



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2017 – 07:08 PM EDT

PDB ID : 4P2V
Title : Structure of the AI-2 processing enzyme LsrF in complex with the product of the LsrG reaction P-HPD
Authors : Miller, S.T.; Oh, I.K.; Xavier, K.B.
Deposited on : unknown
Resolution : 2.51 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

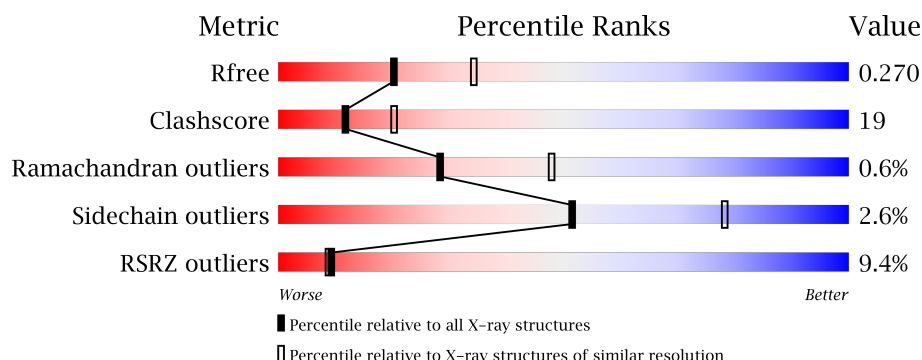
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	293	<div> <div>12%</div> <div>59%</div> <div>34%</div> <div>• •</div> </div>
1	B	293	<div> <div>2%</div> <div>70%</div> <div>25%</div> <div>•</div> </div>
1	C	293	<div> <div>9%</div> <div>66%</div> <div>29%</div> <div>• •</div> </div>
1	D	293	<div> <div>17%</div> <div>51%</div> <div>38%</div> <div>7%</div> <div>•</div> </div>
1	E	293	<div> <div>5%</div> <div>67%</div> <div>29%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	293	<div><div>2%</div><div><div></div><div></div><div></div></div><div>72%</div><div>23%</div><div></div><div>.</div></div>
1	G	293	<div><div>17%</div><div><div></div><div></div><div></div></div><div>59%</div><div>33%</div><div></div><div>.</div><div>.</div><div>.</div></div>
1	H	293	<div><div>13%</div><div><div></div><div></div><div></div></div><div>60%</div><div>35%</div><div></div><div>.</div><div>.</div></div>
1	I	293	<div><div>6%</div><div><div></div><div></div><div></div></div><div>62%</div><div>31%</div><div></div><div>.</div><div>.</div><div>.</div></div>
1	K	293	<div><div>8%</div><div><div></div><div></div><div></div></div><div>61%</div><div>33%</div><div></div><div>.</div><div>.</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22178 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 Uncharacterized aldolase LsrF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	B	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	C	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	D	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	E	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	F	280	Total	C	N	O	S	0	0	0
			2138	1345	377	398	18			
1	G	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	H	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	I	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			
1	K	281	Total	C	N	O	S	0	0	0
			2146	1349	378	401	18			

There are 30 discrepancies between the modelled and reference sequences:

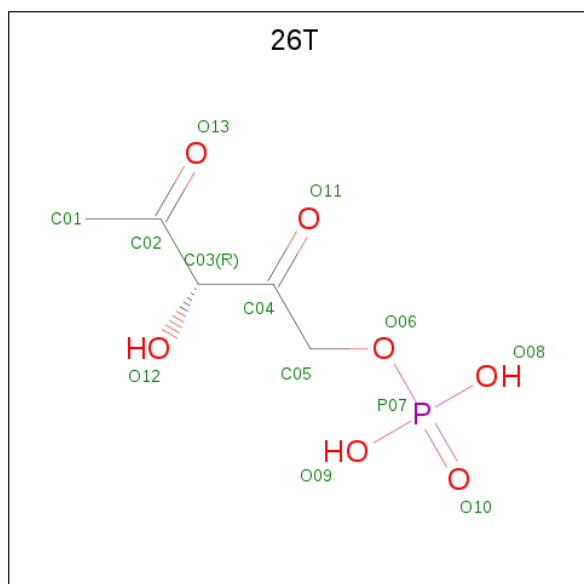
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P76143
A	0	SER	-	expression tag	UNP P76143
A	203	ALA	LYS	engineered mutation	UNP P76143
B	-1	GLY	-	expression tag	UNP P76143
B	0	SER	-	expression tag	UNP P76143
B	203	ALA	LYS	engineered mutation	UNP P76143
C	-1	GLY	-	expression tag	UNP P76143
C	0	SER	-	expression tag	UNP P76143
C	203	ALA	LYS	engineered mutation	UNP P76143

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	expression tag	UNP P76143
D	0	SER	-	expression tag	UNP P76143
D	203	ALA	LYS	engineered mutation	UNP P76143
E	-1	GLY	-	expression tag	UNP P76143
E	0	SER	-	expression tag	UNP P76143
E	203	ALA	LYS	engineered mutation	UNP P76143
F	-1	GLY	-	expression tag	UNP P76143
F	0	SER	-	expression tag	UNP P76143
F	203	ALA	LYS	engineered mutation	UNP P76143
G	-1	GLY	-	expression tag	UNP P76143
G	0	SER	-	expression tag	UNP P76143
G	203	ALA	LYS	engineered mutation	UNP P76143
H	-1	GLY	-	expression tag	UNP P76143
H	0	SER	-	expression tag	UNP P76143
H	203	ALA	LYS	engineered mutation	UNP P76143
I	-1	GLY	-	expression tag	UNP P76143
I	0	SER	-	expression tag	UNP P76143
I	203	ALA	LYS	engineered mutation	UNP P76143
K	-1	GLY	-	expression tag	UNP P76143
K	0	SER	-	expression tag	UNP P76143
K	203	ALA	LYS	engineered mutation	UNP P76143

- Molecule 2 is (3R)-3-hydroxy-2,4-dioxopentyl dihydrogen phosphate (three-letter code: 26T) (formula: C₅H₉O₇P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 13 5 7 1	0	0
2	B	1	Total C O P 13 5 7 1	0	0
2	C	1	Total C O P 13 5 7 1	0	0
2	D	1	Total C O P 13 5 7 1	0	0
2	E	1	Total C O P 13 5 7 1	0	0
2	F	1	Total C O P 13 5 7 1	0	0
2	G	1	Total C O P 13 5 7 1	0	0
2	H	1	Total C O P 13 5 7 1	0	0
2	I	1	Total C O P 13 5 7 1	0	0
2	K	1	Total C O P 13 5 7 1	0	0

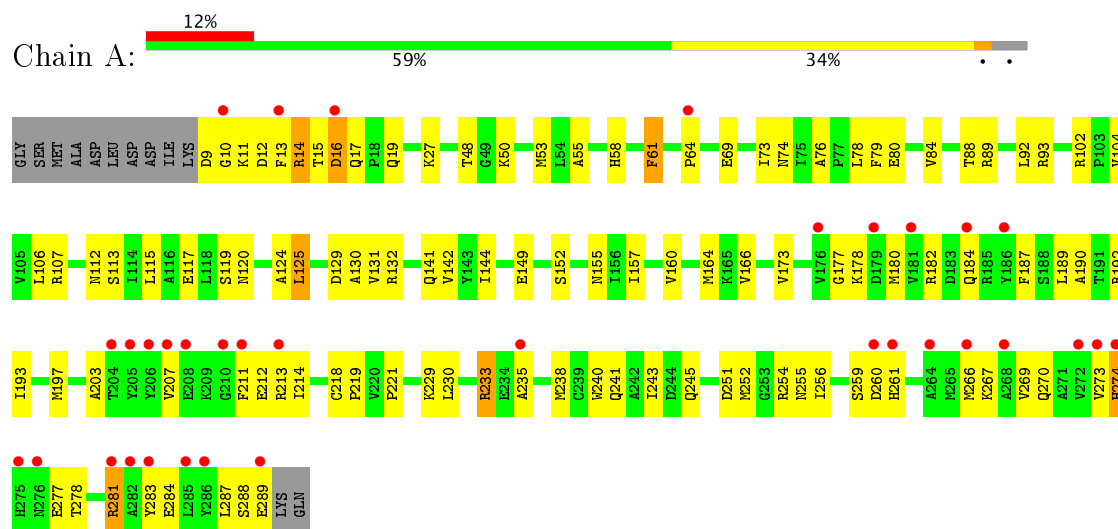
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	47	Total O 47 47	0	0
3	B	73	Total O 73 73	0	0
3	C	66	Total O 66 66	0	0
3	D	38	Total O 38 38	0	0
3	E	71	Total O 71 71	0	0
3	F	85	Total O 85 85	0	0
3	G	47	Total O 47 47	0	0
3	H	47	Total O 47 47	0	0
3	I	80	Total O 80 80	0	0
3	K	42	Total O 42 42	0	0

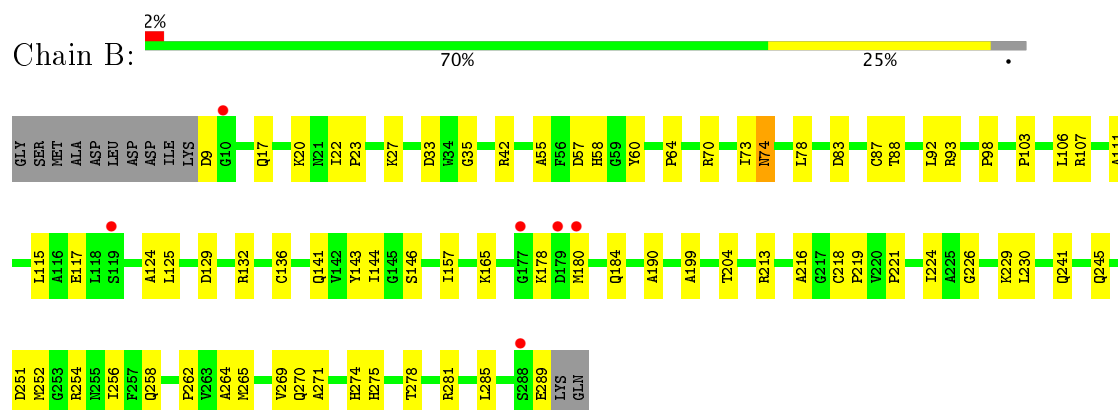
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). 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.

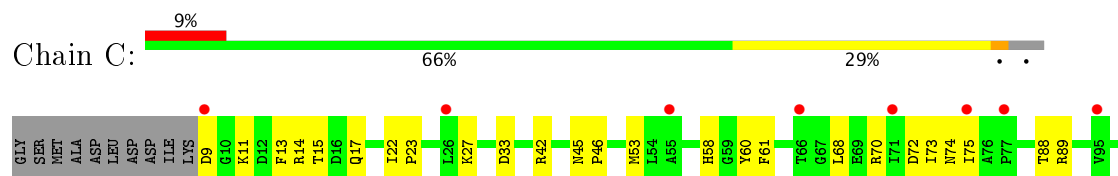
• Molecule 1: Uncharacterized aldolase LsrF

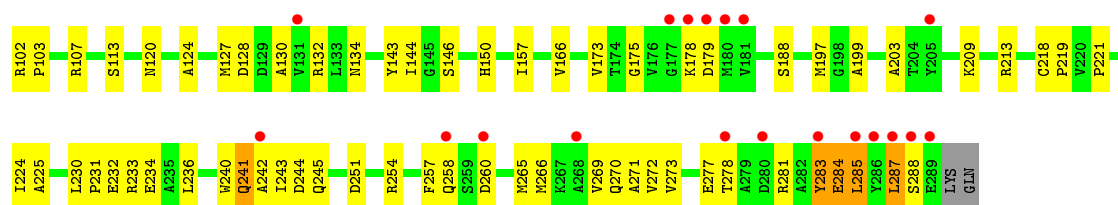


• Molecule 1: Uncharacterized aldolase LsrF

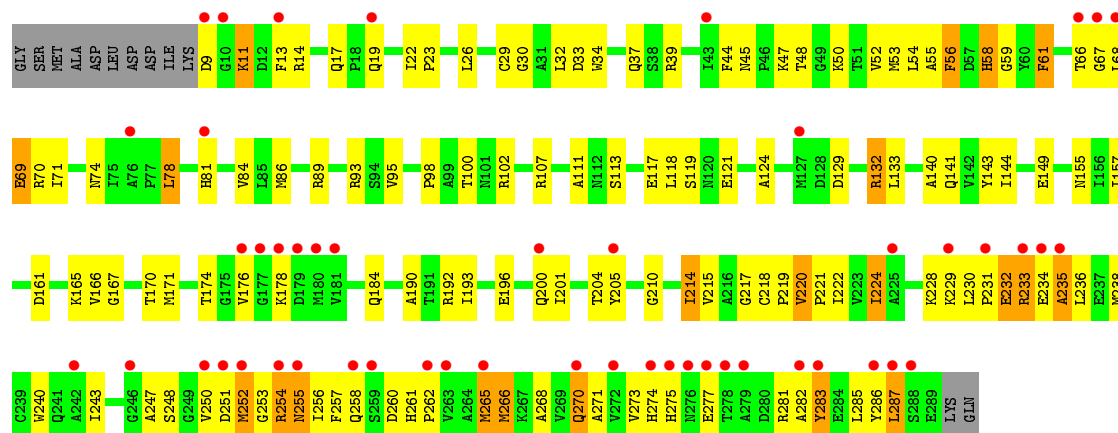


• Molecule 1: Uncharacterized aldolase LsrF

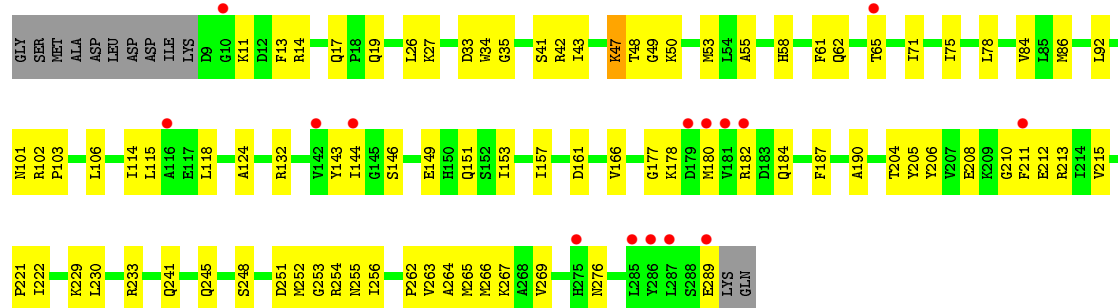




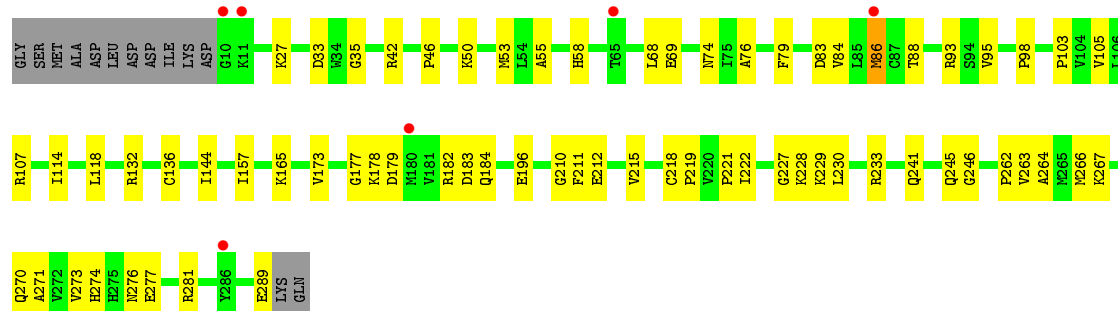
• Molecule 1: Uncharacterized aldolase LsrF



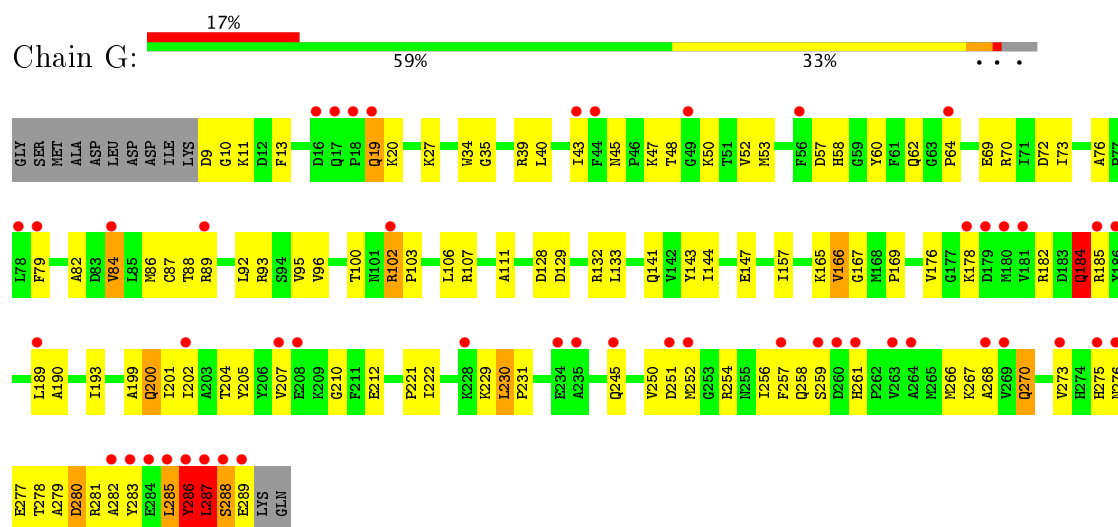
• Molecule 1: Uncharacterized aldolase LsrF



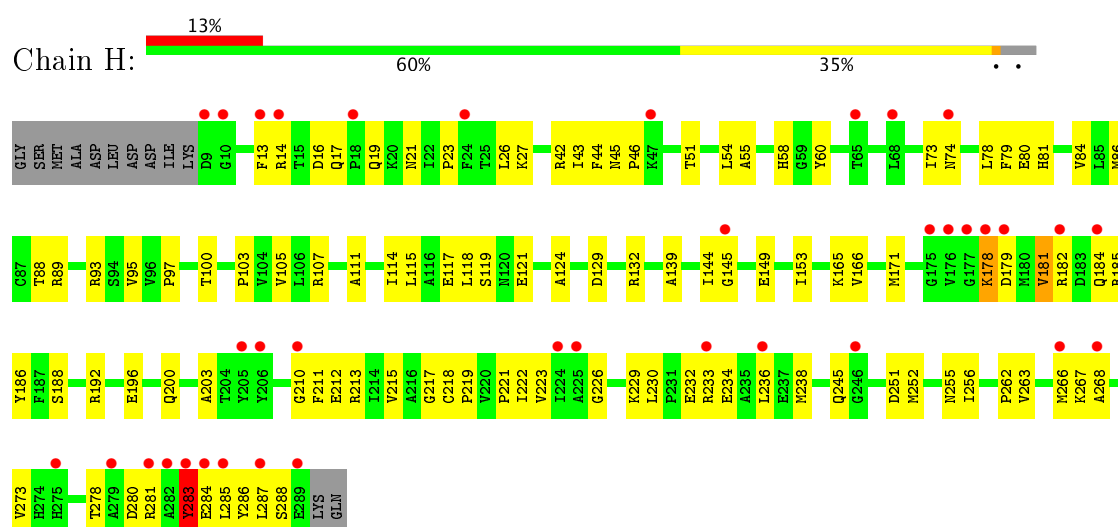
• Molecule 1: Uncharacterized aldolase LsrF



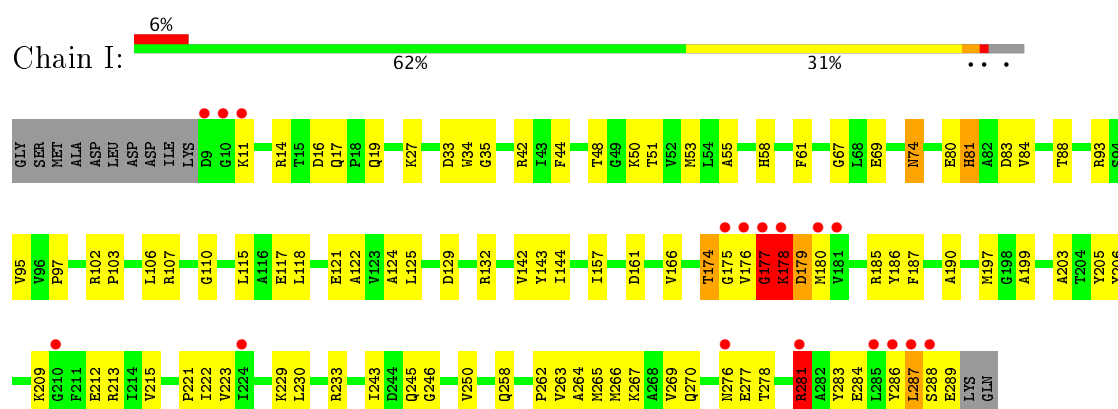
- Molecule 1: Uncharacterized aldolase LsrF



- Molecule 1: Uncharacterized aldolase LsrF

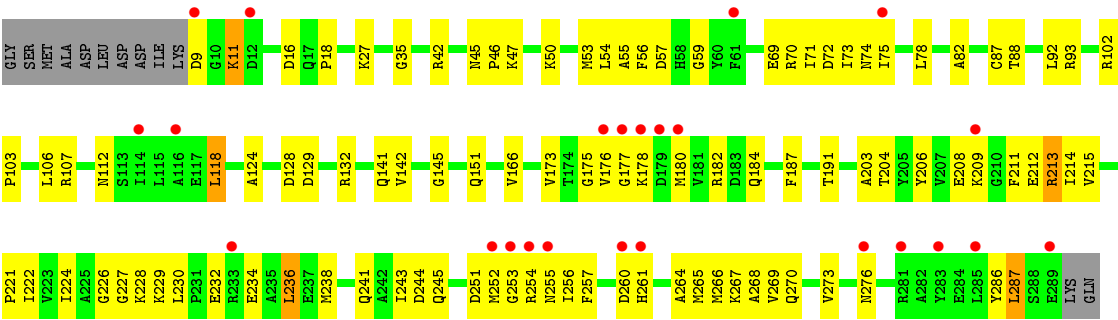


- Molecule 1: Uncharacterized aldolase LsrF



- Molecule 1: Uncharacterized aldolase LsrF





GLOBAL-STATISTICS INFOmissingINFO

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 26T

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.37	0/2185	0.72	3/2957 (0.1%)
1	B	0.27	0/2185	0.54	0/2957
1	C	0.32	0/2185	0.67	3/2957 (0.1%)
1	D	0.43	0/2185	0.76	2/2957 (0.1%)
1	E	0.29	0/2185	0.58	0/2957
1	F	0.28	0/2177	0.55	0/2946
1	G	0.36	0/2185	0.76	3/2957 (0.1%)
1	H	0.39	1/2185 (0.0%)	0.70	0/2957
1	I	0.41	1/2185 (0.0%)	0.70	4/2957 (0.1%)
1	K	0.33	0/2185	0.73	3/2957 (0.1%)
All	All	0.35	2/21842 (0.0%)	0.68	18/29559 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	4
1	I	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	185	ARG	C-N	10.49	1.58	1.34
1	H	283	TYR	CD1-CE1	-6.17	1.30	1.39

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	287	LEU	CA-CB-CG	-10.14	91.98	115.30
1	I	281	ARG	NE-CZ-NH1	-8.64	115.98	120.30
1	K	118	LEU	CA-CB-CG	7.71	133.02	115.30
1	D	287	LEU	CA-CB-CG	-6.43	100.52	115.30
1	G	184	GLN	CA-CB-CG	6.42	127.53	113.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	280	ASP	Peptide
1	G	285	LEU	Peptide
1	G	286	TYR	Peptide
1	G	287	LEU	Peptide
1	I	178	LYS	Peptide

4.2 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	2146	0	2148	98	0
1	B	2146	0	2148	61	0
1	C	2146	0	2148	76	1
1	D	2146	0	2148	182	1
1	E	2146	0	2148	69	0
1	F	2138	0	2144	54	0
1	G	2146	0	2148	113	0
1	H	2146	0	2148	102	0
1	I	2146	0	2148	88	0
1	K	2146	0	2148	89	0
2	A	13	0	9	1	0
2	B	13	0	9	2	0
2	C	13	0	9	0	0
2	D	13	0	9	4	0
2	E	13	0	9	2	0
2	F	13	0	9	1	0
2	G	13	0	9	2	0
2	H	13	0	9	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	13	0	9	3	0
2	K	13	0	9	1	0
3	A	47	0	0	15	0
3	B	73	0	0	14	0
3	C	66	0	0	10	1
3	D	38	0	0	13	0
3	E	71	0	0	17	0
3	F	85	0	0	10	0
3	G	47	0	0	17	0
3	H	47	0	0	14	0
3	I	80	0	0	14	1
3	K	42	0	0	6	0
All	All	22178	0	21566	838	2

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 19.

The worst 5 of 838 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:256:ILE:HG23	1:D:265:MET:SD	1.30	1.64
1:D:256:ILE:CG2	1:D:265:MET:SD	2.20	1.30
1:G:278:THR:OG1	1:G:281:ARG:CG	1.92	1.18
1:G:278:THR:OG1	1:G:281:ARG:HG2	0.99	1.15
1:B:281:ARG:NH1	3:B:402:HOH:O	1.91	1.01

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:287:LEU:O	1:D:47:LYS:NZ[2_454]	2.12	0.08
3:C:401:HOH:O	3:I:403:HOH:O[1_455]	2.19	0.01

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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

of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	279/293 (95%)	267 (96%)	12 (4%)	0	100	100
1	B	279/293 (95%)	269 (96%)	9 (3%)	1 (0%)	38	59
1	C	279/293 (95%)	266 (95%)	11 (4%)	2 (1%)	25	43
1	D	279/293 (95%)	267 (96%)	8 (3%)	4 (1%)	13	23
1	E	279/293 (95%)	268 (96%)	10 (4%)	1 (0%)	38	59
1	F	278/293 (95%)	266 (96%)	11 (4%)	1 (0%)	38	59
1	G	279/293 (95%)	266 (95%)	11 (4%)	2 (1%)	25	43
1	H	279/293 (95%)	265 (95%)	11 (4%)	3 (1%)	17	29
1	I	279/293 (95%)	265 (95%)	10 (4%)	4 (1%)	13	23
1	K	279/293 (95%)	267 (96%)	12 (4%)	0	100	100
All	All	2789/2930 (95%)	2666 (96%)	105 (4%)	18 (1%)	28	48

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	178	LYS
1	D	178	LYS
1	D	286	TYR
1	E	178	LYS
1	F	178	LYS

4.3.2 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	227/237 (96%)	222 (98%)	5 (2%)	57	82
1	B	227/237 (96%)	224 (99%)	3 (1%)	73	90
1	C	227/237 (96%)	224 (99%)	3 (1%)	73	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	227/237 (96%)	210 (92%)	17 (8%)	16	29
1	E	227/237 (96%)	224 (99%)	3 (1%)	73	90
1	F	226/237 (95%)	223 (99%)	3 (1%)	73	90
1	G	227/237 (96%)	219 (96%)	8 (4%)	41	68
1	H	227/237 (96%)	223 (98%)	4 (2%)	64	86
1	I	227/237 (96%)	220 (97%)	7 (3%)	45	73
1	K	227/237 (96%)	221 (97%)	6 (3%)	51	78
All	All	2269/2370 (96%)	2210 (97%)	59 (3%)	51	78

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	270	GLN
1	F	182	ARG
1	K	209	LYS
1	D	283	TYR
1	E	47	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	151	GLN
1	F	276	ASN
1	H	81	HIS
1	D	255	ASN
1	E	101	ASN

4.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

4.6 Ligand geometry [i](#)

10 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	26T	A	301	-	10,12,12	5.54	3 (30%)	9,17,17	2.14	5 (55%)
2	26T	B	301	-	10,12,12	5.53	3 (30%)	9,17,17	2.15	4 (44%)
2	26T	C	301	-	10,12,12	5.40	3 (30%)	9,17,17	2.25	5 (55%)
2	26T	D	301	-	10,12,12	5.80	2 (20%)	9,17,17	2.17	5 (55%)
2	26T	E	301	-	10,12,12	5.49	3 (30%)	9,17,17	2.15	3 (33%)
2	26T	F	301	-	10,12,12	5.79	3 (30%)	9,17,17	2.26	5 (55%)
2	26T	G	301	-	10,12,12	5.36	3 (30%)	9,17,17	2.13	5 (55%)
2	26T	H	301	-	10,12,12	5.64	3 (30%)	9,17,17	2.16	5 (55%)
2	26T	I	301	-	10,12,12	5.66	3 (30%)	9,17,17	2.16	5 (55%)
2	26T	K	301	-	10,12,12	5.63	3 (30%)	9,17,17	2.20	4 (44%)

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	26T	A	301	-	-	0/13/14/14	0/0/0/0
2	26T	B	301	-	-	0/13/14/14	0/0/0/0
2	26T	C	301	-	-	0/13/14/14	0/0/0/0
2	26T	D	301	-	-	0/13/14/14	0/0/0/0
2	26T	E	301	-	-	0/13/14/14	0/0/0/0
2	26T	F	301	-	-	0/13/14/14	0/0/0/0
2	26T	G	301	-	-	0/13/14/14	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	26T	H	301	-	-	0/13/14/14	0/0/0/0
2	26T	I	301	-	-	0/13/14/14	0/0/0/0
2	26T	K	301	-	-	0/13/14/14	0/0/0/0

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	26T	O06-C05	-16.32	1.32	1.43
2	D	301	26T	O06-C05	-16.08	1.32	1.43
2	I	301	26T	O06-C05	-15.30	1.32	1.43
2	K	301	26T	O06-C05	-15.20	1.33	1.43
2	H	301	26T	O06-C05	-14.96	1.33	1.43

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	26T	O13-C02-C01	-3.08	115.41	121.09
2	F	301	26T	O13-C02-C01	-3.08	115.42	121.09
2	C	301	26T	O13-C02-C01	-3.02	115.54	121.09
2	G	301	26T	O13-C02-C01	-3.01	115.56	121.09
2	H	301	26T	O13-C02-C01	-2.98	115.61	121.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	26T	1	0
2	B	301	26T	2	0
2	D	301	26T	4	0
2	E	301	26T	2	0
2	F	301	26T	1	0
2	G	301	26T	2	0
2	H	301	26T	3	0
2	I	301	26T	3	0
2	K	301	26T	1	0

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 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	281/293 (95%)	0.86	34 (12%) 5 4	31, 50, 104, 156	0
1	B	281/293 (95%)	0.25	6 (2%) 64 66	19, 35, 56, 79	0
1	C	281/293 (95%)	0.70	27 (9%) 9 8	31, 49, 85, 145	0
1	D	281/293 (95%)	1.17	50 (17%) 2 1	37, 61, 113, 137	0
1	E	281/293 (95%)	0.41	15 (5%) 27 28	18, 37, 71, 124	0
1	F	280/293 (95%)	0.19	6 (2%) 64 66	19, 33, 53, 99	0
1	G	281/293 (95%)	1.08	49 (17%) 2 1	33, 58, 109, 201	0
1	H	281/293 (95%)	0.80	37 (13%) 4 3	30, 51, 90, 107	0
1	I	281/293 (95%)	0.38	17 (6%) 23 23	20, 37, 77, 147	0
1	K	281/293 (95%)	0.72	24 (8%) 11 11	28, 49, 88, 119	0
All	All	2809/2930 (95%)	0.65	265 (9%) 9 9	18, 45, 92, 201	0

The worst 5 of 265 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	10	GLY	11.5
1	G	287	LEU	9.3
1	H	283	TYR	8.1
1	E	181	VAL	7.9
1	D	287	LEU	7.6

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	26T	B	301	13/13	0.92	0.22	1.04	39,46,55,56	0
2	26T	E	301	13/13	0.88	0.20	0.68	43,49,72,72	0
2	26T	F	301	13/13	0.87	0.18	0.31	37,63,67,69	0
2	26T	C	301	13/13	0.90	0.20	0.27	31,40,93,93	0
2	26T	A	301	13/13	0.84	0.22	0.15	50,55,86,86	0
2	26T	H	301	13/13	0.90	0.22	0.04	53,58,67,68	0
2	26T	I	301	13/13	0.90	0.17	-0.04	40,55,69,69	0
2	26T	K	301	13/13	0.80	0.23	-0.09	47,58,72,73	0
2	26T	G	301	13/13	0.80	0.19	-0.68	45,60,90,91	0
2	26T	D	301	13/13	0.82	0.18	-0.94	49,66,69,72	0

5.5 Other polymers [i](#)

There are no such residues in this entry.