



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 09:32 AM UTC

PDB ID : 1GT7 / pdb_00001gt7
Title : L-rhamnulose-1-phosphate aldolase from Escherichia coli
Authors : Kroemer, M.; Schulz, G.E.
Deposited on : 2002-01-14
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

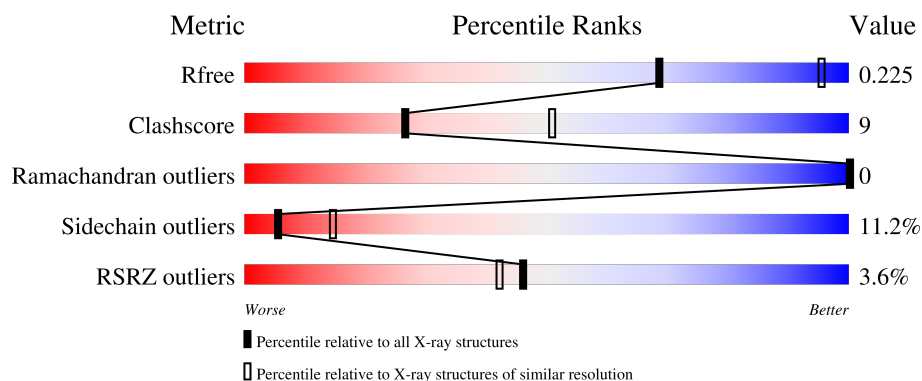
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



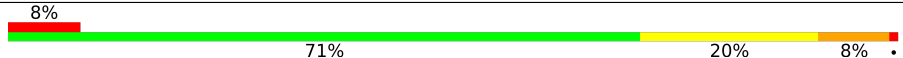
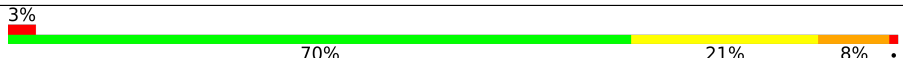
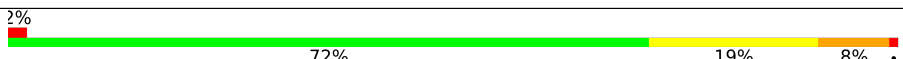
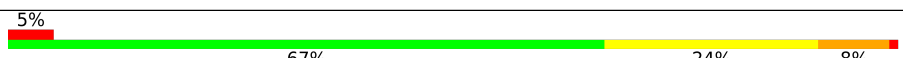
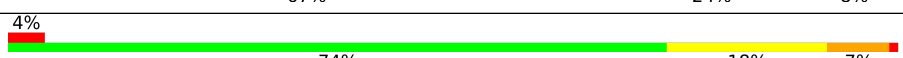
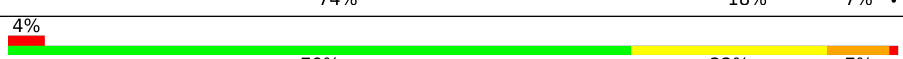
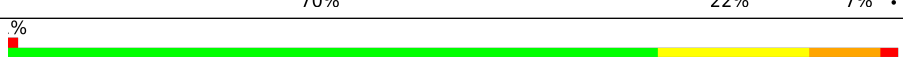
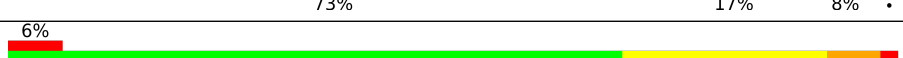
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 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	274	4% 68% 24% 7%
1	B	274	4% 73% 20% 5%
1	C	274	3% 72% 20% 6%
1	D	274	7% 73% 18% 8%
1	E	274	4% 73% 19% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	274	
1	G	274	
1	H	274	
1	I	274	
1	J	274	
1	K	274	
1	L	274	
1	M	274	
1	N	274	
1	O	274	
1	P	274	
1	Q	274	
1	R	274	
1	S	274	
1	T	274	

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
3	PGH	A	300	-	X	-	-
3	PGH	B	300	-	X	-	-
3	PGH	C	300	-	X	-	-
3	PGH	D	300	-	X	-	-
3	PGH	E	300	-	X	-	-
3	PGH	F	300	-	X	-	-
3	PGH	G	300	-	X	-	-
3	PGH	H	300	-	X	-	-
3	PGH	I	300	-	X	-	-
3	PGH	J	300	-	X	-	-
3	PGH	K	300	-	X	-	-
3	PGH	L	300	-	X	-	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PGH	M	300	-	X	-	-
3	PGH	O	300	-	X	-	-
3	PGH	P	300	-	X	-	-
3	PGH	Q	300	-	X	-	-
3	PGH	R	300	-	X	-	-
3	PGH	S	300	-	X	-	-
3	PGH	T	300	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 46180 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 RHAMNULOSE-1-PHOSPHATE ALDOLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	B	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	C	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	D	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	E	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	F	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	G	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	H	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	I	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	J	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	K	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	L	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	M	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	N	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	O	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			
1	P	274	Total	C	N	O	S	0	0	0
			2124	1358	361	394	11			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	274	Total 2124	C 1358	N 361	O 394	S 11	0	0	0
1	R	274	Total 2124	C 1358	N 361	O 394	S 11	0	0	0
1	S	274	Total 2124	C 1358	N 361	O 394	S 11	0	0	0
1	T	274	Total 2124	C 1358	N 361	O 394	S 11	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

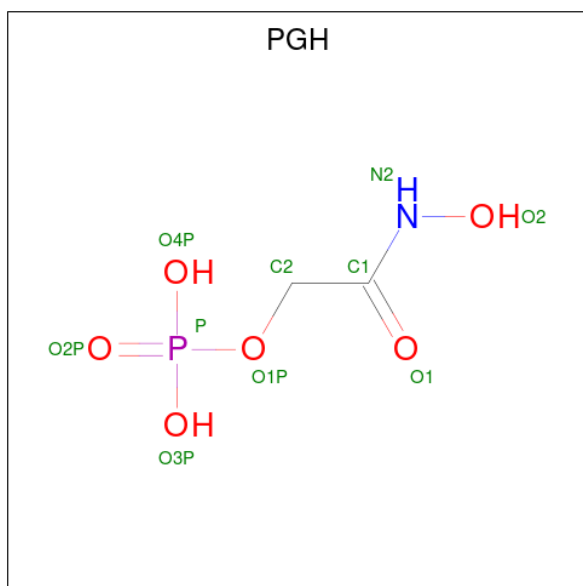
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	E	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0
2	G	1	Total 1	Zn 1	0	0
2	H	1	Total 1	Zn 1	0	0
2	I	1	Total 1	Zn 1	0	0
2	J	1	Total 1	Zn 1	0	0
2	K	1	Total 1	Zn 1	0	0
2	L	1	Total 1	Zn 1	0	0
2	M	1	Total 1	Zn 1	0	0
2	N	1	Total 1	Zn 1	0	0
2	O	1	Total 1	Zn 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	1	Total	Zn	0	0
			1	1		
2	Q	1	Total	Zn	0	0
			1	1		
2	R	1	Total	Zn	0	0
			1	1		
2	S	1	Total	Zn	0	0
			1	1		
2	T	1	Total	Zn	0	0
			1	1		

- Molecule 3 is PHOSPHOGLYCOLOHYDROXAMIC ACID (CCD ID: PGH) (formula: $C_2H_6NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	B	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	C	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	D	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	E	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	F	1	Total	C	N	O	P	0	0
			10	2	1	6	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	H	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	I	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	J	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	K	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	L	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	M	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	N	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	O	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	P	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	Q	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	R	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	S	1	Total	C	N	O	P	0	0
			10	2	1	6	1		
3	T	1	Total	C	N	O	P	0	0
			10	2	1	6	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	177	Total	O	0	0
			177	177		
4	B	174	Total	O	0	0
			174	174		
4	C	173	Total	O	0	0
			173	173		
4	D	173	Total	O	0	0
			173	173		
4	E	179	Total	O	0	0
			179	179		

Continued on next page...

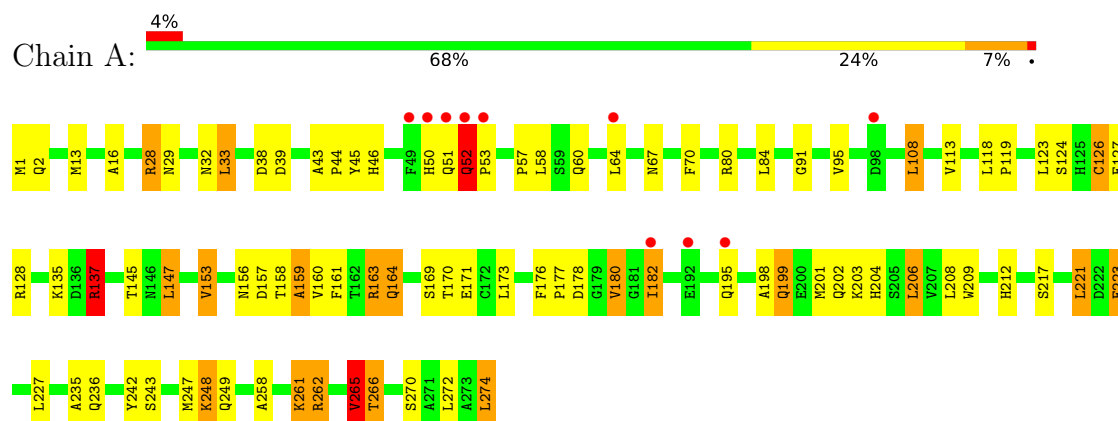
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	174	Total 174	O 174	0	0
4	G	176	Total 176	O 176	0	0
4	H	171	Total 171	O 171	0	0
4	I	177	Total 177	O 177	0	0
4	J	178	Total 178	O 178	0	0
4	K	177	Total 177	O 177	0	0
4	L	167	Total 167	O 167	0	0
4	M	183	Total 183	O 183	0	0
4	N	170	Total 170	O 170	0	0
4	O	175	Total 175	O 175	0	0
4	P	167	Total 167	O 167	0	0
4	Q	176	Total 176	O 176	0	0
4	R	172	Total 172	O 172	0	0
4	S	171	Total 171	O 171	0	0
4	T	170	Total 170	O 170	0	0

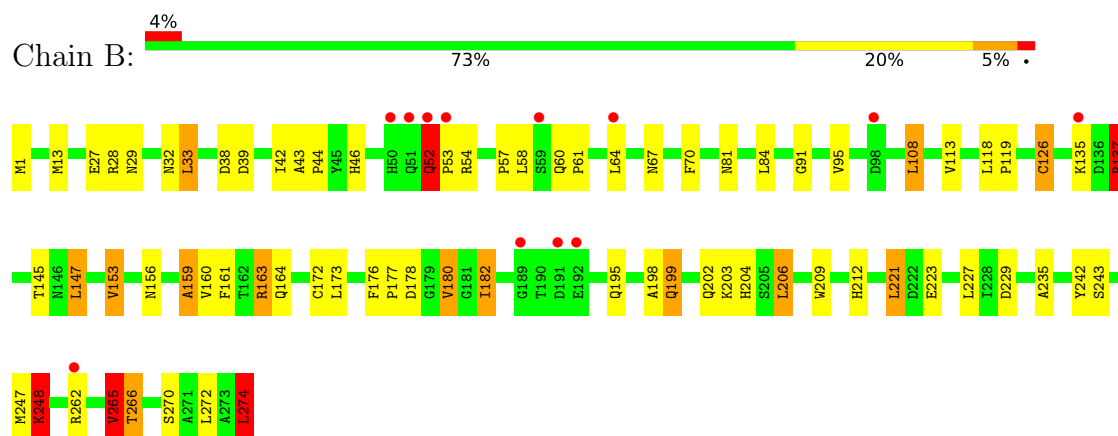
3 Residue-property plots

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.

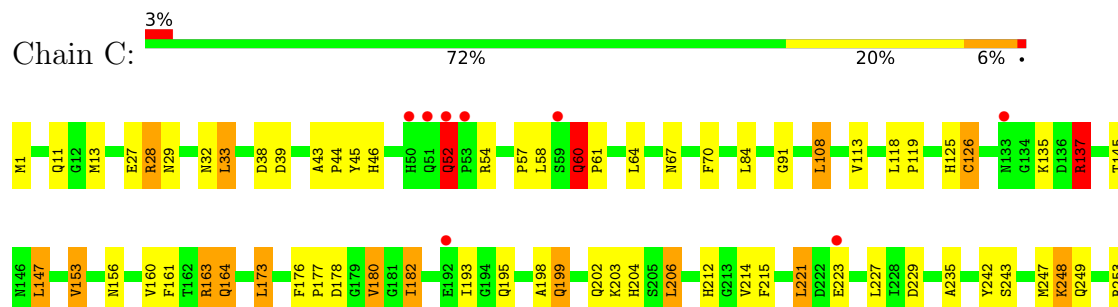
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

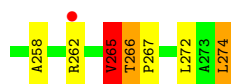


• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

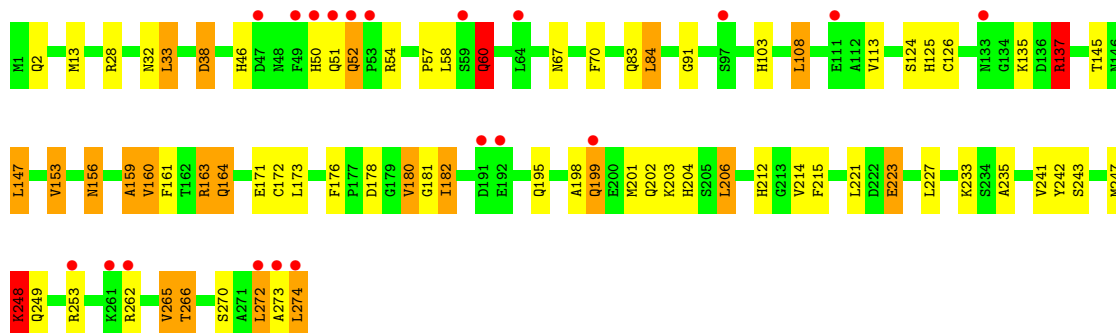
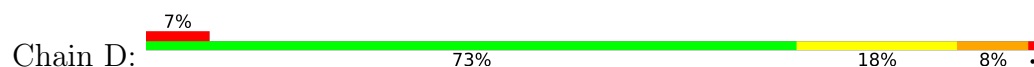


• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

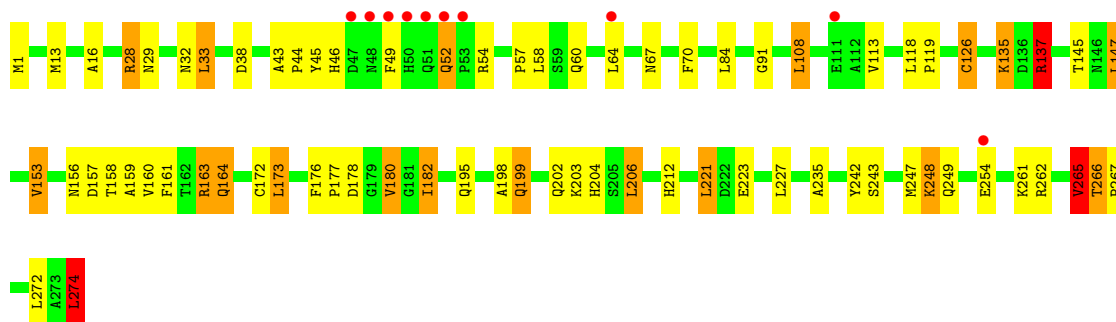




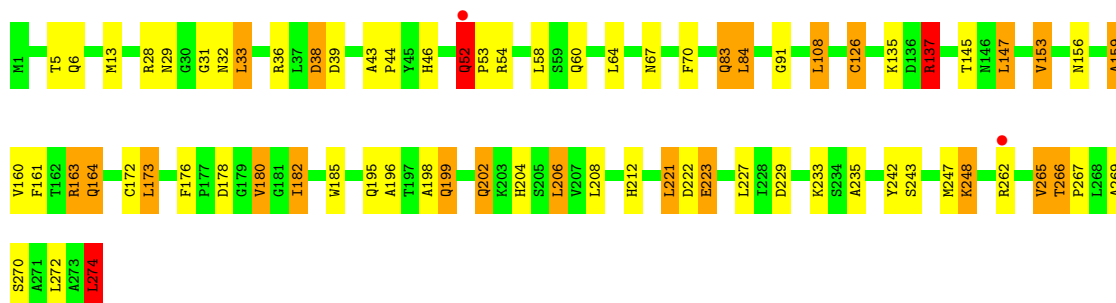
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE



• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

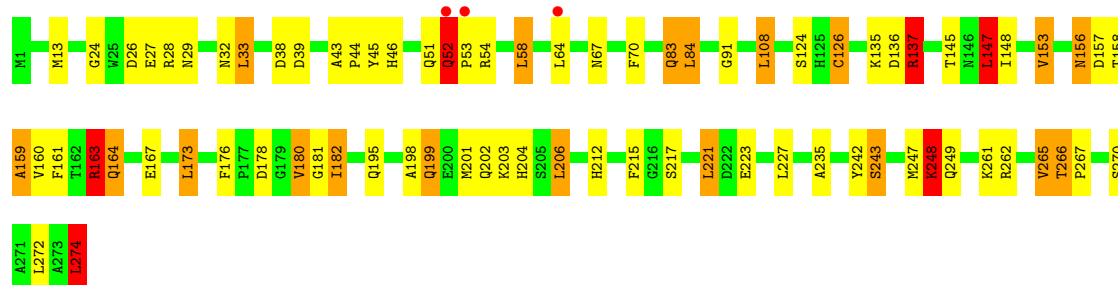


• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

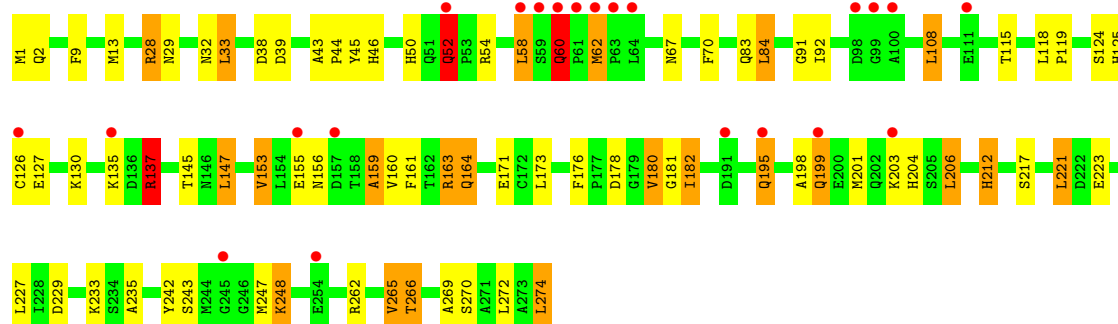


• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

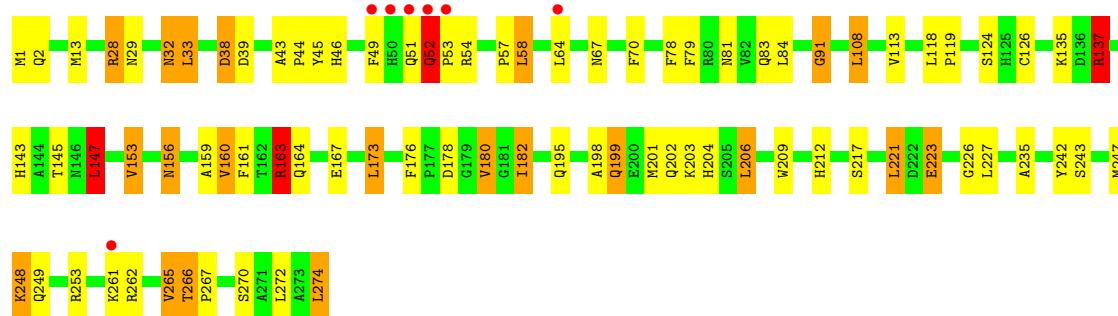




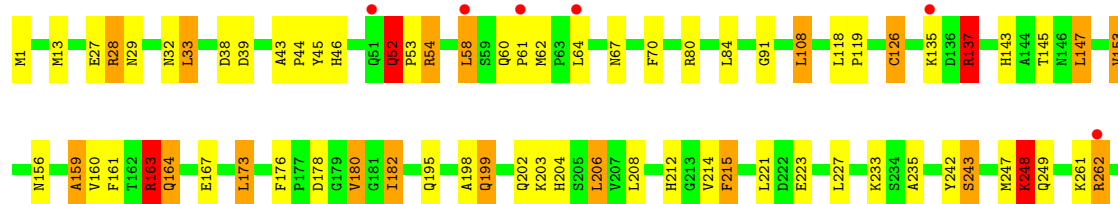
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE



• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE



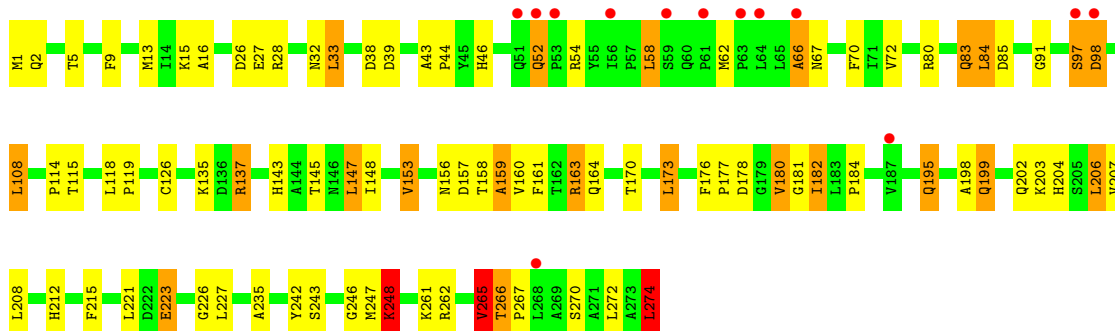
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE





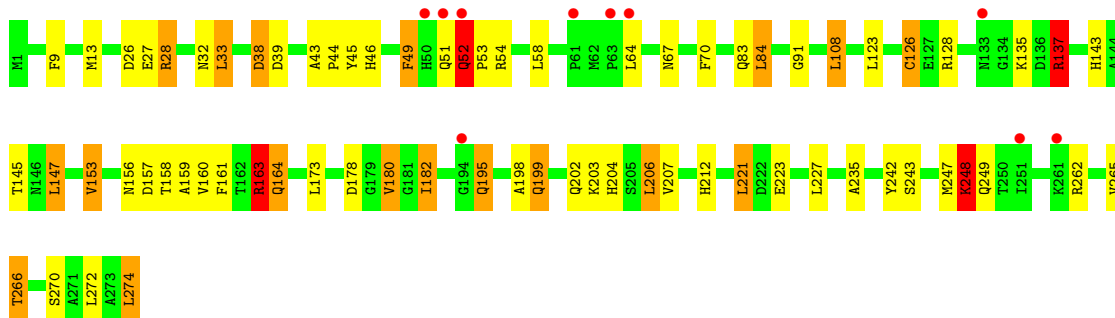
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain K: 5% 67% 24% 8%



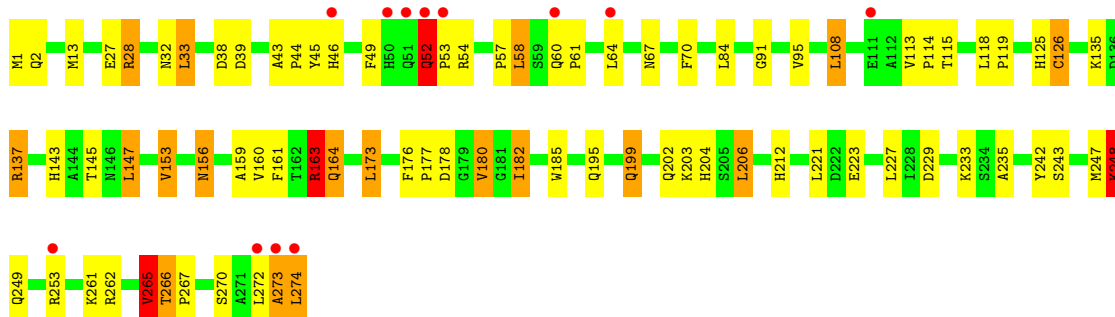
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain L: 4% 74% 18% 7%



• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

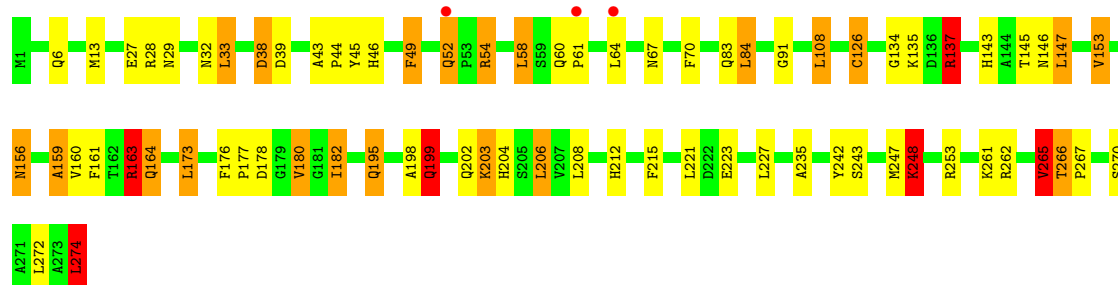
Chain M: 4% 70% 22% 7%



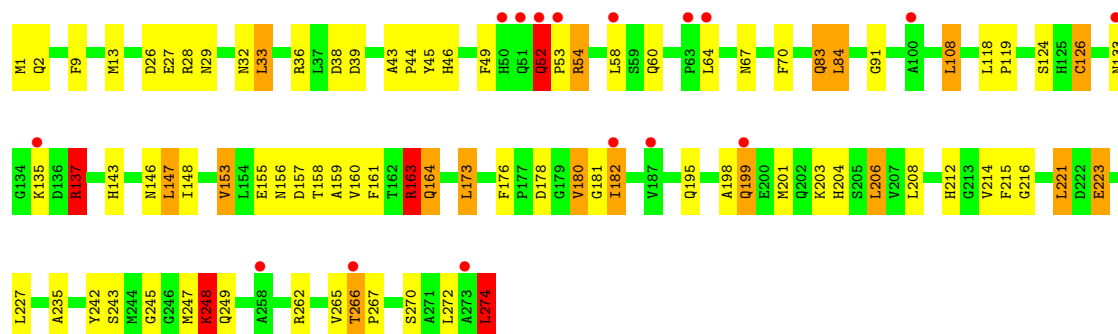
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain N: % 73% 17% 8%

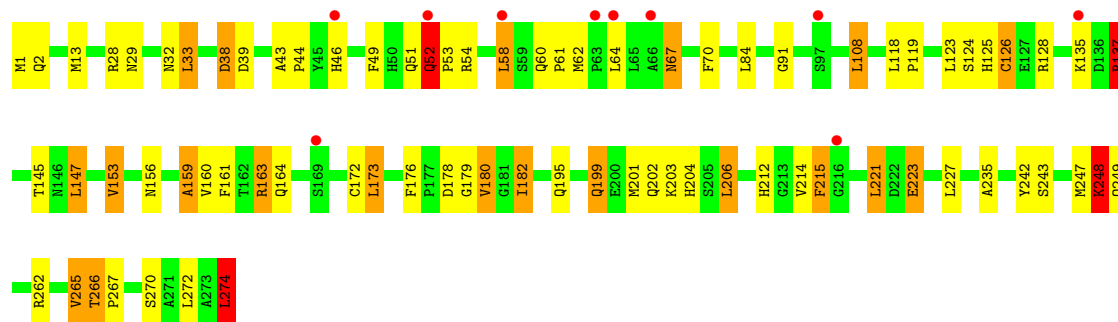




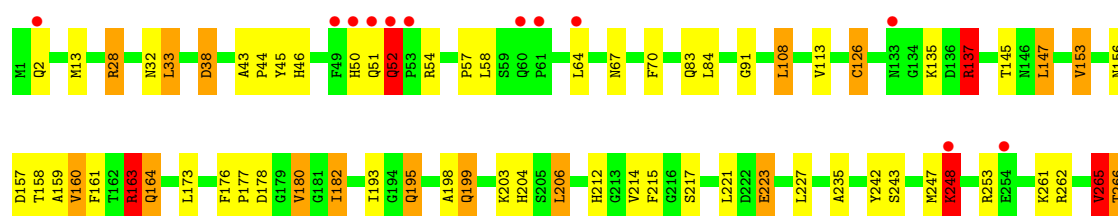
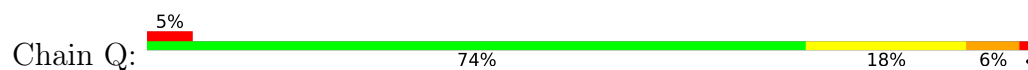
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE



• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE



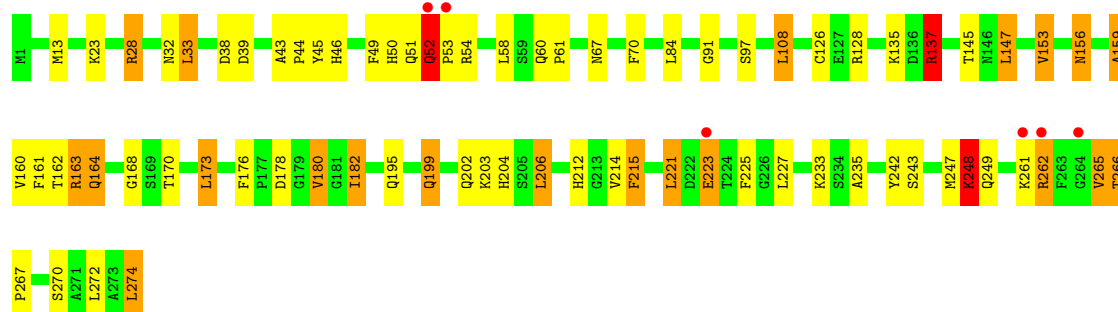
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE





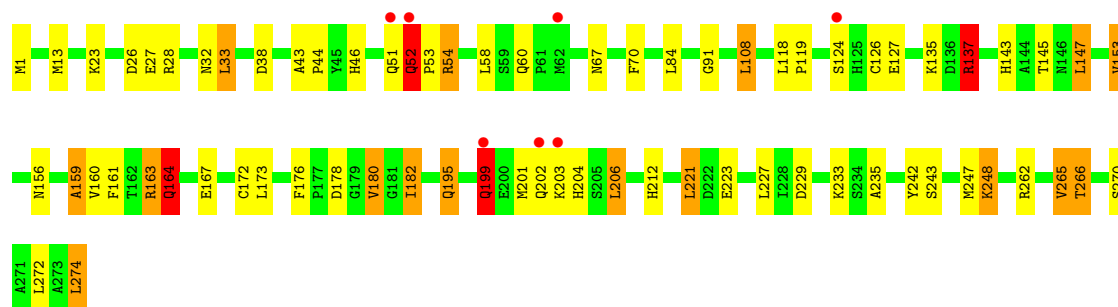
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain R: 2% 73% 19% 8%



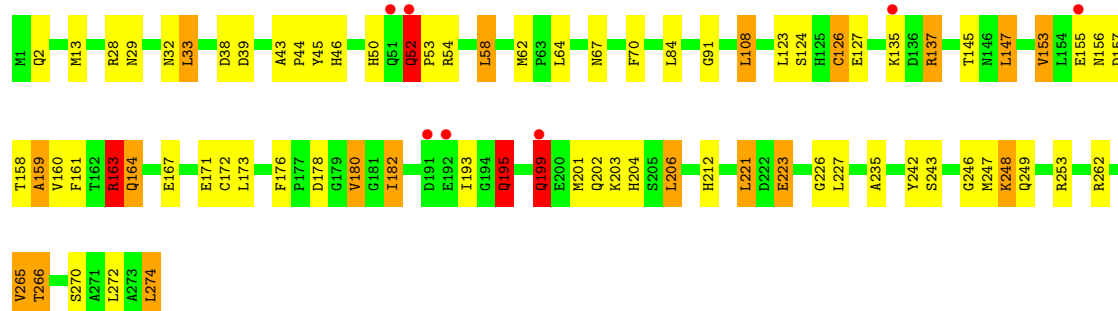
• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain S: 3% 74% 19% 6%



• Molecule 1: RHAMNULOSE-1-PHOSPHATE ALDOLASE

Chain T: 3% 72% 20% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	225.76Å 225.76Å 285.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.00 – 2.70 44.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	90.3 (44.00-2.70) 90.3 (44.00-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.69Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.233 , 0.235 0.219 , 0.225	Depositor DCC
R_{free} test set	1036 reflections (0.50%)	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.003 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	46180	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: ZN, PGH

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	1.05	0/2178	1.74	44/2966 (1.5%)
1	B	1.01	1/2178 (0.0%)	1.71	39/2966 (1.3%)
1	C	1.00	0/2178	1.73	40/2966 (1.3%)
1	D	1.07	0/2178	1.78	48/2966 (1.6%)
1	E	0.99	1/2178 (0.0%)	1.72	37/2966 (1.2%)
1	F	0.95	2/2178 (0.1%)	1.70	40/2966 (1.3%)
1	G	0.95	1/2178 (0.0%)	1.69	42/2966 (1.4%)
1	H	1.04	1/2178 (0.0%)	1.77	49/2966 (1.7%)
1	I	1.00	0/2178	1.71	43/2966 (1.4%)
1	J	1.05	1/2178 (0.0%)	1.69	33/2966 (1.1%)
1	K	1.22	4/2178 (0.2%)	1.79	44/2966 (1.5%)
1	L	1.17	2/2178 (0.1%)	1.73	35/2966 (1.2%)
1	M	0.99	1/2178 (0.0%)	1.72	36/2966 (1.2%)
1	N	1.06	1/2178 (0.0%)	1.70	40/2966 (1.3%)
1	O	1.24	2/2178 (0.1%)	1.76	42/2966 (1.4%)
1	P	1.12	1/2178 (0.0%)	1.69	40/2966 (1.3%)
1	Q	1.05	1/2178 (0.0%)	1.73	41/2966 (1.4%)
1	R	1.01	1/2178 (0.0%)	1.71	44/2966 (1.5%)
1	S	0.99	2/2178 (0.1%)	1.72	37/2966 (1.2%)
1	T	0.99	0/2178	1.72	43/2966 (1.4%)
All	All	1.05	22/43560 (0.1%)	1.73	817/59320 (1.4%)

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	D	0	1
1	F	0	1
1	I	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	1
1	N	0	1
1	P	0	1
1	Q	0	1
All	All	0	7

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	274	LEU	C-OXT	9.70	1.43	1.23
1	P	274	LEU	C-OXT	9.43	1.42	1.23
1	B	274	LEU	C-OXT	9.18	1.42	1.23
1	N	274	LEU	C-OXT	9.09	1.41	1.23
1	K	274	LEU	C-OXT	8.49	1.40	1.23

The worst 5 of 817 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	52	GLN	CB-CG-CD	10.59	130.59	112.60
1	N	52	GLN	CB-CG-CD	10.56	130.55	112.60
1	F	52	GLN	CB-CG-CD	10.37	130.22	112.60
1	H	52	GLN	CB-CG-CD	9.87	129.38	112.60
1	F	266	THR	CB-CA-C	9.76	121.00	110.17

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	38	ASP	Mainchain
1	F	38	ASP	Mainchain
1	I	38	ASP	Mainchain
1	L	38	ASP	Mainchain
1	N	38	ASP	Mainchain

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	2124	0	2097	44	0
1	B	2124	0	2097	37	0
1	C	2124	0	2097	37	0
1	D	2124	0	2097	40	2
1	E	2124	0	2097	36	1
1	F	2124	0	2097	31	0
1	G	2124	0	2097	40	0
1	H	2124	0	2097	43	1
1	I	2124	0	2097	42	0
1	J	2124	0	2097	43	0
1	K	2124	0	2097	45	8
1	L	2124	0	2097	37	2
1	M	2124	0	2097	46	2
1	N	2124	0	2097	42	0
1	O	2124	0	2097	42	0
1	P	2124	0	2097	40	0
1	Q	2124	0	2097	36	0
1	R	2124	0	2097	34	0
1	S	2124	0	2097	36	9
1	T	2124	0	2097	48	3
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
3	A	10	0	3	0	0
3	B	10	0	3	0	0
3	C	10	0	3	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	10	0	3	0	0
3	E	10	0	3	0	0
3	F	10	0	3	0	0
3	G	10	0	3	0	0
3	H	10	0	3	1	0
3	I	10	0	3	0	0
3	J	10	0	3	0	0
3	K	10	0	3	0	0
3	L	10	0	3	0	0
3	M	10	0	3	0	0
3	N	10	0	3	0	0
3	O	10	0	3	0	0
3	P	10	0	3	0	0
3	Q	10	0	3	0	0
3	R	10	0	3	0	0
3	S	10	0	3	0	0
3	T	10	0	3	0	0
4	A	177	0	0	17	0
4	B	174	0	0	16	0
4	C	173	0	0	14	0
4	D	173	0	0	21	0
4	E	179	0	0	16	0
4	F	174	0	0	14	0
4	G	176	0	0	14	0
4	H	171	0	0	19	2
4	I	177	0	0	16	0
4	J	178	0	0	16	0
4	K	177	0	0	22	1
4	L	167	0	0	13	0
4	M	183	0	0	18	0
4	N	170	0	0	16	0
4	O	175	0	0	15	0
4	P	167	0	0	19	0
4	Q	176	0	0	16	0
4	R	172	0	0	14	1
4	S	171	0	0	17	0
4	T	170	0	0	26	0
All	All	46180	0	42000	786	17

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.

The worst 5 of 786 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:K:97:SER:CB	4:K:2077:HOH:O	1.66	1.28
1:T:157:ASP:CG	4:T:2105:HOH:O	1.83	1.20
1:K:97:SER:HB3	4:K:2077:HOH:O	1.28	1.15
1:P:163:ARG:NH2	1:P:274:LEU:OXT	1.91	1.03
1:K:163:ARG:NH2	1:K:274:LEU:OXT	1.93	1.02

The worst 5 of 17 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:K:97:SER:OG	1:S:203:LYS:CD[1_655]	1.44	0.76
1:D:274:LEU:CD1	1:M:253:ARG:NH2[5_555]	1.65	0.55
1:K:66:ALA:CB	1:S:199:GLN:NE2[1_655]	1.67	0.53
1:L:195:GLN:NE2	1:L:195:GLN:NE2[5_555]	1.75	0.45
1:K:98:ASP:N	1:S:203:LYS:NZ[1_655]	1.77	0.43

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	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
1	B	272/274 (99%)	262 (96%)	10 (4%)	0	100	100
1	C	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	D	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
1	E	272/274 (99%)	261 (96%)	11 (4%)	0	100	100
1	F	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
1	G	272/274 (99%)	261 (96%)	11 (4%)	0	100	100
1	H	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	I	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	J	272/274 (99%)	262 (96%)	10 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	L	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	M	272/274 (99%)	261 (96%)	11 (4%)	0	100	100
1	N	272/274 (99%)	263 (97%)	9 (3%)	0	100	100
1	O	272/274 (99%)	262 (96%)	10 (4%)	0	100	100
1	P	272/274 (99%)	265 (97%)	7 (3%)	0	100	100
1	Q	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
1	R	272/274 (99%)	265 (97%)	7 (3%)	0	100	100
1	S	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
1	T	272/274 (99%)	262 (96%)	10 (4%)	0	100	100
All	All	5440/5480 (99%)	5259 (97%)	181 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	228/228 (100%)	203 (89%)	25 (11%)	6	15
1	B	228/228 (100%)	204 (90%)	24 (10%)	6	17
1	C	228/228 (100%)	203 (89%)	25 (11%)	6	15
1	D	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	E	228/228 (100%)	204 (90%)	24 (10%)	6	17
1	F	228/228 (100%)	204 (90%)	24 (10%)	6	17
1	G	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	H	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	I	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	J	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	K	228/228 (100%)	202 (89%)	26 (11%)	5	14

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	228/228 (100%)	201 (88%)	27 (12%)	5	13
1	M	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	N	228/228 (100%)	201 (88%)	27 (12%)	5	13
1	O	228/228 (100%)	201 (88%)	27 (12%)	5	13
1	P	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	Q	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	R	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	S	228/228 (100%)	202 (89%)	26 (11%)	5	14
1	T	228/228 (100%)	204 (90%)	24 (10%)	6	17
All	All	4560/4560 (100%)	4047 (89%)	513 (11%)	5	14

5 of 513 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	32	ASN
1	S	164	GLN
1	R	274	LEU
1	H	221	LEU
1	H	180	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 118 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	156	ASN
1	S	204	HIS
1	M	164	GLN
1	S	195	GLN
1	R	60	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

Of 40 ligands modelled in this entry, 20 are monoatomic - leaving 20 for Mogul analysis.

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	$\# Z > 2$
3	PGH	R	300	2	9,9,9	3.09	5 (55%)	10,12,12	2.08	4 (40%)
3	PGH	G	300	2	9,9,9	3.20	6 (66%)	10,12,12	2.14	3 (30%)
3	PGH	S	300	2	9,9,9	2.94	5 (55%)	10,12,12	2.06	3 (30%)
3	PGH	O	300	2	9,9,9	3.59	5 (55%)	10,12,12	2.90	5 (50%)
3	PGH	J	300	2	9,9,9	3.48	5 (55%)	10,12,12	2.94	6 (60%)
3	PGH	B	300	2	9,9,9	3.08	5 (55%)	10,12,12	2.65	5 (50%)
3	PGH	C	300	2	9,9,9	3.33	5 (55%)	10,12,12	2.14	6 (60%)
3	PGH	F	300	2	9,9,9	2.85	5 (55%)	10,12,12	2.52	3 (30%)
3	PGH	A	300	2	9,9,9	3.06	5 (55%)	10,12,12	2.17	4 (40%)
3	PGH	H	300	2	9,9,9	3.30	6 (66%)	10,12,12	2.14	5 (50%)
3	PGH	P	300	2	9,9,9	3.41	5 (55%)	10,12,12	2.42	3 (30%)
3	PGH	Q	300	2	9,9,9	3.26	5 (55%)	10,12,12	2.45	4 (40%)
3	PGH	N	300	2	9,9,9	3.18	5 (55%)	10,12,12	2.91	3 (30%)
3	PGH	T	300	2	9,9,9	3.35	7 (77%)	10,12,12	2.09	5 (50%)
3	PGH	L	300	2	9,9,9	3.71	5 (55%)	10,12,12	2.60	4 (40%)
3	PGH	D	300	2	9,9,9	3.29	5 (55%)	10,12,12	2.40	4 (40%)
3	PGH	I	300	2	9,9,9	3.01	4 (44%)	10,12,12	2.92	3 (30%)
3	PGH	M	300	2	9,9,9	3.64	5 (55%)	10,12,12	2.73	4 (40%)
3	PGH	E	300	2	9,9,9	3.21	4 (44%)	10,12,12	2.86	6 (60%)
3	PGH	K	300	2	9,9,9	3.30	5 (55%)	10,12,12	2.93	4 (40%)

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
3	PGH	R	300	2	-	5/8/8/8	-
3	PGH	G	300	2	-	4/8/8/8	-
3	PGH	S	300	2	-	5/8/8/8	-
3	PGH	O	300	2	-	5/8/8/8	-
3	PGH	J	300	2	-	5/8/8/8	-
3	PGH	B	300	2	-	5/8/8/8	-
3	PGH	C	300	2	-	5/8/8/8	-
3	PGH	F	300	2	-	5/8/8/8	-
3	PGH	A	300	2	-	5/8/8/8	-
3	PGH	H	300	2	-	5/8/8/8	-
3	PGH	P	300	2	-	5/8/8/8	-
3	PGH	Q	300	2	-	3/8/8/8	-
3	PGH	N	300	2	-	3/8/8/8	-
3	PGH	T	300	2	-	5/8/8/8	-
3	PGH	L	300	2	-	5/8/8/8	-
3	PGH	D	300	2	-	5/8/8/8	-
3	PGH	I	300	2	-	5/8/8/8	-
3	PGH	M	300	2	-	5/8/8/8	-
3	PGH	E	300	2	-	5/8/8/8	-
3	PGH	K	300	2	-	5/8/8/8	-

The worst 5 of 102 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	300	PGH	P-O1P	7.24	1.83	1.60
3	C	300	PGH	P-O1P	7.13	1.82	1.60
3	D	300	PGH	P-O1P	6.63	1.81	1.60
3	A	300	PGH	P-O1P	6.59	1.81	1.60
3	E	300	PGH	P-O1P	6.47	1.80	1.60

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	300	PGH	O1-C1-N2	6.34	131.06	123.27
3	J	300	PGH	O1-C1-N2	6.32	131.03	123.27

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	300	PGH	O1-C1-N2	6.31	131.02	123.27
3	I	300	PGH	O1-C1-N2	6.12	130.78	123.27
3	K	300	PGH	O1-C1-N2	6.06	130.71	123.27

There are no chirality outliers.

5 of 95 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	300	PGH	N2-C1-C2-O1P
3	A	300	PGH	C2-O1P-P-O4P
3	B	300	PGH	N2-C1-C2-O1P
3	B	300	PGH	C2-O1P-P-O3P
3	B	300	PGH	C2-O1P-P-O4P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	300	PGH	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	274/274 (100%)	0.33	10 (3%)	46	42	23, 37, 60, 84	0
1	B	274/274 (100%)	0.27	12 (4%)	39	35	23, 37, 60, 84	0
1	C	274/274 (100%)	0.27	9 (3%)	49	45	23, 37, 60, 84	0
1	D	274/274 (100%)	0.49	20 (7%)	21	18	23, 37, 60, 84	0
1	E	274/274 (100%)	0.24	10 (3%)	46	42	23, 37, 60, 84	0
1	F	274/274 (100%)	0.08	2 (0%)	84	83	23, 37, 60, 84	0
1	G	274/274 (100%)	0.11	3 (1%)	78	76	23, 37, 60, 84	0
1	H	274/274 (100%)	0.41	22 (8%)	18	15	23, 37, 60, 84	0
1	I	274/274 (100%)	0.34	7 (2%)	57	54	23, 37, 60, 84	0
1	J	274/274 (100%)	0.39	6 (2%)	62	59	23, 37, 60, 84	0
1	K	274/274 (100%)	0.84	13 (4%)	36	33	23, 37, 60, 84	0
1	L	274/274 (100%)	0.75	10 (3%)	46	42	23, 37, 60, 84	0
1	M	274/274 (100%)	0.25	12 (4%)	39	35	23, 37, 60, 84	0
1	N	274/274 (100%)	0.30	3 (1%)	78	76	23, 37, 60, 84	0
1	O	274/274 (100%)	0.81	16 (5%)	29	25	23, 37, 60, 84	0
1	P	274/274 (100%)	0.59	10 (3%)	46	42	23, 37, 60, 84	0
1	Q	274/274 (100%)	0.46	15 (5%)	30	27	23, 37, 60, 84	0
1	R	274/274 (100%)	0.20	6 (2%)	62	59	23, 37, 60, 84	0
1	S	274/274 (100%)	0.24	7 (2%)	57	54	23, 37, 60, 84	0
1	T	274/274 (100%)	0.25	7 (2%)	57	54	23, 37, 60, 84	0
All	All	5480/5480 (100%)	0.38	200 (3%)	46	42	23, 37, 60, 84	0

The worst 5 of 200 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	GLN	7.7
1	D	51	GLN	6.7
1	Q	51	GLN	6.6
1	M	273	ALA	6.5
1	M	274	LEU	6.3

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($\text{\AA}^2$)	Q<0.9
3	PGH	L	300	10/10	0.87	0.14	50,52,53,54	0
3	PGH	I	300	10/10	0.90	0.13	50,52,53,54	0
3	PGH	K	300	10/10	0.91	0.11	50,52,53,54	0
3	PGH	O	300	10/10	0.91	0.15	50,52,53,54	0
3	PGH	M	300	10/10	0.92	0.14	50,52,53,54	0
3	PGH	P	300	10/10	0.92	0.13	50,52,53,54	0
3	PGH	N	300	10/10	0.93	0.10	50,52,53,54	0
3	PGH	S	300	10/10	0.93	0.11	50,52,53,54	0
3	PGH	J	300	10/10	0.94	0.12	50,52,53,54	0
3	PGH	E	300	10/10	0.94	0.11	50,52,53,54	0
3	PGH	G	300	10/10	0.94	0.10	50,52,53,54	0
3	PGH	C	300	10/10	0.94	0.12	50,52,53,54	0
3	PGH	A	300	10/10	0.95	0.10	50,52,53,54	0
3	PGH	Q	300	10/10	0.95	0.12	50,52,53,54	0
3	PGH	F	300	10/10	0.95	0.10	50,52,53,54	0
3	PGH	B	300	10/10	0.96	0.08	50,52,53,54	0
3	PGH	H	300	10/10	0.96	0.11	50,52,53,54	0
3	PGH	D	300	10/10	0.96	0.12	50,52,53,54	0
3	PGH	T	300	10/10	0.96	0.11	50,52,53,54	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	K	275	1/1	0.97	0.10	35,35,35,35	0
3	PGH	R	300	10/10	0.97	0.09	50,52,53,54	0
2	ZN	O	275	1/1	0.99	0.12	35,35,35,35	0
2	ZN	P	275	1/1	0.99	0.04	34,34,34,34	0
2	ZN	S	275	1/1	0.99	0.03	33,33,33,33	0
2	ZN	T	275	1/1	0.99	0.04	33,33,33,33	0
2	ZN	J	275	1/1	0.99	0.09	35,35,35,35	0
2	ZN	C	275	1/1	0.99	0.07	32,32,32,32	0
2	ZN	L	275	1/1	0.99	0.09	35,35,35,35	0
2	ZN	N	275	1/1	0.99	0.08	35,35,35,35	0
2	ZN	H	275	1/1	1.00	0.04	32,32,32,32	0
2	ZN	I	275	1/1	1.00	0.05	34,34,34,34	0
2	ZN	B	275	1/1	1.00	0.03	32,32,32,32	0
2	ZN	A	275	1/1	1.00	0.07	32,32,32,32	0
2	ZN	D	275	1/1	1.00	0.04	32,32,32,32	0
2	ZN	M	275	1/1	1.00	0.04	33,33,33,33	0
2	ZN	E	275	1/1	1.00	0.03	32,32,32,32	0
2	ZN	F	275	1/1	1.00	0.02	34,34,34,34	0
2	ZN	G	275	1/1	1.00	0.02	34,34,34,34	0
2	ZN	Q	275	1/1	1.00	0.05	32,32,32,32	0
2	ZN	R	275	1/1	1.00	0.04	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.