



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 04:20 am BST

PDB ID : 3ZQJ
Title : Mycobacterium tuberculosis UvrA
Authors : Rossi, F.; Khanduja, J.S.; Bortoluzzi, A.; Houghton, J.; Sander, P.; Guthlein, C.; Davis, E.O.; Springer, B.; Bottger, E.C.; Relini, A.; Penco, A.; Muniyappa, K.; Rizzi, M.
Deposited on : 2011-06-09
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

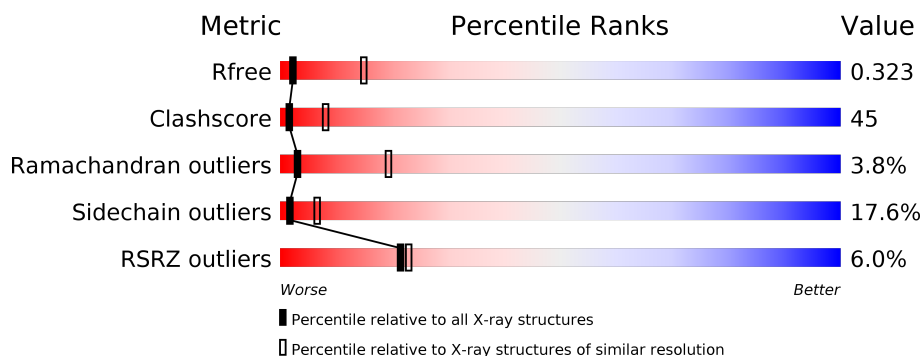
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 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	993	<div> <div>5%</div> <div> <div>42%</div> <div>42%</div> <div>10%</div> <div>• 5%</div> </div> </div>
1	B	993	<div> <div>5%</div> <div> <div>41%</div> <div>41%</div> <div>10%</div> <div>• 8%</div> </div> </div>
1	C	993	<div> <div>4%</div> <div> <div>39%</div> <div>39%</div> <div>10%</div> <div>• 10%</div> </div> </div>
1	D	993	<div> <div>7%</div> <div> <div>39%</div> <div>43%</div> <div>10%</div> <div>• 7%</div> </div> </div>
1	E	993	<div> <div>7%</div> <div> <div>40%</div> <div>41%</div> <div>11%</div> <div>• 7%</div> </div> </div>
1	F	993	<div> <div>5%</div> <div> <div>18%</div> <div>32%</div> <div>10%</div> <div>• 39%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 39998 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 UVRABC SYSTEM PROTEIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	944	Total	C	N	O	S	0	0	0
			7267	4550	1310	1385	22			
1	B	918	Total	C	N	O	S	0	0	0
			7067	4428	1272	1345	22			
1	C	890	Total	C	N	O	S	0	0	0
			6832	4277	1234	1299	22			
1	D	921	Total	C	N	O	S	0	0	0
			7095	4444	1276	1353	22			
1	E	919	Total	C	N	O	S	0	0	0
			7073	4434	1271	1347	21			
1	F	607	Total	C	N	O	S	0	0	0
			4650	2906	844	890	10			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P63380
A	-19	GLY	-	expression tag	UNP P63380
A	-18	HIS	-	expression tag	UNP P63380
A	-17	HIS	-	expression tag	UNP P63380
A	-16	HIS	-	expression tag	UNP P63380
A	-15	HIS	-	expression tag	UNP P63380
A	-14	HIS	-	expression tag	UNP P63380
A	-13	HIS	-	expression tag	UNP P63380
A	-12	HIS	-	expression tag	UNP P63380
A	-11	HIS	-	expression tag	UNP P63380
A	-10	HIS	-	expression tag	UNP P63380
A	-9	HIS	-	expression tag	UNP P63380
A	-8	SER	-	expression tag	UNP P63380
A	-7	SER	-	expression tag	UNP P63380
A	-6	GLY	-	expression tag	UNP P63380
A	-5	HIS	-	expression tag	UNP P63380
A	-4	ILE	-	expression tag	UNP P63380

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLU	-	expression tag	UNP P63380
A	-2	GLY	-	expression tag	UNP P63380
A	-1	ARG	-	expression tag	UNP P63380
A	0	HIS	-	expression tag	UNP P63380
B	-20	MET	-	expression tag	UNP P63380
B	-19	GLY	-	expression tag	UNP P63380
B	-18	HIS	-	expression tag	UNP P63380
B	-17	HIS	-	expression tag	UNP P63380
B	-16	HIS	-	expression tag	UNP P63380
B	-15	HIS	-	expression tag	UNP P63380
B	-14	HIS	-	expression tag	UNP P63380
B	-13	HIS	-	expression tag	UNP P63380
B	-12	HIS	-	expression tag	UNP P63380
B	-11	HIS	-	expression tag	UNP P63380
B	-10	HIS	-	expression tag	UNP P63380
B	-9	HIS	-	expression tag	UNP P63380
B	-8	SER	-	expression tag	UNP P63380
B	-7	SER	-	expression tag	UNP P63380
B	-6	GLY	-	expression tag	UNP P63380
B	-5	HIS	-	expression tag	UNP P63380
B	-4	ILE	-	expression tag	UNP P63380
B	-3	GLU	-	expression tag	UNP P63380
B	-2	GLY	-	expression tag	UNP P63380
B	-1	ARG	-	expression tag	UNP P63380
B	0	HIS	-	expression tag	UNP P63380
C	-20	MET	-	expression tag	UNP P63380
C	-19	GLY	-	expression tag	UNP P63380
C	-18	HIS	-	expression tag	UNP P63380
C	-17	HIS	-	expression tag	UNP P63380
C	-16	HIS	-	expression tag	UNP P63380
C	-15	HIS	-	expression tag	UNP P63380
C	-14	HIS	-	expression tag	UNP P63380
C	-13	HIS	-	expression tag	UNP P63380
C	-12	HIS	-	expression tag	UNP P63380
C	-11	HIS	-	expression tag	UNP P63380
C	-10	HIS	-	expression tag	UNP P63380
C	-9	HIS	-	expression tag	UNP P63380
C	-8	SER	-	expression tag	UNP P63380
C	-7	SER	-	expression tag	UNP P63380
C	-6	GLY	-	expression tag	UNP P63380
C	-5	HIS	-	expression tag	UNP P63380
C	-4	ILE	-	expression tag	UNP P63380

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLU	-	expression tag	UNP P63380
C	-2	GLY	-	expression tag	UNP P63380
C	-1	ARG	-	expression tag	UNP P63380
C	0	HIS	-	expression tag	UNP P63380
D	-20	MET	-	expression tag	UNP P63380
D	-19	GLY	-	expression tag	UNP P63380
D	-18	HIS	-	expression tag	UNP P63380
D	-17	HIS	-	expression tag	UNP P63380
D	-16	HIS	-	expression tag	UNP P63380
D	-15	HIS	-	expression tag	UNP P63380
D	-14	HIS	-	expression tag	UNP P63380
D	-13	HIS	-	expression tag	UNP P63380
D	-12	HIS	-	expression tag	UNP P63380
D	-11	HIS	-	expression tag	UNP P63380
D	-10	HIS	-	expression tag	UNP P63380
D	-9	HIS	-	expression tag	UNP P63380
D	-8	SER	-	expression tag	UNP P63380
D	-7	SER	-	expression tag	UNP P63380
D	-6	GLY	-	expression tag	UNP P63380
D	-5	HIS	-	expression tag	UNP P63380
D	-4	ILE	-	expression tag	UNP P63380
D	-3	GLU	-	expression tag	UNP P63380
D	-2	GLY	-	expression tag	UNP P63380
D	-1	ARG	-	expression tag	UNP P63380
D	0	HIS	-	expression tag	UNP P63380
E	-20	MET	-	expression tag	UNP P63380
E	-19	GLY	-	expression tag	UNP P63380
E	-18	HIS	-	expression tag	UNP P63380
E	-17	HIS	-	expression tag	UNP P63380
E	-16	HIS	-	expression tag	UNP P63380
E	-15	HIS	-	expression tag	UNP P63380
E	-14	HIS	-	expression tag	UNP P63380
E	-13	HIS	-	expression tag	UNP P63380
E	-12	HIS	-	expression tag	UNP P63380
E	-11	HIS	-	expression tag	UNP P63380
E	-10	HIS	-	expression tag	UNP P63380
E	-9	HIS	-	expression tag	UNP P63380
E	-8	SER	-	expression tag	UNP P63380
E	-7	SER	-	expression tag	UNP P63380
E	-6	GLY	-	expression tag	UNP P63380
E	-5	HIS	-	expression tag	UNP P63380
E	-4	ILE	-	expression tag	UNP P63380

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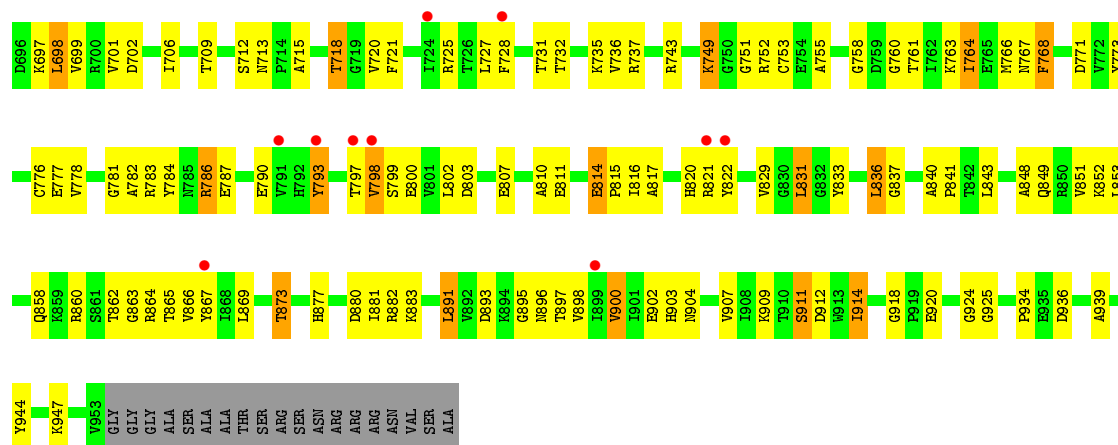
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLU	-	expression tag	UNP P63380
E	-2	GLY	-	expression tag	UNP P63380
E	-1	ARG	-	expression tag	UNP P63380
E	0	HIS	-	expression tag	UNP P63380
F	-20	MET	-	expression tag	UNP P63380
F	-19	GLY	-	expression tag	UNP P63380
F	-18	HIS	-	expression tag	UNP P63380
F	-17	HIS	-	expression tag	UNP P63380
F	-16	HIS	-	expression tag	UNP P63380
F	-15	HIS	-	expression tag	UNP P63380
F	-14	HIS	-	expression tag	UNP P63380
F	-13	HIS	-	expression tag	UNP P63380
F	-12	HIS	-	expression tag	UNP P63380
F	-11	HIS	-	expression tag	UNP P63380
F	-10	HIS	-	expression tag	UNP P63380
F	-9	HIS	-	expression tag	UNP P63380
F	-8	SER	-	expression tag	UNP P63380
F	-7	SER	-	expression tag	UNP P63380
F	-6	GLY	-	expression tag	UNP P63380
F	-5	HIS	-	expression tag	UNP P63380
F	-4	ILE	-	expression tag	UNP P63380
F	-3	GLU	-	expression tag	UNP P63380
F	-2	GLY	-	expression tag	UNP P63380
F	-1	ARG	-	expression tag	UNP P63380
F	0	HIS	-	expression tag	UNP P63380

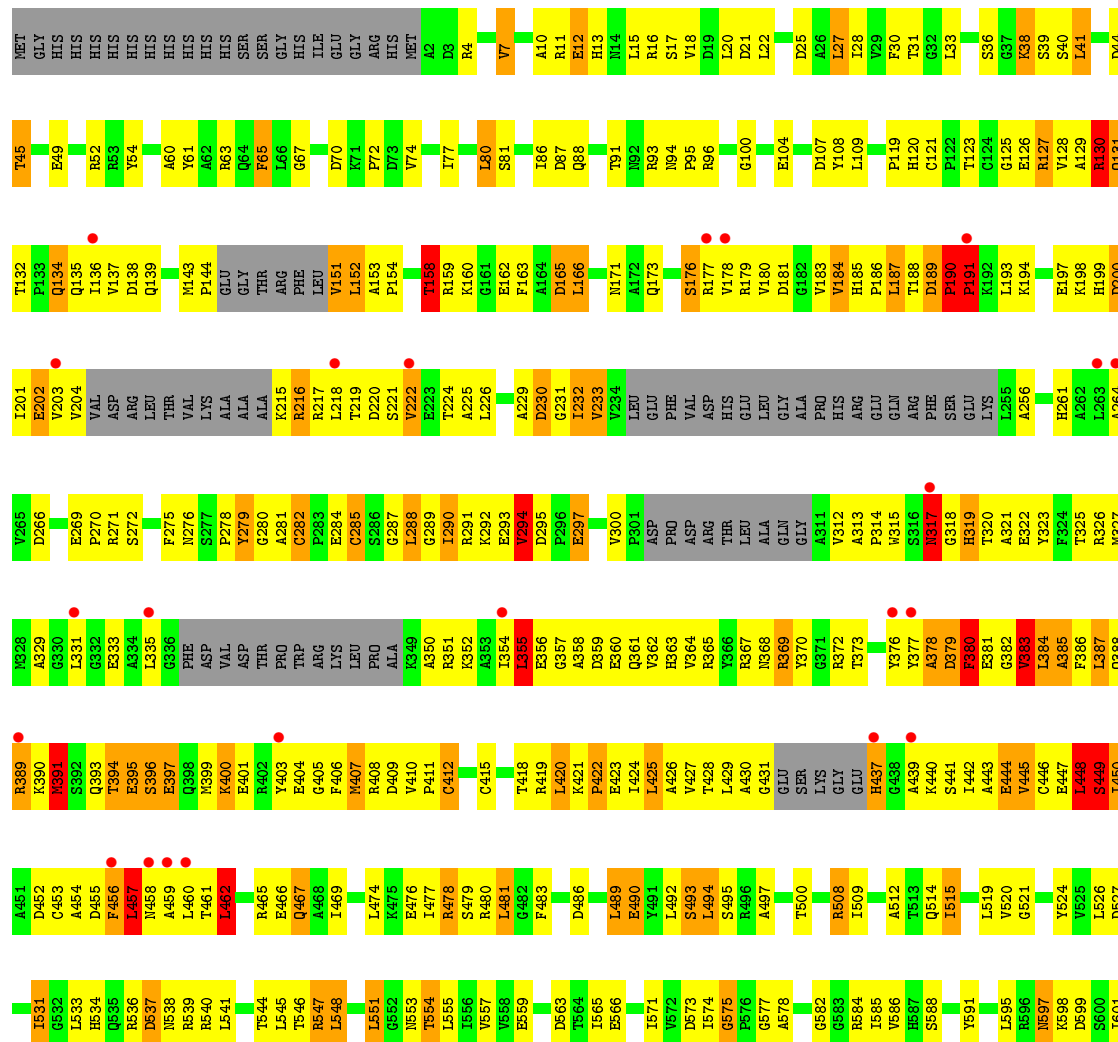
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

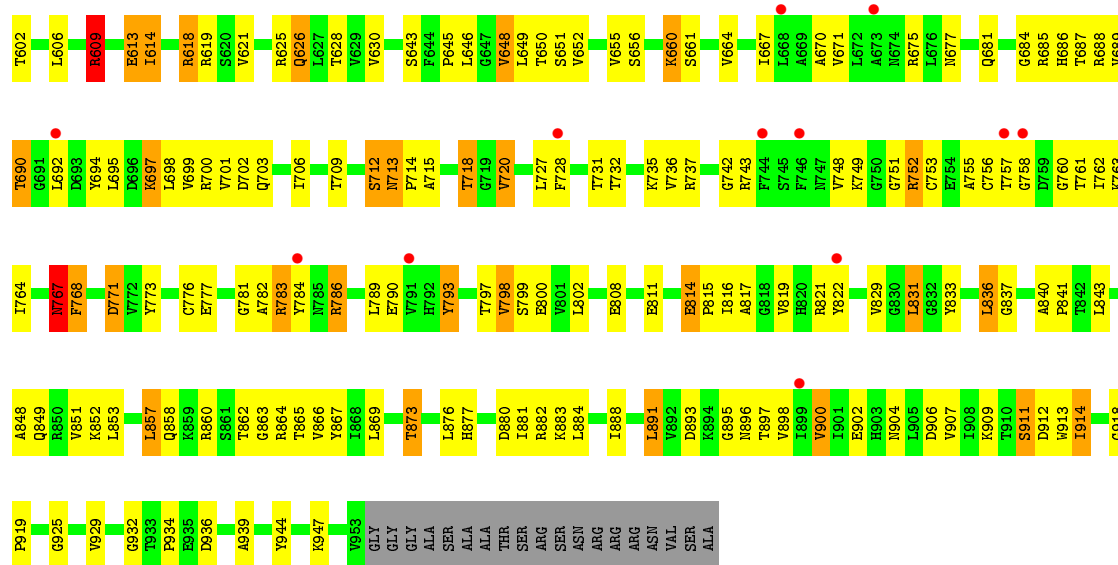
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total 3	Zn 3	0	0
2	A	3	Total 3	Zn 3	0	0
2	D	3	Total 3	Zn 3	0	0
2	C	3	Total 3	Zn 3	0	0
2	E	2	Total 2	Zn 2	0	0



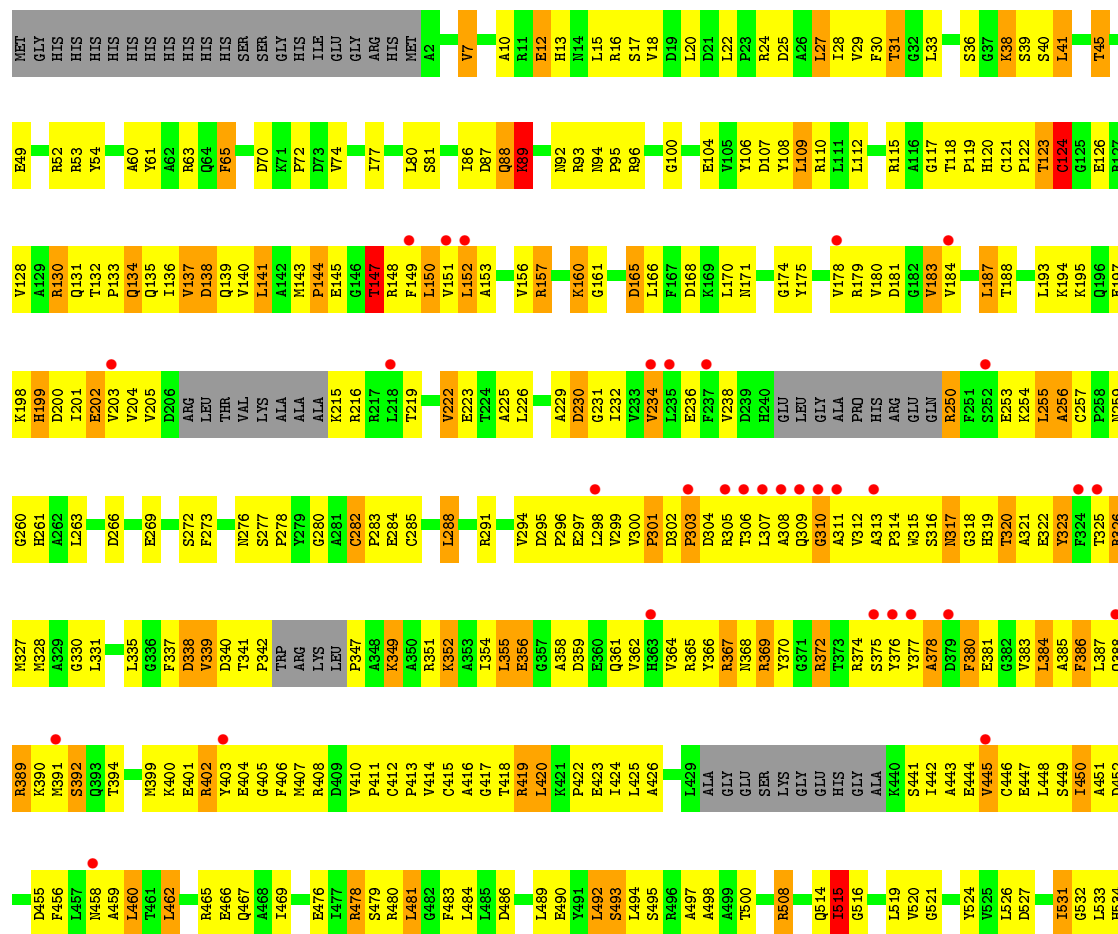


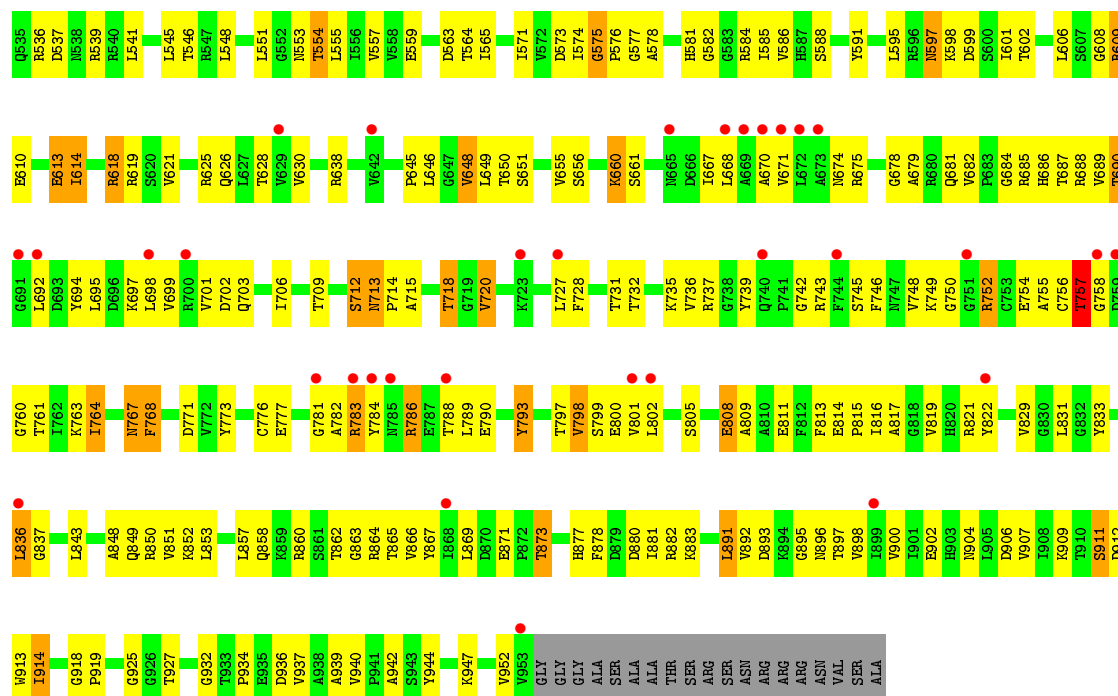
• Molecule 1: UVRABC SYSTEM PROTEIN A



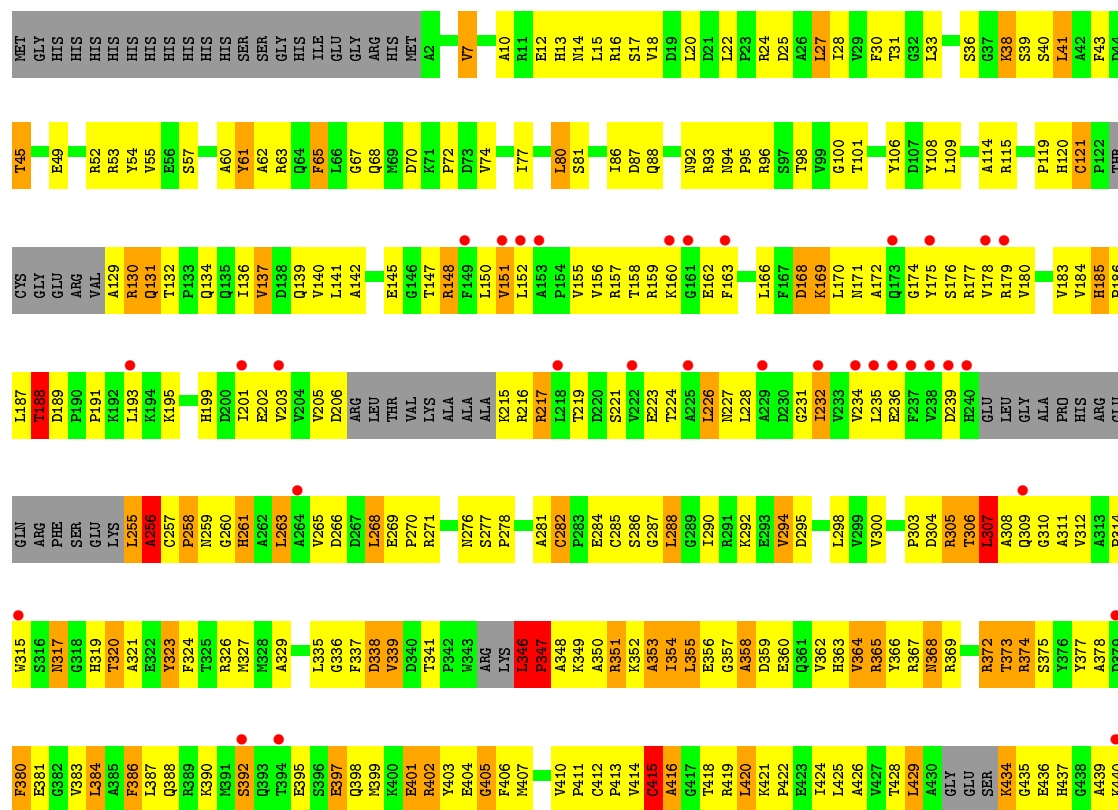


• Molecule 1: UVRABC SYSTEM PROTEIN A





• Molecule 1: UVRABC SYSTEM PROTEIN A







4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	258.23Å 258.23Å 204.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.40 84.52 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.40) 98.5 (84.52-3.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 3.41Å)	Xtriage
Refinement program	REFMAC 5.5.0044	Depositor
R, R_{free}	0.273 , 0.324 0.268 , 0.323	Depositor DCC
R_{free} test set	1067 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	83.7	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 69.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	39998	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.18% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.72	5/7394 (0.1%)	0.95	28/10021 (0.3%)
1	B	0.71	3/7190 (0.0%)	0.87	20/9741 (0.2%)
1	C	0.70	2/6945 (0.0%)	0.87	17/9406 (0.2%)
1	D	0.77	6/7217 (0.1%)	0.87	12/9779 (0.1%)
1	E	0.73	2/7196 (0.0%)	0.91	19/9753 (0.2%)
1	F	0.68	2/4721 (0.0%)	0.92	11/6385 (0.2%)
All	All	0.72	20/40663 (0.0%)	0.90	107/55085 (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	A	0	6
1	B	0	1
1	C	0	6
1	D	0	4
1	E	0	4
1	F	0	6
All	All	0	27

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	256	ALA	C-N	-13.62	1.02	1.34
1	D	124	CYS	C-N	12.92	1.56	1.33
1	D	126	GLU	C-N	-11.61	1.07	1.34
1	B	120	HIS	C-N	-11.33	1.07	1.34
1	A	415	CYS	C-N	11.23	1.59	1.34

The worst 5 of 107 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	478	ARG	NE-CZ-NH1	17.05	128.83	120.30
1	A	478	ARG	NE-CZ-NH2	-16.13	112.23	120.30
1	A	752	ARG	NE-CZ-NH2	-14.18	113.21	120.30
1	A	752	ARG	NE-CZ-NH1	13.59	127.09	120.30
1	E	307	LEU	CB-CA-C	-12.39	86.66	110.20

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	11	ARG	Mainchain
1	A	148	ARG	Sidechain
1	A	213	ALA	Peptide
1	A	373	THR	Peptide
1	A	411	PRO	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7267	0	7280	633	1
1	B	7067	0	7080	707	3
1	C	6832	0	6855	556	0
1	D	7095	0	7100	590	0
1	E	7073	0	7081	602	4
1	F	4650	0	4667	567	1
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	2	0	0	0	0
All	All	39998	0	40063	3590	5

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 45.

The worst 5 of 3590 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:E:442:ILE:HA	1:E:495:SER:CB	1.23	1.62
1:B:299:VAL:HG23	1:B:313:ALA:CB	1.23	1.58
1:D:305:ARG:HA	1:D:311:ALA:CB	1.28	1.57
1:B:299:VAL:CG2	1:B:313:ALA:HB2	1.29	1.56
1:F:412:CYS:SG	1:F:414:VAL:HG22	1.47	1.52

All (5) 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:E:597:ASN:OD1	1:F:16:ARG:NH1[4_554]	2.07	0.13
1:B:398:GLN:OE1	1:E:366:TYR:CB[6_444]	2.09	0.11
1:B:398:GLN:OE1	1:E:366:TYR:CD2[6_444]	2.09	0.11
1:B:398:GLN:OE1	1:E:366:TYR:CG[6_444]	2.09	0.11
1:A:61:TYR:CE2	1:A:767:ASN:O[4_555]	2.10	0.10

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	940/993 (95%)	814 (87%)	105 (11%)	21 (2%)	6	29
1	B	910/993 (92%)	768 (84%)	112 (12%)	30 (3%)	4	22
1	C	876/993 (88%)	730 (83%)	109 (12%)	37 (4%)	3	18
1	D	911/993 (92%)	758 (83%)	123 (14%)	30 (3%)	4	22
1	E	907/993 (91%)	750 (83%)	128 (14%)	29 (3%)	4	22
1	F	595/993 (60%)	449 (76%)	98 (16%)	48 (8%)	1	5
All	All	5139/5958 (86%)	4269 (83%)	675 (13%)	195 (4%)	3	19

5 of 195 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	VAL
1	A	300	VAL
1	A	301	PRO
1	A	382	GLY
1	A	457	LEU

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	778/815 (96%)	648 (83%)	130 (17%)	2	8
1	B	758/815 (93%)	640 (84%)	118 (16%)	2	11
1	C	732/815 (90%)	594 (81%)	138 (19%)	1	4
1	D	763/815 (94%)	642 (84%)	121 (16%)	2	10
1	E	758/815 (93%)	616 (81%)	142 (19%)	1	5
1	F	492/815 (60%)	386 (78%)	106 (22%)	1	3
All	All	4281/4890 (88%)	3526 (82%)	755 (18%)	2	6

5 of 755 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	563	ASP
1	D	263	LEU
1	F	492	LEU
1	C	685	ARG
1	C	911	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	437	HIS
1	D	120	HIS
1	F	92	ASN
1	C	458	ASN

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Mol	Chain	Res	Type
1	C	681	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	3
1	A	2
1	B	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	260:GLY	C	261:HIS	N	1.19
1	A	11:ARG	C	12:GLU	N	1.15
1	A	411:PRO	C	412:CYS	N	1.11
1	B	120:HIS	C	121:CYS	N	1.08
1	D	126:GLU	C	127:ARG	N	1.07

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	944/993 (95%)	0.47	46 (4%) 29 29	16, 55, 94, 112	0
1	B	918/993 (92%)	0.44	53 (5%) 23 24	16, 57, 102, 111	0
1	C	890/993 (89%)	0.37	35 (3%) 39 38	16, 60, 108, 118	0
1	D	921/993 (92%)	0.43	65 (7%) 16 18	16, 60, 103, 114	0
1	E	919/993 (92%)	0.46	68 (7%) 14 16	16, 57, 102, 127	0
1	F	607/993 (61%)	0.53	45 (7%) 14 16	45, 79, 112, 117	0
All	All	5199/5958 (87%)	0.44	312 (6%) 21 23	16, 61, 104, 127	0

The worst 5 of 312 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	357	GLY	7.0
1	E	239	ASP	6.8
1	D	235	LEU	6.7
1	A	308	ALA	6.5
1	A	307	LEU	6.1

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. 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(\AA^2)	Q<0.9
2	ZN	A	1954	1/1	0.75	0.20	65,65,65,65	0
2	ZN	B	1955	1/1	0.80	0.26	116,116,116,116	0
2	ZN	A	1955	1/1	0.83	0.21	116,116,116,116	0
2	ZN	E	1955	1/1	0.85	0.24	116,116,116,116	0
2	ZN	D	1955	1/1	0.89	0.23	116,116,116,116	0
2	ZN	C	1955	1/1	0.93	0.23	116,116,116,116	0
2	ZN	A	1956	1/1	0.94	0.21	48,48,48,48	0
2	ZN	B	1956	1/1	0.95	0.19	44,44,44,44	0
2	ZN	B	1954	1/1	0.95	0.21	65,65,65,65	0
2	ZN	D	1954	1/1	0.96	0.13	66,66,66,66	0
2	ZN	E	1954	1/1	0.98	0.17	66,66,66,66	0
2	ZN	D	1956	1/1	0.99	0.16	59,59,59,59	0
2	ZN	C	1954	1/1	0.99	0.17	65,65,65,65	0
2	ZN	C	1956	1/1	0.99	0.18	76,76,76,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.