



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 12:06 am BST

PDB ID : 1AW1  
Title : TRIOSEPHOSPHATE ISOMERASE OF VIBRIO MARINUS COMPLEXED WITH 2-PHOSPHOGLYCOLATE  
Authors : Maes, D.; Zeelen, J.P.; Wierenga, R.K.  
Deposited on : 1997-10-09  
Resolution : 2.70 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](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.

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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)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

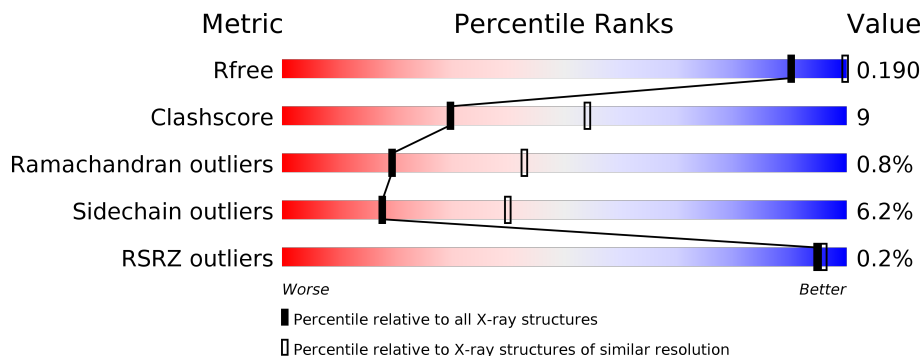
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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	256	 77% 21%
1	B	256	 80% 16%
1	D	256	 77% 21%
1	E	256	 80% 15%
1	G	256	 77% 21%
1	H	256	 80% 15%

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Mol	Chain	Length	Quality of chain
1	J	256	 77% 21% .
1	K	256	 80% 14% . .

## 2 Entry composition

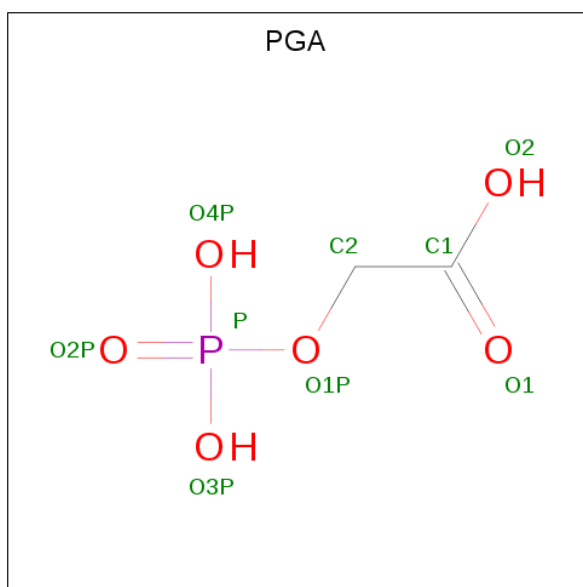
There are 3 unique types of molecules in this entry. The entry contains 15324 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	255	Total 1871	C 1172	N 323	O 369	S 7	2	0	0
1	B	254	Total 1865	C 1169	N 322	O 367	S 7	1	0	0
1	D	255	Total 1871	C 1172	N 323	O 369	S 7	2	0	0
1	E	254	Total 1865	C 1169	N 322	O 367	S 7	1	0	0
1	G	255	Total 1871	C 1172	N 323	O 369	S 7	2	0	0
1	H	254	Total 1865	C 1169	N 322	O 367	S 7	1	0	0
1	J	255	Total 1871	C 1172	N 323	O 369	S 7	2	0	0
1	K	254	Total 1865	C 1169	N 322	O 367	S 7	1	0	0

- 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
2	A	1	Total	C	O	P	0	0
			9	2	6	1		
2	B	1	Total	C	O	P	0	0
			9	2	6	1		
2	D	1	Total	C	O	P	0	0
			9	2	6	1		
2	E	1	Total	C	O	P	0	0
			9	2	6	1		
2	G	1	Total	C	O	P	0	0
			9	2	6	1		
2	H	1	Total	C	O	P	0	0
			9	2	6	1		
2	J	1	Total	C	O	P	0	0
			9	2	6	1		
2	K	1	Total	C	O	P	0	0
			9	2	6	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	44	Total	O	0	0
			44	44		
3	B	34	Total	O	0	0
			34	34		
3	D	42	Total	O	0	0
			42	42		
3	E	33	Total	O	0	0
			33	33		

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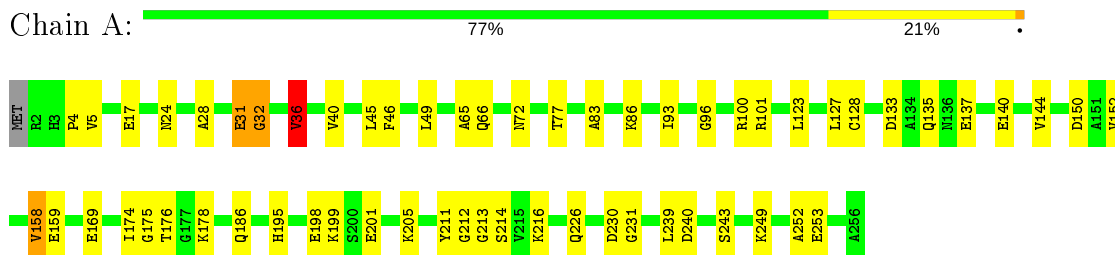
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	G	44	Total 44	O 44	0	0
3	H	34	Total 34	O 34	0	0
3	J	44	Total 44	O 44	0	0
3	K	33	Total 33	O 33	0	0

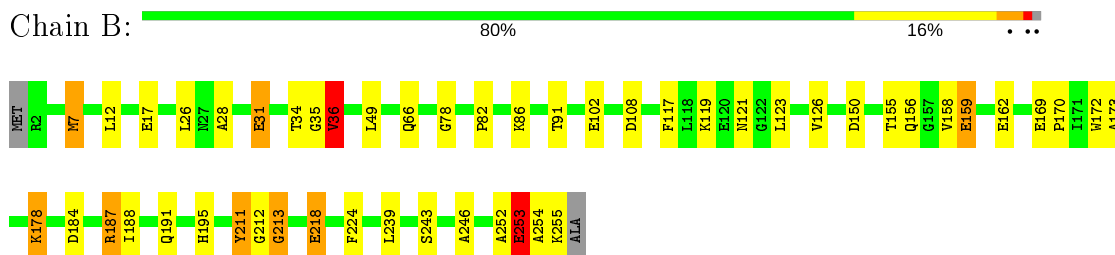
### 3 Residue-property plots i

These plots are drawn for all protein, RNA and DNA 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.

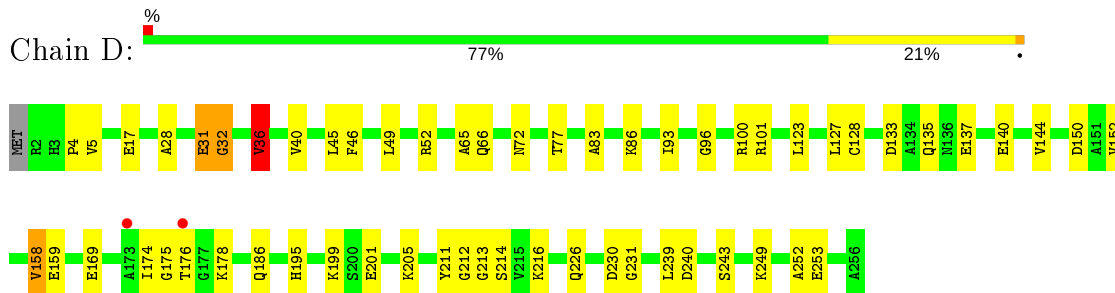
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



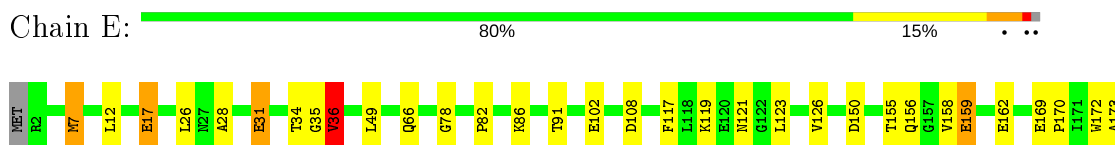
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

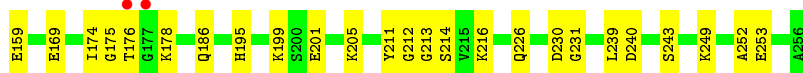
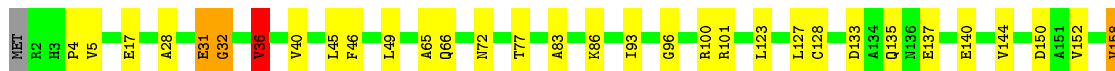
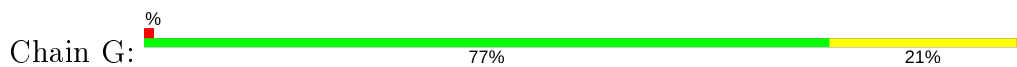


- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

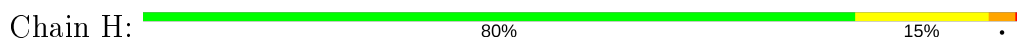




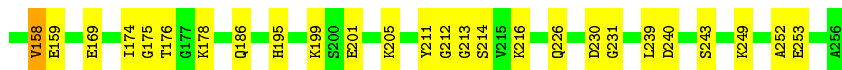
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



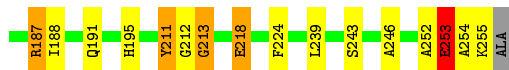
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE



- 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, $\alpha$ , $\beta$ , $\gamma$	89.51Å 138.08Å 89.52Å 90.00° 91.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.70 24.20 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (8.00-2.70) 99.9 (24.20-2.70)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.49 (at 2.71Å)	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.192 , 0.215 0.170 , 0.190	Depositor DCC
$R_{free}$ test set	2980 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.3	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 20.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.188 for l,k,-h 0.187 for h,-k,-l 0.479 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	15324	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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	0.70	0/1900	0.81	1/2576 (0.0%)
1	B	0.69	2/1894 (0.1%)	0.79	2/2569 (0.1%)
1	D	0.70	0/1900	0.81	1/2576 (0.0%)
1	E	0.69	2/1894 (0.1%)	0.79	2/2569 (0.1%)
1	G	0.70	0/1900	0.81	1/2576 (0.0%)
1	H	0.69	2/1894 (0.1%)	0.79	2/2569 (0.1%)
1	J	0.70	0/1900	0.81	1/2576 (0.0%)
1	K	0.69	2/1894 (0.1%)	0.79	1/2569 (0.0%)
All	All	0.70	8/15176 (0.1%)	0.80	11/20580 (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	B	0	1
1	E	0	1
1	H	0	1
1	K	0	1
All	All	0	4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	102	GLU	CG-CD	5.76	1.60	1.51
1	B	102	GLU	CG-CD	5.69	1.60	1.51
1	H	102	GLU	CG-CD	5.69	1.60	1.51
1	K	102	GLU	CG-CD	5.68	1.60	1.51
1	K	253	GLU	CG-CD	5.31	1.59	1.51
1	H	253	GLU	CG-CD	5.29	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	253	GLU	CG-CD	5.25	1.59	1.51
1	E	253	GLU	CG-CD	5.25	1.59	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	36	VAL	CB-CA-C	-7.60	96.95	111.40
1	J	36	VAL	CB-CA-C	-7.60	96.96	111.40
1	A	36	VAL	CB-CA-C	-7.58	96.99	111.40
1	G	36	VAL	CB-CA-C	-7.58	97.00	111.40
1	E	36	VAL	CB-CA-C	-5.45	101.05	111.40
1	K	36	VAL	CB-CA-C	-5.44	101.07	111.40
1	H	36	VAL	CB-CA-C	-5.43	101.08	111.40
1	B	36	VAL	CB-CA-C	-5.43	101.09	111.40
1	H	108	ASP	CB-CG-OD1	5.06	122.85	118.30
1	E	108	ASP	CB-CG-OD1	5.06	122.85	118.30
1	B	108	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	211	TYR	Sidechain
1	E	211	TYR	Sidechain
1	H	211	TYR	Sidechain
1	K	211	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	1871	0	1848	35	3
1	B	1865	0	1843	39	0
1	D	1871	0	1848	40	0
1	E	1865	0	1843	41	0
1	G	1871	0	1848	33	3
1	H	1865	0	1843	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1871	0	1848	40	0
1	K	1865	0	1843	38	0
2	A	9	0	2	1	0
2	B	9	0	2	0	0
2	D	9	0	2	1	0
2	E	9	0	2	0	0
2	G	9	0	2	1	0
2	H	9	0	2	0	0
2	J	9	0	2	1	0
2	K	9	0	2	0	0
3	A	44	0	0	2	0
3	B	34	0	0	0	0
3	D	42	0	0	2	0
3	E	33	0	0	0	0
3	G	44	0	0	2	0
3	H	34	0	0	0	0
3	J	44	0	0	2	0
3	K	33	0	0	0	0
All	All	15324	0	14780	280	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 9.

All (280) 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:D:32:GLY:HA2	1:J:253:GLU:OE2	1.26	1.32
1:D:32:GLY:CA	1:J:253:GLU:OE2	1.87	1.23
1:D:253:GLU:OE2	1:J:32:GLY:HA2	1.42	1.18
1:H:169:GLU:HG2	1:H:212:GLY:HA3	1.31	1.12
1:B:169:GLU:HG2	1:B:212:GLY:HA3	1.31	1.12
1:E:169:GLU:HG2	1:E:212:GLY:HA3	1.31	1.10
1:K:169:GLU:HG2	1:K:212:GLY:HA3	1.31	1.10
1:D:253:GLU:OE2	1:J:32:GLY:CA	2.14	0.96
1:A:66:GLN:HE21	1:B:78:GLY:H	1.21	0.89
1:G:66:GLN:HE21	1:H:78:GLY:H	1.21	0.88
1:D:169:GLU:HG2	1:D:212:GLY:HA3	1.55	0.87
1:J:66:GLN:HE21	1:K:78:GLY:H	1.21	0.87
1:J:169:GLU:HG2	1:J:212:GLY:HA3	1.55	0.86
1:D:66:GLN:HE21	1:E:78:GLY:H	1.21	0.86
1:G:169:GLU:HG2	1:G:212:GLY:HA3	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLU:HG2	1:A:212:GLY:HA3	1.55	0.86
1:D:66:GLN:NE2	1:E:78:GLY:H	1.74	0.85
1:D:32:GLY:N	1:J:253:GLU:OE2	2.09	0.84
1:J:66:GLN:NE2	1:K:78:GLY:H	1.74	0.84
1:G:66:GLN:NE2	1:H:78:GLY:H	1.74	0.84
1:A:66:GLN:NE2	1:B:78:GLY:H	1.74	0.83
1:K:211:TYR:OH	1:K:213:GLY:HA3	1.79	0.83
1:E:211:TYR:OH	1:E:213:GLY:HA3	1.79	0.83
1:H:211:TYR:OH	1:H:213:GLY:HA3	1.79	0.81
1:B:211:TYR:OH	1:B:213:GLY:HA3	1.79	0.81
1:A:36:VAL:HG22	1:A:252:ALA:HB2	1.66	0.77
1:G:36:VAL:HG22	1:G:252:ALA:HB2	1.66	0.76
1:D:36:VAL:HG22	1:D:252:ALA:HB2	1.66	0.75
1:J:36:VAL:HG22	1:J:252:ALA:HB2	1.66	0.75
1:E:169:GLU:CG	1:E:212:GLY:HA3	2.18	0.69
1:H:169:GLU:CG	1:H:212:GLY:HA3	2.18	0.69
1:K:169:GLU:CG	1:K:212:GLY:HA3	2.18	0.69
1:B:169:GLU:CG	1:B:212:GLY:HA3	2.18	0.68
1:D:201:GLU:O	1:D:205:LYS:HG2	1.94	0.67
1:B:159:GLU:O	1:B:162:GLU:HG2	1.94	0.67
1:A:174:ILE:O	1:A:176:THR:HG23	1.95	0.67
1:H:159:GLU:O	1:H:162:GLU:HG2	1.95	0.67
1:G:174:ILE:O	1:G:176:THR:HG23	1.95	0.67
1:G:201:GLU:O	1:G:205:LYS:HG2	1.94	0.66
1:J:201:GLU:O	1:J:205:LYS:HG2	1.94	0.66
1:A:201:GLU:O	1:A:205:LYS:HG2	1.94	0.66
1:J:174:ILE:O	1:J:176:THR:HG23	1.95	0.66
1:D:174:ILE:O	1:D:176:THR:HG23	1.95	0.66
1:K:159:GLU:O	1:K:162:GLU:HG2	1.95	0.66
1:E:159:GLU:O	1:E:162:GLU:HG2	1.94	0.65
1:K:7:MET:HE1	1:K:126:VAL:HG21	1.81	0.63
1:E:7:MET:HE1	1:E:126:VAL:HG21	1.81	0.63
1:H:155:THR:HG23	1:H:156:GLN:HG3	1.81	0.63
1:K:253:GLU:HG2	1:K:254:ALA:N	2.14	0.63
1:B:155:THR:HG23	1:B:156:GLN:HG3	1.81	0.63
1:E:253:GLU:HG2	1:E:254:ALA:N	2.14	0.63
1:B:253:GLU:HG2	1:B:254:ALA:N	2.14	0.62
1:E:155:THR:HG23	1:E:156:GLN:HG3	1.81	0.62
1:K:155:THR:HG23	1:K:156:GLN:HG3	1.81	0.62
1:H:253:GLU:HG2	1:H:254:ALA:N	2.14	0.62
1:A:133:ASP:O	1:A:137:GLU:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:133:ASP:O	1:G:137:GLU:HG3	2.00	0.62
1:D:133:ASP:O	1:D:137:GLU:HG3	2.00	0.61
1:J:133:ASP:O	1:J:137:GLU:HG3	2.00	0.61
1:B:28:ALA:O	1:B:31:GLU:HB2	2.01	0.60
1:H:7:MET:HE1	1:H:126:VAL:HG21	1.83	0.60
1:H:28:ALA:O	1:H:31:GLU:HB2	2.01	0.60
1:K:28:ALA:O	1:K:31:GLU:HB2	2.01	0.60
1:B:243:SER:O	1:B:246:ALA:HB3	2.02	0.60
1:H:243:SER:O	1:H:246:ALA:HB3	2.02	0.60
1:E:243:SER:O	1:E:246:ALA:HB3	2.02	0.60
1:E:28:ALA:O	1:E:31:GLU:HB2	2.01	0.59
1:K:243:SER:O	1:K:246:ALA:HB3	2.02	0.59
1:A:46:PHE:HA	3:A:306:HOH:O	2.02	0.59
1:D:46:PHE:HA	3:D:305:HOH:O	2.02	0.59
1:G:46:PHE:HA	3:G:306:HOH:O	2.02	0.59
1:J:46:PHE:HA	3:J:307:HOH:O	2.02	0.59
1:K:150:ASP:OD1	1:K:195:HIS:HE1	1.87	0.57
1:G:66:GLN:HE21	1:H:78:GLY:N	1.98	0.57
1:B:150:ASP:OD1	1:B:195:HIS:HE1	1.87	0.57
1:E:150:ASP:OD1	1:E:195:HIS:HE1	1.88	0.57
1:A:66:GLN:HE21	1:B:78:GLY:N	1.97	0.56
1:H:150:ASP:OD1	1:H:195:HIS:HE1	1.88	0.56
1:A:198:GLU:OE2	1:D:52:ARG:NH2	2.34	0.55
1:J:66:GLN:HE21	1:K:78:GLY:N	1.97	0.55
1:B:7:MET:HE1	1:B:126:VAL:HG21	1.89	0.55
1:H:34:THR:HG22	1:H:35:GLY:N	2.22	0.55
1:A:77:THR:HG23	1:B:66:GLN:HB3	1.89	0.55
1:B:34:THR:HG22	1:B:35:GLY:N	2.22	0.55
1:D:77:THR:HG23	1:E:66:GLN:HB3	1.89	0.55
1:G:77:THR:HG23	1:H:66:GLN:HB3	1.89	0.55
1:A:17:GLU:CD	1:A:17:GLU:H	2.10	0.54
1:D:66:GLN:HE21	1:E:78:GLY:N	1.97	0.54
1:G:17:GLU:CD	1:G:17:GLU:H	2.10	0.54
1:J:77:THR:HG23	1:K:66:GLN:HB3	1.89	0.54
1:E:34:THR:HG22	1:E:35:GLY:N	2.22	0.54
1:K:34:THR:HG22	1:K:35:GLY:N	2.22	0.54
1:D:17:GLU:H	1:D:17:GLU:CD	2.10	0.54
1:J:17:GLU:CD	1:J:17:GLU:H	2.10	0.54
1:J:240:ASP:HB3	1:J:243:SER:HB2	1.90	0.53
1:D:240:ASP:HB3	1:D:243:SER:HB2	1.91	0.52
1:J:159:GLU:CD	1:J:159:GLU:H	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:ASP:HB3	1:A:243:SER:HB2	1.91	0.52
1:G:240:ASP:HB3	1:G:243:SER:HB2	1.90	0.52
1:D:159:GLU:H	1:D:159:GLU:CD	2.12	0.52
1:G:159:GLU:H	1:G:159:GLU:CD	2.12	0.52
1:H:211:TYR:CZ	1:H:213:GLY:HA3	2.44	0.52
1:B:211:TYR:CZ	1:B:213:GLY:HA3	2.44	0.52
1:D:249:LYS:O	1:D:253:GLU:HG2	2.10	0.52
1:E:211:TYR:CZ	1:E:213:GLY:HA3	2.44	0.52
1:B:36:VAL:HG22	1:B:252:ALA:HB2	1.91	0.51
1:K:211:TYR:CZ	1:K:213:GLY:HA3	2.44	0.51
1:A:159:GLU:H	1:A:159:GLU:CD	2.12	0.51
1:K:36:VAL:HG22	1:K:252:ALA:HB2	1.91	0.51
1:E:36:VAL:HG22	1:E:252:ALA:HB2	1.91	0.51
1:J:249:LYS:O	1:J:253:GLU:HG2	2.10	0.51
1:A:249:LYS:O	1:A:253:GLU:HG2	2.10	0.51
1:D:5:VAL:O	1:D:231:GLY:HA3	2.11	0.51
1:H:36:VAL:HG22	1:H:252:ALA:HB2	1.91	0.51
1:J:5:VAL:O	1:J:231:GLY:HA3	2.11	0.51
1:A:5:VAL:O	1:A:231:GLY:HA3	2.11	0.51
1:G:249:LYS:O	1:G:253:GLU:HG2	2.10	0.51
1:G:5:VAL:O	1:G:231:GLY:HA3	2.11	0.51
1:K:184:ASP:O	1:K:188:ILE:HG13	2.12	0.50
1:E:184:ASP:O	1:E:188:ILE:HG13	2.12	0.50
1:B:212:GLY:O	1:B:213:GLY:O	2.30	0.50
1:K:172:TRP:CZ3	1:K:178:LYS:HD3	2.47	0.49
1:K:187:ARG:HH11	1:K:187:ARG:HG3	1.77	0.49
1:E:172:TRP:CZ3	1:E:178:LYS:HD3	2.47	0.49
1:E:187:ARG:O	1:E:191:GLN:HG3	2.12	0.49
1:H:212:GLY:O	1:H:213:GLY:O	2.30	0.49
1:K:187:ARG:O	1:K:191:GLN:HG3	2.12	0.49
1:G:211:TYR:OH	1:G:213:GLY:HA3	2.12	0.49
1:A:211:TYR:OH	1:A:213:GLY:HA3	2.12	0.49
1:J:211:TYR:OH	1:J:213:GLY:HA3	2.12	0.49
1:B:172:TRP:CZ3	1:B:178:LYS:HD3	2.47	0.49
1:K:212:GLY:O	1:K:213:GLY:O	2.30	0.49
1:D:211:TYR:OH	1:D:213:GLY:HA3	2.12	0.49
1:H:172:TRP:CZ3	1:H:178:LYS:HD3	2.47	0.49
1:E:187:ARG:HG3	1:E:187:ARG:HH11	1.77	0.49
1:H:86:LYS:HE2	1:H:121:ASN:O	2.13	0.49
1:H:187:ARG:O	1:H:191:GLN:HG3	2.12	0.49
1:B:86:LYS:HE2	1:B:121:ASN:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:GLU:CG	1:B:254:ALA:N	2.76	0.48
1:E:212:GLY:O	1:E:213:GLY:O	2.30	0.48
1:B:184:ASP:O	1:B:188:ILE:HG13	2.12	0.48
1:H:211:TYR:HH	1:H:213:GLY:HA3	1.77	0.48
1:B:187:ARG:HH11	1:B:187:ARG:HG3	1.77	0.48
1:B:187:ARG:O	1:B:191:GLN:HG3	2.12	0.48
1:H:187:ARG:HH11	1:H:187:ARG:HG3	1.77	0.48
1:D:178:LYS:C	1:D:178:LYS:HD3	2.34	0.48
1:H:253:GLU:CG	1:H:254:ALA:N	2.76	0.48
1:B:211:TYR:HH	1:B:213:GLY:HA3	1.77	0.48
1:D:150:ASP:OD1	1:D:195:HIS:HE1	1.97	0.48
1:H:224:PHE:O	1:H:255:LYS:HE2	2.14	0.48
1:H:184:ASP:O	1:H:188:ILE:HG13	2.12	0.47
1:J:178:LYS:C	1:J:178:LYS:HD3	2.34	0.47
1:J:150:ASP:OD1	1:J:195:HIS:HE1	1.97	0.47
1:K:253:GLU:CG	1:K:254:ALA:N	2.76	0.47
1:B:224:PHE:O	1:B:255:LYS:HE2	2.14	0.47
1:E:86:LYS:HE2	1:E:121:ASN:O	2.13	0.47
1:G:150:ASP:OD1	1:G:195:HIS:HE1	1.97	0.47
1:G:178:LYS:HD3	1:G:178:LYS:C	2.34	0.47
1:E:253:GLU:CG	1:E:254:ALA:N	2.76	0.47
1:K:86:LYS:HE2	1:K:121:ASN:O	2.13	0.47
1:A:169:GLU:HG2	1:A:212:GLY:CA	2.38	0.47
1:A:86:LYS:HG3	1:A:123:LEU:HD21	1.96	0.46
1:A:178:LYS:C	1:A:178:LYS:HD3	2.34	0.46
1:H:91:THR:HA	1:H:123:LEU:HD12	1.97	0.46
1:K:91:THR:HA	1:K:123:LEU:HD12	1.97	0.46
1:K:224:PHE:O	1:K:255:LYS:HE2	2.14	0.46
1:A:150:ASP:OD1	1:A:195:HIS:HE1	1.97	0.46
1:B:91:THR:HA	1:B:123:LEU:HD12	1.97	0.46
1:D:86:LYS:HG3	1:D:123:LEU:HD21	1.97	0.46
1:D:186:GLN:HB2	1:D:226:GLN:HG3	1.98	0.46
1:E:224:PHE:O	1:E:255:LYS:HE2	2.14	0.46
1:E:91:THR:HA	1:E:123:LEU:HD12	1.97	0.46
1:G:86:LYS:HG3	1:G:123:LEU:HD21	1.97	0.46
1:J:86:LYS:HG3	1:J:123:LEU:HD21	1.96	0.46
1:G:72:ASN:ND2	1:G:83:ALA:H	2.14	0.46
1:H:212:GLY:O	1:H:213:GLY:C	2.55	0.46
1:E:170:PRO:HG2	1:E:173:ALA:HB3	1.98	0.46
1:K:170:PRO:HG2	1:K:173:ALA:HB3	1.98	0.46
1:A:72:ASN:ND2	1:A:83:ALA:H	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:186:GLN:HB2	1:J:226:GLN:HG3	1.98	0.45
1:J:72:ASN:ND2	1:J:83:ALA:H	2.14	0.45
1:B:170:PRO:HG2	1:B:173:ALA:HB3	1.98	0.45
1:B:218:GLU:H	1:B:218:GLU:CD	2.19	0.45
1:D:72:ASN:ND2	1:D:83:ALA:H	2.14	0.45
1:H:170:PRO:HG2	1:H:173:ALA:HB3	1.98	0.45
1:K:187:ARG:HH11	1:K:187:ARG:CG	2.30	0.45
1:H:218:GLU:H	1:H:218:GLU:CD	2.19	0.45
1:E:187:ARG:CG	1:E:187:ARG:HH11	2.30	0.45
1:D:169:GLU:HG2	1:D:212:GLY:CA	2.38	0.45
1:H:187:ARG:HH11	1:H:187:ARG:CG	2.30	0.45
1:K:218:GLU:H	1:K:218:GLU:CD	2.19	0.45
1:E:218:GLU:CD	1:E:218:GLU:H	2.19	0.45
1:J:169:GLU:HG2	1:J:212:GLY:CA	2.38	0.45
1:A:186:GLN:HB2	1:A:226:GLN:HG3	1.98	0.44
1:B:212:GLY:O	1:B:213:GLY:C	2.55	0.44
1:B:187:ARG:HH11	1:B:187:ARG:CG	2.30	0.44
1:J:24:ASN:HD22	1:J:24:ASN:HA	1.68	0.44
1:K:212:GLY:O	1:K:213:GLY:C	2.55	0.44
1:G:169:GLU:HG2	1:G:212:GLY:CA	2.38	0.44
1:E:212:GLY:O	1:E:213:GLY:C	2.55	0.44
1:G:186:GLN:HB2	1:G:226:GLN:HG3	1.98	0.44
1:H:169:GLU:HG2	1:H:212:GLY:CA	2.23	0.44
1:K:253:GLU:OE2	1:K:254:ALA:HB2	2.18	0.44
1:E:159:GLU:H	1:E:159:GLU:HG2	1.64	0.43
1:E:253:GLU:OE2	1:E:254:ALA:HB2	2.19	0.43
1:J:28:ALA:O	1:J:31:GLU:HB2	2.18	0.43
1:B:12:LEU:HD12	1:B:12:LEU:HA	1.89	0.43
1:D:28:ALA:O	1:D:31:GLU:HB2	2.19	0.43
1:D:96:GLY:O	1:D:101:ARG:HD2	2.18	0.43
1:G:214:SER:HB3	1:G:216:LYS:HE2	1.99	0.43
1:A:214:SER:HB3	1:A:216:LYS:HE2	1.99	0.43
1:D:101:ARG:NH2	3:D:296:HOH:O	2.52	0.43
1:D:77:THR:CG2	1:E:66:GLN:HB3	2.48	0.43
1:G:28:ALA:O	1:G:31:GLU:HB2	2.18	0.43
1:J:96:GLY:O	1:J:101:ARG:HD2	2.18	0.43
1:J:77:THR:CG2	1:K:66:GLN:HB3	2.48	0.43
1:A:28:ALA:O	1:A:31:GLU:HB2	2.18	0.43
1:A:101:ARG:NH2	3:A:297:HOH:O	2.52	0.43
1:J:101:ARG:NH2	3:J:298:HOH:O	2.52	0.43
1:D:214:SER:HB3	1:D:216:LYS:HE2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLY:O	1:A:101:ARG:HD2	2.18	0.43
1:A:158:VAL:HG11	1:A:199:LYS:HB2	2.01	0.43
1:G:96:GLY:O	1:G:101:ARG:HD2	2.18	0.43
1:G:77:THR:CG2	1:H:66:GLN:HB3	2.48	0.43
1:A:169:GLU:OE2	2:A:290:PGA:O1	2.37	0.42
1:A:77:THR:CG2	1:B:66:GLN:HB3	2.48	0.42
1:G:101:ARG:NH2	3:G:297:HOH:O	2.52	0.42
1:J:214:SER:HB3	1:J:216:LYS:HE2	2.00	0.42
1:J:65:ALA:HB3	1:J:93:ILE:HD12	2.01	0.42
1:K:119:LYS:HD2	1:K:119:LYS:HA	1.82	0.42
1:G:169:GLU:OE2	2:G:290:PGA:O1	2.37	0.42
1:J:169:GLU:OE2	2:J:290:PGA:O1	2.37	0.42
1:B:253:GLU:OE2	1:B:254:ALA:HB2	2.18	0.42
1:D:65:ALA:HB3	1:D:93:ILE:HD12	2.01	0.42
1:G:158:VAL:HG11	1:G:199:LYS:HB2	2.01	0.42
1:H:253:GLU:OE2	1:H:254:ALA:HB2	2.18	0.42
1:B:169:GLU:HG2	1:B:212:GLY:CA	2.23	0.42
1:E:169:GLU:HG2	1:E:212:GLY:CA	2.23	0.42
1:K:17:GLU:H	1:K:17:GLU:HG3	1.62	0.42
1:G:101:ARG:NH1	1:G:128:CYS:O	2.53	0.42
1:G:65:ALA:HB3	1:G:93:ILE:HD12	2.01	0.42
1:D:169:GLU:OE2	2:D:290:PGA:O1	2.37	0.42
1:H:7:MET:HE2	1:H:7:MET:HB2	1.96	0.42
1:A:101:ARG:NH1	1:A:128:CYS:O	2.53	0.42
1:A:65:ALA:HB3	1:A:93:ILE:HD12	2.01	0.42
1:E:172:TRP:HZ3	1:E:178:LYS:HD3	1.84	0.42
1:A:4:PRO:HA	1:A:230:ASP:O	2.20	0.41
1:E:218:GLU:CD	1:E:218:GLU:N	2.74	0.41
1:J:4:PRO:HA	1:J:230:ASP:O	2.20	0.41
1:B:119:LYS:HA	1:B:119:LYS:HD2	1.82	0.41
1:D:4:PRO:HA	1:D:230:ASP:O	2.20	0.41
1:J:158:VAL:HG11	1:J:199:LYS:HB2	2.01	0.41
1:K:218:GLU:N	1:K:218:GLU:CD	2.74	0.41
1:G:4:PRO:HA	1:G:230:ASP:O	2.20	0.41
1:H:82:PRO:HG2	1:H:117:PHE:CE2	2.55	0.41
1:H:119:LYS:HA	1:H:119:LYS:HD2	1.82	0.41
1:D:158:VAL:HG11	1:D:199:LYS:HB2	2.01	0.41
1:D:72:ASN:HD22	1:D:72:ASN:HA	1.70	0.41
1:E:17:GLU:H	1:E:17:GLU:HG3	1.62	0.41
1:B:218:GLU:CD	1:B:218:GLU:N	2.74	0.41
1:E:12:LEU:HD12	1:E:12:LEU:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:PRO:HG2	1:B:117:PHE:CE2	2.55	0.41
1:D:101:ARG:NH1	1:D:128:CYS:O	2.53	0.41
1:J:101:ARG:NH1	1:J:128:CYS:O	2.53	0.41
1:K:172:TRP:HZ3	1:K:178:LYS:HD3	1.84	0.41
1:E:82:PRO:HG2	1:E:117:PHE:CE2	2.55	0.41
1:H:159:GLU:H	1:H:159:GLU:HG2	1.64	0.41
1:H:218:GLU:N	1:H:218:GLU:CD	2.74	0.41
1:K:82:PRO:HG2	1:K:117:PHE:CE2	2.55	0.41
1:A:24:ASN:HA	1:A:24:ASN:HD22	1.68	0.41
1:K:169:GLU:HG2	1:K:212:GLY:CA	2.23	0.41
1:E:119:LYS:HA	1:E:119:LYS:HD2	1.82	0.40
1:D:135:GLN:CD	1:D:144:VAL:HG21	2.42	0.40
1:J:135:GLN:CD	1:J:144:VAL:HG21	2.42	0.40
1:B:172:TRP:HZ3	1:B:178:LYS:HD3	1.84	0.40
1:A:135:GLN:CD	1:A:144:VAL:HG21	2.42	0.40
1:J:72:ASN:HD22	1:J:72:ASN:HA	1.69	0.40
1:E:7:MET:HE2	1:E:7:MET:HB2	1.99	0.40
1:G:135:GLN:CD	1:G:144:VAL:HG21	2.42	0.40
1:H:172:TRP:HZ3	1:H:178:LYS:HD3	1.84	0.40

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:A:253:GLU:OE2	1:G:32:GLY:CA[2_646]	1.87	0.33
1:A:253:GLU:OE2	1:G:32:GLY:N[2_646]	2.08	0.12
1:A:32:GLY:CA	1:G:253:GLU:OE2[2_646]	2.14	0.06

## 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	253/256 (99%)	244 (96%)	6 (2%)	3 (1%)	13	32
1	B	252/256 (98%)	238 (94%)	13 (5%)	1 (0%)	34	60
1	D	253/256 (99%)	244 (96%)	6 (2%)	3 (1%)	13	32
1	E	252/256 (98%)	238 (94%)	13 (5%)	1 (0%)	34	60
1	G	253/256 (99%)	244 (96%)	6 (2%)	3 (1%)	13	32
1	H	252/256 (98%)	238 (94%)	13 (5%)	1 (0%)	34	60
1	J	253/256 (99%)	244 (96%)	6 (2%)	3 (1%)	13	32
1	K	252/256 (98%)	238 (94%)	13 (5%)	1 (0%)	34	60
All	All	2020/2048 (99%)	1928 (95%)	76 (4%)	16 (1%)	19	43

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
1	D	31	GLU
1	G	31	GLU
1	J	31	GLU
1	B	213	GLY
1	E	213	GLY
1	H	213	GLY
1	K	213	GLY
1	A	32	GLY
1	D	32	GLY
1	G	32	GLY
1	J	32	GLY
1	A	175	GLY
1	D	175	GLY
1	G	175	GLY
1	J	175	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	184/185 (100%)	174 (95%)	10 (5%)	22	47
1	B	184/185 (100%)	171 (93%)	13 (7%)	14	34
1	D	184/185 (100%)	174 (95%)	10 (5%)	22	47
1	E	184/185 (100%)	171 (93%)	13 (7%)	14	34
1	G	184/185 (100%)	174 (95%)	10 (5%)	22	47
1	H	184/185 (100%)	171 (93%)	13 (7%)	14	34
1	J	184/185 (100%)	174 (95%)	10 (5%)	22	47
1	K	184/185 (100%)	171 (93%)	13 (7%)	14	34
All	All	1472/1480 (100%)	1380 (94%)	92 (6%)	18	40

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	40	VAL
1	A	45	LEU
1	A	49	LEU
1	A	100	ARG
1	A	127	LEU
1	A	140	GLU
1	A	152	VAL
1	A	158	VAL
1	A	239	LEU
1	B	7	MET
1	B	17	GLU
1	B	26	LEU
1	B	31	GLU
1	B	36	VAL
1	B	49	LEU
1	B	158	VAL
1	B	159	GLU
1	B	178	LYS
1	B	187	ARG
1	B	218	GLU
1	B	239	LEU
1	B	253	GLU
1	D	36	VAL
1	D	40	VAL
1	D	45	LEU
1	D	49	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	100	ARG
1	D	127	LEU
1	D	140	GLU
1	D	152	VAL
1	D	158	VAL
1	D	239	LEU
1	E	7	MET
1	E	17	GLU
1	E	26	LEU
1	E	31	GLU
1	E	36	VAL
1	E	49	LEU
1	E	158	VAL
1	E	159	GLU
1	E	178	LYS
1	E	187	ARG
1	E	218	GLU
1	E	239	LEU
1	E	253	GLU
1	G	36	VAL
1	G	40	VAL
1	G	45	LEU
1	G	49	LEU
1	G	100	ARG
1	G	127	LEU
1	G	140	GLU
1	G	152	VAL
1	G	158	VAL
1	G	239	LEU
1	H	7	MET
1	H	17	GLU
1	H	26	LEU
1	H	31	GLU
1	H	36	VAL
1	H	49	LEU
1	H	158	VAL
1	H	159	GLU
1	H	178	LYS
1	H	187	ARG
1	H	218	GLU
1	H	239	LEU
1	H	253	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	36	VAL
1	J	40	VAL
1	J	45	LEU
1	J	49	LEU
1	J	100	ARG
1	J	127	LEU
1	J	140	GLU
1	J	152	VAL
1	J	158	VAL
1	J	239	LEU
1	K	7	MET
1	K	17	GLU
1	K	26	LEU
1	K	31	GLU
1	K	36	VAL
1	K	49	LEU
1	K	158	VAL
1	K	159	GLU
1	K	178	LYS
1	K	187	ARG
1	K	218	GLU
1	K	239	LEU
1	K	253	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	24	ASN
1	A	66	GLN
1	A	72	ASN
1	A	121	ASN
1	A	195	HIS
1	A	210	GLN
1	B	3	HIS
1	B	92	HIS
1	B	154	ASN
1	B	195	HIS
1	D	24	ASN
1	D	66	GLN
1	D	72	ASN
1	D	121	ASN
1	D	195	HIS

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Mol	Chain	Res	Type
1	D	210	GLN
1	E	3	HIS
1	E	92	HIS
1	E	154	ASN
1	E	195	HIS
1	G	24	ASN
1	G	66	GLN
1	G	72	ASN
1	G	121	ASN
1	G	195	HIS
1	G	210	GLN
1	H	3	HIS
1	H	92	HIS
1	H	154	ASN
1	H	195	HIS
1	J	24	ASN
1	J	66	GLN
1	J	72	ASN
1	J	121	ASN
1	J	195	HIS
1	J	210	GLN
1	K	3	HIS
1	K	92	HIS
1	K	154	ASN
1	K	195	HIS

### 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 carbohydrates in this entry.



## 5.6 Ligand geometry

8 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	A	290	-	5,8,8	0.52	0	6,11,11	0.64	0
2	PGA	J	290	-	5,8,8	0.53	0	6,11,11	0.64	0
2	PGA	H	290	-	5,8,8	0.64	0	6,11,11	0.70	0
2	PGA	G	290	-	5,8,8	0.53	0	6,11,11	0.64	0
2	PGA	D	290	-	5,8,8	0.52	0	6,11,11	0.64	0
2	PGA	B	290	-	5,8,8	0.65	0	6,11,11	0.70	0
2	PGA	K	290	-	5,8,8	0.65	0	6,11,11	0.69	0
2	PGA	E	290	-	5,8,8	0.65	0	6,11,11	0.70	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	PGA	A	290	-	-	0/4/6/6	-
2	PGA	J	290	-	-	0/4/6/6	-
2	PGA	H	290	-	-	3/4/6/6	-
2	PGA	G	290	-	-	0/4/6/6	-
2	PGA	D	290	-	-	0/4/6/6	-
2	PGA	B	290	-	-	3/4/6/6	-
2	PGA	K	290	-	-	3/4/6/6	-
2	PGA	E	290	-	-	3/4/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	290	PGA	C2-O1P-P-O2P
2	H	290	PGA	C2-O1P-P-O3P
2	H	290	PGA	C2-O1P-P-O4P
2	B	290	PGA	C2-O1P-P-O2P
2	B	290	PGA	C2-O1P-P-O3P
2	B	290	PGA	C2-O1P-P-O4P
2	K	290	PGA	C2-O1P-P-O2P
2	K	290	PGA	C2-O1P-P-O3P
2	K	290	PGA	C2-O1P-P-O4P
2	E	290	PGA	C2-O1P-P-O2P
2	E	290	PGA	C2-O1P-P-O3P
2	E	290	PGA	C2-O1P-P-O4P

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	290	PGA	1	0
2	J	290	PGA	1	0
2	G	290	PGA	1	0
2	D	290	PGA	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, 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	255/256 (99%)	-0.71	0 <a href="#">100</a>   <a href="#">100</a>	2, 8, 26, 42	1 (0%)
1	B	254/256 (99%)	-0.67	0 <a href="#">100</a>   <a href="#">100</a>	3, 12, 30, 45	1 (0%)
1	D	255/256 (99%)	-0.75	2 (0%) <a href="#">86</a>   <a href="#">87</a>	2, 8, 26, 42	1 (0%)
1	E	254/256 (99%)	-0.64	0 <a href="#">100</a>   <a href="#">100</a>	3, 12, 30, 45	1 (0%)
1	G	255/256 (99%)	-0.70	2 (0%) <a href="#">86</a>   <a href="#">87</a>	2, 8, 26, 42	1 (0%)
1	H	254/256 (99%)	-0.65	0 <a href="#">100</a>   <a href="#">100</a>	3, 12, 30, 45	1 (0%)
1	J	255/256 (99%)	-0.74	0 <a href="#">100</a>   <a href="#">100</a>	2, 8, 26, 42	1 (0%)
1	K	254/256 (99%)	-0.66	0 <a href="#">100</a>   <a href="#">100</a>	3, 12, 30, 45	1 (0%)
All	All	2036/2048 (99%)	-0.69	4 (0%) <a href="#">95</a>   <a href="#">96</a>	2, 10, 30, 45	8 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	176	THR	3.2
1	G	176	THR	2.9
1	G	177	GLY	2.3
1	D	173	ALA	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 carbohydrates 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, 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	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	PGA	G	290	9/9	0.92	0.23	26,28,30,30	0
2	PGA	D	290	9/9	0.94	0.22	26,28,30,30	0
2	PGA	J	290	9/9	0.96	0.18	26,28,30,30	0
2	PGA	A	290	9/9	0.97	0.18	26,28,30,30	0
2	PGA	B	290	9/9	0.97	0.13	22,24,29,29	0
2	PGA	H	290	9/9	0.98	0.13	22,24,29,29	0
2	PGA	K	290	9/9	0.98	0.14	22,24,29,29	0
2	PGA	E	290	9/9	0.98	0.12	22,24,29,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.