



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:07 AM UTC

PDB ID : 6NPF / pdb_00006npf
Title : Structure of E.coli enolase in complex with an analog of the natural product SF-2312 metabolite.
Authors : Erlandsen, H.; Krucinska, J.; Lombardo, M.; Wright, D.
Deposited on : 2019-01-17
Resolution : 2.57 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

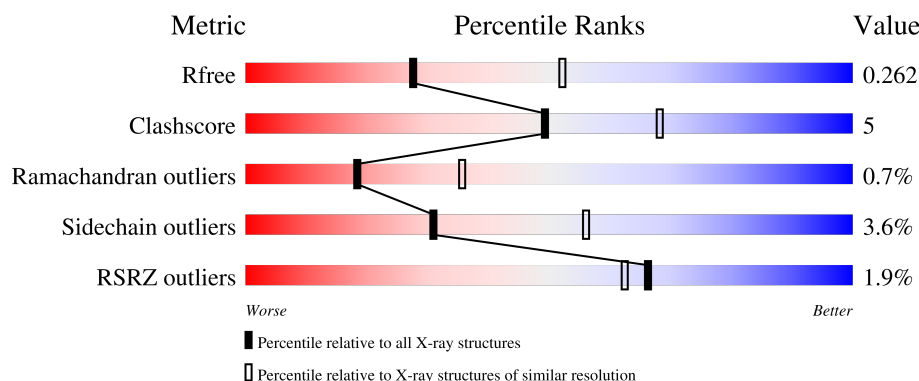
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	449	2% 86% 10% ..
1	B	449	86% 10% ..
1	C	449	2% 81% 16% .
1	D	449	3% 82% 13% ..
1	E	449	3% 79% 14% . 5%

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Mol	Chain	Length	Quality of chain
1	F	449	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TLA	C	703	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19725 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 Enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3249	2033	558	643	15			
1	B	436	Total	C	N	O	S	0	0	0
			3234	2024	554	641	15			
1	C	438	Total	C	N	O	S	0	0	0
			3249	2033	558	643	15			
1	D	432	Total	C	N	O	S	0	0	0
			3206	2008	549	634	15			
1	F	434	Total	C	N	O	S	0	0	0
			3219	2015	551	638	15			
1	E	426	Total	C	N	O	S	0	0	0
			3168	1988	542	623	15			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	GLY	-	expression tag	UNP B7MLA0
A	-16	SER	-	expression tag	UNP B7MLA0
A	-15	HIS	-	expression tag	UNP B7MLA0
A	-14	MET	-	expression tag	UNP B7MLA0
A	-13	ALA	-	expression tag	UNP B7MLA0
A	-12	SER	-	expression tag	UNP B7MLA0
A	-11	MET	-	expression tag	UNP B7MLA0
A	-10	THR	-	expression tag	UNP B7MLA0
A	-9	GLY	-	expression tag	UNP B7MLA0
A	-8	GLY	-	expression tag	UNP B7MLA0
A	-7	GLN	-	expression tag	UNP B7MLA0
A	-6	GLN	-	expression tag	UNP B7MLA0
A	-5	MET	-	expression tag	UNP B7MLA0
A	-4	GLY	-	expression tag	UNP B7MLA0
A	-3	ARG	-	expression tag	UNP B7MLA0
A	-2	GLY	-	expression tag	UNP B7MLA0
A	-1	SER	-	expression tag	UNP B7MLA0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	GLY	-	expression tag	UNP B7MLA0
B	-16	SER	-	expression tag	UNP B7MLA0
B	-15	HIS	-	expression tag	UNP B7MLA0
B	-14	MET	-	expression tag	UNP B7MLA0
B	-13	ALA	-	expression tag	UNP B7MLA0
B	-12	SER	-	expression tag	UNP B7MLA0
B	-11	MET	-	expression tag	UNP B7MLA0
B	-10	THR	-	expression tag	UNP B7MLA0
B	-9	GLY	-	expression tag	UNP B7MLA0
B	-8	GLY	-	expression tag	UNP B7MLA0
B	-7	GLN	-	expression tag	UNP B7MLA0
B	-6	GLN	-	expression tag	UNP B7MLA0
B	-5	MET	-	expression tag	UNP B7MLA0
B	-4	GLY	-	expression tag	UNP B7MLA0
B	-3	ARG	-	expression tag	UNP B7MLA0
B	-2	GLY	-	expression tag	UNP B7MLA0
B	-1	SER	-	expression tag	UNP B7MLA0
C	-17	GLY	-	expression tag	UNP B7MLA0
C	-16	SER	-	expression tag	UNP B7MLA0
C	-15	HIS	-	expression tag	UNP B7MLA0
C	-14	MET	-	expression tag	UNP B7MLA0
C	-13	ALA	-	expression tag	UNP B7MLA0
C	-12	SER	-	expression tag	UNP B7MLA0
C	-11	MET	-	expression tag	UNP B7MLA0
C	-10	THR	-	expression tag	UNP B7MLA0
C	-9	GLY	-	expression tag	UNP B7MLA0
C	-8	GLY	-	expression tag	UNP B7MLA0
C	-7	GLN	-	expression tag	UNP B7MLA0
C	-6	GLN	-	expression tag	UNP B7MLA0
C	-5	MET	-	expression tag	UNP B7MLA0
C	-4	GLY	-	expression tag	UNP B7MLA0
C	-3	ARG	-	expression tag	UNP B7MLA0
C	-2	GLY	-	expression tag	UNP B7MLA0
C	-1	SER	-	expression tag	UNP B7MLA0
D	-17	GLY	-	expression tag	UNP B7MLA0
D	-16	SER	-	expression tag	UNP B7MLA0
D	-15	HIS	-	expression tag	UNP B7MLA0
D	-14	MET	-	expression tag	UNP B7MLA0
D	-13	ALA	-	expression tag	UNP B7MLA0
D	-12	SER	-	expression tag	UNP B7MLA0
D	-11	MET	-	expression tag	UNP B7MLA0
D	-10	THR	-	expression tag	UNP B7MLA0

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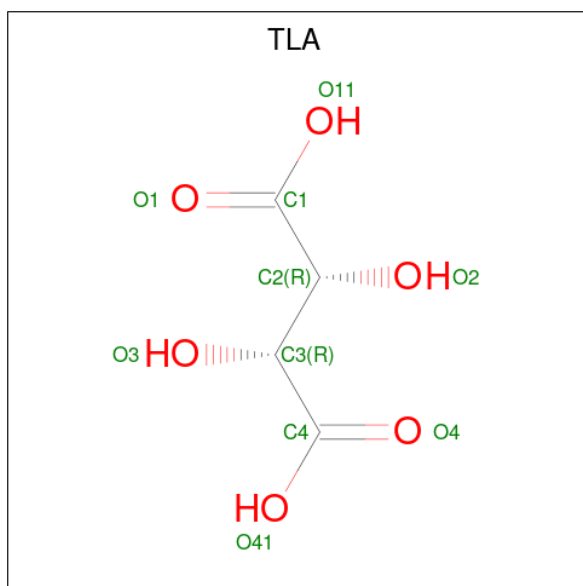
Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	GLY	-	expression tag	UNP B7MLA0
D	-8	GLY	-	expression tag	UNP B7MLA0
D	-7	GLN	-	expression tag	UNP B7MLA0
D	-6	GLN	-	expression tag	UNP B7MLA0
D	-5	MET	-	expression tag	UNP B7MLA0
D	-4	GLY	-	expression tag	UNP B7MLA0
D	-3	ARG	-	expression tag	UNP B7MLA0
D	-2	GLY	-	expression tag	UNP B7MLA0
D	-1	SER	-	expression tag	UNP B7MLA0
F	-17	GLY	-	expression tag	UNP B7MLA0
F	-16	SER	-	expression tag	UNP B7MLA0
F	-15	HIS	-	expression tag	UNP B7MLA0
F	-14	MET	-	expression tag	UNP B7MLA0
F	-13	ALA	-	expression tag	UNP B7MLA0
F	-12	SER	-	expression tag	UNP B7MLA0
F	-11	MET	-	expression tag	UNP B7MLA0
F	-10	THR	-	expression tag	UNP B7MLA0
F	-9	GLY	-	expression tag	UNP B7MLA0
F	-8	GLY	-	expression tag	UNP B7MLA0
F	-7	GLN	-	expression tag	UNP B7MLA0
F	-6	GLN	-	expression tag	UNP B7MLA0
F	-5	MET	-	expression tag	UNP B7MLA0
F	-4	GLY	-	expression tag	UNP B7MLA0
F	-3	ARG	-	expression tag	UNP B7MLA0
F	-2	GLY	-	expression tag	UNP B7MLA0
F	-1	SER	-	expression tag	UNP B7MLA0
E	-17	GLY	-	expression tag	UNP B7MLA0
E	-16	SER	-	expression tag	UNP B7MLA0
E	-15	HIS	-	expression tag	UNP B7MLA0
E	-14	MET	-	expression tag	UNP B7MLA0
E	-13	ALA	-	expression tag	UNP B7MLA0
E	-12	SER	-	expression tag	UNP B7MLA0
E	-11	MET	-	expression tag	UNP B7MLA0
E	-10	THR	-	expression tag	UNP B7MLA0
E	-9	GLY	-	expression tag	UNP B7MLA0
E	-8	GLY	-	expression tag	UNP B7MLA0
E	-7	GLN	-	expression tag	UNP B7MLA0
E	-6	GLN	-	expression tag	UNP B7MLA0
E	-5	MET	-	expression tag	UNP B7MLA0
E	-4	GLY	-	expression tag	UNP B7MLA0
E	-3	ARG	-	expression tag	UNP B7MLA0
E	-2	GLY	-	expression tag	UNP B7MLA0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	expression tag	UNP B7MLA0

- Molecule 2 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	4	6		
2	B	1	Total	C	O	0	0
			10	4	6		
2	C	1	Total	C	O	0	0
			10	4	6		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

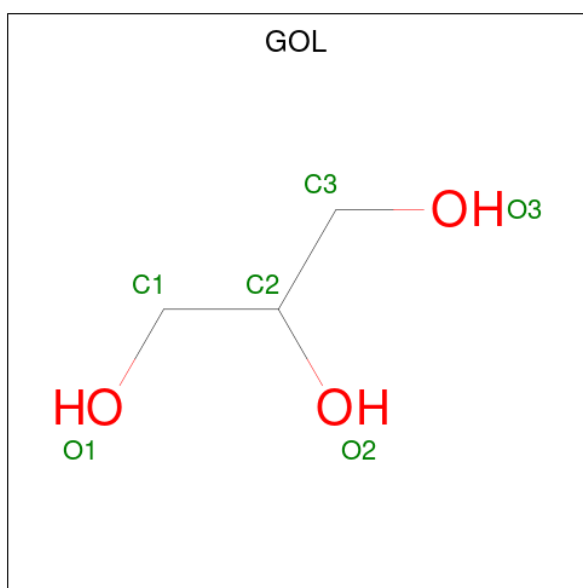
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

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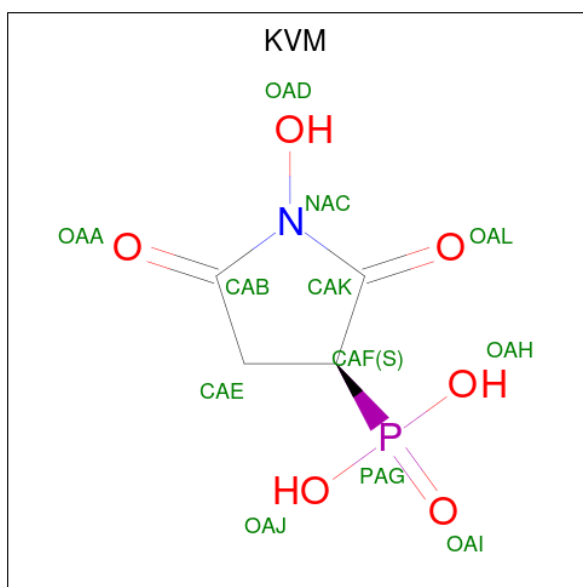
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		
4	F	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is [(3S)-1-hydroxy-2,5-dioxopyrrolidin-3-yl]phosphonic acid (CCD ID: KVM) (formula: $C_4H_6NO_6P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	D	1	Total	C	N	O	P	0	0
			12	4	1	6	1		
6	F	1	Total	C	N	O	P	0	0
			12	4	1	6	1		
6	E	1	Total	C	N	O	P	0	0
			12	4	1	6	1		

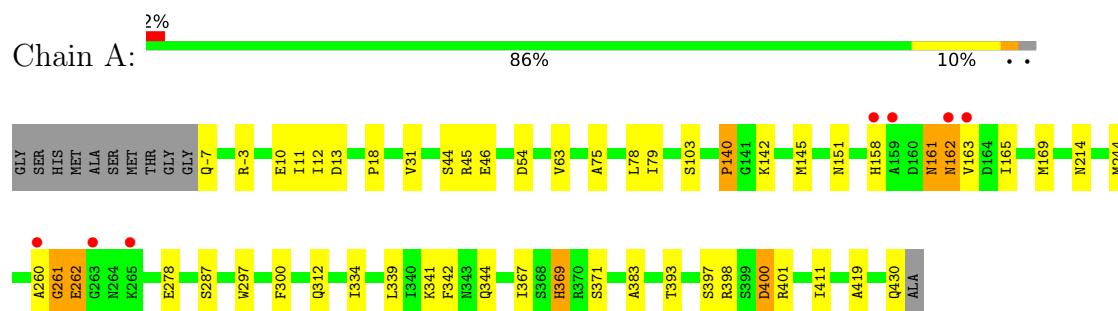
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	53	Total	O	0	0
			53	53		
7	B	36	Total	O	0	0
			36	36		
7	C	49	Total	O	0	0
			49	49		
7	D	46	Total	O	0	0
			46	46		
7	F	39	Total	O	0	0
			39	39		
7	E	26	Total	O	0	0
			26	26		

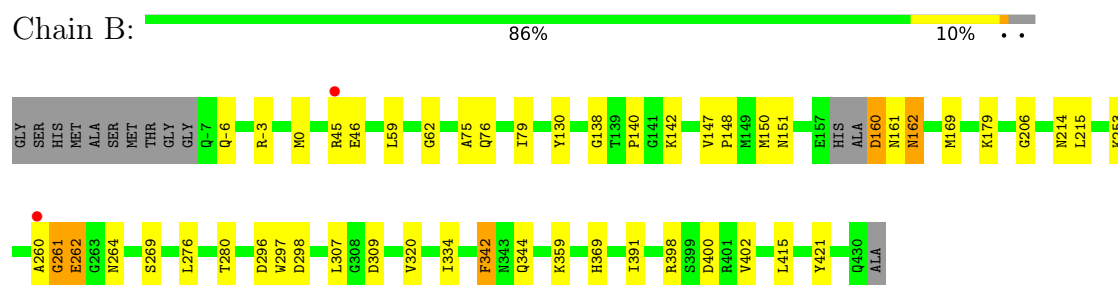
3 Residue-property plots [i](#)

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 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.

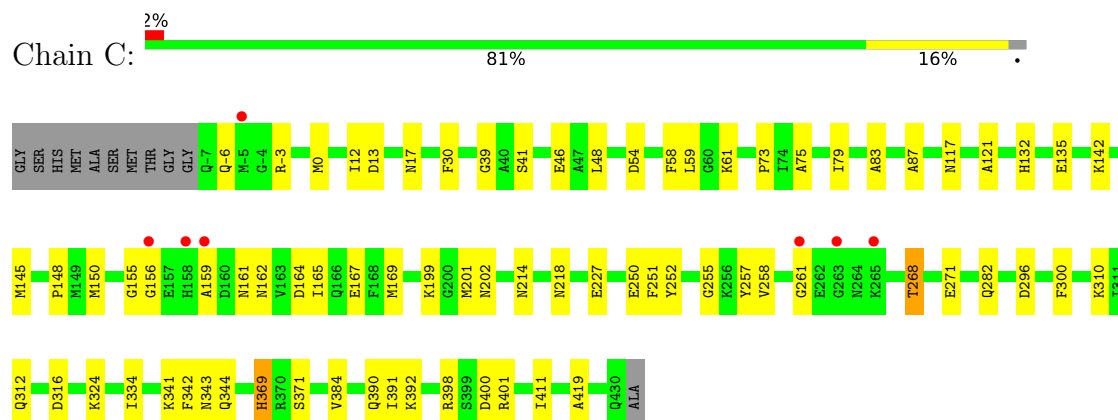
• Molecule 1: Enolase



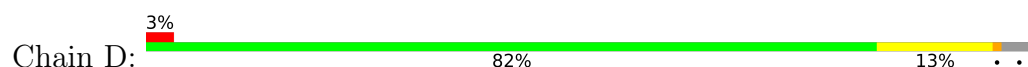
• Molecule 1: Enolase

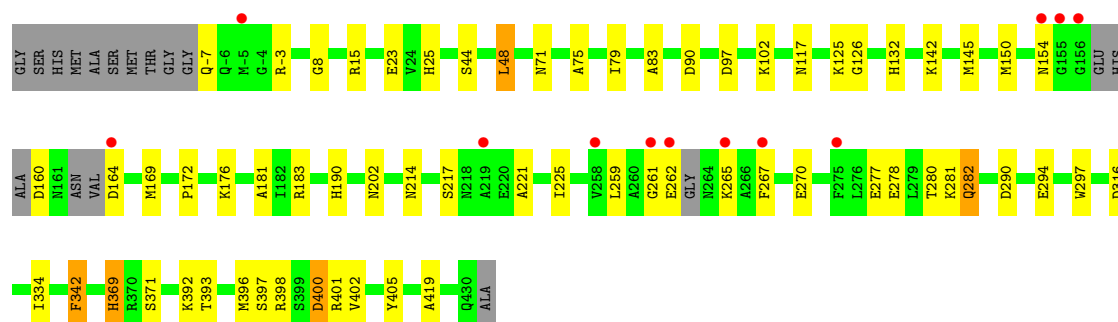


• Molecule 1: Enolase

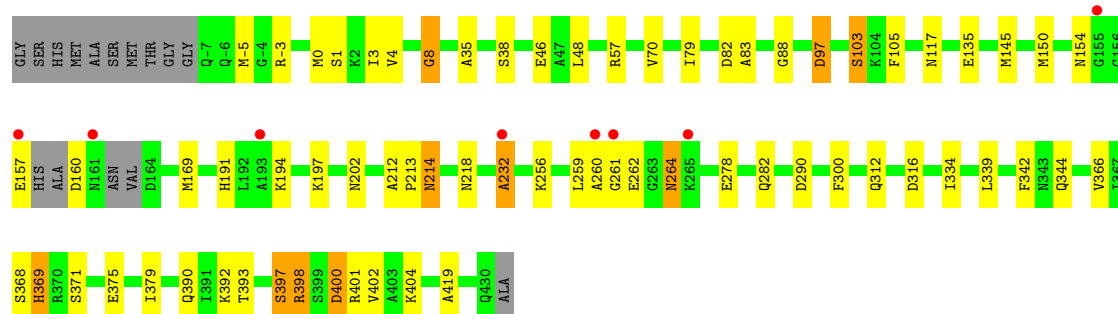
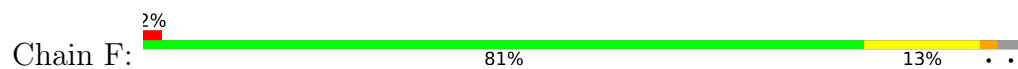


• Molecule 1: Enolase

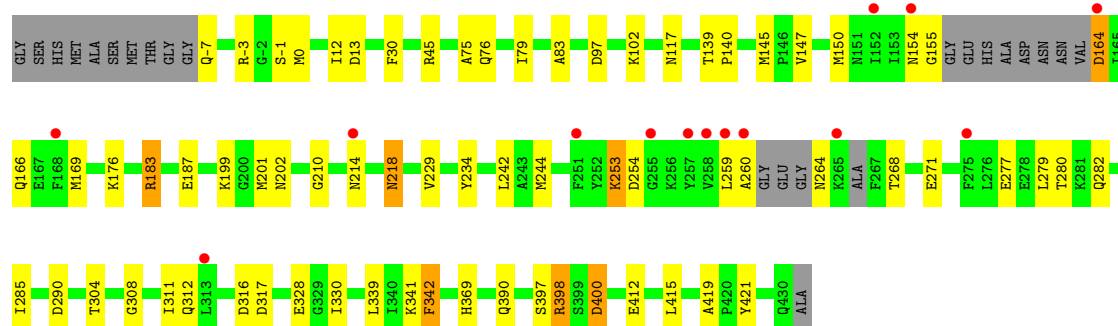
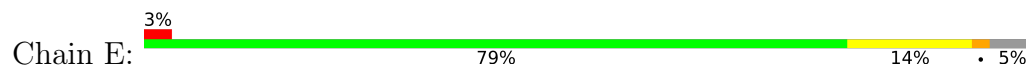




● Molecule 1: Enolase



● Molecule 1: Enolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.18Å 143.11Å 206.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.03 – 2.57 93.03 – 2.57	Depositor EDS
% Data completeness (in resolution range)	99.1 (93.03-2.57) 99.1 (93.03-2.57)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.191 , 0.256 0.200 , 0.262	Depositor DCC
R_{free} test set	4924 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19725	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: MG, TLA, SO4, GOL, KVM

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	1.10	0/3291	1.58	8/4428 (0.2%)
1	B	1.10	0/3274	1.54	10/4403 (0.2%)
1	C	1.10	1/3291 (0.0%)	1.54	5/4428 (0.1%)
1	D	1.11	0/3244	1.53	6/4359 (0.1%)
1	E	1.16	0/3206	1.59	12/4308 (0.3%)
1	F	1.12	0/3258	1.53	8/4379 (0.2%)
All	All	1.12	1/19564 (0.0%)	1.55	49/26305 (0.2%)

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	F	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	161	ASN	C-O	-5.63	1.20	1.24

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	-5	MET	CA-C-N	6.65	126.42	120.10
1	F	-5	MET	C-N-CA	6.65	126.42	120.10
1	E	342	PHE	CA-CB-CG	6.24	120.03	113.80
1	D	160	ASP	CA-CB-CG	5.97	118.57	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	HIS	CB-CA-C	5.90	119.34	111.14
1	A	400	ASP	CA-CB-CG	5.90	118.50	112.60
1	C	161	ASN	CA-C-O	-5.71	115.03	120.56
1	D	342	PHE	CA-CB-CG	5.68	119.48	113.80
1	D	400	ASP	CA-CB-CG	5.67	118.28	112.60
1	E	317	ASP	CA-C-N	5.63	127.83	120.28
1	E	317	ASP	C-N-CA	5.63	127.83	120.28
1	E	279	LEU	CA-C-N	5.61	128.35	120.28
1	E	279	LEU	C-N-CA	5.61	128.35	120.28
1	C	87	ALA	CA-C-N	5.52	126.07	119.94
1	C	87	ALA	C-N-CA	5.52	126.07	119.94
1	A	214	ASN	CB-CA-C	5.51	119.91	110.81
1	D	90	ASP	CB-CA-C	5.45	119.43	110.88
1	C	73	PRO	CA-C-N	5.43	127.51	120.56
1	C	73	PRO	C-N-CA	5.43	127.51	120.56
1	E	13	ASP	CA-CB-CG	5.38	117.98	112.60
1	A	140	PRO	CA-C-O	-5.35	115.50	121.23
1	B	342	PHE	CA-C-O	-5.35	113.02	119.49
1	B	298	ASP	CA-C-N	5.32	126.00	119.99
1	B	298	ASP	C-N-CA	5.32	126.00	119.99
1	B	206	GLY	CA-C-N	5.29	127.36	120.28
1	B	206	GLY	C-N-CA	5.29	127.36	120.28
1	F	214	ASN	CB-CA-C	5.25	119.47	110.81
1	F	88	GLY	CA-C-N	5.21	127.07	120.72
1	F	88	GLY	C-N-CA	5.21	127.07	120.72
1	A	54	ASP	CA-C-N	5.20	127.50	120.38
1	A	54	ASP	C-N-CA	5.20	127.50	120.38
1	E	328	GLU	CA-C-N	5.20	125.72	120.00
1	E	328	GLU	C-N-CA	5.20	125.72	120.00
1	B	62	GLY	CA-C-O	-5.19	115.49	122.24
1	E	330	ILE	CA-C-N	5.18	127.22	120.28
1	E	330	ILE	C-N-CA	5.18	127.22	120.28
1	B	307	LEU	CA-C-N	5.16	125.81	120.03
1	B	307	LEU	C-N-CA	5.16	125.81	120.03
1	D	48	LEU	CA-C-N	5.15	128.17	120.95
1	D	48	LEU	C-N-CA	5.15	128.17	120.95
1	E	218	ASN	CA-C-N	5.14	127.42	120.38
1	E	218	ASN	C-N-CA	5.14	127.42	120.38
1	A	31	VAL	CA-C-N	5.11	125.12	121.65
1	A	31	VAL	C-N-CA	5.11	125.12	121.65
1	F	35	ALA	CA-C-N	5.09	127.47	120.39
1	F	35	ALA	C-N-CA	5.09	127.47	120.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	359	LYS	CA-C-N	5.09	127.61	120.28
1	B	359	LYS	C-N-CA	5.09	127.61	120.28
1	F	8	GLY	CA-C-O	-5.07	116.31	120.92

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	261	GLY	Peptide
1	F	160	ASP	Peptide
1	F	232	ALA	Peptide

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	3249	0	3274	31	0
1	B	3234	0	3261	27	0
1	C	3249	0	3274	51	0
1	D	3206	0	3235	38	0
1	E	3168	0	3208	41	0
1	F	3219	0	3245	39	0
2	A	10	0	4	0	0
2	B	10	0	4	0	0
2	C	10	0	4	4	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
3	C	10	0	0	0	0
3	D	15	0	0	1	0
3	F	15	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	6	0	8	0	0
5	C	6	0	8	0	0
5	D	6	0	8	0	0
6	D	12	0	0	1	0
6	E	12	0	0	1	0
6	F	12	0	0	1	0
7	A	53	0	0	3	0
7	B	36	0	0	1	0
7	C	49	0	0	1	0
7	D	46	0	0	4	0
7	E	26	0	0	1	0
7	F	39	0	0	1	0
All	All	19725	0	19541	210	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 5.

All (210) 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:C:312:GLN:HE22	1:C:390:GLN:HE22	1.15	0.93
1:F:312:GLN:HE22	1:F:390:GLN:HE22	1.01	0.90
1:E:154:ASN:ND2	1:E:210:GLY:O	2.12	0.83
1:E:164:ASP:HB3	1:E:218:ASN:HD21	1.47	0.80
1:C:369:HIS:CD2	1:C:401:ARG:HH11	2.02	0.77
1:F:312:GLN:HE22	1:F:390:GLN:NE2	1.84	0.73
1:E:312:GLN:HE22	1:E:390:GLN:HE22	1.33	0.72
1:F:312:GLN:NE2	1:F:390:GLN:HE22	1.84	0.70
1:C:75:ALA:O	1:C:79:ILE:HG12	1.90	0.69
1:F:369:HIS:CD2	1:F:401:ARG:HH11	2.09	0.69
1:E:164:ASP:CB	1:E:218:ASN:HD21	2.06	0.69
1:B:160:ASP:N	1:B:160:ASP:OD1	2.25	0.67
1:E:398:ARG:HB3	1:E:400:ASP:OD1	1.96	0.66
1:D:-7:GLN:OE1	7:D:701:HOH:O	2.13	0.65
1:D:44:SER:OG	1:D:294:GLU:OE2	2.14	0.65
1:D:172:PRO:HG2	1:D:181:ALA:HB1	1.78	0.65
1:D:392:LYS:NZ	6:D:601:KVM:OAD	2.31	0.63
1:F:202:ASN:ND2	1:E:202:ASN:HD21	1.98	0.62
1:C:145:MET:HE3	1:C:419:ALA:CB	2.29	0.62
6:E:602:KVM:OAA	7:E:701:HOH:O	2.16	0.62
1:C:164:ASP:H	1:C:218:ASN:HD21	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:75:ALA:O	1:D:79:ILE:HG12	1.99	0.62
1:A:297:TRP:CE3	1:A:334:ILE:HD12	2.36	0.61
1:A:260:ALA:O	1:A:261:GLY:O	2.19	0.61
1:C:83:ALA:HA	1:C:117:ASN:HD21	1.65	0.61
1:F:290:ASP:OD2	1:F:316:ASP:HB3	2.00	0.61
1:C:162:ASN:N	1:C:214:ASN:ND2	2.50	0.60
1:E:83:ALA:HA	1:E:117:ASN:HD21	1.67	0.60
1:D:8:GLY:H	1:D:71:ASN:HD21	1.50	0.59
1:E:229:VAL:HG12	1:E:234:TYR:O	2.03	0.59
1:C:312:GLN:NE2	1:C:390:GLN:HE22	1.93	0.59
1:D:8:GLY:H	1:D:71:ASN:ND2	2.01	0.59
1:B:75:ALA:O	1:B:79:ILE:HG12	2.04	0.58
1:F:218:ASN:HD22	1:F:262:GLU:HG3	1.68	0.58
1:E:268:THR:HG22	1:E:271:GLU:CD	2.29	0.58
1:A:161:ASN:O	1:A:162:ASN:HB2	2.03	0.57
1:A:430:GLN:C	7:A:713:HOH:O	2.48	0.57
1:F:278:GLU:OE2	1:F:282:GLN:NE2	2.38	0.57
1:C:145:MET:HE3	1:C:419:ALA:HB1	1.87	0.56
1:D:15:ARG:NH1	7:D:703:HOH:O	2.38	0.56
1:E:259:LEU:N	1:E:259:LEU:HD12	2.21	0.56
1:F:4:VAL:O	1:F:79:ILE:HD12	2.06	0.55
1:F:194:LYS:O	1:F:197:LYS:HE3	2.07	0.55
1:B:-6:GLN:HE22	1:D:-3:ARG:NH2	2.04	0.55
1:E:312:GLN:HE22	1:E:390:GLN:NE2	2.05	0.54
1:E:183:ARG:NH1	1:E:187:GLU:OE2	2.40	0.54
1:E:155:GLY:N	1:E:166:GLN:O	2.40	0.54
1:E:75:ALA:O	1:E:79:ILE:HG12	2.06	0.54
1:C:41:SER:HB2	1:C:250:GLU:OE2	2.08	0.54
1:C:61:LYS:NZ	7:C:801:HOH:O	2.41	0.53
1:D:297:TRP:CE3	1:D:334:ILE:HD13	2.43	0.53
1:E:150:MET:O	1:E:169:MET:HA	2.09	0.53
1:C:300:PHE:HB3	1:C:334:ILE:HG23	1.90	0.53
1:E:154:ASN:HD21	1:E:210:GLY:C	2.15	0.53
1:B:162:ASN:HB2	1:B:215:LEU:O	2.09	0.52
1:C:268:THR:HG22	1:C:271:GLU:CD	2.34	0.52
1:E:97:ASP:OD2	1:E:102:LYS:HA	2.10	0.52
1:F:339:LEU:HG	1:F:368:SER:HB2	1.91	0.52
1:D:277:GLU:O	1:D:280:THR:HB	2.10	0.52
1:E:199:LYS:HB3	1:E:201:MET:HE3	1.92	0.52
1:C:148:PRO:HG2	1:C:150:MET:HE3	1.91	0.51
1:D:97:ASP:OD2	1:D:102:LYS:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:MET:HE3	1:D:419:ALA:HB1	1.93	0.51
1:B:46:GLU:CD	1:B:344:GLN:HG2	2.36	0.51
1:D:150:MET:O	1:D:169:MET:HA	2.11	0.51
1:A:297:TRP:CE3	1:A:334:ILE:CD1	2.94	0.51
1:A:369:HIS:CD2	1:A:401:ARG:HH11	2.29	0.51
1:F:83:ALA:HA	1:F:117:ASN:HD21	1.76	0.51
1:B:-6:GLN:HE22	1:D:-3:ARG:HH21	1.60	0.50
1:C:316:ASP:CG	1:C:341:LYS:HZ2	2.19	0.50
1:E:-3:ARG:HA	1:E:0:MET:HE2	1.93	0.50
1:A:151:ASN:HA	1:A:169:MET:HG2	1.92	0.50
1:E:154:ASN:ND2	1:E:210:GLY:C	2.70	0.50
1:E:164:ASP:HB3	1:E:218:ASN:ND2	2.23	0.50
1:B:147:VAL:HG22	1:B:421:TYR:CZ	2.46	0.50
1:C:252:TYR:CZ	1:C:255:GLY:HA2	2.47	0.50
1:F:57:ARG:HA	1:E:183:ARG:NH1	2.27	0.49
1:A:287:SER:HA	1:A:312:GLN:O	2.12	0.49
1:D:217:SER:HB2	1:D:262:GLU:OE2	2.12	0.49
1:A:165:ILE:HG21	1:A:244:MET:HE2	1.95	0.49
1:F:46:GLU:CD	1:F:344:GLN:HG2	2.38	0.49
1:F:145:MET:HE3	1:F:419:ALA:CB	2.43	0.49
1:D:369:HIS:CD2	1:D:401:ARG:HH11	2.30	0.49
1:E:259:LEU:O	1:E:260:ALA:C	2.56	0.49
1:A:10:GLU:OE1	1:B:179:LYS:NZ	2.39	0.49
1:C:341:LYS:NZ	2:C:703:TLA:H2	2.28	0.49
1:A:75:ALA:O	1:A:79:ILE:HG12	2.12	0.48
1:A:145:MET:HE1	1:A:411:ILE:HG22	1.95	0.48
1:A:11:ILE:O	1:A:18:PRO:HA	2.13	0.48
3:D:603:SO4:O1	7:D:702:HOH:O	2.19	0.48
1:D:83:ALA:HA	1:D:117:ASN:HD21	1.77	0.48
1:F:402:VAL:CG1	1:E:12:ILE:HB	2.44	0.48
1:A:367:ILE:HG13	1:A:383:ALA:HA	1.96	0.48
1:A:-3:ARG:HD2	1:C:-6:GLN:NE2	2.29	0.48
1:D:297:TRP:CE3	1:D:334:ILE:CD1	2.96	0.48
1:C:150:MET:O	1:C:169:MET:HA	2.14	0.48
1:F:259:LEU:HD12	1:F:259:LEU:N	2.28	0.48
1:A:261:GLY:O	1:A:262:GLU:C	2.57	0.47
1:B:-3:ARG:HG2	1:B:0:MET:HE3	1.96	0.47
1:D:132:HIS:HE1	7:D:726:HOH:O	1.96	0.47
1:D:396:MET:HE1	1:D:405:TYR:CD2	2.49	0.47
1:E:277:GLU:O	1:E:280:THR:HB	2.14	0.47
1:A:145:MET:HE3	1:A:419:ALA:CB	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:191:HIS:NE2	1:F:232:ALA:CB	2.78	0.47
1:C:-3:ARG:HA	1:C:0:MET:HE2	1.96	0.47
1:C:41:SER:CB	1:C:250:GLU:OE2	2.63	0.47
1:D:23:GLU:OE1	1:D:25:HIS:HE1	1.97	0.47
1:A:46:GLU:CD	1:A:344:GLN:HG2	2.40	0.47
1:C:169:MET:SD	1:C:392:LYS:HD2	2.55	0.47
1:E:145:MET:SD	1:E:412:GLU:HB2	2.54	0.47
1:F:191:HIS:NE2	1:F:232:ALA:HB3	2.30	0.46
1:E:147:VAL:HG22	1:E:421:TYR:CZ	2.49	0.46
1:F:-3:ARG:HA	1:F:0:MET:HE2	1.96	0.46
1:A:63:VAL:HA	7:A:720:HOH:O	2.15	0.46
1:E:415:LEU:HD13	1:E:419:ALA:HB2	1.97	0.46
1:F:375:GLU:H	1:F:375:GLU:CD	2.23	0.46
1:F:157:GLU:N	7:F:804:HOH:O	2.49	0.46
1:F:379:ILE:HD11	1:F:404:LYS:HG2	1.97	0.46
1:E:280:THR:HG23	1:E:311:ILE:HD11	1.98	0.46
1:A:12:ILE:HB	1:B:402:VAL:CG1	2.46	0.45
1:C:30:PHE:HA	1:E:-7:GLN:O	2.16	0.45
1:C:145:MET:CE	1:C:419:ALA:HB1	2.46	0.45
1:C:199:LYS:NZ	1:C:227:GLU:OE2	2.49	0.45
1:F:97:ASP:HB2	1:F:105:PHE:CD2	2.52	0.45
1:D:290:ASP:OD2	1:D:316:ASP:HB3	2.16	0.45
1:B:261:GLY:O	1:B:262:GLU:CG	2.65	0.45
1:F:212:ALA:N	1:F:213:PRO:CD	2.79	0.45
1:C:202:ASN:HD21	1:D:202:ASN:HD21	1.65	0.45
1:B:297:TRP:CE3	1:B:334:ILE:HD12	2.52	0.45
1:C:341:LYS:HZ3	2:C:703:TLA:C2	2.30	0.45
1:C:369:HIS:CD2	1:C:401:ARG:NH1	2.80	0.45
1:F:392:LYS:HE3	6:F:703:KVM:OAA	2.17	0.45
1:E:253:LYS:HE3	1:E:253:LYS:HA	1.99	0.45
1:C:257:TYR:OH	1:C:296:ASP:OD2	2.30	0.44
1:B:297:TRP:CE3	1:B:334:ILE:CD1	3.01	0.44
1:D:369:HIS:CD2	1:D:393:THR:HA	2.51	0.44
1:C:39:GLY:HA2	2:C:703:TLA:O41	2.17	0.44
1:C:54:ASP:C	1:C:54:ASP:OD1	2.61	0.44
1:B:161:ASN:HB2	1:B:214:ASN:HA	2.00	0.44
1:E:290:ASP:OD2	1:E:316:ASP:HB3	2.18	0.44
1:E:339:LEU:HD23	1:E:341:LYS:NZ	2.33	0.44
1:D:125:LYS:NZ	1:D:132:HIS:HD2	2.16	0.44
1:A:369:HIS:HE1	7:A:706:HOH:O	2.01	0.43
1:C:162:ASN:N	1:C:214:ASN:HD21	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:VAL:O	1:B:320:VAL:HG23	2.19	0.43
1:F:397:SER:O	1:F:398:ARG:HB2	2.18	0.43
1:C:167:GLU:OE1	1:C:392:LYS:NZ	2.48	0.43
1:A:151:ASN:CA	1:A:169:MET:HG2	2.48	0.43
1:C:83:ALA:CA	1:C:117:ASN:HD21	2.30	0.43
1:D:145:MET:HE3	1:D:419:ALA:CB	2.48	0.43
1:B:162:ASN:ND2	1:B:261:GLY:CA	2.82	0.43
1:C:155:GLY:O	1:C:165:ILE:O	2.36	0.43
1:D:278:GLU:O	1:D:281:LYS:O	2.35	0.43
1:D:281:LYS:O	1:D:282:GLN:HB3	2.17	0.43
1:F:1:SER:OG	1:F:82:ASP:OD1	2.35	0.43
1:E:244:MET:HE3	1:E:285:ILE:HD13	1.99	0.43
1:B:162:ASN:ND2	1:B:261:GLY:HA2	2.33	0.43
1:C:59:LEU:N	1:C:59:LEU:HD12	2.34	0.43
1:C:199:LYS:HD3	1:C:201:MET:CE	2.48	0.43
1:C:341:LYS:HZ3	2:C:703:TLA:H2	1.84	0.43
1:B:269:SER:OG	1:B:296:ASP:OD2	2.36	0.43
1:C:12:ILE:HB	1:D:402:VAL:CG1	2.48	0.42
1:C:46:GLU:CD	1:C:344:GLN:HG2	2.44	0.42
1:F:3:ILE:HD11	1:F:117:ASN:ND2	2.34	0.42
1:F:369:HIS:CD2	1:F:393:THR:HA	2.55	0.42
1:E:214:ASN:HD22	1:E:214:ASN:HA	1.70	0.42
1:E:304:THR:O	1:E:308:GLY:HA3	2.20	0.42
1:A:78:LEU:O	1:A:79:ILE:C	2.63	0.42
1:C:148:PRO:HA	1:C:391:ILE:O	2.20	0.42
1:A:339:LEU:HD23	1:A:341:LYS:HE3	2.01	0.42
1:B:138:GLY:HA2	7:B:603:HOH:O	2.20	0.42
1:B:161:ASN:CB	1:B:214:ASN:HA	2.50	0.42
1:C:251:PHE:HB2	1:C:258:VAL:O	2.18	0.42
1:D:126:GLY:O	1:E:-1:SER:HA	2.20	0.42
1:C:83:ALA:CB	1:C:117:ASN:HD21	2.32	0.42
1:B:130:TYR:CE1	1:B:415:LEU:HD11	2.55	0.42
1:C:58:PHE:CE1	1:D:183:ARG:HA	2.54	0.42
1:D:259:LEU:N	1:D:259:LEU:HD12	2.35	0.42
1:F:339:LEU:HD12	1:F:366:VAL:HB	2.02	0.42
1:A:369:HIS:CD2	1:A:393:THR:HA	2.55	0.41
1:E:139:THR:N	1:E:140:PRO:HD3	2.35	0.41
1:A:278:GLU:OE1	1:A:278:GLU:HA	2.19	0.41
1:B:276:LEU:O	1:B:280:THR:HG23	2.21	0.41
1:A:140:PRO:HG3	1:F:135:GLU:O	2.20	0.41
1:B:150:MET:O	1:B:169:MET:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:-3:ARG:HD2	1:C:-6:GLN:HE22	1.85	0.41
1:A:13:ASP:OD1	1:A:13:ASP:C	2.64	0.41
1:C:13:ASP:OD1	1:C:13:ASP:C	2.61	0.41
1:C:384:VAL:HG11	1:C:411:ILE:HG21	2.02	0.41
1:F:8:GLY:CA	1:F:70:VAL:HG11	2.51	0.41
1:F:48:LEU:HD23	1:F:103:SER:HA	2.01	0.41
1:A:-7:GLN:O	1:E:30:PHE:HA	2.20	0.41
1:C:121:ALA:HB3	1:C:132:HIS:CE1	2.56	0.41
1:C:162:ASN:H	1:C:214:ASN:ND2	2.19	0.41
1:D:164:ASP:OD2	1:D:259:LEU:HB3	2.20	0.41
1:F:259:LEU:O	1:F:264:ASN:HA	2.20	0.41
1:B:140:PRO:HG3	1:C:135:GLU:O	2.20	0.41
1:E:176:LYS:HE2	1:E:176:LYS:HA	2.03	0.41
1:D:396:MET:HE1	1:D:405:TYR:CE2	2.56	0.41
1:F:150:MET:O	1:F:169:MET:HA	2.21	0.41
1:C:17:ASN:HD21	1:D:190:HIS:CE1	2.39	0.41
1:B:59:LEU:HD12	1:B:59:LEU:N	2.35	0.40
1:F:202:ASN:HD21	1:E:202:ASN:HD21	1.68	0.40
1:B:148:PRO:HA	1:B:391:ILE:O	2.21	0.40
1:B:151:ASN:HA	1:B:169:MET:HG2	2.03	0.40
1:D:259:LEU:HD13	1:D:267:PHE:CE1	2.57	0.40
1:A:300:PHE:HB3	1:A:334:ILE:HG23	2.03	0.40
1:D:221:ALA:O	1:D:225:ILE:HG13	2.21	0.40
1:F:300:PHE:HB3	1:F:334:ILE:HG23	2.04	0.40
1:F:398:ARG:HB3	1:F:400:ASP:OD1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	436/449 (97%)	411 (94%)	21 (5%)	4 (1%)	14 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	432/449 (96%)	412 (95%)	17 (4%)	3 (1%)	18	36
1	C	436/449 (97%)	414 (95%)	18 (4%)	4 (1%)	14	29
1	D	424/449 (94%)	404 (95%)	17 (4%)	3 (1%)	18	36
1	E	418/449 (93%)	391 (94%)	26 (6%)	1 (0%)	43	63
1	F	428/449 (95%)	399 (93%)	26 (6%)	3 (1%)	18	36
All	All	2574/2694 (96%)	2431 (94%)	125 (5%)	18 (1%)	18	36

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	261	GLY
1	B	262	GLU
1	A	262	GLU
1	A	162	ASN
1	B	260	ALA
1	D	261	GLY
1	D	282	GLN
1	B	398	ARG
1	F	261	GLY
1	A	398	ARG
1	F	260	ALA
1	F	398	ARG
1	E	398	ARG
1	C	159	ALA
1	C	261	GLY
1	C	398	ARG
1	D	398	ARG
1	C	156	GLY

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	331/337 (98%)	320 (97%)	11 (3%)	33	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	330/337 (98%)	319 (97%)	11 (3%)	33	59
1	C	331/337 (98%)	320 (97%)	11 (3%)	33	59
1	D	327/337 (97%)	315 (96%)	12 (4%)	30	55
1	E	324/337 (96%)	311 (96%)	13 (4%)	28	52
1	F	328/337 (97%)	316 (96%)	12 (4%)	30	55
All	All	1971/2022 (98%)	1901 (96%)	70 (4%)	31	56

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	SER
1	A	45	ARG
1	A	103	SER
1	A	142	LYS
1	A	161	ASN
1	A	163	VAL
1	A	342	PHE
1	A	369	HIS
1	A	371	SER
1	A	397	SER
1	A	400	ASP
1	B	45	ARG
1	B	76	GLN
1	B	142	LYS
1	B	160	ASP
1	B	162	ASN
1	B	253	LYS
1	B	264	ASN
1	B	309	ASP
1	B	342	PHE
1	B	369	HIS
1	B	400	ASP
1	C	48	LEU
1	C	142	LYS
1	C	268	THR
1	C	282	GLN
1	C	310	LYS
1	C	324	LYS
1	C	342	PHE
1	C	343	ASN

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Mol	Chain	Res	Type
1	C	369	HIS
1	C	371	SER
1	C	400	ASP
1	D	48	LEU
1	D	142	LYS
1	D	154	ASN
1	D	176	LYS
1	D	214	ASN
1	D	265	LYS
1	D	270	GLU
1	D	342	PHE
1	D	369	HIS
1	D	371	SER
1	D	397	SER
1	D	400	ASP
1	F	38	SER
1	F	97	ASP
1	F	103	SER
1	F	154	ASN
1	F	214	ASN
1	F	256	LYS
1	F	264	ASN
1	F	342	PHE
1	F	369	HIS
1	F	371	SER
1	F	397	SER
1	F	400	ASP
1	E	45	ARG
1	E	76	GLN
1	E	164	ASP
1	E	183	ARG
1	E	242	LEU
1	E	253	LYS
1	E	254	ASP
1	E	264	ASN
1	E	282	GLN
1	E	342	PHE
1	E	369	HIS
1	E	397	SER
1	E	400	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	154	ASN
1	A	161	ASN
1	A	190	HIS
1	A	264	ASN
1	A	369	HIS
1	B	-6	GLN
1	B	17	ASN
1	B	101	ASN
1	B	154	ASN
1	B	162	ASN
1	B	190	HIS
1	B	202	ASN
1	B	312	GLN
1	B	369	HIS
1	B	390	GLN
1	C	17	ASN
1	C	117	ASN
1	C	132	HIS
1	C	202	ASN
1	C	214	ASN
1	C	218	ASN
1	C	312	GLN
1	C	369	HIS
1	C	430	GLN
1	D	17	ASN
1	D	25	HIS
1	D	71	ASN
1	D	117	ASN
1	D	132	HIS
1	D	191	HIS
1	D	214	ASN
1	D	282	GLN
1	D	303	GLN
1	D	369	HIS
1	F	25	HIS
1	F	117	ASN
1	F	132	HIS
1	F	137	ASN
1	F	202	ASN
1	F	218	ASN
1	F	312	GLN
1	F	369	HIS

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Mol	Chain	Res	Type
1	E	117	ASN
1	E	137	ASN
1	E	151	ASN
1	E	202	ASN
1	E	214	ASN
1	E	218	ASN
1	E	390	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 27 ligands modelled in this entry, 6 are monoatomic - leaving 21 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	SO4	C	701	-	4,4,4	0.24	0	6,6,6	0.18	0
3	SO4	F	705	-	4,4,4	0.25	0	6,6,6	0.15	0
3	SO4	B	504	-	4,4,4	0.26	0	6,6,6	0.21	0
5	GOL	A	605	-	5,5,5	0.20	0	5,5,5	0.44	0
3	SO4	A	602	-	4,4,4	0.28	0	6,6,6	0.11	0
3	SO4	F	704	-	4,4,4	0.29	0	6,6,6	0.16	0
5	GOL	D	605	-	5,5,5	0.16	0	5,5,5	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	606	-	4,4,4	0.35	0	6,6,6	0.13	0
3	SO4	A	604	-	4,4,4	0.30	0	6,6,6	0.19	0
2	TLA	A	601	4	9,9,9	2.42	2 (22%)	12,12,12	1.90	3 (25%)
6	KVM	F	703	4	9,12,12	5.14	6 (66%)	12,19,19	2.99	6 (50%)
3	SO4	F	701	-	4,4,4	0.33	0	6,6,6	0.10	0
2	TLA	C	703	4	9,9,9	1.88	2 (22%)	12,12,12	1.75	3 (25%)
3	SO4	C	704	-	4,4,4	0.30	0	6,6,6	0.16	0
3	SO4	D	603	-	4,4,4	0.34	0	6,6,6	0.10	0
6	KVM	D	601	4	9,12,12	5.88	6 (66%)	12,19,19	4.34	6 (50%)
5	GOL	B	503	-	5,5,5	0.16	0	5,5,5	0.36	0
6	KVM	E	602	4	9,12,12	7.42	6 (66%)	12,19,19	2.55	7 (58%)
2	TLA	B	501	4	9,9,9	2.47	3 (33%)	12,12,12	2.93	5 (41%)
5	GOL	C	705	-	5,5,5	0.17	0	5,5,5	0.38	0
3	SO4	D	602	-	4,4,4	0.25	0	6,6,6	0.14	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
6	KVM	D	601	4	-	6/6/22/22	0/1/1/1
5	GOL	B	503	-	-	0/4/4/4	-
5	GOL	D	605	-	-	2/4/4/4	-
6	KVM	E	602	4	-	0/6/22/22	0/1/1/1
2	TLA	B	501	4	-	4/12/12/12	-
2	TLA	C	703	4	-	8/12/12/12	-
5	GOL	C	705	-	-	4/4/4/4	-
2	TLA	A	601	4	-	2/12/12/12	-
6	KVM	F	703	4	-	6/6/22/22	0/1/1/1
5	GOL	A	605	-	-	4/4/4/4	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	602	KVM	OAD-NAC	-16.99	1.18	1.38
6	D	601	KVM	OAD-NAC	11.62	1.52	1.38
6	F	703	KVM	OAD-NAC	11.09	1.51	1.38
6	D	601	KVM	CAE-CAB	-9.57	1.35	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	602	KVM	CAE-CAB	-8.87	1.36	1.50
6	F	703	KVM	CAE-CAB	-8.00	1.38	1.50
6	E	602	KVM	PAG-CAF	-7.44	1.71	1.81
6	E	602	KVM	PAG-OAI	7.01	1.61	1.49
2	B	501	TLA	C2-C1	-6.16	1.43	1.52
6	D	601	KVM	PAG-OAI	5.54	1.58	1.49
2	A	601	TLA	C2-C1	-5.35	1.45	1.52
6	D	601	KVM	PAG-OAJ	-4.60	1.47	1.54
6	D	601	KVM	PAG-OAH	4.18	1.61	1.54
2	C	703	TLA	C3-C4	-4.10	1.46	1.52
6	F	703	KVM	PAG-OAH	3.92	1.61	1.54
6	F	703	KVM	PAG-OAJ	3.85	1.61	1.54
2	A	601	TLA	O11-C1	-3.82	1.18	1.30
6	E	602	KVM	CAK-NAC	-3.77	1.32	1.37
6	F	703	KVM	PAG-CAF	3.42	1.86	1.81
6	D	601	KVM	CAK-NAC	-3.35	1.33	1.37
6	E	602	KVM	PAG-OAJ	-2.74	1.50	1.54
6	F	703	KVM	CAK-NAC	-2.62	1.34	1.37
2	B	501	TLA	O11-C1	-2.32	1.23	1.30
2	B	501	TLA	O3-C3	2.28	1.46	1.42
2	C	703	TLA	O41-C4	-2.13	1.23	1.30

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	601	KVM	OAD-NAC-CAB	9.80	134.06	122.09
6	D	601	KVM	OAD-NAC-CAK	-7.71	116.00	122.14
2	B	501	TLA	O2-C2-C1	-7.41	94.85	110.69
6	F	703	KVM	OAD-NAC-CAB	7.27	130.97	122.09
6	D	601	KVM	OAA-CAB-CAE	-5.58	119.12	127.28
6	E	602	KVM	OAD-NAC-CAB	4.55	127.65	122.09
2	B	501	TLA	O2-C2-C3	4.54	119.40	110.17
6	F	703	KVM	OAA-CAB-CAE	-4.46	120.76	127.28
2	A	601	TLA	O2-C2-C1	-4.01	102.13	110.69
2	A	601	TLA	O2-C2-C3	3.72	117.73	110.17
6	E	602	KVM	PAG-CAF-CAK	3.55	121.88	114.55
6	D	601	KVM	OAJ-PAG-OAI	-3.52	104.61	113.45
6	F	703	KVM	OAD-NAC-CAK	-3.51	119.34	122.14
6	D	601	KVM	OAL-CAK-NAC	-3.41	121.26	124.48
6	E	602	KVM	CAE-CAF-CAK	3.25	105.23	103.72
6	E	602	KVM	OAJ-PAG-OAH	3.13	116.07	107.58
2	B	501	TLA	O3-C3-C2	3.04	116.36	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	703	TLA	C2-C3-C4	-3.01	103.15	109.82
6	E	602	KVM	OAA-CAB-CAE	-2.94	122.98	127.28
6	F	703	KVM	OAL-CAK-NAC	-2.58	122.04	124.48
2	C	703	TLA	O2-C2-C3	-2.57	104.93	110.17
6	E	602	KVM	OAH-PAG-OAI	-2.57	107.02	113.45
6	F	703	KVM	CAE-CAF-CAK	-2.56	102.54	103.72
2	A	601	TLA	O41-C4-C3	2.44	120.10	113.31
2	B	501	TLA	O1-C1-C2	-2.32	115.45	121.62
2	C	703	TLA	O3-C3-C4	-2.28	105.82	110.69
2	B	501	TLA	O11-C1-O1	2.24	129.17	124.08
6	D	601	KVM	OAH-PAG-OAI	-2.13	108.10	113.45
6	F	703	KVM	CAF-CAK-NAC	2.12	111.30	107.88
6	E	602	KVM	CAF-CAE-CAB	-2.05	102.61	105.41

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	605	GOL	O1-C1-C2-C3
5	C	705	GOL	O1-C1-C2-C3
5	C	705	GOL	C1-C2-C3-O3
5	C	705	GOL	O2-C2-C3-O3
5	D	605	GOL	C1-C2-C3-O3
6	D	601	KVM	CAE-CAF-PAG-OAH
6	D	601	KVM	CAK-CAF-PAG-OAH
6	D	601	KVM	CAE-CAF-PAG-OAI
6	D	601	KVM	CAK-CAF-PAG-OAI
6	D	601	KVM	CAE-CAF-PAG-OAJ
6	D	601	KVM	CAK-CAF-PAG-OAJ
6	F	703	KVM	CAE-CAF-PAG-OAH
6	F	703	KVM	CAK-CAF-PAG-OAH
6	F	703	KVM	CAE-CAF-PAG-OAI
6	F	703	KVM	CAK-CAF-PAG-OAI
6	F	703	KVM	CAE-CAF-PAG-OAJ
6	F	703	KVM	CAK-CAF-PAG-OAJ
2	A	601	TLA	O1-C1-C2-O2
2	A	601	TLA	O11-C1-C2-O2
2	C	703	TLA	O2-C2-C3-C4
2	B	501	TLA	O11-C1-C2-O2
2	C	703	TLA	C1-C2-C3-C4
2	B	501	TLA	O1-C1-C2-O2
5	A	605	GOL	O1-C1-C2-O2

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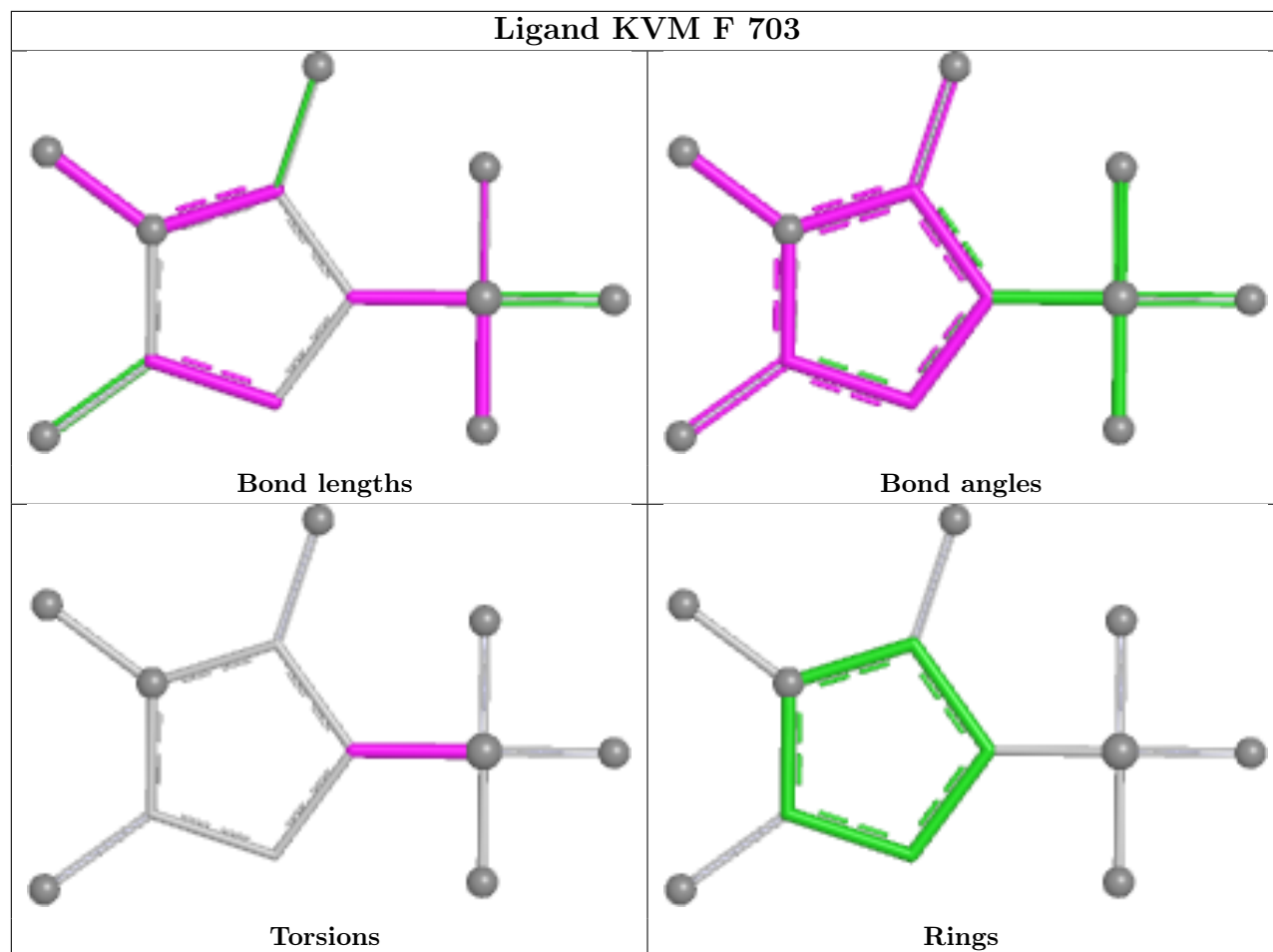
Mol	Chain	Res	Type	Atoms
2	C	703	TLA	O2-C2-C3-O3
2	C	703	TLA	C1-C2-C3-O3
5	A	605	GOL	O2-C2-C3-O3
5	C	705	GOL	O1-C1-C2-O2
5	D	605	GOL	O2-C2-C3-O3
2	C	703	TLA	O11-C1-C2-O2
2	B	501	TLA	O1-C1-C2-C3
2	C	703	TLA	O11-C1-C2-C3
2	C	703	TLA	O1-C1-C2-C3
5	A	605	GOL	C1-C2-C3-O3
2	C	703	TLA	O1-C1-C2-O2
2	B	501	TLA	O11-C1-C2-C3

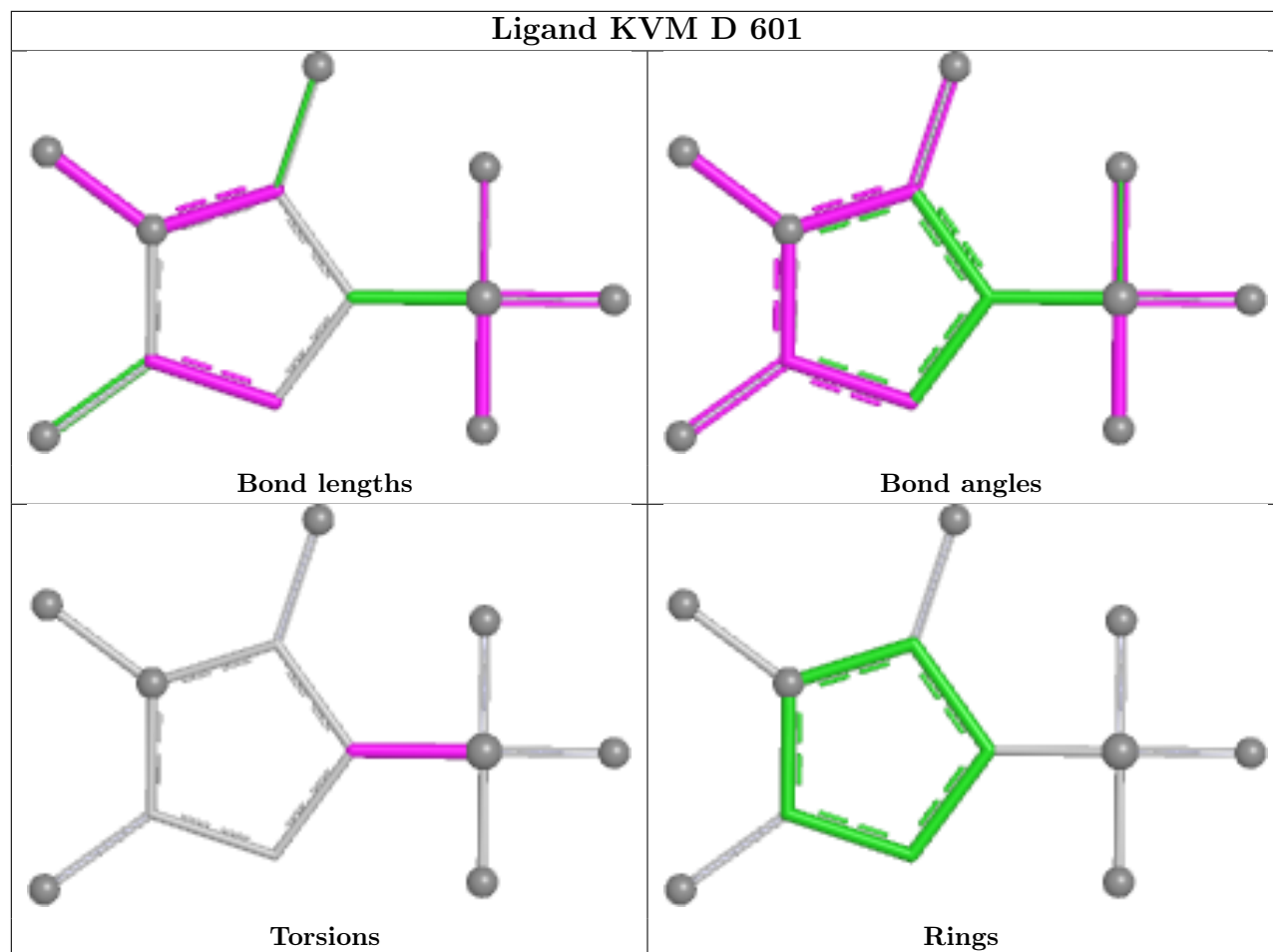
There are no ring outliers.

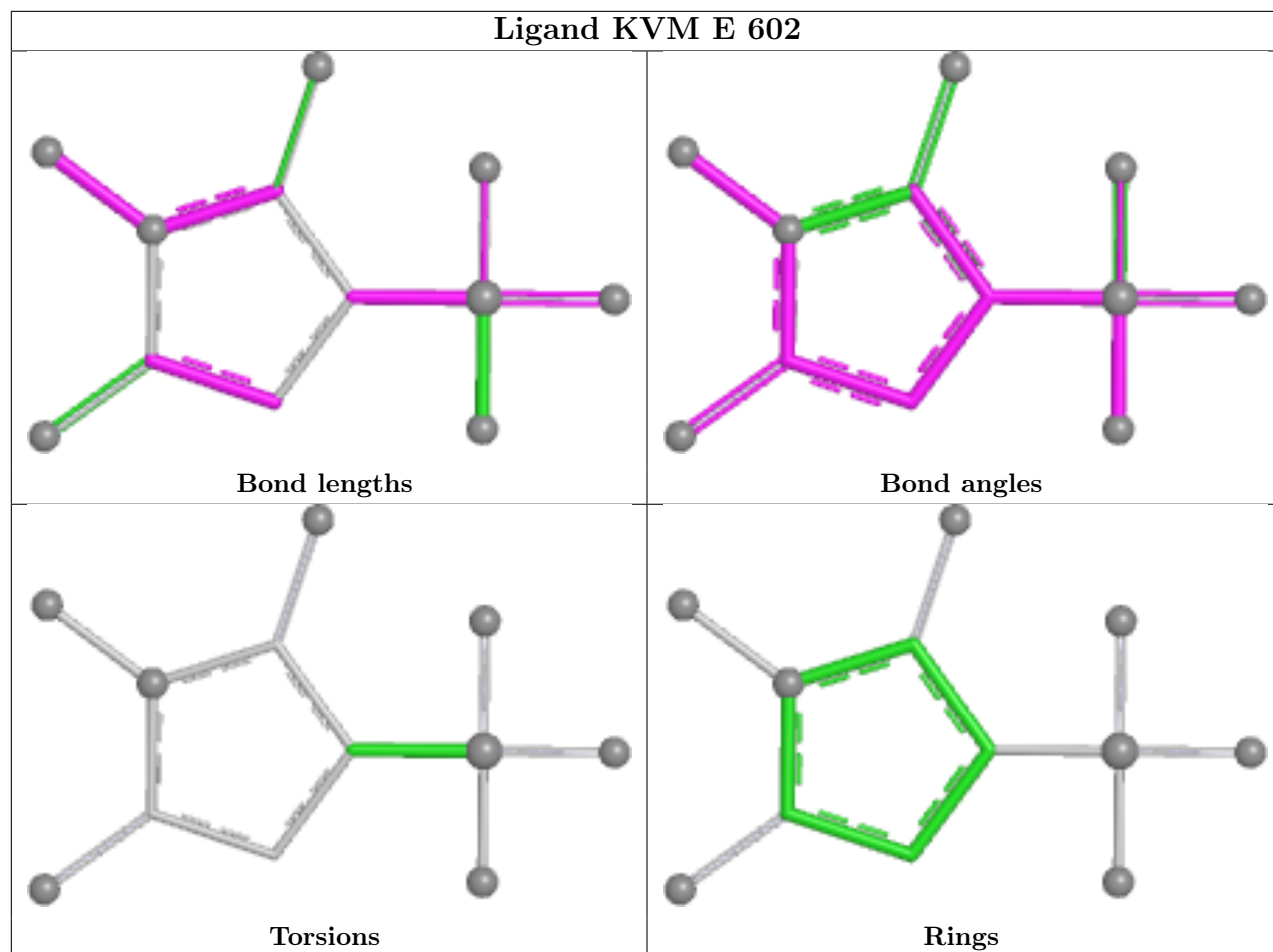
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	703	KVM	1	0
2	C	703	TLA	4	0
3	D	603	SO4	1	0
6	D	601	KVM	1	0
6	E	602	KVM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	438/449 (97%)	-0.21	7 (1%) 70 67	28, 41, 66, 109	0
1	B	436/449 (97%)	-0.10	2 (0%) 87 86	31, 45, 70, 98	0
1	C	438/449 (97%)	-0.21	7 (1%) 70 67	29, 42, 68, 113	0
1	D	432/449 (96%)	0.05	12 (2%) 55 50	30, 48, 84, 128	0
1	E	426/449 (94%)	0.46	14 (3%) 49 44	34, 59, 91, 106	0
1	F	434/449 (96%)	0.12	8 (1%) 67 64	33, 50, 78, 104	0
All	All	2604/2694 (96%)	0.02	50 (1%) 66 62	28, 47, 80, 128	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	163	VAL	3.6
1	A	159	ALA	3.5
1	C	158	HIS	3.5
1	D	156	GLY	3.4
1	A	263	GLY	3.4
1	E	260	ALA	3.3
1	D	261	GLY	3.3
1	D	-5	MET	3.2
1	D	262	GLU	3.1
1	D	265	LYS	3.1
1	D	258	VAL	3.1
1	F	232	ALA	3.1
1	E	168	PHE	3.0
1	F	161	ASN	3.0
1	F	157	GLU	2.9
1	E	258	VAL	2.9
1	F	193	ALA	2.8
1	F	265	LYS	2.8
1	D	164	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	158	HIS	2.8
1	F	155	GLY	2.8
1	E	265	LYS	2.8
1	D	219	ALA	2.7
1	E	154	ASN	2.7
1	F	260	ALA	2.7
1	E	164	ASP	2.6
1	E	259	LEU	2.6
1	E	255	GLY	2.6
1	E	313	LEU	2.5
1	E	152	ILE	2.5
1	A	162	ASN	2.5
1	A	260	ALA	2.4
1	F	261	GLY	2.4
1	B	45	ARG	2.4
1	A	265	LYS	2.3
1	E	257	TYR	2.3
1	C	261	GLY	2.3
1	C	263	GLY	2.3
1	E	275	PHE	2.3
1	C	159	ALA	2.2
1	D	267	PHE	2.2
1	B	260	ALA	2.2
1	C	156	GLY	2.2
1	D	154	ASN	2.2
1	D	155	GLY	2.1
1	D	275	PHE	2.1
1	E	251	PHE	2.1
1	C	265	LYS	2.1
1	C	-5	MET	2.1
1	E	214	ASN	2.0

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 ⓘ

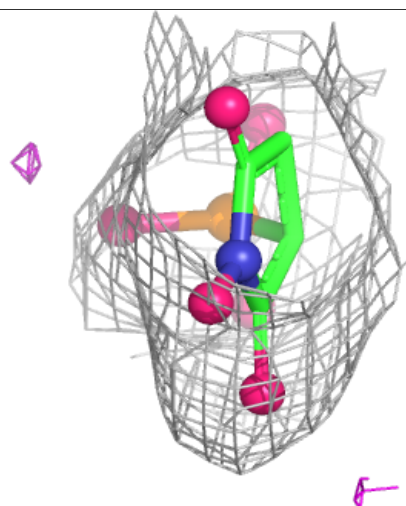
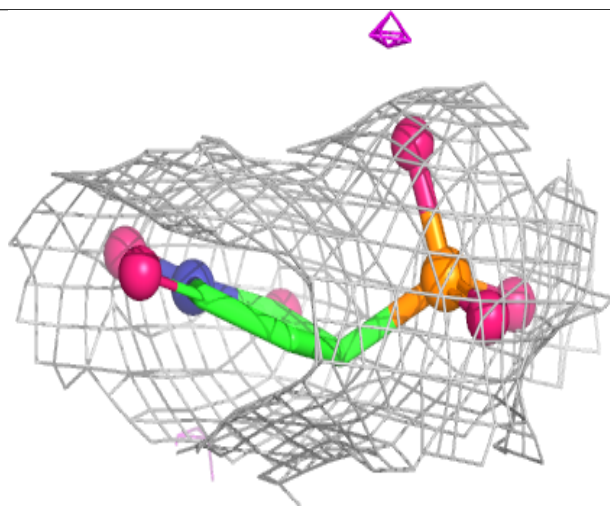
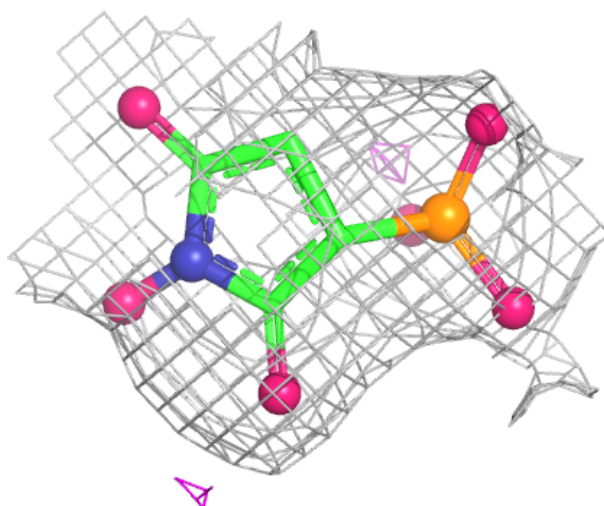
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	C	704	5/5	0.64	0.14	120,120,133,140	0
5	GOL	C	705	6/6	0.72	0.22	56,63,66,66	0
3	SO4	B	504	5/5	0.74	0.14	75,89,101,104	0
5	GOL	B	503	6/6	0.76	0.20	94,101,106,108	0
5	GOL	D	605	6/6	0.79	0.16	54,68,72,73	0
3	SO4	F	705	5/5	0.81	0.14	78,84,93,93	0
5	GOL	A	605	6/6	0.82	0.17	72,80,86,86	0
3	SO4	F	704	5/5	0.83	0.12	84,103,111,111	0
3	SO4	D	603	5/5	0.87	0.10	81,83,93,98	0
6	KVM	E	602	12/12	0.88	0.10	64,83,92,97	0
3	SO4	D	606	5/5	0.92	0.13	81,90,97,103	0
3	SO4	D	602	5/5	0.93	0.10	55,62,63,67	0
3	SO4	F	701	5/5	0.93	0.14	63,76,81,94	0
6	KVM	D	601	12/12	0.93	0.09	53,61,70,70	0
3	SO4	C	701	5/5	0.93	0.11	49,58,62,63	0
2	TLA	C	703	10/10	0.94	0.07	37,41,44,48	0
2	TLA	B	501	10/10	0.94	0.07	34,41,45,50	0
6	KVM	F	703	12/12	0.95	0.08	60,67,79,81	0
2	TLA	A	601	10/10	0.95	0.07	32,35,38,39	0
3	SO4	A	602	5/5	0.96	0.10	62,64,72,73	0
3	SO4	A	604	5/5	0.97	0.07	51,54,61,63	0
4	MG	E	601	1/1	0.99	0.02	42,42,42,42	0
4	MG	B	502	1/1	0.99	0.02	30,30,30,30	0
4	MG	C	702	1/1	0.99	0.02	25,25,25,25	0
4	MG	F	702	1/1	0.99	0.02	40,40,40,40	0
4	MG	D	604	1/1	1.00	0.02	39,39,39,39	0
4	MG	A	603	1/1	1.00	0.01	21,21,21,21	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

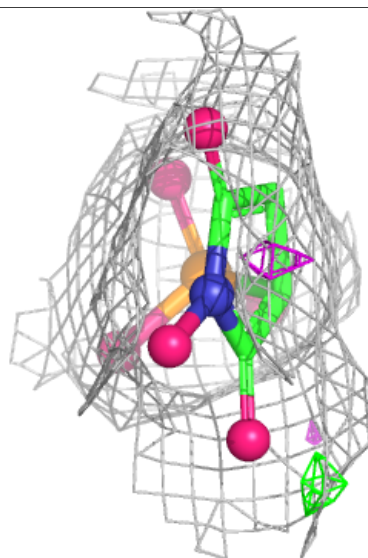
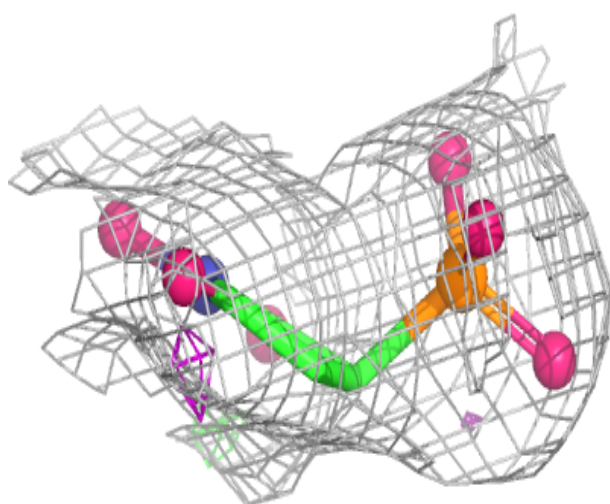
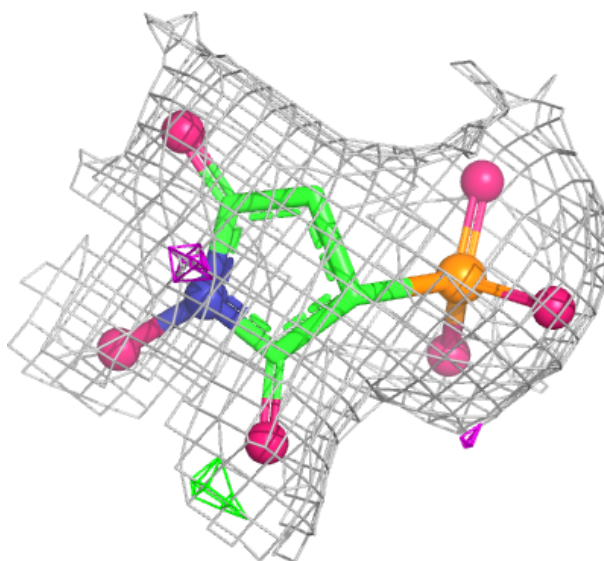
Electron density around KVM E 602:

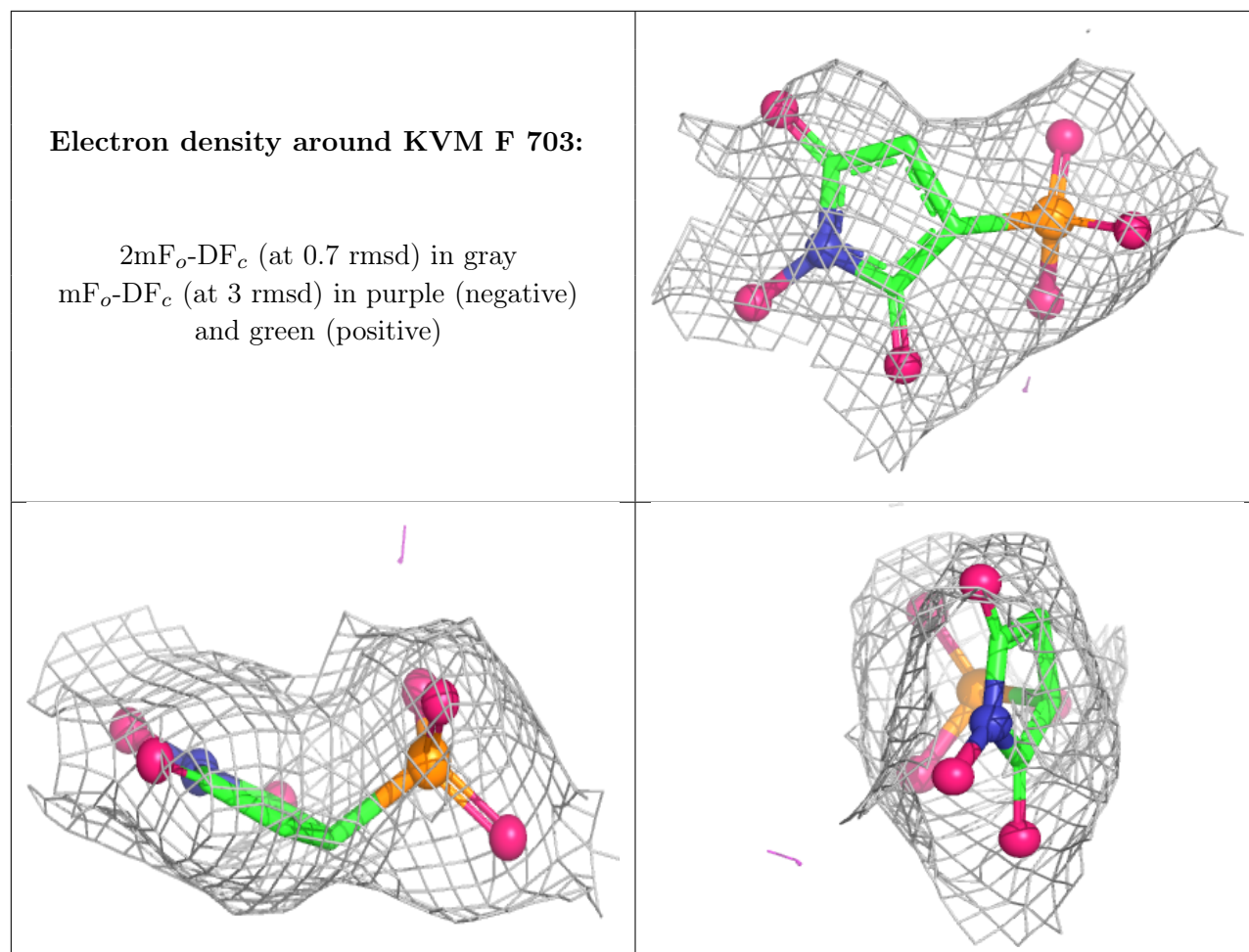
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around KVM D 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.