG:NH2	1:B:204:ILE:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ILE:HD12	1:A:161:ILE:N	2.28	0.48
1:B:26:SER:OG	1:B:238:GLU:HG2	2.14	0.48
1:A:21:LYS:O	1:A:21:LYS:HG2	2.14	0.47
1:B:118:LYS:HB2	1:B:118:LYS:HZ2	1.79	0.46
1:B:96:PHE:CB	1:B:167:LEU:HD21	2.45	0.46
1:A:199:LYS:HD3	1:A:203:GLN:NE2	2.30	0.46
1:A:9:ALA:CB	1:A:235:SER:HB2	2.45	0.46
1:B:71:ASN:HD21	1:B:82:ILE:HG13	1.80	0.46
1:B:144:THR:HA	1:B:191:ILE:HD13	1.99	0.45
1:B:231:VAL:CG1	1:B:234:ALA:HB3	2.47	0.45
1:A:113:LEU:HD23	1:A:150:PHE:HB2	1.99	0.45
1:B:68:LYS:HB2	1:B:111:GLU:HB3	1.97	0.44
1:B:136:GLN:HB2	1:B:138:LYS:HG3	2.00	0.44
1:A:245:LYS:O	1:A:248:MET:HG2	2.17	0.44
1:A:21:LYS:HA	1:A:54:LEU:HD13	2.00	0.43
1:A:69:PHE:CG	1:A:74:TYR:CE2	3.06	0.43
1:B:33:ASP:HA	1:B:34:PRO:HD2	1.93	0.43
1:B:199:LYS:HB3	1:B:200:GLN:OE1	2.18	0.43
1:A:231:VAL:CG1	1:A:234:ALA:HB3	2.48	0.43
1:A:6:PHE:CD2	1:A:207:LEU:HD11	2.54	0.43
1:B:65:ASN:HD21	1:B:112:LYS:HZ2	1.64	0.43
1:A:21:LYS:O	1:A:25:ASN:ND2	2.48	0.43
1:B:9:ALA:CB	1:B:235:SER:HB2	2.47	0.43
1:B:110:ARG:HG2	1:B:153:LEU:HD11	2.01	0.43
1:A:6:PHE:HB3	1:A:207:LEU:HD21	2.01	0.42
1:A:128:GLY:HA3	1:A:165:GLU:O	2.18	0.42
1:B:66:VAL:CG1	1:B:91:VAL:CG1	2.97	0.42
1:B:189:ARG:HD2	1:B:225:ASP:OD1	2.19	0.42
1:A:67:SER:HB2	1:A:77:GLU:HB3	2.01	0.42
1:A:129:GLU:OE2	1:A:134:ARG:NH1	2.52	0.42
1:B:156:ASN:C	1:B:156:ASN:HD22	2.27	0.42
1:A:168:TRP:CE3	1:A:169:ALA:HB2	2.55	0.42
1:A:136:GLN:OE1	1:A:138:LYS:HD2	2.19	0.42
1:B:118:LYS:HB2	1:B:118:LYS:HZ3	1.81	0.42
1:A:136:GLN:O	1:A:137:ASN:C	2.62	0.41
1:A:64:GLN:HB3	1:B:75:THR:HG23	2.02	0.41
1:A:69:PHE:CD2	1:A:74:TYR:CD2	3.08	0.41
1:B:193:LYS:HG3	1:B:198:GLU:HA	2.02	0.41
1:A:106:ASP:O	1:A:109:VAL:HB	2.20	0.41
1:B:148:LYS:HD2	3:B:612:HOH:O	2.20	0.41
1:A:87:ASN:OD1	1:A:87:ASN:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:THR:OG1	1:B:180:GLN:HG3	2.20	0.41
1:B:132:GLU:O	1:B:136:GLN:CG	2.69	0.40
1:B:42:PHE:CE2	1:B:92:ILE:HG13	2.56	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	244/248 (98%)	233 (96%)	10 (4%)	1 (0%)	30	43
1	B	244/248 (98%)	229 (94%)	15 (6%)	0	100	100
All	All	488/496 (98%)	462 (95%)	25 (5%)	1 (0%)	43	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	SER

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	219/220 (100%)	213 (97%)	6 (3%)	39	62
1	B	219/220 (100%)	203 (93%)	16 (7%)	13	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	438/440 (100%)	416 (95%)	22 (5%)	22	38

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	LEU
1	A	81	GLU
1	A	117	LEU
1	A	205	ARG
1	A	211	SER
1	A	229	PHE
1	B	25	ASN
1	B	49	ASP
1	B	54	LEU
1	B	86	LEU
1	B	107	GLU
1	B	111	GLU
1	B	118	LYS
1	B	136	GLN
1	B	156	ASN
1	B	179	GLU
1	B	186	LYS
1	B	187	GLU
1	B	194	ASP
1	B	195	THR
1	B	203	GLN
1	B	205	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	87	ASN
1	A	119	ASN
1	A	120	ASN
1	A	159	ASN
1	A	202	ASN
1	A	223	GLN
1	B	14	ASN
1	B	25	ASN
1	B	29	ASN

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Mol	Chain	Res	Type
1	B	56	GLN
1	B	65	ASN
1	B	71	ASN
1	B	87	ASN
1	B	136	GLN
1	B	156	ASN
1	B	185	HIS
1	B	223	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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	G3H	A	5401	-	8,9,9	6.17	3 (37%)	7,12,12	4.42	1 (14%)
2	G3H	B	6401	-	8,9,9	6.22	3 (37%)	7,12,12	4.36	1 (14%)

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	G3H	A	5401	-	-	5/7/8/8	-
2	G3H	B	6401	-	-	5/7/8/8	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6401	G3H	C3-C2	12.24	1.69	1.51
2	A	5401	G3H	C3-C2	11.82	1.68	1.51
2	A	5401	G3H	O1P-C3	-11.39	1.01	1.44
2	B	6401	G3H	O1P-C3	-11.22	1.02	1.44
2	A	5401	G3H	O1-C1	-5.56	0.98	1.20
2	B	6401	G3H	O1-C1	-5.49	0.99	1.20

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5401	G3H	O2-C2-C1	11.59	133.98	109.03
2	B	6401	G3H	O2-C2-C1	11.43	133.63	109.03

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5401	G3H	C1-C2-C3-O1P
2	A	5401	G3H	O2-C2-C3-O1P
2	A	5401	G3H	C3-O1P-P-O4P
2	B	6401	G3H	C1-C2-C3-O1P
2	B	6401	G3H	O2-C2-C3-O1P
2	B	6401	G3H	C3-O1P-P-O4P
2	A	5401	G3H	C3-O1P-P-O3P
2	B	6401	G3H	C3-O1P-P-O3P
2	A	5401	G3H	C3-O1P-P-O2P
2	B	6401	G3H	C3-O1P-P-O2P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	6401	G3H	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	246/248 (99%)	-0.41	0	100 100	10, 23, 46, 63	0
1	B	246/248 (99%)	-0.42	1 (0%)	88 86	8, 20, 44, 60	0
All	All	492/496 (99%)	-0.42	1 (0%)	91 89	8, 21, 46, 63	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	199	LYS	2.2

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	G3H	A	5401	10/10	0.72	0.19	58,75,85,86	10
2	G3H	B	6401	10/10	0.76	0.20	60,74,83,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.