



# wwPDB X-ray Structure Validation Summary Report

Jul 31, 2023 – 12:42 AM EDT

PDB ID : 1ML1  
Title : PROTEIN ENGINEERING WITH MONOMERIC TRIOSEPHOSPHATE ISOMERASE: THE MODELLING AND STRUCTURE VERIFICATION OF A SEVEN RESIDUE LOOP  
Authors : Thanki, N.; Zeelen, J.P.; Mathieu, M.; Jaenicke, R.; Abagyan, R.A.; Wierenga, R.; Schliebs, W.  
Deposited on : 1996-09-27  
Resolution : 2.60 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.34  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.34

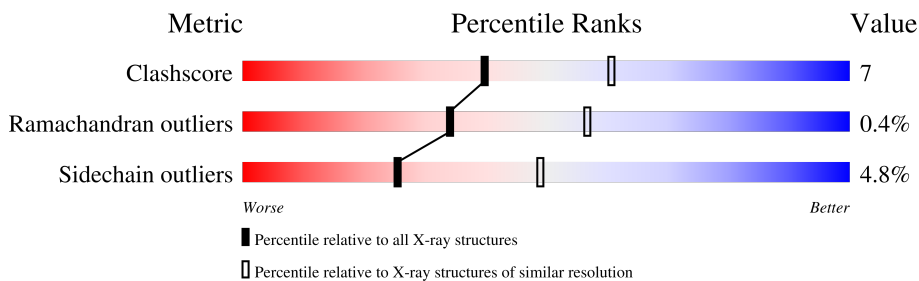
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain	
1	A	243	79%	19% ..
1	C	243	78%	20% ..
1	E	243	77%	21% ..
1	G	243	77%	21% ..
1	I	243	77%	21% ..
1	K	243	77%	21% ..

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11063 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
			Total	C	N	O	S			
1	A	241	1826	1160	321	341	4	0	0	0
1	C	241	1826	1160	321	341	4	0	0	0
1	E	241	1826	1160	321	341	4	0	0	0
1	G	241	1826	1160	321	341	4	0	0	0
1	I	241	1826	1160	321	341	4	0	0	0
1	K	241	1826	1160	321	341	4	0	0	0

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	SER	ASN	conflict	UNP P04789
A	18	PRO	GLN	conflict	UNP P04789
A	19	ASP	GLN	conflict	UNP P04789
A	68	GLY	ILE	conflict	UNP P04789
A	69	ASN	ALA	conflict	UNP P04789
A	70	ALA	LYS	conflict	UNP P04789
A	71	ASP	SER	conflict	UNP P04789
A	72	ALA	GLY	conflict	UNP P04789
A	?	-	ALA	deletion	UNP P04789
A	?	-	PHE	deletion	UNP P04789
A	?	-	THR	deletion	UNP P04789
A	?	-	GLU	deletion	UNP P04789
A	?	-	VAL	deletion	UNP P04789
A	?	-	SER	deletion	UNP P04789
A	81	ALA	PRO	conflict	UNP P04789
A	82	SER	ILE	conflict	UNP P04789
A	100	TRP	ALA	conflict	UNP P04789

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Chain	Residue	Modelled	Actual	Comment	Reference
C	15	SER	ASN	conflict	UNP P04789
C	18	PRO	GLN	conflict	UNP P04789
C	19	ASP	GLN	conflict	UNP P04789
C	68	GLY	ILE	conflict	UNP P04789
C	69	ASN	ALA	conflict	UNP P04789
C	70	ALA	LYS	conflict	UNP P04789
C	71	ASP	SER	conflict	UNP P04789
C	72	ALA	GLY	conflict	UNP P04789
C	?	-	ALA	deletion	UNP P04789
C	?	-	PHE	deletion	UNP P04789
C	?	-	THR	deletion	UNP P04789
C	?	-	GLU	deletion	UNP P04789
C	?	-	VAL	deletion	UNP P04789
C	?	-	SER	deletion	UNP P04789
C	81	ALA	PRO	conflict	UNP P04789
C	82	SER	ILE	conflict	UNP P04789
C	100	TRP	ALA	conflict	UNP P04789
E	15	SER	ASN	conflict	UNP P04789
E	18	PRO	GLN	conflict	UNP P04789
E	19	ASP	GLN	conflict	UNP P04789
E	68	GLY	ILE	conflict	UNP P04789
E	69	ASN	ALA	conflict	UNP P04789
E	70	ALA	LYS	conflict	UNP P04789
E	71	ASP	SER	conflict	UNP P04789
E	72	ALA	GLY	conflict	UNP P04789
E	?	-	ALA	deletion	UNP P04789
E	?	-	PHE	deletion	UNP P04789
E	?	-	THR	deletion	UNP P04789
E	?	-	GLU	deletion	UNP P04789
E	?	-	VAL	deletion	UNP P04789
E	?	-	SER	deletion	UNP P04789
E	81	ALA	PRO	conflict	UNP P04789
E	82	SER	ILE	conflict	UNP P04789
E	100	TRP	ALA	conflict	UNP P04789
G	15	SER	ASN	conflict	UNP P04789
G	18	PRO	GLN	conflict	UNP P04789
G	19	ASP	GLN	conflict	UNP P04789
G	68	GLY	ILE	conflict	UNP P04789
G	69	ASN	ALA	conflict	UNP P04789
G	70	ALA	LYS	conflict	UNP P04789
G	71	ASP	SER	conflict	UNP P04789
G	72	ALA	GLY	conflict	UNP P04789

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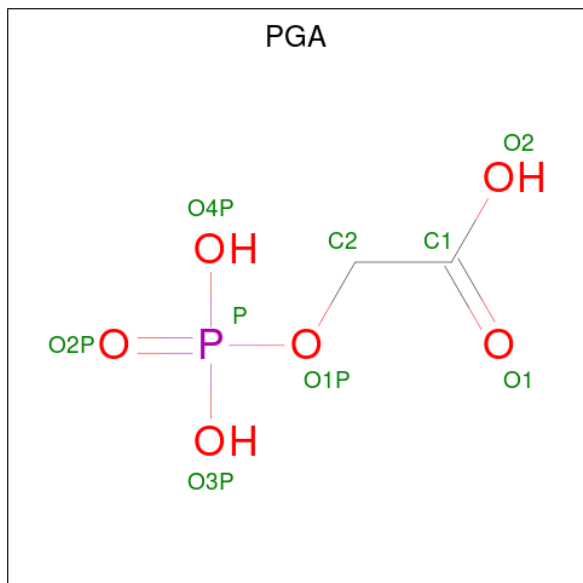
Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	ALA	deletion	UNP P04789
G	?	-	PHE	deletion	UNP P04789
G	?	-	THR	deletion	UNP P04789
G	?	-	GLU	deletion	UNP P04789
G	?	-	VAL	deletion	UNP P04789
G	?	-	SER	deletion	UNP P04789
G	81	ALA	PRO	conflict	UNP P04789
G	82	SER	ILE	conflict	UNP P04789
G	100	TRP	ALA	conflict	UNP P04789
I	15	SER	ASN	conflict	UNP P04789
I	18	PRO	GLN	conflict	UNP P04789
I	19	ASP	GLN	conflict	UNP P04789
I	68	GLY	ILE	conflict	UNP P04789
I	69	ASN	ALA	conflict	UNP P04789
I	70	ALA	LYS	conflict	UNP P04789
I	71	ASP	SER	conflict	UNP P04789
I	72	ALA	GLY	conflict	UNP P04789
I	?	-	ALA	deletion	UNP P04789
I	?	-	PHE	deletion	UNP P04789
I	?	-	THR	deletion	UNP P04789
I	?	-	GLU	deletion	UNP P04789
I	?	-	VAL	deletion	UNP P04789
I	?	-	SER	deletion	UNP P04789
I	81	ALA	PRO	conflict	UNP P04789
I	82	SER	ILE	conflict	UNP P04789
I	100	TRP	ALA	conflict	UNP P04789
K	15	SER	ASN	conflict	UNP P04789
K	18	PRO	GLN	conflict	UNP P04789
K	19	ASP	GLN	conflict	UNP P04789
K	68	GLY	ILE	conflict	UNP P04789
K	69	ASN	ALA	conflict	UNP P04789
K	70	ALA	LYS	conflict	UNP P04789
K	71	ASP	SER	conflict	UNP P04789
K	72	ALA	GLY	conflict	UNP P04789
K	?	-	ALA	deletion	UNP P04789
K	?	-	PHE	deletion	UNP P04789
K	?	-	THR	deletion	UNP P04789
K	?	-	GLU	deletion	UNP P04789
K	?	-	VAL	deletion	UNP P04789
K	?	-	SER	deletion	UNP P04789
K	81	ALA	PRO	conflict	UNP P04789
K	82	SER	ILE	conflict	UNP P04789

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Chain	Residue	Modelled	Actual	Comment	Reference
K	100	TRP	ALA	conflict	UNP P04789

- Molecule 2 is 2-PHOSPHOGLYCOLIC ACID (three-letter code: PGA) (formula: C<sub>2</sub>H<sub>5</sub>O<sub>6</sub>P).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	10	10	10	0	0
3	C	7	7	7	0	0
3	E	8	8	8	0	0

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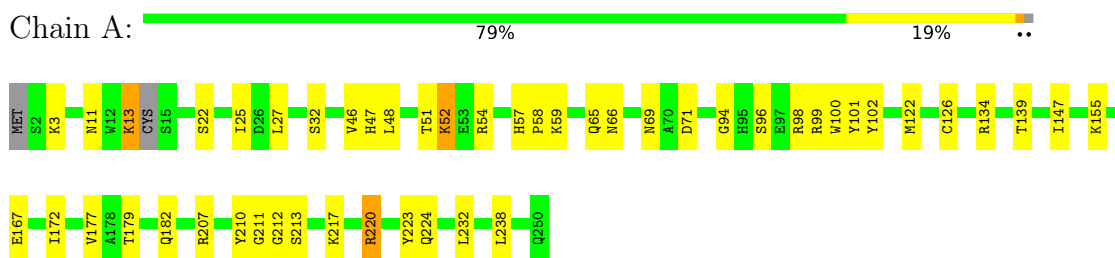
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	G	9	Total O 9 9	0	0
3	I	12	Total O 12 12	0	0
3	K	7	Total O 7 7	0	0

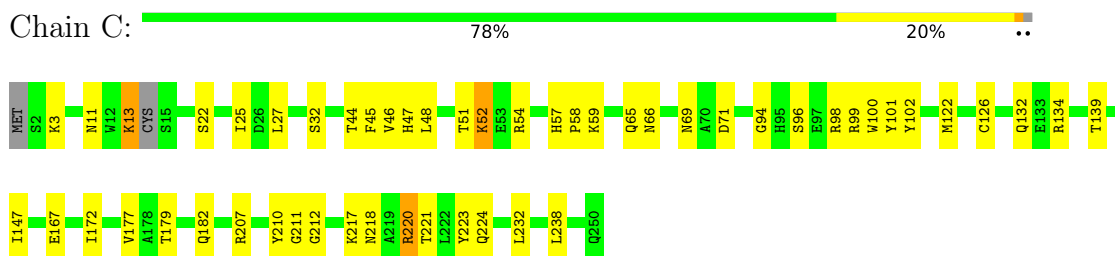
### 3 Residue-property plots [i](#)

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.

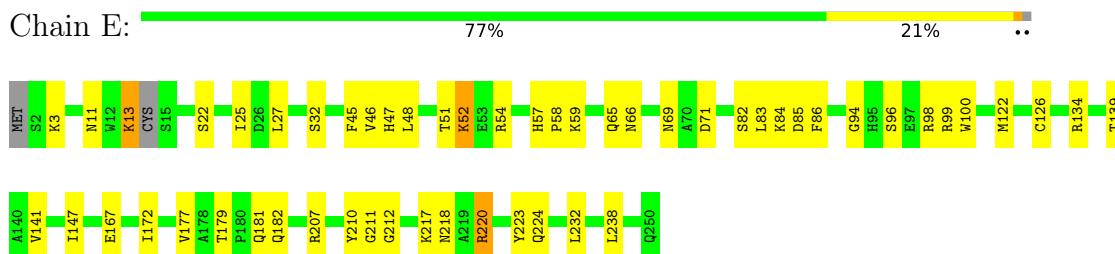
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



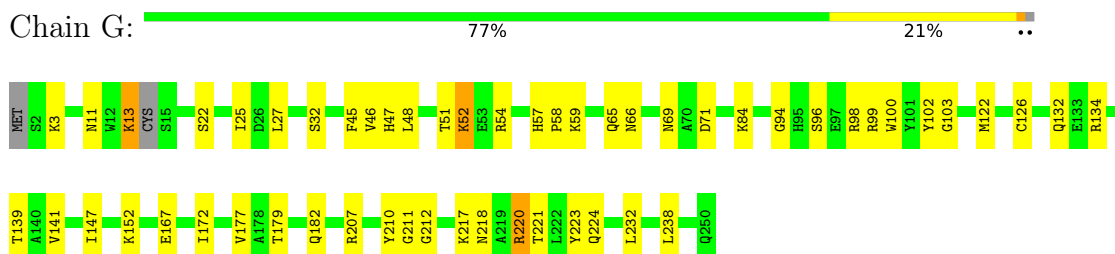
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE




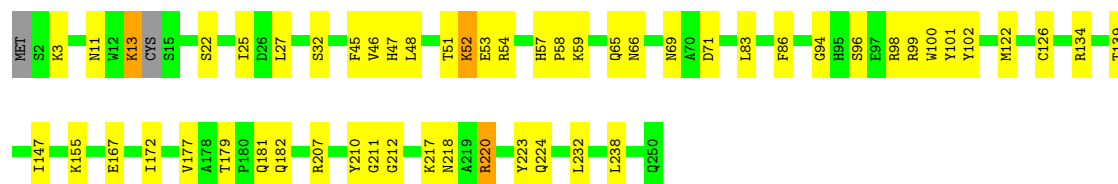
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE






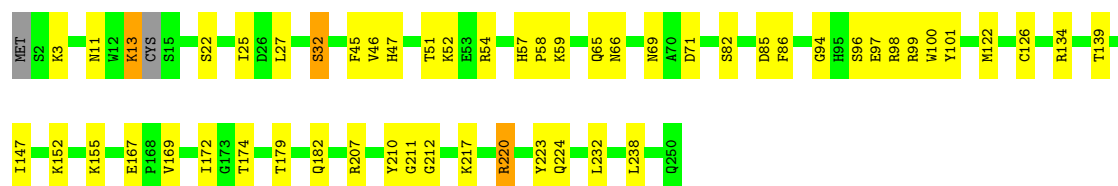
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain I:  77% 21% ..



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain K:  77% 21% ..



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	165.23Å 165.23Å 51.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.00 – 2.60 6.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	94.6 (32.00-2.60) 94.8 (6.00-2.65)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.19 (at 2.66Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.231 , 0.247 0.216 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.7	Xtrriage
Anisotropy	0.242	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 25.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.054 for -h,-k,l 0.046 for h,-h-k,-l 0.154 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11063	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.18% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>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: 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	0.53	0/1861	0.70	2/2526 (0.1%)
1	C	0.54	0/1861	0.70	2/2526 (0.1%)
1	E	0.55	0/1861	0.71	2/2526 (0.1%)
1	G	0.55	0/1861	0.71	2/2526 (0.1%)
1	I	0.53	0/1861	0.70	2/2526 (0.1%)
1	K	0.55	0/1861	0.70	2/2526 (0.1%)
All	All	0.54	0/11166	0.70	12/15156 (0.1%)

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
1	C	0	1
1	E	0	1
1	G	0	1
1	I	0	1
1	K	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	232	LEU	N-CA-C	-5.38	96.46	111.00
1	K	232	LEU	N-CA-C	-5.38	96.46	111.00
1	C	232	LEU	N-CA-C	-5.38	96.47	111.00
1	A	232	LEU	N-CA-C	-5.38	96.48	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	232	LEU	N-CA-C	-5.37	96.50	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	TYR	Sidechain
1	C	210	TYR	Sidechain
1	E	210	TYR	Sidechain
1	G	210	TYR	Sidechain
1	I	210	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	1826	0	1845	27	0
1	C	1826	0	1845	32	1
1	E	1826	0	1845	29	2
1	G	1826	0	1845	36	2
1	I	1826	0	1845	31	1
1	K	1826	0	1845	36	0
2	A	9	0	2	1	0
2	C	9	0	2	1	0
2	E	9	0	2	1	0
2	G	9	0	2	1	0
2	I	9	0	2	1	0
2	K	9	0	2	1	0
3	A	10	0	0	0	0
3	C	7	0	0	0	0
3	E	8	0	0	0	0
3	G	9	0	0	0	0
3	I	12	0	0	0	0
3	K	7	0	0	1	0
All	All	11063	0	11082	161	3

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.

The worst 5 of 161 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:G:100:TRP:HA	1:K:82:SER:HB2	1.33	1.10
1:C:102:TYR:OH	1:E:45:PHE:CE1	2.25	0.90
1:A:101:TYR:CD1	1:C:45:PHE:HB3	2.09	0.88
1:A:101:TYR:CG	1:C:45:PHE:HB3	2.15	0.81
1:G:102:TYR:OH	1:K:45:PHE:CE1	2.36	0.77

All (3) 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:C:221:THR:OG1	1:I:181:GLN:NE2[2_654]	1.03	1.17
1:E:181:GLN:NE2	1:G:221:THR:OG1[1_554]	1.09	1.11
1:E:181:GLN:NE2	1:G:221:THR:CB[1_554]	2.10	0.10

## 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	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
1	C	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
1	E	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
1	G	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
1	I	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
1	K	239/243 (98%)	232 (97%)	6 (2%)	1 (0%)	34	57
All	All	1434/1458 (98%)	1392 (97%)	36 (2%)	6 (0%)	34	57

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	GLY
1	C	212	GLY
1	E	212	GLY
1	G	212	GLY
1	I	212	GLY

### 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	189/191 (99%)	180 (95%)	9 (5%)	25	49
1	C	189/191 (99%)	180 (95%)	9 (5%)	25	49
1	E	189/191 (99%)	180 (95%)	9 (5%)	25	49
1	G	189/191 (99%)	180 (95%)	9 (5%)	25	49
1	I	189/191 (99%)	180 (95%)	9 (5%)	25	49
1	K	189/191 (99%)	180 (95%)	9 (5%)	25	49
All	All	1134/1146 (99%)	1080 (95%)	54 (5%)	25	49

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	27	LEU
1	G	238	LEU
1	K	98	ARG
1	G	32	SER
1	G	147	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	224	GLN
1	I	224	GLN
1	K	224	GLN
1	C	224	GLN

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Mol	Chain	Res	Type
1	A	224	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

6 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	PGA	E	600	-	8,8,8	1.80	2 (25%)	10,11,11	1.09	1 (10%)
2	PGA	K	600	-	8,8,8	1.84	2 (25%)	10,11,11	1.09	1 (10%)
2	PGA	I	600	-	8,8,8	1.83	2 (25%)	10,11,11	1.09	1 (10%)
2	PGA	C	600	-	8,8,8	1.81	2 (25%)	10,11,11	1.09	1 (10%)
2	PGA	G	600	-	8,8,8	1.83	2 (25%)	10,11,11	1.09	1 (10%)
2	PGA	A	600	-	8,8,8	1.84	2 (25%)	10,11,11	1.09	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	E	600	-	-	0/6/6/6	-
2	PGA	K	600	-	-	0/6/6/6	-
2	PGA	I	600	-	-	0/6/6/6	-
2	PGA	C	600	-	-	0/6/6/6	-
2	PGA	G	600	-	-	0/6/6/6	-
2	PGA	A	600	-	-	0/6/6/6	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	600	PGA	O1P-C2	-3.95	1.40	1.43
2	A	600	PGA	O1P-C2	-3.92	1.40	1.43
2	I	600	PGA	O1P-C2	-3.90	1.40	1.43
2	G	600	PGA	O1P-C2	-3.88	1.40	1.43
2	C	600	PGA	O1P-C2	-3.82	1.40	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	600	PGA	O1-C1-C2	-2.18	114.24	122.44
2	K	600	PGA	O1-C1-C2	-2.18	114.24	122.44
2	I	600	PGA	O1-C1-C2	-2.18	114.27	122.44
2	A	600	PGA	O1-C1-C2	-2.17	114.29	122.44
2	C	600	PGA	O1-C1-C2	-2.17	114.31	122.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	600	PGA	1	0
2	K	600	PGA	1	0
2	I	600	PGA	1	0
2	C	600	PGA	1	0
2	G	600	PGA	1	0
2	A	600	PGA	1	0

## 5.7 Other polymers [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.