



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2025 – 02:13 PM JST

PDB ID : 9KS0 / pdb_00009ks0
Title : E. coli MaeB PTA domain apo form
Authors : Sassa, M.; Yamato, H.; Tanino, H.; Fukuda, Y.; Inoue, T.
Deposited on : 2024-11-29
Resolution : 2.80 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

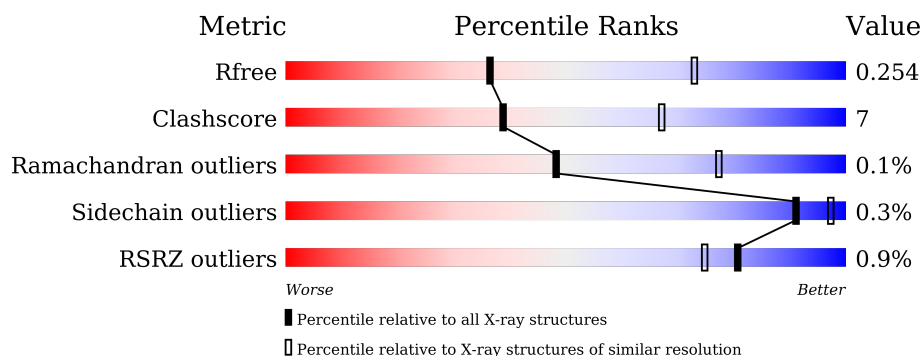
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	164625	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)

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	E	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 17%, green 72%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 72% 17% 11% </div> </div>
1	F	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 76%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 76% 13% 11% </div> </div>
1	G	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 78%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 78% 13% 9% </div> </div>
1	H	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 75%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 75% 14% 11% </div> </div>
1	I	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 10%, green 79%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 10% 11% </div> </div>
2	J	372	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 79%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 12% 9% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15580 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 NADP-dependent malic enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	332	Total	C	N	O	S	0	0	0
			2550	1602	454	477	17			
1	F	331	Total	C	N	O	S	0	0	0
			2546	1600	453	476	17			
1	G	338	Total	C	N	O	S	0	0	0
			2607	1640	462	488	17			
1	H	332	Total	C	N	O	S	0	0	0
			2550	1602	454	477	17			
1	I	331	Total	C	N	O	S	0	0	0
			2546	1600	453	476	17			

There are 205 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	388	MET	-	initiating methionine	UNP P76558
E	389	GLY	-	expression tag	UNP P76558
E	390	SER	-	expression tag	UNP P76558
E	391	SER	-	expression tag	UNP P76558
E	392	HIS	-	expression tag	UNP P76558
E	393	HIS	-	expression tag	UNP P76558
E	394	HIS	-	expression tag	UNP P76558
E	395	HIS	-	expression tag	UNP P76558
E	396	HIS	-	expression tag	UNP P76558
E	397	HIS	-	expression tag	UNP P76558
E	398	SER	-	expression tag	UNP P76558
E	399	SER	-	expression tag	UNP P76558
E	400	GLY	-	expression tag	UNP P76558
E	401	LEU	-	expression tag	UNP P76558
E	402	VAL	-	expression tag	UNP P76558
E	403	PRO	-	expression tag	UNP P76558
E	404	ARG	-	expression tag	UNP P76558
E	405	GLY	-	expression tag	UNP P76558
E	406	SER	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
E	407	HIS	-	expression tag	UNP P76558
E	408	MET	-	expression tag	UNP P76558
E	409	ALA	-	expression tag	UNP P76558
E	410	SER	-	expression tag	UNP P76558
E	411	MET	-	expression tag	UNP P76558
E	412	THR	-	expression tag	UNP P76558
E	413	GLY	-	expression tag	UNP P76558
E	414	GLY	-	expression tag	UNP P76558
E	415	GLN	-	expression tag	UNP P76558
E	416	GLN	-	expression tag	UNP P76558
E	417	MET	-	expression tag	UNP P76558
E	418	GLY	-	expression tag	UNP P76558
E	419	ARG	-	expression tag	UNP P76558
E	420	GLY	-	expression tag	UNP P76558
E	421	SER	-	expression tag	UNP P76558
E	422	GLU	-	expression tag	UNP P76558
E	423	ASN	-	expression tag	UNP P76558
E	424	LEU	-	expression tag	UNP P76558
E	425	TYR	-	expression tag	UNP P76558
E	426	PHE	-	expression tag	UNP P76558
E	427	GLN	-	expression tag	UNP P76558
E	428	GLY	-	expression tag	UNP P76558
F	388	MET	-	initiating methionine	UNP P76558
F	389	GLY	-	expression tag	UNP P76558
F	390	SER	-	expression tag	UNP P76558
F	391	SER	-	expression tag	UNP P76558
F	392	HIS	-	expression tag	UNP P76558
F	393	HIS	-	expression tag	UNP P76558
F	394	HIS	-	expression tag	UNP P76558
F	395	HIS	-	expression tag	UNP P76558
F	396	HIS	-	expression tag	UNP P76558
F	397	HIS	-	expression tag	UNP P76558
F	398	SER	-	expression tag	UNP P76558
F	399	SER	-	expression tag	UNP P76558
F	400	GLY	-	expression tag	UNP P76558
F	401	LEU	-	expression tag	UNP P76558
F	402	VAL	-	expression tag	UNP P76558
F	403	PRO	-	expression tag	UNP P76558
F	404	ARG	-	expression tag	UNP P76558
F	405	GLY	-	expression tag	UNP P76558
F	406	SER	-	expression tag	UNP P76558
F	407	HIS	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
F	408	MET	-	expression tag	UNP P76558
F	409	ALA	-	expression tag	UNP P76558
F	410	SER	-	expression tag	UNP P76558
F	411	MET	-	expression tag	UNP P76558
F	412	THR	-	expression tag	UNP P76558
F	413	GLY	-	expression tag	UNP P76558
F	414	GLY	-	expression tag	UNP P76558
F	415	GLN	-	expression tag	UNP P76558
F	416	GLN	-	expression tag	UNP P76558
F	417	MET	-	expression tag	UNP P76558
F	418	GLY	-	expression tag	UNP P76558
F	419	ARG	-	expression tag	UNP P76558
F	420	GLY	-	expression tag	UNP P76558
F	421	SER	-	expression tag	UNP P76558
F	422	GLU	-	expression tag	UNP P76558
F	423	ASN	-	expression tag	UNP P76558
F	424	LEU	-	expression tag	UNP P76558
F	425	TYR	-	expression tag	UNP P76558
F	426	PHE	-	expression tag	UNP P76558
F	427	GLN	-	expression tag	UNP P76558
F	428	GLY	-	expression tag	UNP P76558
G	388	MET	-	initiating methionine	UNP P76558
G	389	GLY	-	expression tag	UNP P76558
G	390	SER	-	expression tag	UNP P76558
G	391	SER	-	expression tag	UNP P76558
G	392	HIS	-	expression tag	UNP P76558
G	393	HIS	-	expression tag	UNP P76558
G	394	HIS	-	expression tag	UNP P76558
G	395	HIS	-	expression tag	UNP P76558
G	396	HIS	-	expression tag	UNP P76558
G	397	HIS	-	expression tag	UNP P76558
G	398	SER	-	expression tag	UNP P76558
G	399	SER	-	expression tag	UNP P76558
G	400	GLY	-	expression tag	UNP P76558
G	401	LEU	-	expression tag	UNP P76558
G	402	VAL	-	expression tag	UNP P76558
G	403	PRO	-	expression tag	UNP P76558
G	404	ARG	-	expression tag	UNP P76558
G	405	GLY	-	expression tag	UNP P76558
G	406	SER	-	expression tag	UNP P76558
G	407	HIS	-	expression tag	UNP P76558
G	408	MET	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
G	409	ALA	-	expression tag	UNP P76558
G	410	SER	-	expression tag	UNP P76558
G	411	MET	-	expression tag	UNP P76558
G	412	THR	-	expression tag	UNP P76558
G	413	GLY	-	expression tag	UNP P76558
G	414	GLY	-	expression tag	UNP P76558
G	415	GLN	-	expression tag	UNP P76558
G	416	GLN	-	expression tag	UNP P76558
G	417	MET	-	expression tag	UNP P76558
G	418	GLY	-	expression tag	UNP P76558
G	419	ARG	-	expression tag	UNP P76558
G	420	GLY	-	expression tag	UNP P76558
G	421	SER	-	expression tag	UNP P76558
G	422	GLU	-	expression tag	UNP P76558
G	423	ASN	-	expression tag	UNP P76558
G	424	LEU	-	expression tag	UNP P76558
G	425	TYR	-	expression tag	UNP P76558
G	426	PHE	-	expression tag	UNP P76558
G	427	GLN	-	expression tag	UNP P76558
G	428	GLY	-	expression tag	UNP P76558
H	388	MET	-	initiating methionine	UNP P76558
H	389	GLY	-	expression tag	UNP P76558
H	390	SER	-	expression tag	UNP P76558
H	391	SER	-	expression tag	UNP P76558
H	392	HIS	-	expression tag	UNP P76558
H	393	HIS	-	expression tag	UNP P76558
H	394	HIS	-	expression tag	UNP P76558
H	395	HIS	-	expression tag	UNP P76558
H	396	HIS	-	expression tag	UNP P76558
H	397	HIS	-	expression tag	UNP P76558
H	398	SER	-	expression tag	UNP P76558
H	399	SER	-	expression tag	UNP P76558
H	400	GLY	-	expression tag	UNP P76558
H	401	LEU	-	expression tag	UNP P76558
H	402	VAL	-	expression tag	UNP P76558
H	403	PRO	-	expression tag	UNP P76558
H	404	ARG	-	expression tag	UNP P76558
H	405	GLY	-	expression tag	UNP P76558
H	406	SER	-	expression tag	UNP P76558
H	407	HIS	-	expression tag	UNP P76558
H	408	MET	-	expression tag	UNP P76558
H	409	ALA	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
H	410	SER	-	expression tag	UNP P76558
H	411	MET	-	expression tag	UNP P76558
H	412	THR	-	expression tag	UNP P76558
H	413	GLY	-	expression tag	UNP P76558
H	414	GLY	-	expression tag	UNP P76558
H	415	GLN	-	expression tag	UNP P76558
H	416	GLN	-	expression tag	UNP P76558
H	417	MET	-	expression tag	UNP P76558
H	418	GLY	-	expression tag	UNP P76558
H	419	ARG	-	expression tag	UNP P76558
H	420	GLY	-	expression tag	UNP P76558
H	421	SER	-	expression tag	UNP P76558
H	422	GLU	-	expression tag	UNP P76558
H	423	ASN	-	expression tag	UNP P76558
H	424	LEU	-	expression tag	UNP P76558
H	425	TYR	-	expression tag	UNP P76558
H	426	PHE	-	expression tag	UNP P76558
H	427	GLN	-	expression tag	UNP P76558
H	428	GLY	-	expression tag	UNP P76558
I	388	MET	-	initiating methionine	UNP P76558
I	389	GLY	-	expression tag	UNP P76558
I	390	SER	-	expression tag	UNP P76558
I	391	SER	-	expression tag	UNP P76558
I	392	HIS	-	expression tag	UNP P76558
I	393	HIS	-	expression tag	UNP P76558
I	394	HIS	-	expression tag	UNP P76558
I	395	HIS	-	expression tag	UNP P76558
I	396	HIS	-	expression tag	UNP P76558
I	397	HIS	-	expression tag	UNP P76558
I	398	SER	-	expression tag	UNP P76558
I	399	SER	-	expression tag	UNP P76558
I	400	GLY	-	expression tag	UNP P76558
I	401	LEU	-	expression tag	UNP P76558
I	402	VAL	-	expression tag	UNP P76558
I	403	PRO	-	expression tag	UNP P76558
I	404	ARG	-	expression tag	UNP P76558
I	405	GLY	-	expression tag	UNP P76558
I	406	SER	-	expression tag	UNP P76558
I	407	HIS	-	expression tag	UNP P76558
I	408	MET	-	expression tag	UNP P76558
I	409	ALA	-	expression tag	UNP P76558
I	410	SER	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
I	411	MET	-	expression tag	UNP P76558
I	412	THR	-	expression tag	UNP P76558
I	413	GLY	-	expression tag	UNP P76558
I	414	GLY	-	expression tag	UNP P76558
I	415	GLN	-	expression tag	UNP P76558
I	416	GLN	-	expression tag	UNP P76558
I	417	MET	-	expression tag	UNP P76558
I	418	GLY	-	expression tag	UNP P76558
I	419	ARG	-	expression tag	UNP P76558
I	420	GLY	-	expression tag	UNP P76558
I	421	SER	-	expression tag	UNP P76558
I	422	GLU	-	expression tag	UNP P76558
I	423	ASN	-	expression tag	UNP P76558
I	424	LEU	-	expression tag	UNP P76558
I	425	TYR	-	expression tag	UNP P76558
I	426	PHE	-	expression tag	UNP P76558
I	427	GLN	-	expression tag	UNP P76558
I	428	GLY	-	expression tag	UNP P76558

- Molecule 2 is a protein called NADP-dependent malic enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	338	Total	C	N	O	S	0	0	0
			2608	1640	462	489	17			

There are 41 discrepancies between the modelled and reference sequences:

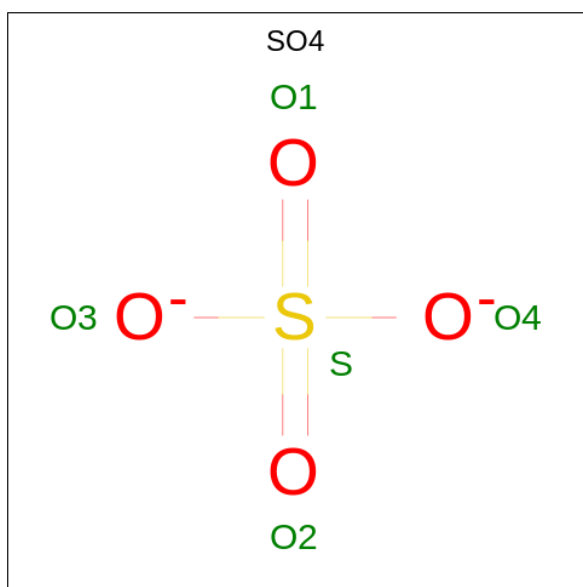
Chain	Residue	Modelled	Actual	Comment	Reference
J	388	MET	-	initiating methionine	UNP P76558
J	389	GLY	-	expression tag	UNP P76558
J	390	SER	-	expression tag	UNP P76558
J	391	SER	-	expression tag	UNP P76558
J	392	HIS	-	expression tag	UNP P76558
J	393	HIS	-	expression tag	UNP P76558
J	394	HIS	-	expression tag	UNP P76558
J	395	HIS	-	expression tag	UNP P76558
J	396	HIS	-	expression tag	UNP P76558
J	397	HIS	-	expression tag	UNP P76558
J	398	SER	-	expression tag	UNP P76558
J	399	SER	-	expression tag	UNP P76558
J	400	GLY	-	expression tag	UNP P76558
J	401	LEU	-	expression tag	UNP P76558

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Chain	Residue	Modelled	Actual	Comment	Reference
J	402	VAL	-	expression tag	UNP P76558
J	403	PRO	-	expression tag	UNP P76558
J	404	ARG	-	expression tag	UNP P76558
J	405	GLY	-	expression tag	UNP P76558
J	406	SER	-	expression tag	UNP P76558
J	407	HIS	-	expression tag	UNP P76558
J	408	MET	-	expression tag	UNP P76558
J	409	ALA	-	expression tag	UNP P76558
J	410	SER	-	expression tag	UNP P76558
J	411	MET	-	expression tag	UNP P76558
J	412	THR	-	expression tag	UNP P76558
J	413	GLY	-	expression tag	UNP P76558
J	414	GLY	-	expression tag	UNP P76558
J	415	GLN	-	expression tag	UNP P76558
J	416	GLN	-	expression tag	UNP P76558
J	417	MET	-	expression tag	UNP P76558
J	418	GLY	-	expression tag	UNP P76558
J	419	ARG	-	expression tag	UNP P76558
J	420	GLY	-	expression tag	UNP P76558
J	421	SER	-	expression tag	UNP P76558
J	422	GLU	-	expression tag	UNP P76558
J	423	ASN	-	expression tag	UNP P76558
J	424	LEU	-	expression tag	UNP P76558
J	425	TYR	-	expression tag	UNP P76558
J	426	PHE	-	expression tag	UNP P76558
J	427	GLN	-	expression tag	UNP P76558
J	428	GLY	-	expression tag	UNP P76558

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		

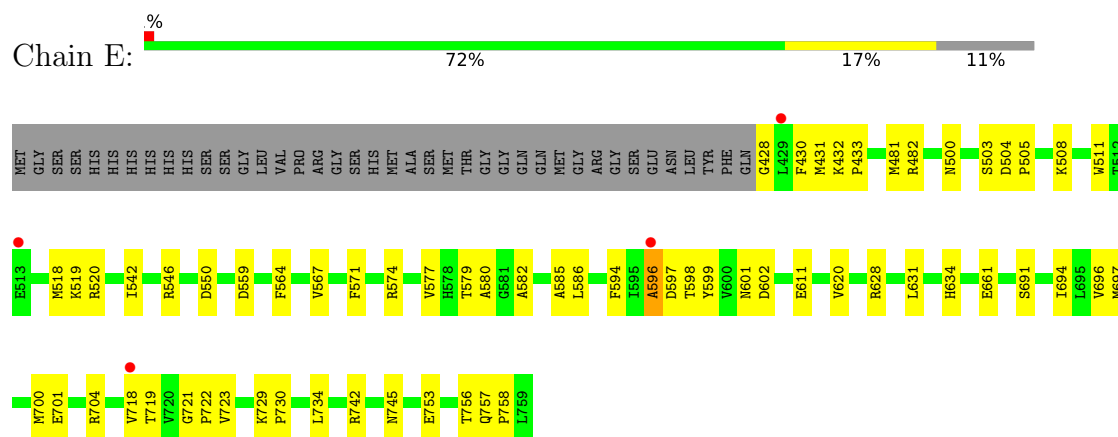
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	28	Total	O	0	0
			28	28		
4	F	26	Total	O	0	0
			26	26		
4	G	21	Total	O	0	0
			21	21		
4	H	28	Total	O	0	0
			28	28		
4	I	36	Total	O	0	0
			36	36		
4	J	24	Total	O	0	0
			24	24		

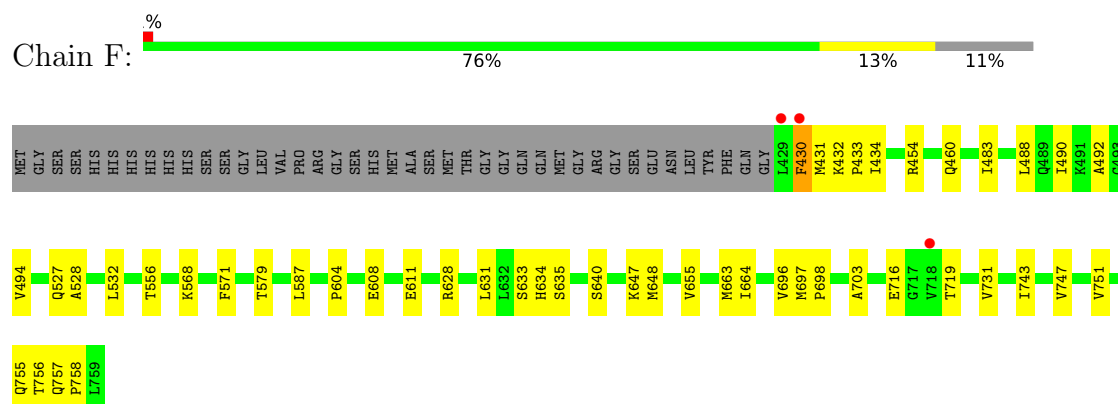
3 Residue-property plots [i](#)

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.

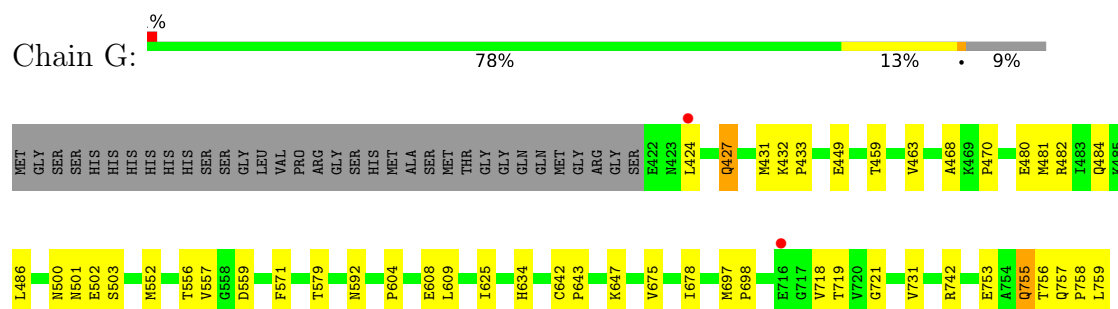
- Molecule 1: NADP-dependent malic enzyme




- Molecule 1: NADP-dependent malic enzyme

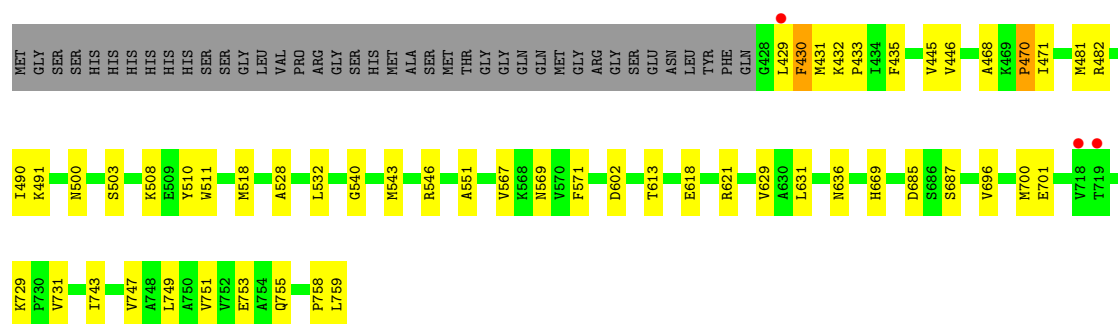


- Molecule 1: NADP-dependent malic enzyme




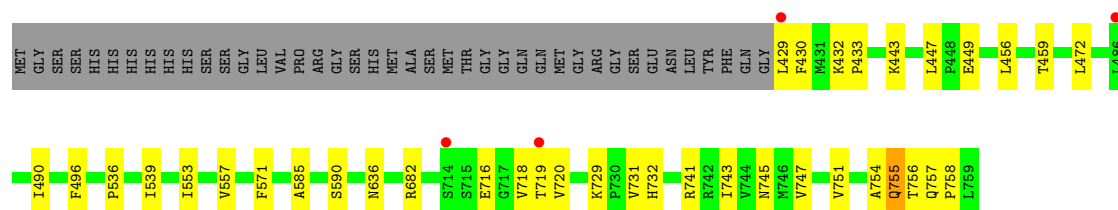
- Molecule 1: NADP-dependent malic enzyme

Chain H: 




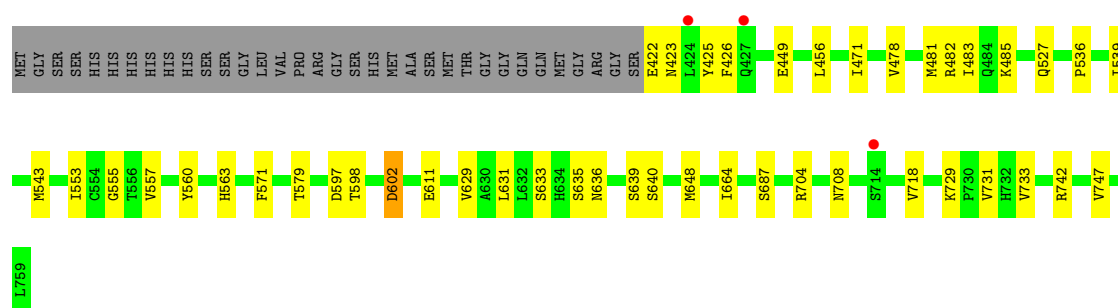
- Molecule 1: NADP-dependent malic enzyme

Chain I: 



- Molecule 2: NADP-dependent malic enzyme

Chain J: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.07Å 130.03Å 169.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.88 – 2.80 47.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.88-2.80) 99.9 (47.88-2.80)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.214 , 0.259 0.214 , 0.254	Depositor DCC
R_{free} test set	2971 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15580	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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: CSO, SO4

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	E	0.90	0/2592	1.32	2/3508 (0.1%)
1	F	0.98	0/2588	1.43	2/3503 (0.1%)
1	G	0.97	0/2651	1.42	2/3588 (0.1%)
1	H	0.99	0/2592	1.41	2/3508 (0.1%)
1	I	0.99	0/2588	1.45	3/3503 (0.1%)
2	J	0.98	0/2644	1.46	1/3576 (0.0%)
All	All	0.97	0/15655	1.41	12/21186 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	755	GLN	N-CA-C	-7.08	101.69	110.41
1	G	556	THR	N-CA-C	-6.98	104.77	113.28
1	G	755	GLN	N-CA-C	-6.78	102.07	110.41
1	I	755	GLN	N-CA-C	-6.48	101.41	110.35
1	E	634	HIS	N-CA-C	-6.12	104.88	112.90
1	H	470	PRO	N-CA-C	5.59	120.27	111.38
1	H	430	PHE	N-CA-C	-5.49	106.54	113.18
1	I	756	THR	CB-CA-C	-5.33	110.45	116.63
2	J	633	SER	O-C-N	5.24	128.76	123.26
1	F	634	HIS	N-CA-C	-5.22	105.59	111.28
1	E	756	THR	O-C-N	5.07	124.58	120.83
1	I	716	GLU	CB-CA-C	-5.01	110.77	116.54

There are no chirality outliers.

There are no planarity outliers.

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	E	2550	0	2595	45	0
1	F	2546	0	2592	32	0
1	G	2607	0	2644	41	0
1	H	2550	0	2595	40	0
1	I	2546	0	2592	29	0
2	J	2608	0	2643	27	0
3	E	5	0	0	0	0
3	I	5	0	0	0	0
4	E	28	0	0	0	0
4	F	26	0	0	0	0
4	G	21	0	0	3	0
4	H	28	0	0	7	0
4	I	36	0	0	0	0
4	J	24	0	0	0	0
All	All	15580	0	15661	207	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 7.

All (207) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:759:LEU:HA	4:G:806:HOH:O	1.45	1.16
1:F:579:THR:HG21	1:F:608:GLU:HG2	1.40	1.03
1:I:585:ALA:HB3	1:I:718:VAL:HG11	1.42	1.00
1:E:596:ALA:HB2	1:E:696:VAL:HA	1.45	0.96
1:G:759:LEU:HD12	4:G:806:HOH:O	1.64	0.95
1:I:429:LEU:HB3	1:I:432:LYS:HE2	1.55	0.87
1:E:428:GLY:HA3	1:E:719:THR:HG21	1.60	0.83
2:J:481:MET:HE2	2:J:482:ARG:HD2	1.60	0.82
1:E:586:LEU:HD23	1:E:718:VAL:HG22	1.65	0.79
1:E:602:ASP:HA	1:E:700:MET:HE2	1.65	0.78
1:F:579:THR:CG2	1:F:608:GLU:HG2	2.14	0.78
1:G:424:LEU:HD13	1:G:625:ILE:HG21	1.66	0.77
1:F:757:GLN:HG3	1:F:758:PRO:HD2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:449:GLU:HG2	1:G:557:VAL:HG22	1.68	0.75
1:I:585:ALA:CB	1:I:718:VAL:HG11	2.17	0.74
1:I:571:PHE:CE2	1:I:731:VAL:HG21	2.23	0.73
1:H:687:SER:CB	4:H:804:HOH:O	2.38	0.71
2:J:718:VAL:HG23	2:J:742:ARG:HD3	1.72	0.71
1:I:490:ILE:HG12	1:I:496:PHE:CD1	2.27	0.69
2:J:449:GLU:HG2	2:J:557:VAL:HG12	1.73	0.68
1:I:490:ILE:HG12	1:I:496:PHE:HD1	1.60	0.67
1:E:481:MET:HG3	1:E:482:ARG:N	2.10	0.67
1:H:687:SER:HB3	4:H:804:HOH:O	1.93	0.66
1:E:428:GLY:CA	1:E:719:THR:HG21	2.25	0.66
1:E:628:ARG:NH1	1:E:691:SER:O	2.28	0.66
1:I:429:LEU:CB	1:I:432:LYS:HE2	2.24	0.66
1:E:596:ALA:CB	1:E:697:MET:H	2.09	0.65
1:I:429:LEU:HD21	1:I:719:THR:HG21	1.78	0.65
1:F:430:PHE:HE1	1:F:719:THR:HB	1.60	0.64
1:I:449:GLU:HG2	1:I:557:VAL:HG22	1.78	0.64
1:E:631:LEU:HD23	1:E:696:VAL:HB	1.78	0.64
1:F:432:LYS:HB3	1:F:433:PRO:HD3	1.80	0.64
1:G:634:HIS:CD2	1:H:700:MET:HE2	2.33	0.63
1:E:585:ALA:O	1:E:718:VAL:HG13	1.99	0.63
2:J:571:PHE:CE2	2:J:731:VAL:HG21	2.34	0.63
1:H:468:ALA:O	1:H:470:PRO:HD3	1.98	0.62
1:H:510:TYR:HE1	1:H:546:ARG:HD3	1.64	0.62
1:I:718:VAL:HG12	1:I:720:VAL:H	1.64	0.62
1:I:757:GLN:HB3	1:I:758:PRO:HD2	1.80	0.62
1:H:571:PHE:CE2	1:H:731:VAL:HG21	2.35	0.61
1:G:721:GLY:O	1:G:742:ARG:HD3	1.99	0.61
1:I:743:ILE:O	1:I:747:VAL:HG23	2.01	0.61
1:E:597:ASP:OD2	1:E:601:ASN:N	2.33	0.61
1:G:698:PRO:HG3	1:H:701:GLU:HG2	1.82	0.61
1:H:429:LEU:HG	1:H:431:MET:HB2	1.84	0.59
1:G:753:GLU:HG2	1:G:758:PRO:HA	1.82	0.59
1:G:642:CYS:SG	4:G:813:HOH:O	2.47	0.57
2:J:478:VAL:O	2:J:482:ARG:HG2	2.04	0.57
2:J:456:LEU:HD22	2:J:483:ILE:HD11	1.87	0.56
1:E:564:PHE:HA	1:E:567:VAL:HG22	1.88	0.56
1:H:432:LYS:HB3	1:H:433:PRO:HD3	1.87	0.55
1:H:430:PHE:O	1:H:433:PRO:HD2	2.06	0.55
1:E:599:TYR:HA	1:E:704:ARG:HH21	1.72	0.55
1:I:490:ILE:HG23	1:I:496:PHE:HE1	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:758:PRO:O	1:G:759:LEU:HB2	2.06	0.55
1:F:430:PHE:CE1	1:F:719:THR:HB	2.39	0.55
1:F:571:PHE:CE2	1:F:731:VAL:HG21	2.42	0.54
1:E:508:LYS:HA	1:E:511:TRP:CD1	2.41	0.54
1:H:743:ILE:O	1:H:747:VAL:HG23	2.07	0.54
1:E:432:LYS:HB2	1:E:433:PRO:HD3	1.90	0.54
1:E:596:ALA:O	1:E:598:THR:HG23	2.07	0.54
2:J:425:TYR:O	2:J:426:PHE:CG	2.61	0.54
1:H:567:VAL:HG13	1:H:571:PHE:HD2	1.72	0.53
1:F:743:ILE:O	1:F:747:VAL:HG23	2.09	0.53
1:F:527:GLN:HE22	1:G:559:ASP:CG	2.16	0.53
2:J:422:GLU:HG2	2:J:423:ASN:N	2.24	0.53
1:F:628:ARG:HG2	1:F:663:MET:SD	2.49	0.52
1:E:428:GLY:HA3	1:E:719:THR:CG2	2.35	0.52
1:F:587:LEU:HD23	1:F:716:GLU:CG	2.40	0.52
2:J:718:VAL:HG21	2:J:742:ARG:NH1	2.25	0.52
1:E:721:GLY:O	1:E:742:ARG:HD3	2.10	0.52
1:H:471:ILE:HG21	1:H:543:MET:HE1	1.92	0.52
1:H:510:TYR:CE1	1:H:546:ARG:HD3	2.45	0.51
1:I:443:LYS:HD2	1:I:754:ALA:HB1	1.93	0.51
1:E:701:GLU:OE1	1:F:633:SER:HA	2.11	0.51
1:F:587:LEU:HD23	1:F:716:GLU:HG3	1.93	0.51
1:F:631:LEU:HB3	1:F:648:MET:HE3	1.92	0.50
1:I:490:ILE:HG23	1:I:496:PHE:CE1	2.46	0.50
1:E:500:ASN:HB3	1:E:503:SER:O	2.12	0.50
1:E:508:LYS:HA	1:E:511:TRP:NE1	2.25	0.50
2:J:471:ILE:HG21	2:J:543:MET:HE1	1.94	0.50
1:I:430:PHE:HZ	1:I:720:VAL:CG2	2.24	0.50
1:H:431:MET:HB3	1:H:435:PHE:CE2	2.46	0.50
1:I:571:PHE:CD1	1:I:729:LYS:HG3	2.47	0.50
1:I:757:GLN:HE21	1:I:758:PRO:HD2	1.76	0.50
1:G:424:LEU:HD13	1:G:625:ILE:HD13	1.94	0.49
1:H:685:ASP:HB2	4:H:809:HOH:O	2.11	0.49
1:I:430:PHE:HZ	1:I:720:VAL:HG22	1.76	0.49
1:I:536:PRO:HA	1:I:539:ILE:HD12	1.95	0.49
1:H:508:LYS:HA	1:H:511:TRP:CD1	2.48	0.49
1:H:569:ASN:ND2	4:H:801:HOH:O	2.34	0.49
1:E:757:GLN:HG3	1:E:758:PRO:HD2	1.94	0.49
1:H:508:LYS:HA	1:H:511:TRP:NE1	2.27	0.49
1:I:432:LYS:N	1:I:433:PRO:HD2	2.27	0.49
1:G:675:VAL:HB	1:G:678:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:574:ARG:O	1:E:577:VAL:HG22	2.13	0.48
1:G:424:LEU:HD11	1:G:592:ASN:O	2.13	0.48
1:G:459:THR:HG23	1:G:470:PRO:HG2	1.95	0.48
1:I:456:LEU:O	1:I:459:THR:HG22	2.13	0.48
1:E:596:ALA:O	1:E:597:ASP:C	2.57	0.48
1:G:604:PRO:O	1:G:647:LYS:HD2	2.14	0.47
1:G:718:VAL:HG12	1:G:719:THR:N	2.28	0.47
1:E:550:ASP:O	1:E:730:PRO:HG2	2.15	0.47
1:G:427:GLN:H	1:G:427:GLN:HG3	1.53	0.47
1:G:459:THR:O	1:G:463:VAL:HG23	2.15	0.47
1:G:480:GLU:O	1:G:481:MET:C	2.57	0.47
1:G:500:ASN:HB3	1:G:503:SER:O	2.15	0.47
1:G:501:ASN:OD1	1:G:502:GLU:HG3	2.15	0.47
1:F:635:SER:HB2	1:F:640:SER:HB3	1.96	0.47
1:G:424:LEU:HD12	1:G:592:ASN:HB2	1.96	0.47
1:H:631:LEU:HD23	1:H:696:VAL:HB	1.95	0.47
1:H:685:ASP:CB	4:H:809:HOH:O	2.63	0.46
1:F:483:ILE:HG23	1:F:488:LEU:HB2	1.97	0.46
1:H:429:LEU:CG	1:H:431:MET:HB2	2.46	0.46
2:J:456:LEU:HD22	2:J:483:ILE:CD1	2.45	0.46
1:H:753:GLU:HB3	1:H:758:PRO:HA	1.97	0.46
1:I:447:LEU:HB2	1:I:472:LEU:HD23	1.96	0.46
1:F:697:MET:HE2	1:F:703:ALA:HA	1.97	0.46
2:J:636:ASN:H	2:J:639:SER:HB3	1.80	0.46
1:I:443:LYS:HE2	1:I:755:GLN:HG2	1.97	0.46
1:F:579:THR:HG21	1:F:608:GLU:CG	2.29	0.45
2:J:704:ARG:HG3	2:J:708:ASN:ND2	2.31	0.45
1:F:604:PRO:O	1:F:647:LYS:HD2	2.16	0.45
1:H:528:ALA:O	1:H:532:LEU:HD23	2.16	0.45
1:F:756:THR:OG1	1:F:757:GLN:N	2.50	0.45
2:J:571:PHE:CD1	2:J:729:LYS:HG3	2.51	0.45
1:H:636:ASN:HB2	1:H:669:HIS:CE1	2.52	0.45
1:E:542:ILE:O	1:E:546:ARG:HG3	2.17	0.45
1:I:636:ASN:O	1:I:682:ARG:NH1	2.50	0.45
1:E:718:VAL:HG11	1:E:742:ARG:HH22	1.82	0.45
1:G:642:CYS:HB3	1:G:643:PRO:HD2	1.98	0.45
2:J:536:PRO:HA	2:J:539:ILE:HD12	1.99	0.45
1:G:424:LEU:CD1	1:G:625:ILE:HD13	2.46	0.45
1:H:445:VAL:HG22	1:H:551:ALA:HB3	1.98	0.44
1:H:751:VAL:O	1:H:755:GLN:HG3	2.17	0.44
1:G:579:THR:HG21	1:G:608:GLU:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:698:PRO:HG3	1:H:701:GLU:CG	2.48	0.44
1:H:602:ASP:HA	1:H:700:MET:HB2	2.00	0.44
1:E:431:MET:HE2	1:E:745:ASN:O	2.18	0.44
1:G:756:THR:OG1	1:G:757:GLN:N	2.50	0.44
1:E:430:PHE:O	1:E:433:PRO:HD2	2.18	0.44
1:G:753:GLU:CG	1:G:758:PRO:HA	2.45	0.44
1:E:596:ALA:HB3	1:E:697:MET:H	1.81	0.44
1:G:697:MET:HB3	1:G:698:PRO:HD2	1.99	0.44
2:J:449:GLU:HG2	2:J:557:VAL:CG1	2.46	0.43
2:J:597:ASP:OD1	2:J:598:THR:N	2.51	0.43
1:F:631:LEU:HD23	1:F:696:VAL:HB	2.00	0.43
1:H:490:ILE:C	1:H:491:LYS:HD2	2.44	0.43
1:F:460:GLN:NE2	1:F:490:ILE:HG23	2.34	0.43
1:G:609:LEU:HD12	1:G:647:LYS:HG2	2.00	0.43
1:G:634:HIS:CD2	1:H:700:MET:CE	3.02	0.43
1:H:500:ASN:ND2	1:H:503:SER:HB3	2.33	0.43
2:J:481:MET:HE3	2:J:485:LYS:HD2	1.99	0.43
1:E:518:MET:HE3	1:E:518:MET:HB3	1.85	0.43
1:F:492:ALA:C	1:F:494:VAL:N	2.76	0.43
1:E:582:ALA:HA	1:E:723:VAL:O	2.19	0.43
2:J:555:GLY:HA2	2:J:563:HIS:CD2	2.54	0.43
1:F:568:LYS:C	1:F:568:LYS:HD3	2.43	0.43
1:E:504:ASP:OD1	1:E:505:PRO:HD2	2.19	0.42
1:E:585:ALA:HB2	1:E:594:PHE:CD2	2.54	0.42
1:G:571:PHE:CE2	1:G:731:VAL:HG21	2.54	0.42
1:E:571:PHE:CD1	1:E:729:LYS:HG3	2.55	0.42
1:E:596:ALA:HB2	1:E:697:MET:H	1.80	0.42
1:E:753:GLU:HG2	1:E:758:PRO:HA	2.01	0.42
1:F:492:ALA:C	1:F:494:VAL:H	2.26	0.42
1:E:722:PRO:HD2	1:E:734:LEU:HA	2.00	0.42
1:F:528:ALA:O	1:F:532:LEU:HD23	2.19	0.42
1:G:552:MET:HB3	1:G:731:VAL:HG22	1.99	0.42
1:H:571:PHE:CD1	1:H:729:LYS:HG3	2.54	0.42
2:J:629:VAL:HG11	2:J:664:ILE:HD12	2.01	0.42
1:F:697:MET:HB3	1:F:698:PRO:HD2	2.00	0.42
1:I:747:VAL:O	1:I:751:VAL:HG23	2.19	0.42
1:E:559:ASP:CG	2:J:527:GLN:HE22	2.28	0.42
1:H:685:ASP:CG	4:H:809:HOH:O	2.61	0.42
1:E:519:LYS:HG3	1:E:520:ARG:HG3	2.01	0.42
1:H:618:GLU:OE1	1:H:621:ARG:NH1	2.53	0.42
2:J:635:SER:HB2	2:J:640:SER:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:446:VAL:HG11	1:H:540:GLY:HA2	2.02	0.42
2:J:553:ILE:HG13	2:J:747:VAL:HG22	2.00	0.41
2:J:602:ASP:N	2:J:602:ASP:OD1	2.52	0.41
1:E:579:THR:HG22	1:E:611:GLU:OE2	2.21	0.41
1:E:580:ALA:O	1:E:601:ASN:ND2	2.53	0.41
1:E:661:GLU:OE2	1:E:661:GLU:N	2.52	0.41
1:G:431:MET:HE3	1:G:431:MET:HB3	1.97	0.41
1:H:518:MET:HE2	4:H:801:HOH:O	2.20	0.41
1:G:757:GLN:HG3	1:G:758:PRO:CD	2.50	0.41
2:J:579:THR:HG21	2:J:611:GLU:HB2	2.02	0.41
1:F:655:VAL:HG11	1:F:664:ILE:HD13	2.01	0.41
1:G:755:GLN:O	1:G:756:THR:OG1	2.34	0.41
1:F:431:MET:O	1:F:434:ILE:N	2.54	0.41
1:F:454:ARG:NH2	1:F:556:THR:HB	2.36	0.41
1:H:481:MET:CE	1:H:482:ARG:HG3	2.51	0.41
1:I:553:ILE:CD1	1:I:732:HIS:HB2	2.50	0.41
1:I:751:VAL:O	1:I:754:ALA:HB3	2.20	0.41
2:J:560:TYR:CE2	2:J:733:VAL:HB	2.55	0.41
1:E:620:VAL:HG21	1:E:694:ILE:HD11	2.03	0.41
1:G:432:LYS:HB3	1:G:433:PRO:HD3	2.03	0.40
2:J:631:LEU:HB3	2:J:648:MET:HE3	2.02	0.40
1:E:718:VAL:HG12	1:E:719:THR:N	2.35	0.40
1:G:480:GLU:HG3	1:G:484:GLN:OE1	2.22	0.40
1:G:482:ARG:O	1:G:486:LEU:HG	2.22	0.40
1:H:749:LEU:HD11	1:H:759:LEU:HD11	2.03	0.40
1:I:741:ARG:HG3	1:I:745:ASN:HD21	1.86	0.40
1:F:579:THR:HG23	1:F:611:GLU:OE2	2.22	0.40
1:F:747:VAL:O	1:F:751:VAL:HG23	2.21	0.40
1:G:468:ALA:O	1:G:470:PRO:HD3	2.22	0.40
1:H:613:THR:HG23	1:H:629:VAL:HG11	2.03	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	E	330/372 (89%)	321 (97%)	8 (2%)	1 (0%)	37	67
1	F	329/372 (88%)	320 (97%)	9 (3%)	0	100	100
1	G	336/372 (90%)	329 (98%)	7 (2%)	0	100	100
1	H	330/372 (89%)	324 (98%)	6 (2%)	0	100	100
1	I	329/372 (88%)	324 (98%)	5 (2%)	0	100	100
2	J	335/372 (90%)	328 (98%)	7 (2%)	0	100	100
All	All	1989/2232 (89%)	1946 (98%)	42 (2%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	596	ALA

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	E	276/308 (90%)	276 (100%)	0	100	100
1	F	276/308 (90%)	275 (100%)	1 (0%)	89	96
1	G	282/308 (92%)	281 (100%)	1 (0%)	89	96
1	H	276/308 (90%)	276 (100%)	0	100	100
1	I	276/308 (90%)	275 (100%)	1 (0%)	89	96
2	J	281/307 (92%)	279 (99%)	2 (1%)	81	94
All	All	1667/1847 (90%)	1662 (100%)	5 (0%)	91	97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	430	PHE

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Mol	Chain	Res	Type
1	G	427	GLN
1	I	590	SER
2	J	602	ASP
2	J	687	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	561	HIS
1	E	680	ASN
1	G	427	GLN
1	G	757	GLN
1	H	500	ASN
1	H	516	GLN
1	H	545	GLN
1	I	501	ASN
1	I	516	GLN
1	I	535	ASN
1	I	757	GLN
2	J	484	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CSO	J	642	2	3,6,7	0.72	0	0,6,8	-	-

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	CSO	J	642	2	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	I	801	-	4,4,4	0.39	0	6,6,6	0.06	0
3	SO4	E	801	-	4,4,4	0.39	0	6,6,6	0.06	0

There are no bond length outliers.

There are no bond angle outliers.

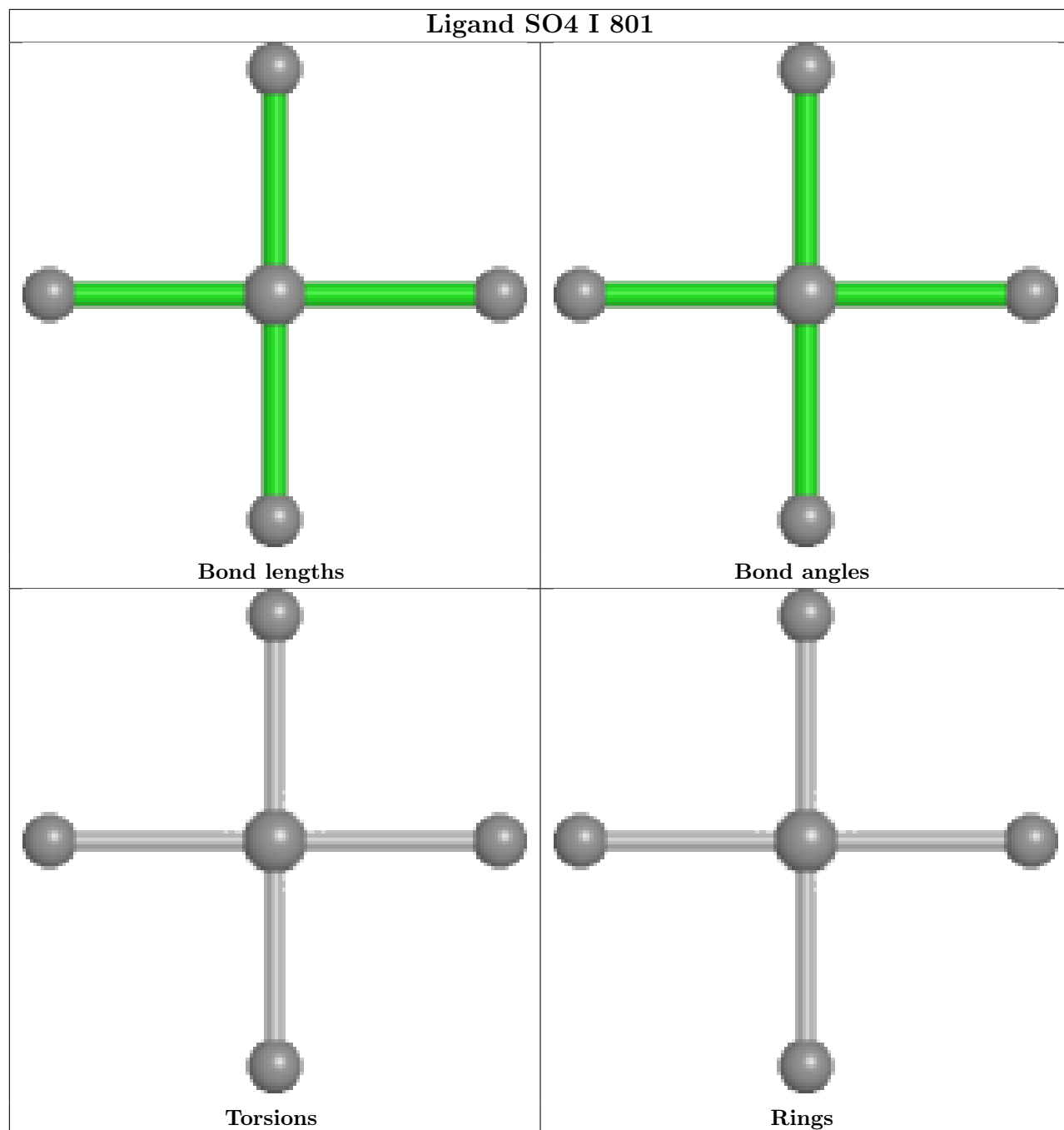
There are no chirality outliers.

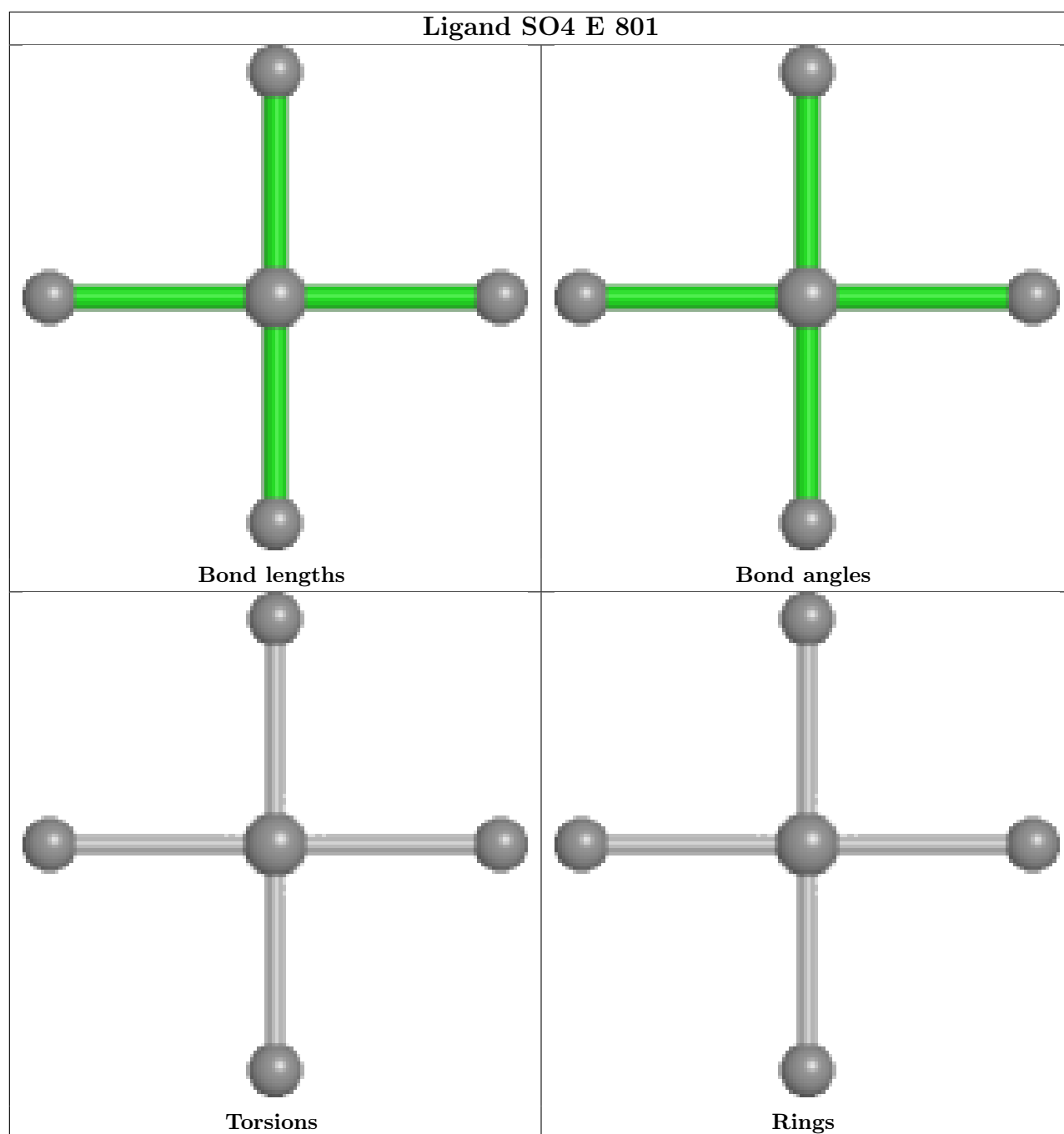
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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(Å²)	Q<0.9	
1	E	332/372 (89%)	-0.19	4 (1%)	76	69	30, 58, 84, 112	0
1	F	331/372 (88%)	-0.21	3 (0%)	81	75	44, 63, 86, 120	0
1	G	338/372 (90%)	-0.13	2 (0%)	85	81	44, 65, 95, 113	0
1	H	332/372 (89%)	-0.18	3 (0%)	81	75	41, 60, 97, 121	0
1	I	331/372 (88%)	-0.13	4 (1%)	76	69	36, 59, 101, 120	0
2	J	337/372 (90%)	-0.18	3 (0%)	81	75	42, 59, 92, 106	0
All	All	2001/2232 (89%)	-0.17	19 (0%)	81	75	30, 61, 93, 121	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	596	ALA	4.4
1	F	429	LEU	4.1
1	I	429	LEU	3.7
1	G	424	LEU	3.2
1	H	429	LEU	3.1
1	E	429	LEU	3.0
2	J	714	SER	2.9
1	I	486	LEU	2.7
1	I	719	THR	2.6
1	F	718	VAL	2.6
1	E	718	VAL	2.4
1	H	718	VAL	2.4
1	I	714	SER	2.3
2	J	427	GLN	2.2
1	F	430	PHE	2.2
1	G	716	GLU	2.1
1	H	719	THR	2.1
1	E	513	GLU	2.1
2	J	424	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CSO	J	642	7/8	0.86	0.09	56,63,84,88	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

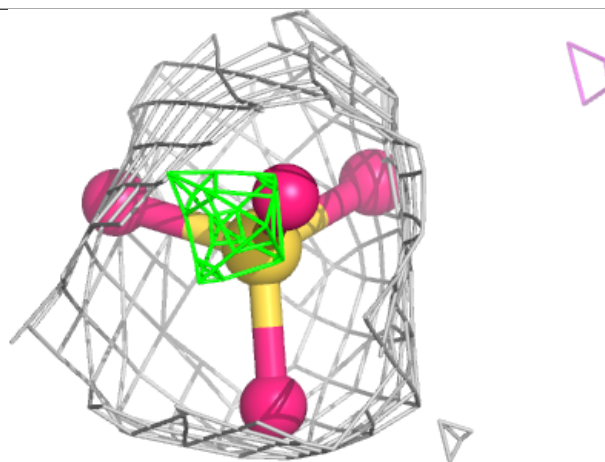
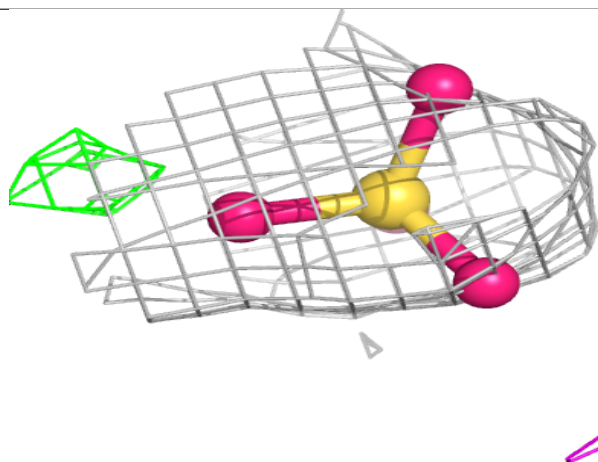
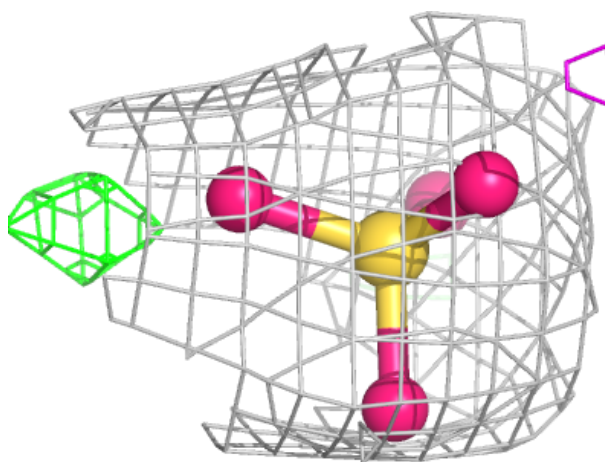
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	E	801	5/5	0.71	0.16	121,123,126,128	0
3	SO4	I	801	5/5	0.93	0.10	85,87,88,92	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.

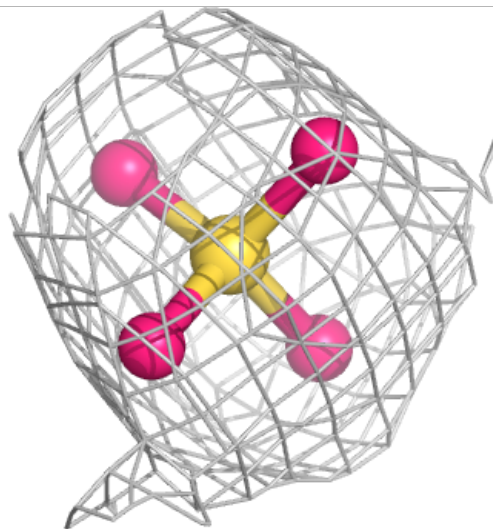
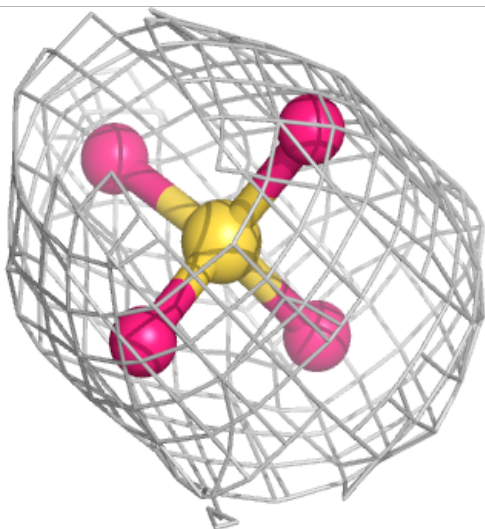
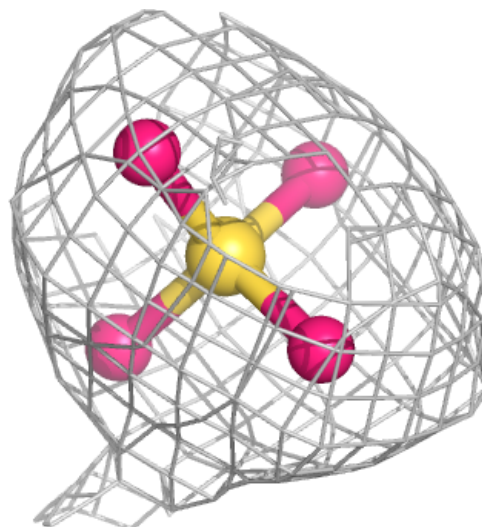
Electron density around SO4 E 801:

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



Electron density around SO4 I 801:

$2mF_o-DF_c$ (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.