



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 21, 2024 – 08:21 PM EDT

PDB ID : 3D01
Title : Crystal structure of the protein Atu1372 with unknown function from *Agrobacterium tumefaciens*
Authors : Zhang, R.; Xu, X.; Gu, J.; Savchenko, A.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2008-04-30
Resolution : 1.70 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 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

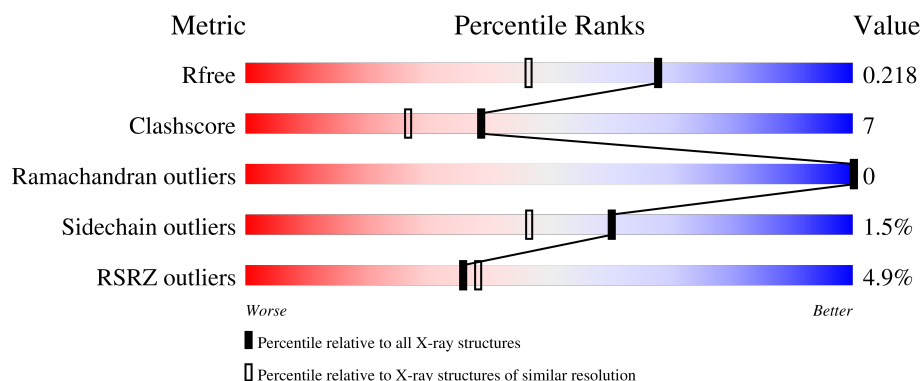
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	165	 5% 85% 10% • 5%
1	B	165	 2% 86% 8% • 5%
1	C	165	 5% 84% 10% • 5%
1	D	165	 4% 88% 5% • 5%
1	E	165	 3% 83% 10% • 6%

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Mol	Chain	Length	Quality of chain
1	F	165	
1	G	165	
1	H	165	
1	I	165	
1	J	165	
1	K	165	
1	L	165	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PG5	F	166	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15234 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 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	158	Total	C	N	O	S	Se	0	0	0
			1170	744	202	220	1	3			
1	B	157	Total	C	N	O	S	Se	0	0	0
			1163	740	201	218	1	3			
1	C	157	Total	C	N	O	S	Se	0	0	0
			1167	742	201	220	1	3			
1	D	156	Total	C	N	O	S	Se	0	0	0
			1159	738	200	217	1	3			
1	E	155	Total	C	N	O	S	Se	0	0	0
			1151	732	199	216	1	3			
1	F	158	Total	C	N	O	S	Se	0	0	0
			1174	746	202	222	1	3			
1	G	157	Total	C	N	O	S	Se	0	0	0
			1164	740	201	219	1	3			
1	H	157	Total	C	N	O	S	Se	0	0	0
			1167	742	201	220	1	3			
1	I	159	Total	C	N	O	S	Se	0	0	0
			1179	749	203	223	1	3			
1	J	157	Total	C	N	O	S	Se	0	0	0
			1167	742	201	220	1	3			
1	K	157	Total	C	N	O	S	Se	0	0	0
			1169	743	201	221	1	3			
1	L	160	Total	C	N	O	S	Se	0	0	0
			1186	754	204	224	1	3			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A9CJ63
A	2	THR	-	expression tag	UNP A9CJ63
A	3	GLU	-	expression tag	UNP A9CJ63
A	4	ASN	-	expression tag	UNP A9CJ63
A	5	LEU	-	expression tag	UNP A9CJ63

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Chain	Residue	Modelled	Actual	Comment	Reference
A	6	TYR	-	expression tag	UNP A9CJ63
A	7	PHE	-	expression tag	UNP A9CJ63
A	8	GLN	-	expression tag	UNP A9CJ63
A	9	GLY	-	expression tag	UNP A9CJ63
B	1	GLY	-	expression tag	UNP A9CJ63
B	2	THR	-	expression tag	UNP A9CJ63
B	3	GLU	-	expression tag	UNP A9CJ63
B	4	ASN	-	expression tag	UNP A9CJ63
B	5	LEU	-	expression tag	UNP A9CJ63
B	6	TYR	-	expression tag	UNP A9CJ63
B	7	PHE	-	expression tag	UNP A9CJ63
B	8	GLN	-	expression tag	UNP A9CJ63
B	9	GLY	-	expression tag	UNP A9CJ63
C	1	GLY	-	expression tag	UNP A9CJ63
C	2	THR	-	expression tag	UNP A9CJ63
C	3	GLU	-	expression tag	UNP A9CJ63
C	4	ASN	-	expression tag	UNP A9CJ63
C	5	LEU	-	expression tag	UNP A9CJ63
C	6	TYR	-	expression tag	UNP A9CJ63
C	7	PHE	-	expression tag	UNP A9CJ63
C	8	GLN	-	expression tag	UNP A9CJ63
C	9	GLY	-	expression tag	UNP A9CJ63
D	1	GLY	-	expression tag	UNP A9CJ63
D	2	THR	-	expression tag	UNP A9CJ63
D	3	GLU	-	expression tag	UNP A9CJ63
D	4	ASN	-	expression tag	UNP A9CJ63
D	5	LEU	-	expression tag	UNP A9CJ63
D	6	TYR	-	expression tag	UNP A9CJ63
D	7	PHE	-	expression tag	UNP A9CJ63
D	8	GLN	-	expression tag	UNP A9CJ63
D	9	GLY	-	expression tag	UNP A9CJ63
E	1	GLY	-	expression tag	UNP A9CJ63
E	2	THR	-	expression tag	UNP A9CJ63
E	3	GLU	-	expression tag	UNP A9CJ63
E	4	ASN	-	expression tag	UNP A9CJ63
E	5	LEU	-	expression tag	UNP A9CJ63
E	6	TYR	-	expression tag	UNP A9CJ63
E	7	PHE	-	expression tag	UNP A9CJ63
E	8	GLN	-	expression tag	UNP A9CJ63
E	9	GLY	-	expression tag	UNP A9CJ63
F	1	GLY	-	expression tag	UNP A9CJ63
F	2	THR	-	expression tag	UNP A9CJ63

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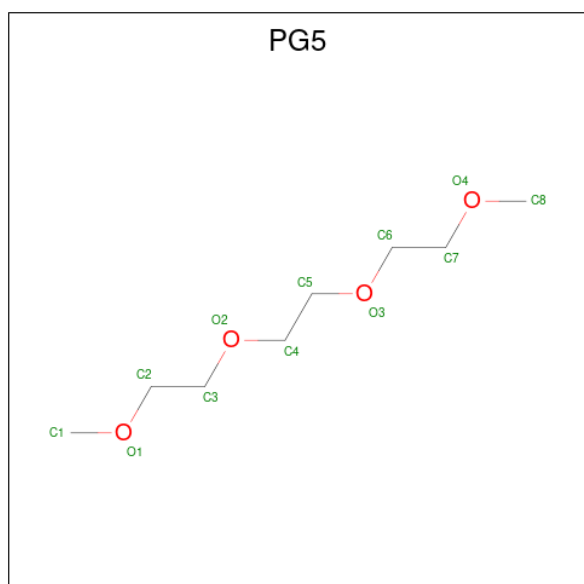
Chain	Residue	Modelled	Actual	Comment	Reference
F	3	GLU	-	expression tag	UNP A9CJ63
F	4	ASN	-	expression tag	UNP A9CJ63
F	5	LEU	-	expression tag	UNP A9CJ63
F	6	TYR	-	expression tag	UNP A9CJ63
F	7	PHE	-	expression tag	UNP A9CJ63
F	8	GLN	-	expression tag	UNP A9CJ63
F	9	GLY	-	expression tag	UNP A9CJ63
G	1	GLY	-	expression tag	UNP A9CJ63
G	2	THR	-	expression tag	UNP A9CJ63
G	3	GLU	-	expression tag	UNP A9CJ63
G	4	ASN	-	expression tag	UNP A9CJ63
G	5	LEU	-	expression tag	UNP A9CJ63
G	6	TYR	-	expression tag	UNP A9CJ63
G	7	PHE	-	expression tag	UNP A9CJ63
G	8	GLN	-	expression tag	UNP A9CJ63
G	9	GLY	-	expression tag	UNP A9CJ63
H	1	GLY	-	expression tag	UNP A9CJ63
H	2	THR	-	expression tag	UNP A9CJ63
H	3	GLU	-	expression tag	UNP A9CJ63
H	4	ASN	-	expression tag	UNP A9CJ63
H	5	LEU	-	expression tag	UNP A9CJ63
H	6	TYR	-	expression tag	UNP A9CJ63
H	7	PHE	-	expression tag	UNP A9CJ63
H	8	GLN	-	expression tag	UNP A9CJ63
H	9	GLY	-	expression tag	UNP A9CJ63
I	1	GLY	-	expression tag	UNP A9CJ63
I	2	THR	-	expression tag	UNP A9CJ63
I	3	GLU	-	expression tag	UNP A9CJ63
I	4	ASN	-	expression tag	UNP A9CJ63
I	5	LEU	-	expression tag	UNP A9CJ63
I	6	TYR	-	expression tag	UNP A9CJ63
I	7	PHE	-	expression tag	UNP A9CJ63
I	8	GLN	-	expression tag	UNP A9CJ63
I	9	GLY	-	expression tag	UNP A9CJ63
J	1	GLY	-	expression tag	UNP A9CJ63
J	2	THR	-	expression tag	UNP A9CJ63
J	3	GLU	-	expression tag	UNP A9CJ63
J	4	ASN	-	expression tag	UNP A9CJ63
J	5	LEU	-	expression tag	UNP A9CJ63
J	6	TYR	-	expression tag	UNP A9CJ63
J	7	PHE	-	expression tag	UNP A9CJ63
J	8	GLN	-	expression tag	UNP A9CJ63

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Chain	Residue	Modelled	Actual	Comment	Reference
J	9	GLY	-	expression tag	UNP A9CJ63
K	1	GLY	-	expression tag	UNP A9CJ63
K	2	THR	-	expression tag	UNP A9CJ63
K	3	GLU	-	expression tag	UNP A9CJ63
K	4	ASN	-	expression tag	UNP A9CJ63
K	5	LEU	-	expression tag	UNP A9CJ63
K	6	TYR	-	expression tag	UNP A9CJ63
K	7	PHE	-	expression tag	UNP A9CJ63
K	8	GLN	-	expression tag	UNP A9CJ63
K	9	GLY	-	expression tag	UNP A9CJ63
L	1	GLY	-	expression tag	UNP A9CJ63
L	2	THR	-	expression tag	UNP A9CJ63
L	3	GLU	-	expression tag	UNP A9CJ63
L	4	ASN	-	expression tag	UNP A9CJ63
L	5	LEU	-	expression tag	UNP A9CJ63
L	6	TYR	-	expression tag	UNP A9CJ63
L	7	PHE	-	expression tag	UNP A9CJ63
L	8	GLN	-	expression tag	UNP A9CJ63
L	9	GLY	-	expression tag	UNP A9CJ63

- Molecule 2 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (three-letter code: PG5) (formula: C₈H₁₈O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	8	4		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 12 8 4	0	0
2	C	1	Total C O 12 8 4	0	0
2	E	1	Total C O 12 8 4	0	0
2	F	1	Total C O 12 8 4	0	0
2	G	1	Total C O 12 8 4	0	0
2	H	1	Total C O 12 8 4	0	0
2	I	1	Total C O 12 8 4	0	0
2	J	1	Total C O 12 8 4	0	0
2	J	1	Total C O 12 8 4	0	0
2	K	1	Total C O 12 8 4	0	0
2	L	1	Total C O 12 8 4	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	107	Total O 107 107	0	0
3	B	91	Total O 91 91	0	0
3	C	95	Total O 95 95	0	0
3	D	91	Total O 91 91	0	0
3	E	82	Total O 82 82	0	0
3	F	86	Total O 86 86	0	0
3	G	88	Total O 88 88	0	0
3	H	97	Total O 97 97	0	0

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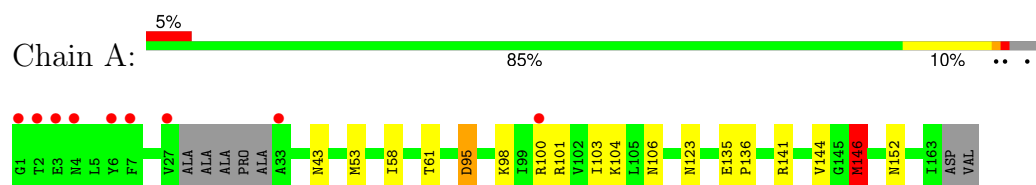
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	77	Total 77	O 77	0	0
3	J	94	Total 94	O 94	0	0
3	K	85	Total 85	O 85	0	0
3	L	81	Total 81	O 81	0	0

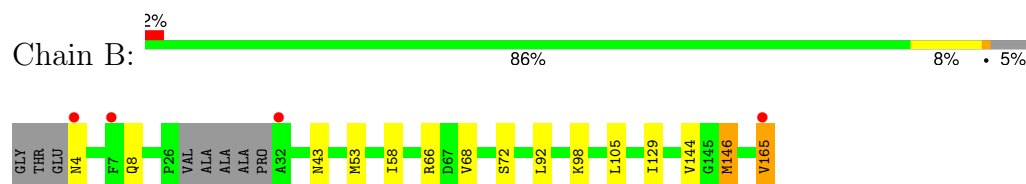
3 Residue-property plots [i](#)

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.

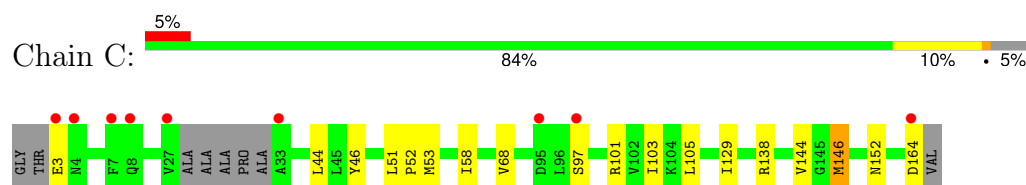
- Molecule 1: Uncharacterized protein



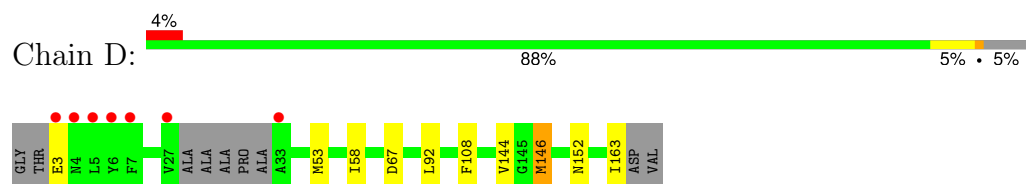
- Molecule 1: Uncharacterized protein



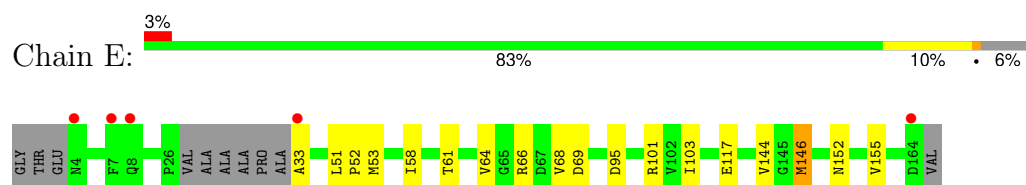
- Molecule 1: Uncharacterized protein



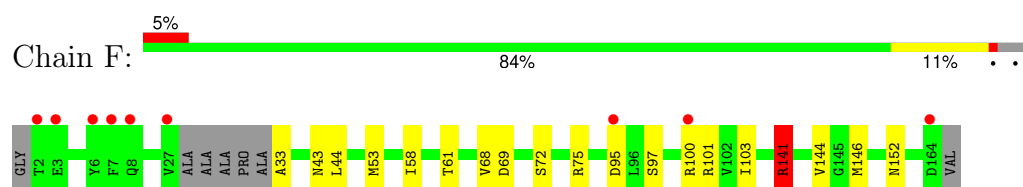
- Molecule 1: Uncharacterized protein



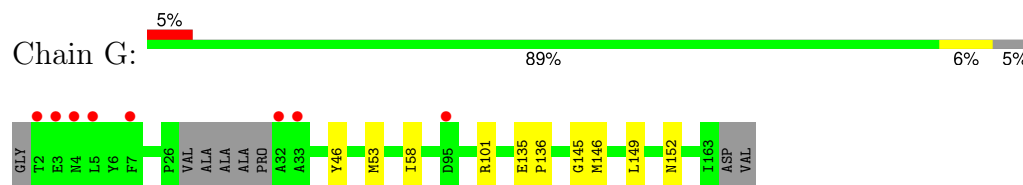
- Molecule 1: Uncharacterized protein



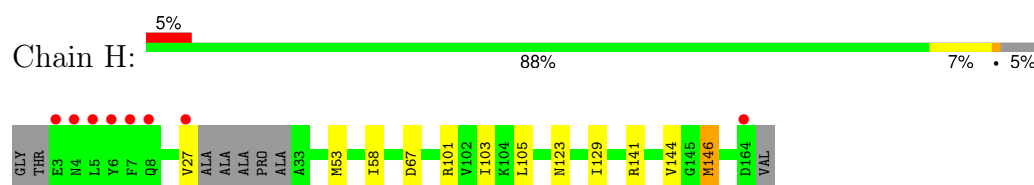
- Molecule 1: Uncharacterized protein



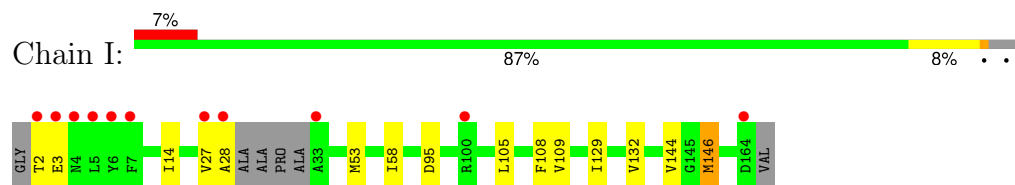
- Molecule 1: Uncharacterized protein



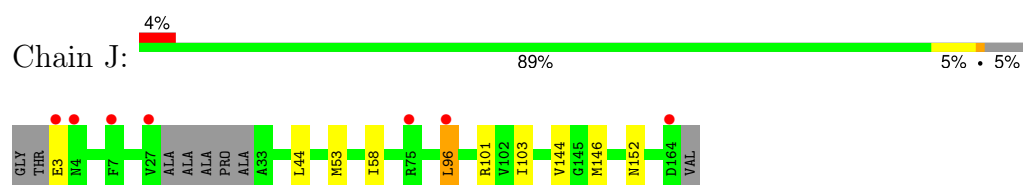
- Molecule 1: Uncharacterized protein



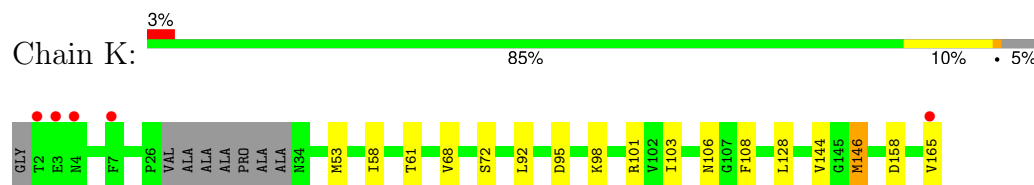
- Molecule 1: Uncharacterized protein



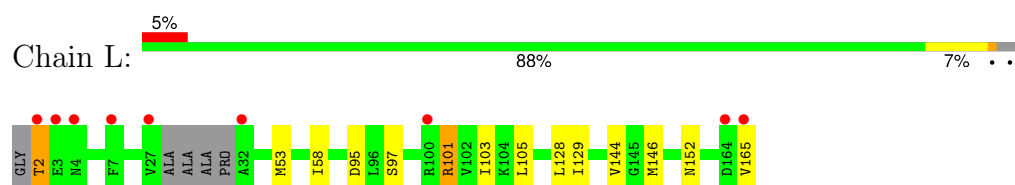
- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	93.62Å 93.60Å 93.63Å 68.20° 67.87° 68.14°	Depositor
Resolution (Å)	46.13 – 1.70 46.13 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.0 (46.13-1.70) 97.0 (46.13-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.179 , 0.214 0.184 , 0.218	Depositor DCC
R_{free} test set	14230 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.61$, $\langle L^2 \rangle = 0.47$	Xtriage
Estimated twinning fraction	0.034 for l,h,k 0.034 for k,l,h 0.034 for -k,-h,-l 0.038 for -h,-l,-k 0.038 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	15234	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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 47.76 % 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 9.4742e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: PG5

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	0.76	1/1182 (0.1%)	0.73	0/1598
1	B	0.70	0/1175	0.74	2/1589 (0.1%)
1	C	0.76	1/1179 (0.1%)	0.74	0/1594
1	D	0.74	0/1171	0.71	0/1583
1	E	0.71	0/1163	0.76	2/1572 (0.1%)
1	F	0.77	0/1186	0.97	3/1604 (0.2%)
1	G	0.68	0/1176	0.72	0/1590
1	H	0.75	0/1179	0.78	1/1594 (0.1%)
1	I	0.73	0/1191	0.77	0/1611
1	J	0.72	0/1179	0.76	0/1594
1	K	0.68	0/1181	0.75	0/1597
1	L	0.70	0/1198	0.74	0/1621
All	All	0.72	2/14160 (0.0%)	0.77	8/19147 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	MSE	SE-CE	-6.50	1.57	1.95
1	C	68	VAL	CB-CG2	-5.68	1.41	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	141	ARG	NE-CZ-NH1	16.99	128.80	120.30
1	F	141	ARG	NE-CZ-NH2	-15.75	112.42	120.30
1	H	146	MSE	CG-SE-CE	-7.57	82.24	98.90
1	B	66	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	E	69	ASP	CB-CG-OD1	5.69	123.42	118.30

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	A	1170	0	1204	19	0
1	B	1163	0	1194	14	0
1	C	1167	0	1195	15	0
1	D	1159	0	1191	10	0
1	E	1151	0	1180	25	0
1	F	1174	0	1202	22	0
1	G	1164	0	1194	8	0
1	H	1167	0	1195	9	0
1	I	1179	0	1207	19	0
1	J	1167	0	1195	14	0
1	K	1169	0	1197	12	0
1	L	1186	0	1216	13	0
2	A	12	0	18	4	0
2	B	12	0	18	1	0
2	C	12	0	18	5	0
2	E	12	0	18	5	0
2	F	12	0	18	7	0
2	G	12	0	18	0	0
2	H	12	0	18	3	0
2	I	12	0	18	1	0
2	J	24	0	36	6	0
2	K	12	0	18	3	0
2	L	12	0	18	4	0
3	A	107	0	0	3	0
3	B	91	0	0	4	0
3	C	95	0	0	8	0
3	D	91	0	0	4	0
3	E	82	0	0	4	0
3	F	86	0	0	8	0
3	G	88	0	0	3	0
3	H	97	0	0	3	0
3	I	77	0	0	3	0
3	J	94	0	0	5	0
3	K	85	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	81	0	0	1	0
All	All	15234	0	14586	192	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.

The worst 5 of 192 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:53:MSE:CE	1:E:58:ILE:HD13	1.31	1.53
1:E:53:MSE:HE1	1:E:58:ILE:CD1	1.51	1.41
1:I:144:VAL:O	1:I:146:MSE:HE1	1.46	1.13
2:C:166:PG5:H13	3:C:222:HOH:O	1.57	1.02
1:A:53:MSE:SE	1:A:58:ILE:HD13	2.16	0.96

There are no symmetry-related clashes.

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	154/165 (93%)	150 (97%)	4 (3%)	0	100	100
1	B	153/165 (93%)	150 (98%)	3 (2%)	0	100	100
1	C	153/165 (93%)	151 (99%)	2 (1%)	0	100	100
1	D	152/165 (92%)	149 (98%)	3 (2%)	0	100	100
1	E	151/165 (92%)	148 (98%)	3 (2%)	0	100	100
1	F	154/165 (93%)	151 (98%)	3 (2%)	0	100	100
1	G	153/165 (93%)	151 (99%)	2 (1%)	0	100	100
1	H	153/165 (93%)	150 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	155/165 (94%)	153 (99%)	2 (1%)	0	100	100
1	J	153/165 (93%)	151 (99%)	2 (1%)	0	100	100
1	K	153/165 (93%)	150 (98%)	3 (2%)	0	100	100
1	L	156/165 (94%)	152 (97%)	4 (3%)	0	100	100
All	All	1840/1980 (93%)	1806 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	124/124 (100%)	122 (98%)	2 (2%)	58	44
1	B	123/124 (99%)	121 (98%)	2 (2%)	58	44
1	C	124/124 (100%)	122 (98%)	2 (2%)	58	44
1	D	123/124 (99%)	122 (99%)	1 (1%)	79	71
1	E	122/124 (98%)	120 (98%)	2 (2%)	58	44
1	F	125/124 (101%)	124 (99%)	1 (1%)	79	71
1	G	123/124 (99%)	121 (98%)	2 (2%)	58	44
1	H	124/124 (100%)	124 (100%)	0	100	100
1	I	125/124 (101%)	123 (98%)	2 (2%)	58	44
1	J	124/124 (100%)	122 (98%)	2 (2%)	58	44
1	K	125/124 (101%)	122 (98%)	3 (2%)	44	27
1	L	126/124 (102%)	123 (98%)	3 (2%)	44	27
All	All	1488/1488 (100%)	1466 (98%)	22 (2%)	60	47

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	96	LEU

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Mol	Chain	Res	Type
1	K	146	MSE
1	K	95	ASP
1	K	165	VAL
1	D	146	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	83	ASN
1	L	83	ASN
1	I	106	ASN
1	J	152	ASN
1	L	152	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	PG5	C	166	-	11,11,11	0.31	0	10,10,10	0.84	0
2	PG5	E	166	-	11,11,11	0.37	0	10,10,10	0.35	0
2	PG5	H	166	-	11,11,11	0.38	0	10,10,10	0.54	0
2	PG5	J	166	-	11,11,11	0.47	0	10,10,10	0.49	0
2	PG5	I	166	-	11,11,11	0.49	0	10,10,10	0.34	0
2	PG5	F	166	-	11,11,11	0.38	0	10,10,10	0.46	0
2	PG5	K	166	-	11,11,11	0.34	0	10,10,10	1.19	2 (20%)
2	PG5	A	166	-	11,11,11	0.52	0	10,10,10	0.99	1 (10%)
2	PG5	G	166	-	11,11,11	0.48	0	10,10,10	0.56	0
2	PG5	B	166	-	11,11,11	0.47	0	10,10,10	0.52	0
2	PG5	L	166	-	11,11,11	0.56	0	10,10,10	0.48	0
2	PG5	J	167	-	11,11,11	0.38	0	10,10,10	0.95	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PG5	C	166	-	-	4/9/9/9	-
2	PG5	E	166	-	-	4/9/9/9	-
2	PG5	H	166	-	-	4/9/9/9	-
2	PG5	J	166	-	-	4/9/9/9	-
2	PG5	I	166	-	-	2/9/9/9	-
2	PG5	F	166	-	-	6/9/9/9	-
2	PG5	K	166	-	-	5/9/9/9	-
2	PG5	A	166	-	-	7/9/9/9	-
2	PG5	G	166	-	-	2/9/9/9	-
2	PG5	B	166	-	-	3/9/9/9	-
2	PG5	L	166	-	-	4/9/9/9	-
2	PG5	J	167	-	-	5/9/9/9	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	166	PG5	O3-C5-C4	2.62	122.28	110.35
2	K	166	PG5	O2-C4-C5	-2.22	100.24	110.35
2	K	166	PG5	O3-C5-C4	-2.03	101.09	110.35

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	166	PG5	O3-C6-C7-O4
2	J	167	PG5	O3-C6-C7-O4
2	A	166	PG5	O2-C4-C5-O3
2	K	166	PG5	O1-C2-C3-O2
2	C	166	PG5	C3-C2-O1-C1

There are no ring outliers.

11 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	166	PG5	5	0
2	E	166	PG5	5	0
2	H	166	PG5	3	0
2	J	166	PG5	1	0
2	I	166	PG5	1	0
2	F	166	PG5	7	0
2	K	166	PG5	3	0
2	A	166	PG5	4	0
2	B	166	PG5	1	0
2	L	166	PG5	4	0
2	J	167	PG5	5	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	155/165 (93%)	-0.08	9 (5%) 30 31	13, 22, 40, 54	0
1	B	154/165 (93%)	-0.28	4 (2%) 57 60	11, 18, 34, 44	0
1	C	154/165 (93%)	-0.17	9 (5%) 30 31	12, 19, 36, 51	0
1	D	153/165 (92%)	-0.24	7 (4%) 38 41	11, 18, 35, 51	0
1	E	152/165 (92%)	-0.21	5 (3%) 49 52	14, 21, 34, 40	0
1	F	155/165 (93%)	-0.17	9 (5%) 30 31	11, 19, 37, 54	0
1	G	154/165 (93%)	-0.12	8 (5%) 34 36	14, 20, 40, 53	0
1	H	154/165 (93%)	-0.16	8 (5%) 34 36	12, 19, 38, 51	0
1	I	156/165 (94%)	0.00	11 (7%) 23 24	13, 20, 39, 56	0
1	J	154/165 (93%)	-0.17	7 (4%) 39 41	12, 19, 36, 52	0
1	K	154/165 (93%)	-0.06	5 (3%) 50 53	14, 21, 39, 55	0
1	L	157/165 (95%)	-0.08	9 (5%) 30 32	13, 22, 41, 55	0
All	All	1852/1980 (93%)	-0.14	91 (4%) 36 38	11, 20, 38, 56	0

The worst 5 of 91 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	28	ALA	7.5
1	L	32	ALA	6.6
1	F	2	THR	5.6
1	C	27	VAL	4.7
1	I	164	ASP	4.6

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 monosaccharides 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
2	PG5	G	166	12/12	0.85	0.15	26,32,38,39	0
2	PG5	C	166	12/12	0.87	0.17	29,32,37,40	0
2	PG5	E	166	12/12	0.87	0.18	31,35,43,43	0
2	PG5	A	166	12/12	0.87	0.16	31,35,39,42	0
2	PG5	F	166	12/12	0.88	0.15	27,32,35,37	0
2	PG5	B	166	12/12	0.88	0.13	22,27,40,40	0
2	PG5	K	166	12/12	0.88	0.13	25,31,37,37	0
2	PG5	L	166	12/12	0.88	0.14	25,29,34,37	0
2	PG5	H	166	12/12	0.89	0.14	26,32,40,43	0
2	PG5	J	167	12/12	0.90	0.14	29,32,42,43	0
2	PG5	I	166	12/12	0.91	0.12	23,28,35,37	0
2	PG5	J	166	12/12	0.92	0.11	25,29,39,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.