



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2017 – 03:07 PM EDT

PDB ID : 5ECK
Title : Crystal Structure of FIN219-FIP1 complex with JA, Ile and ATP
Authors : Chen, C.Y.; Cheng, Y.S.
Deposited on : 2015-10-20
Resolution : 1.54 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-20029077
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-20029077

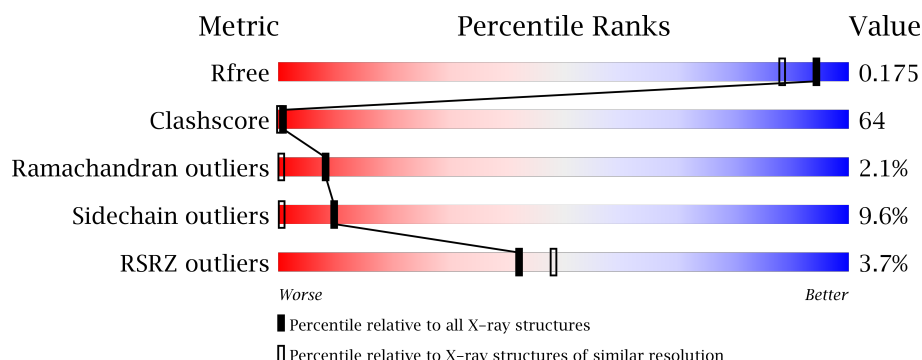
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.54 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	1773 (1.56-1.52)
Clashscore	112137	1845 (1.56-1.52)
Ramachandran outliers	110173	1810 (1.56-1.52)
Sidechain outliers	110143	1808 (1.56-1.52)
RSRZ outliers	101464	1774 (1.56-1.52)

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	575	<div> <div>5%</div> <div>26%</div> <div>63%</div> <div>9%</div> <div>..</div> </div>
1	D	575	<div> <div>4%</div> <div>22%</div> <div>66%</div> <div>10%</div> <div>..</div> </div>
2	B	223	<div> <div>3%</div> <div>27%</div> <div>63%</div> <div>5%</div> <div>.</div> </div>
2	C	223	<div> <div>2%</div> <div>36%</div> <div>53%</div> <div>6%</div> <div>.</div> </div>
2	E	223	<div> <div>0%</div> <div>27%</div> <div>63%</div> <div>5%</div> <div>.</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	223	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ILE	A	601	-	-	X	-
3	ILE	D	601	-	-	X	-
4	ATP	A	602	-	-	X	-
4	ATP	D	603	-	-	X	-
5	JAA	A	603	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 18113 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 Jasmonic acid-amido synthetase JAR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	569	Total	C	N	O	S	0	0	0
			4479	2859	748	850	22			
1	D	569	Total	C	N	O	S	0	0	0
			4479	2859	748	850	22			

- Molecule 2 is a protein called Glutathione S-transferase U20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1748	1136	284	323	5			
2	C	214	Total	C	N	O	S	0	0	0
			1748	1136	284	323	5			
2	E	214	Total	C	N	O	S	0	0	0
			1748	1136	284	323	5			
2	F	214	Total	C	N	O	S	0	0	0
			1748	1136	284	323	5			

There are 24 discrepancies between the modelled and reference sequences:

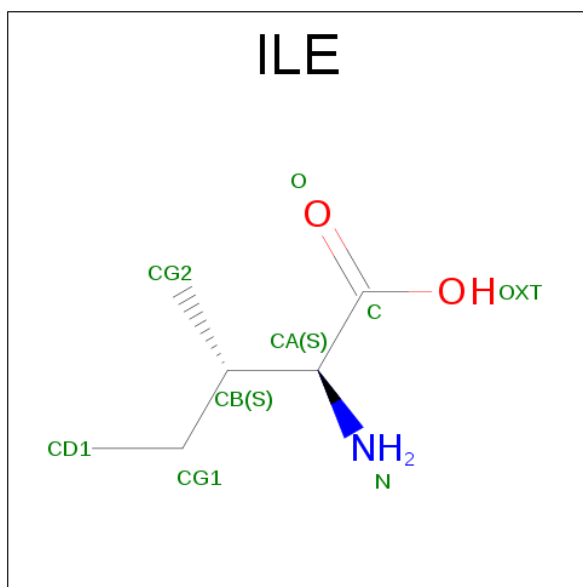
Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	expression tag	UNP Q8L7C9
B	-4	HIS	-	expression tag	UNP Q8L7C9
B	-3	HIS	-	expression tag	UNP Q8L7C9
B	-2	HIS	-	expression tag	UNP Q8L7C9
B	-1	HIS	-	expression tag	UNP Q8L7C9
B	0	HIS	-	expression tag	UNP Q8L7C9
C	-5	HIS	-	expression tag	UNP Q8L7C9
C	-4	HIS	-	expression tag	UNP Q8L7C9
C	-3	HIS	-	expression tag	UNP Q8L7C9
C	-2	HIS	-	expression tag	UNP Q8L7C9
C	-1	HIS	-	expression tag	UNP Q8L7C9
C	0	HIS	-	expression tag	UNP Q8L7C9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	HIS	-	expression tag	UNP Q8L7C9
E	-4	HIS	-	expression tag	UNP Q8L7C9
E	-3	HIS	-	expression tag	UNP Q8L7C9
E	-2	HIS	-	expression tag	UNP Q8L7C9
E	-1	HIS	-	expression tag	UNP Q8L7C9
E	0	HIS	-	expression tag	UNP Q8L7C9
F	-5	HIS	-	expression tag	UNP Q8L7C9
F	-4	HIS	-	expression tag	UNP Q8L7C9
F	-3	HIS	-	expression tag	UNP Q8L7C9
F	-2	HIS	-	expression tag	UNP Q8L7C9
F	-1	HIS	-	expression tag	UNP Q8L7C9
F	0	HIS	-	expression tag	UNP Q8L7C9

- Molecule 3 is ISOLEUCINE (three-letter code: ILE) (formula: $C_6H_{13}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	6	1	2		
3	D	1	Total	C	N	O	0	0
			9	6	1	2		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
4	D	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 5 is {(1R,2R)-3-oxo-2-[(2Z)-pent-2-en-1-yl]cyclopentyl}acetic acid (three-letter code: JAA) (formula: C₁₂H₁₈O₃).



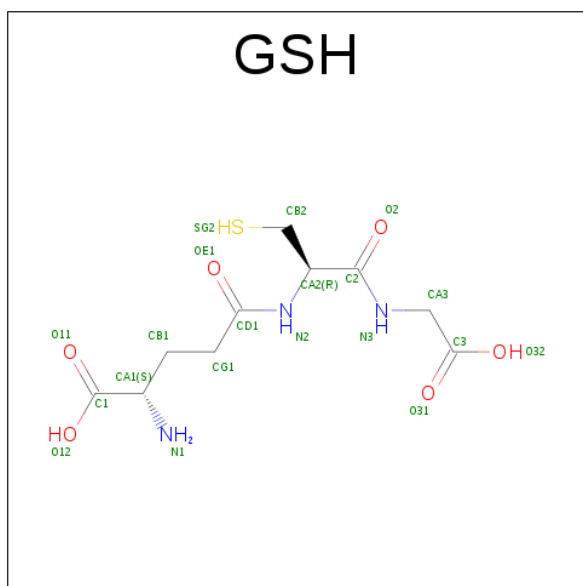
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			15	12	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			15	12	3		

- Molecule 6 is GLUTATHIONE (three-letter code: GSH) (formula: C₁₀H₁₇N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
6	C	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
6	E	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
6	F	1	Total	C	N	O	S	0	0
			20	10	3	6	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	453	Total	O	0	0
			453	453		
7	B	258	Total	O	0	0
			258	258		
7	C	230	Total	O	0	0
			230	230		
7	D	528	Total	O	0	0
			528	528		

Continued on next page...

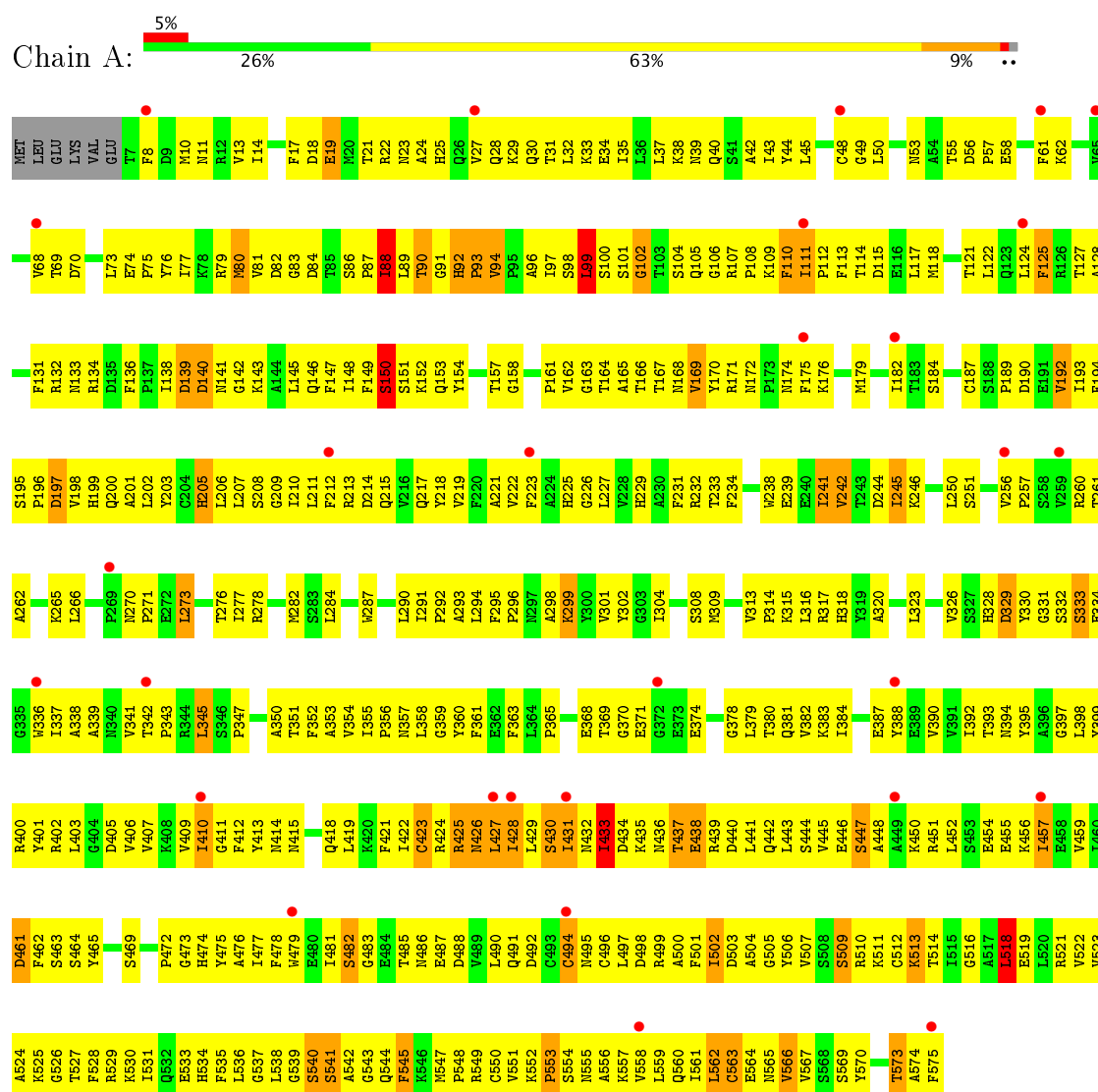
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	E	258	Total	O	0	0
			258	258		
7	F	246	Total	O	0	0
			246	246		

3 Residue-property plots

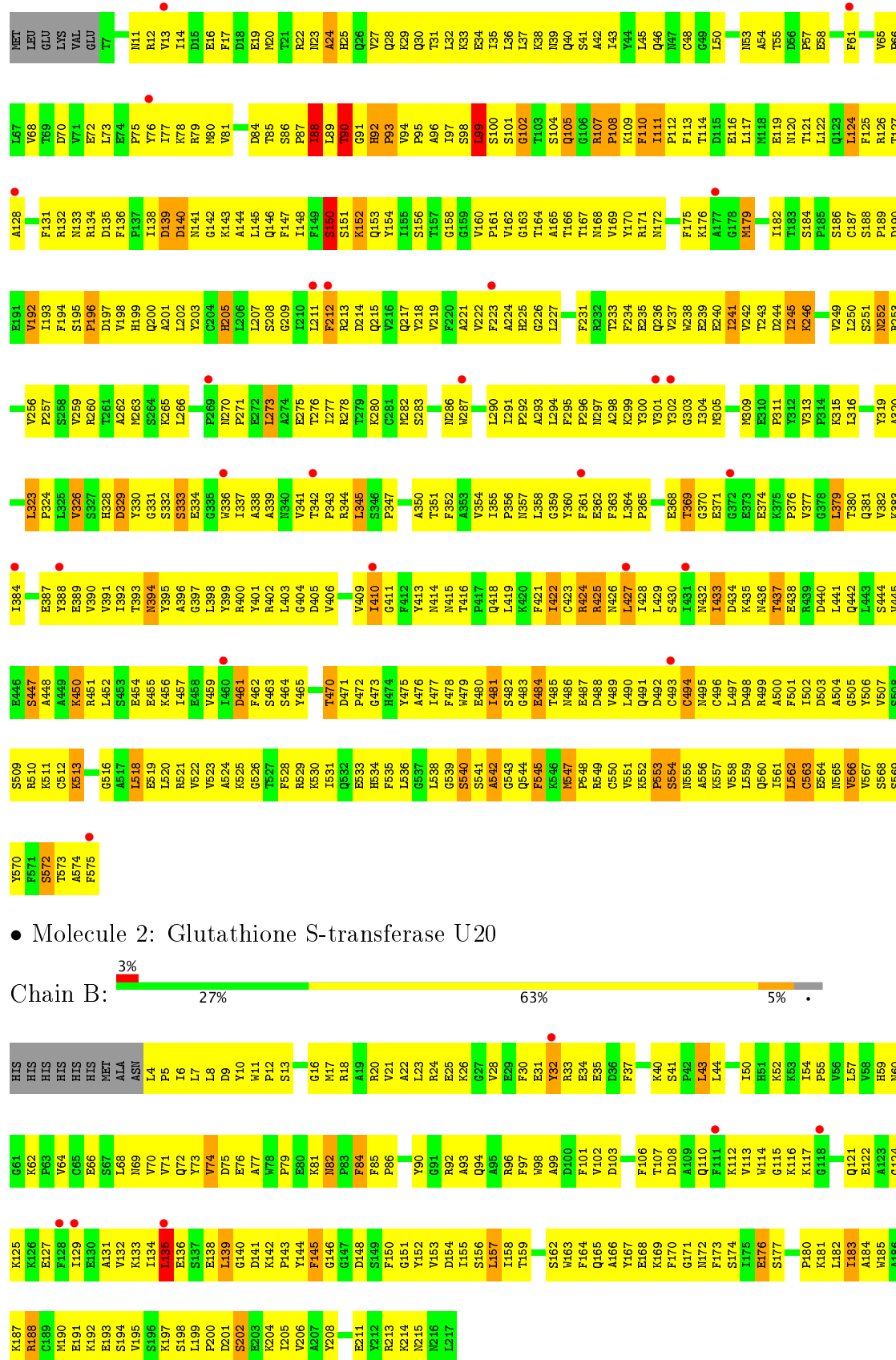
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ($RSRZ > 2$). 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.

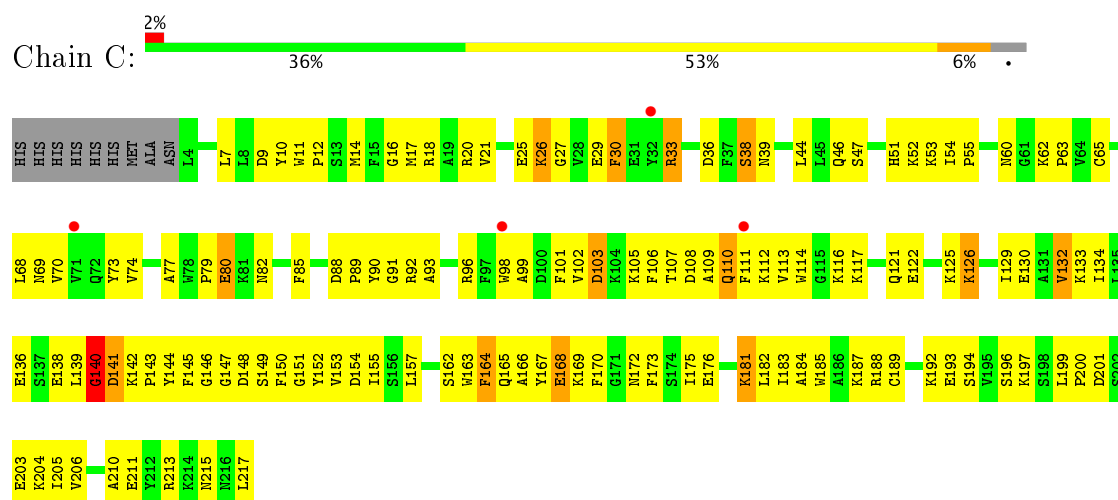
- Molecule 1: Jasmonic acid-amido synthetase JAR1



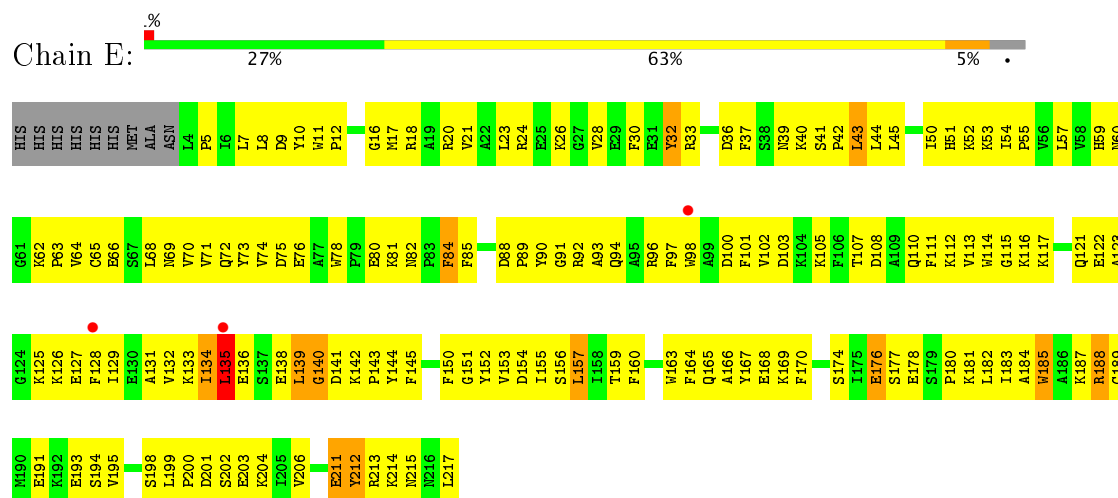
- Molecule 1: Jasmonic acid-amido synthetase JAR1



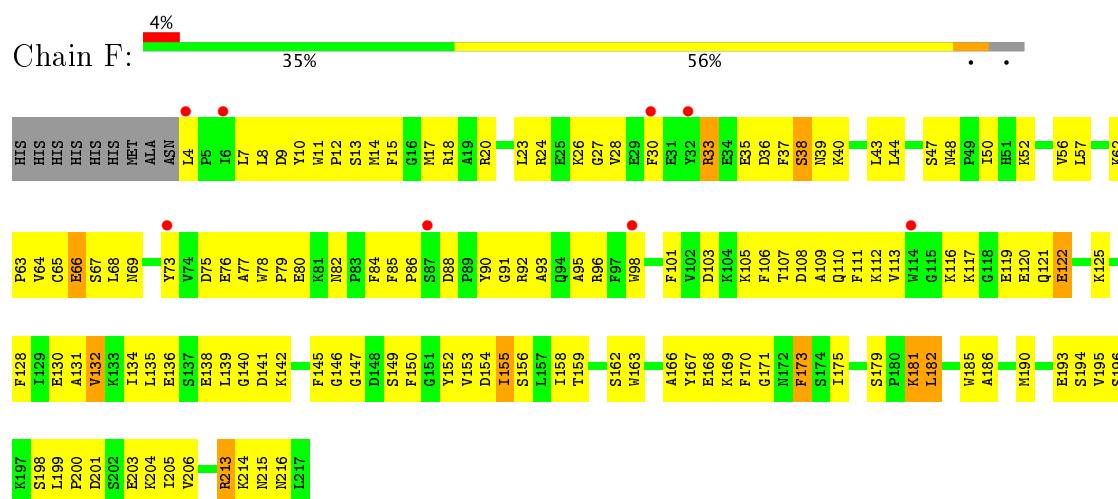




• Molecule 2: Glutathione S-transferase U20



• Molecule 2: Glutathione S-transferase U20



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.86Å 53.85Å 196.40Å 92.33° 97.16° 113.48°	Depositor
Resolution (Å)	24.24 – 1.54 24.24 – 1.47	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.24-1.54) 91.2 (24.24-1.47)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 1.47Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692+SVN)	Depositor
R, R_{free}	0.162 , 0.175 0.162 , 0.175	Depositor DCC
R_{free} test set	29521 reflections (10.02%)	DCC
Wilson B-factor (Å ²)	-1.6	Xtriage
Anisotropy	-0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.60 , 264.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.053 for k,h,-h-k-l 0.000 for -k,-h,l 0.000 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	18113	wwPDB-VP
Average B, all atoms (Å ²)	6.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 71.06 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.8038e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GSH, ATP, JAA

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	0.55	0/4581	0.79	4/6219 (0.1%)
1	D	0.56	0/4581	0.80	2/6219 (0.0%)
2	B	0.65	0/1799	0.81	3/2428 (0.1%)
2	C	0.54	0/1799	0.66	1/2428 (0.0%)
2	E	0.65	0/1799	0.77	3/2428 (0.1%)
2	F	0.57	0/1799	0.67	0/2428
All	All	0.58	0/16358	0.77	13/22150 (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	A	0	1
2	C	0	2
2	F	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	188	ARG	NE-CZ-NH1	-9.17	115.72	120.30
2	B	135	LEU	CB-CG-CD1	-8.81	96.02	111.00
2	E	188	ARG	NE-CZ-NH1	-8.56	116.02	120.30
1	A	99	LEU	CA-CB-CG	8.09	133.91	115.30
2	E	135	LEU	CB-CG-CD1	-7.24	98.70	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	427	LEU	Peptide
2	C	140	GLY	Peptide
2	C	165	GLN	Sidechain
2	F	140	GLY	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	4479	0	4433	617	2
1	D	4479	0	4433	707	2
2	B	1748	0	1704	247	1
2	C	1748	0	1704	175	0
2	E	1748	0	1704	235	1
2	F	1748	0	1704	161	1
3	A	9	0	10	11	0
3	D	9	0	10	6	0
4	A	31	0	2	21	0
4	D	31	0	2	21	0
5	A	15	0	0	7	0
5	D	15	0	0	5	0
6	B	20	0	15	0	0
6	C	20	0	15	1	0
6	E	20	0	15	4	0
6	F	20	0	15	1	0
7	A	453	0	0	90	5
7	B	258	0	0	68	3
7	C	230	0	0	45	4
7	D	528	0	0	146	4
7	E	258	0	0	52	1
7	F	246	0	0	39	2
All	All	18113	0	15766	2052	18

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 64.

The worst 5 of 2052 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:A:176:LYS:NZ	1:A:190:ASP:OD2	1.61	1.34
1:D:176:LYS:NZ	1:D:190:ASP:OD2	1.61	1.31
1:D:456:LYS:NZ	2:E:201:ASP:OD2	1.79	1.15
1:D:107:ARG:HH11	1:D:107:ARG:HG3	1.02	1.13
1:D:499:ARG:O	2:E:188:ARG:NH1	1.85	1.09

The worst 5 of 18 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:D:270:ASN:O	1:D:511:LYS:NZ[1_565]	2.00	0.20
1:A:278:ARG:NH2	2:B:141:ASP:OD2[1_565]	2.05	0.15
1:A:270:ASN:ND2	1:A:510:ARG:O[1_565]	2.07	0.13
7:D:979:HOH:O	7:D:1014:HOH:O[1_445]	2.09	0.11
7:A:924:HOH:O	7:A:929:HOH:O[1_545]	2.10	0.10

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	567/575 (99%)	506 (89%)	47 (8%)	14 (2%)	6	0
1	D	567/575 (99%)	505 (89%)	43 (8%)	19 (3%)	4	0
2	B	212/223 (95%)	196 (92%)	14 (7%)	2 (1%)	20	3
2	C	212/223 (95%)	199 (94%)	10 (5%)	3 (1%)	13	1
2	E	212/223 (95%)	192 (91%)	19 (9%)	1 (0%)	32	9
2	F	212/223 (95%)	196 (92%)	14 (7%)	2 (1%)	20	3
All	All	1982/2042 (97%)	1794 (90%)	147 (7%)	41 (2%)	8	0

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	THR
1	A	513	LYS
1	A	540	SER
1	A	542	ALA
1	D	369	THR

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	499/505 (99%)	444 (89%)	55 (11%)	7	0
1	D	499/505 (99%)	444 (89%)	55 (11%)	7	0
2	B	187/195 (96%)	171 (91%)	16 (9%)	12	1
2	C	187/195 (96%)	172 (92%)	15 (8%)	14	1
2	E	187/195 (96%)	173 (92%)	14 (8%)	16	1
2	F	187/195 (96%)	174 (93%)	13 (7%)	18	1
All	All	1746/1790 (98%)	1578 (90%)	168 (10%)	10	0

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	46	GLN
1	D	111	ILE
2	F	33	ARG
2	C	110	GLN
2	C	197	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	72	GLN
2	C	121	GLN
1	D	495	ASN
2	C	51	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	544	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
3	ILE	A	601	-	5,8,8	0.64	0	4,10,10	0.52	0
4	ATP	A	602	-	27,33,33	4.62	17 (62%)	25,52,52	3.90	11 (44%)
5	JAA	A	603	-	12,15,15	5.85	7 (58%)	12,19,19	2.75	7 (58%)
6	GSH	B	301	-	11,19,19	1.70	4 (36%)	14,24,24	2.81	5 (35%)
6	GSH	C	301	-	11,19,19	1.72	4 (36%)	14,24,24	3.07	8 (57%)
3	ILE	D	601	-	5,8,8	0.45	0	4,10,10	0.43	0
5	JAA	D	602	-	12,15,15	5.88	7 (58%)	12,19,19	2.82	8 (66%)
4	ATP	D	603	-	27,33,33	4.82	14 (51%)	25,52,52	3.80	9 (36%)
6	GSH	E	301	-	11,19,19	1.59	3 (27%)	14,24,24	3.33	7 (50%)
6	GSH	F	301	-	11,19,19	1.67	4 (36%)	14,24,24	2.72	7 (50%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ILE	A	601	-	-	0/6/10/10	0/0/0/0
4	ATP	A	602	-	-	0/18/38/38	0/3/3/3
5	JAA	A	603	-	-	0/7/22/22	0/1/1/1
6	GSH	B	301	-	-	0/18/24/24	0/0/0/0
6	GSH	C	301	-	-	0/18/24/24	0/0/0/0
3	ILE	D	601	-	-	0/6/10/10	0/0/0/0
5	JAA	D	602	-	-	0/7/22/22	0/1/1/1
4	ATP	D	603	-	-	0/18/38/38	0/3/3/3
6	GSH	E	301	-	-	0/18/24/24	0/0/0/0
6	GSH	F	301	-	-	0/18/24/24	0/0/0/0

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	602	JAA	C05-C08	-13.91	1.30	1.52
5	A	603	JAA	C05-C08	-13.08	1.31	1.52
4	D	603	ATP	C5'-C4'	-11.27	1.16	1.51
4	A	602	ATP	C5'-C4'	-11.01	1.16	1.51
5	A	603	JAA	C06-C04	-10.86	1.25	1.53

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	602	ATP	C4-C5-N7	-11.04	98.74	109.41
4	D	603	ATP	C4-C5-N7	-10.44	99.33	109.41
4	D	603	ATP	C4'-O4'-C1'	-9.13	100.05	109.77
4	A	602	ATP	N3-C2-N1	-9.10	120.93	128.86
6	E	301	GSH	CA3-N3-C2	-8.64	110.69	122.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	ILE	11	0
4	A	602	ATP	21	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	603	JAA	7	0
6	C	301	GSH	1	0
3	D	601	ILE	6	0
5	D	602	JAA	5	0
4	D	603	ATP	21	0
6	E	301	GSH	4	0
6	F	301	GSH	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	569/575 (98%)	0.77	29 (5%)	29 32	3, 7, 7, 16	0
1	D	569/575 (98%)	0.77	24 (4%)	37 41	3, 7, 7, 16	0
2	B	214/223 (95%)	0.59	6 (2%)	53 60	2, 3, 7, 11	0
2	C	214/223 (95%)	0.78	4 (1%)	67 72	7, 7, 7, 7	0
2	E	214/223 (95%)	0.57	3 (1%)	75 79	2, 3, 7, 11	0
2	F	214/223 (95%)	0.75	8 (3%)	42 48	7, 7, 7, 7	0
All	All	1994/2042 (97%)	0.73	74 (3%)	42 48	2, 7, 7, 16	0

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	427	LEU	4.2
1	D	212	PHE	3.3
2	B	129	ILE	3.0
1	D	372	GLY	2.9
1	A	431	ILE	2.9

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(Å ²)	Q<0.9
6	GSH	B	301	20/20	0.96	0.12	0.78	6,7,7,7	0
5	JAA	D	602	15/15	0.96	0.13	0.63	6,7,7,7	0
6	GSH	E	301	20/20	0.96	0.12	0.19	6,6,7,7	0
4	ATP	D	603	31/31	0.96	0.12	0.16	6,7,7,7	0
6	GSH	C	301	20/20	0.97	0.13	-0.07	6,7,7,7	0
5	JAA	A	603	15/15	0.96	0.12	-0.09	6,7,7,7	0
4	ATP	A	602	31/31	0.96	0.11	-0.32	6,7,7,7	0
3	ILE	D	601	9/9	0.97	0.12	-0.33	6,6,7,7	0
6	GSH	F	301	20/20	0.97	0.12	-0.62	6,7,7,7	0
3	ILE	A	601	9/9	0.97	0.11	-1.07	6,6,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.