



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 23, 2026 – 08:58 AM UTC

PDB ID : 8BLM / pdb_00008blm
Title : Structure of RutB
Authors : Rajendran, C.
Deposited on : 2022-11-09
Resolution : 1.90 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

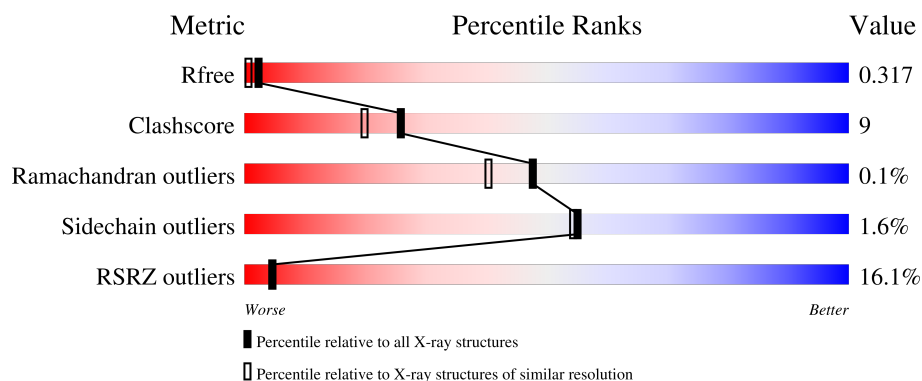
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	230	<div> <div>9%</div> <div>76%</div> <div>20%</div> <div>..</div> </div>
1	B	230	<div> <div>9%</div> <div>80%</div> <div>16%</div> <div>..</div> </div>
1	C	230	<div> <div>11%</div> <div>76%</div> <div>20%</div> <div>..</div> </div>
1	D	230	<div> <div>14%</div> <div>82%</div> <div>13%</div> <div>..</div> </div>
1	E	230	<div> <div>18%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	230	
1	G	230	
1	H	230	
1	I	230	
1	J	230	
1	K	230	
1	L	230	
1	M	230	
1	N	230	
1	O	230	
1	P	230	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 28516 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 Ureidoacrylate amidohydrolase RutB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1709	1098	285	321	5			
1	B	222	Total	C	N	O	S	0	0	0
			1715	1104	285	321	5			
1	C	222	Total	C	N	O	S	0	0	0
			1715	1104	285	321	5			
1	D	220	Total	C	N	O	S	0	0	0
			1702	1096	283	318	5			
1	E	222	Total	C	N	O	S	0	0	0
			1703	1098	283	317	5			
1	F	220	Total	C	N	O	S	0	0	0
			1694	1092	282	315	5			
1	G	222	Total	C	N	O	S	0	0	0
			1711	1101	284	321	5			
1	H	222	Total	C	N	O	S	0	0	0
			1715	1104	285	321	5			
1	I	222	Total	C	N	O	S	0	0	0
			1708	1099	285	319	5			
1	J	222	Total	C	N	O	S	0	0	0
			1696	1091	281	319	5			
1	K	220	Total	C	N	O	S	0	0	0
			1692	1091	282	314	5			
1	L	220	Total	C	N	O	S	0	0	0
			1702	1096	283	318	5			
1	M	222	Total	C	N	O	S	0	0	0
			1713	1103	285	320	5			
1	N	222	Total	C	N	O	S	0	0	0
			1711	1102	284	320	5			
1	O	222	Total	C	N	O	S	0	0	0
			1715	1104	285	321	5			
1	P	220	Total	C	N	O	S	0	0	0
			1683	1085	279	314	5			

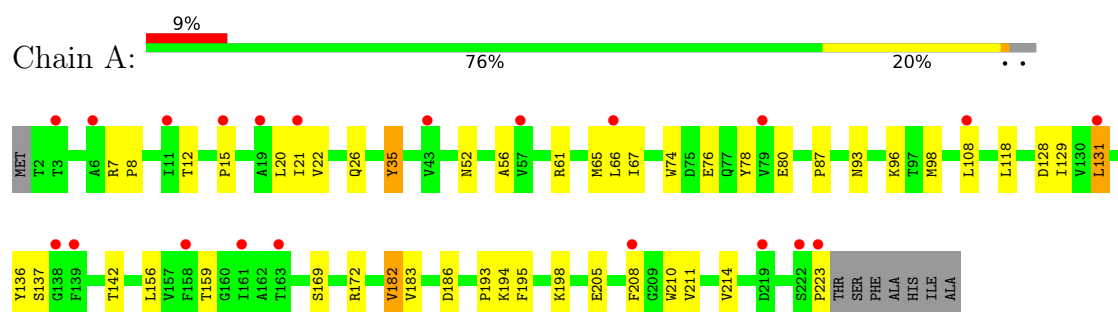
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	95	Total 95	O 95	0	0
2	B	87	Total 87	O 87	0	0
2	C	96	Total 96	O 96	0	0
2	D	81	Total 81	O 81	0	0
2	E	78	Total 78	O 78	0	0
2	F	70	Total 70	O 70	0	0
2	G	78	Total 78	O 78	0	0
2	H	81	Total 81	O 81	0	0
2	I	93	Total 93	O 93	0	0
2	J	84	Total 84	O 84	0	0
2	K	71	Total 71	O 71	0	0
2	L	82	Total 82	O 82	0	0
2	M	68	Total 68	O 68	0	0
2	N	48	Total 48	O 48	0	0
2	O	62	Total 62	O 62	0	0
2	P	58	Total 58	O 58	0	0

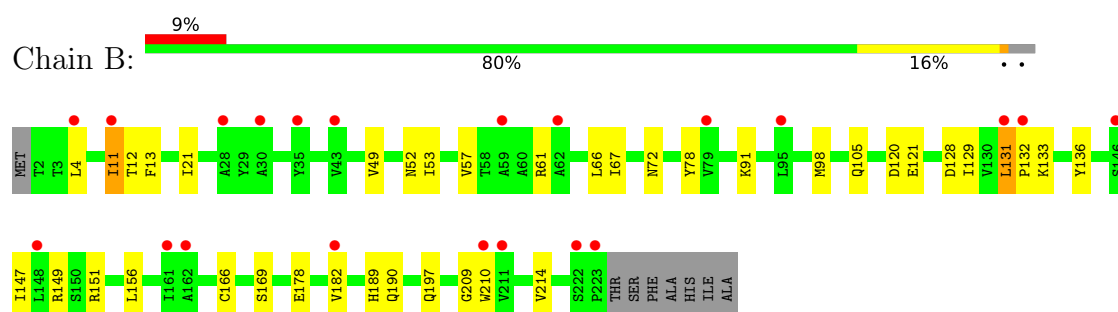
3 Residue-property plots [i](#)

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.

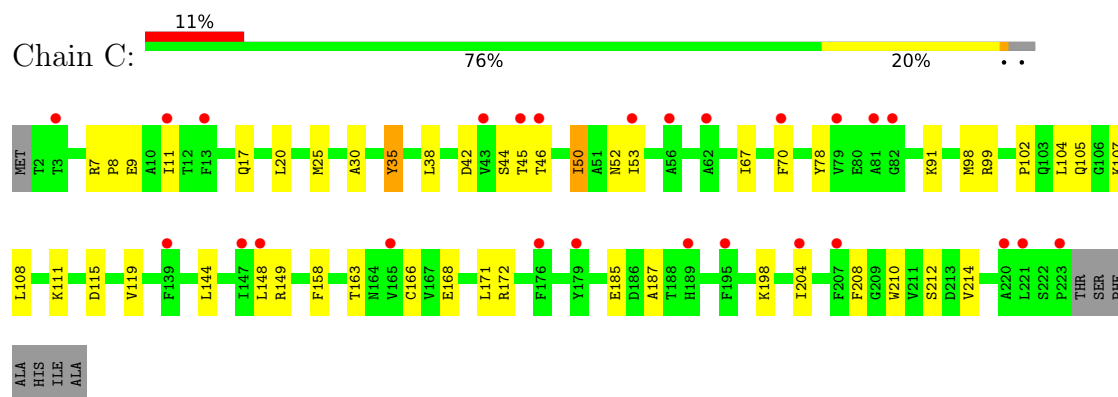
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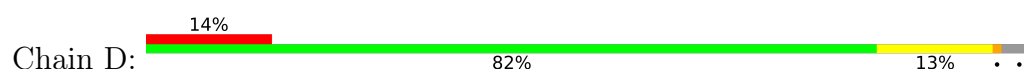
• Molecule 1: Ureidoacrylate amidohydrolase RutB

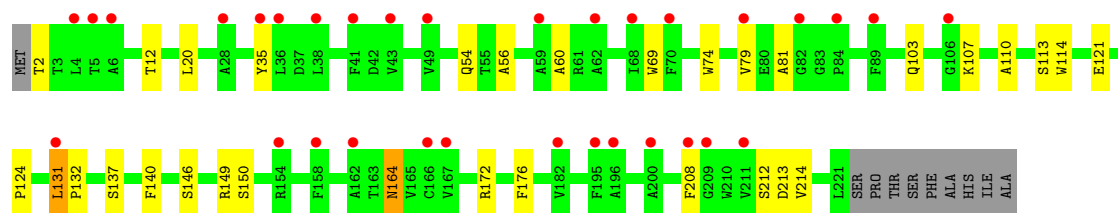


• Molecule 1: Ureidoacrylate amidohydrolase RutB

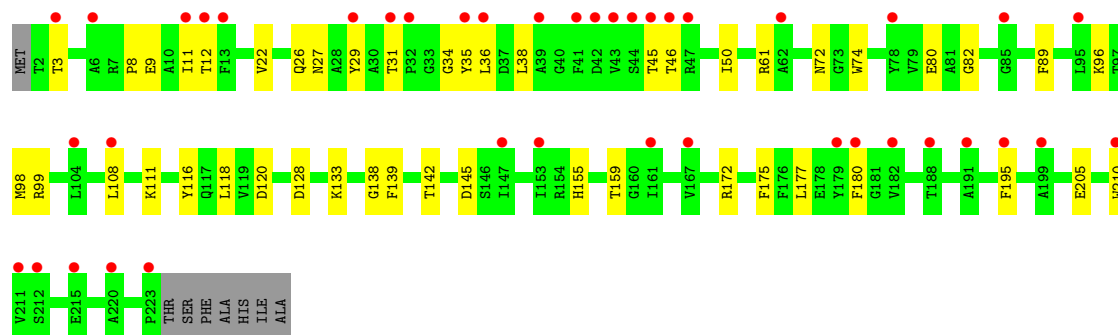
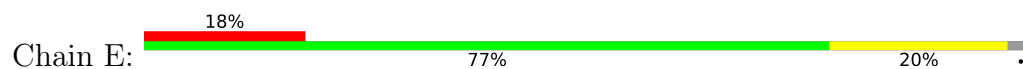


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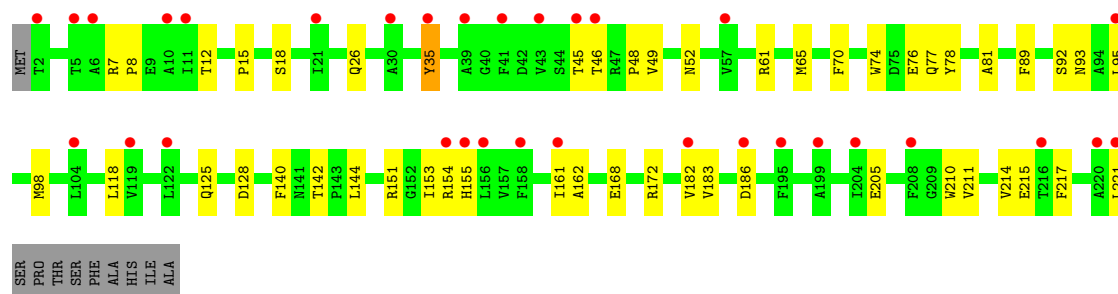
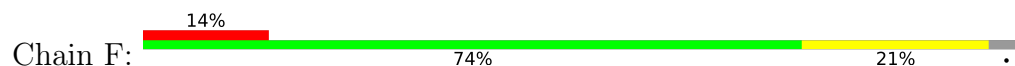




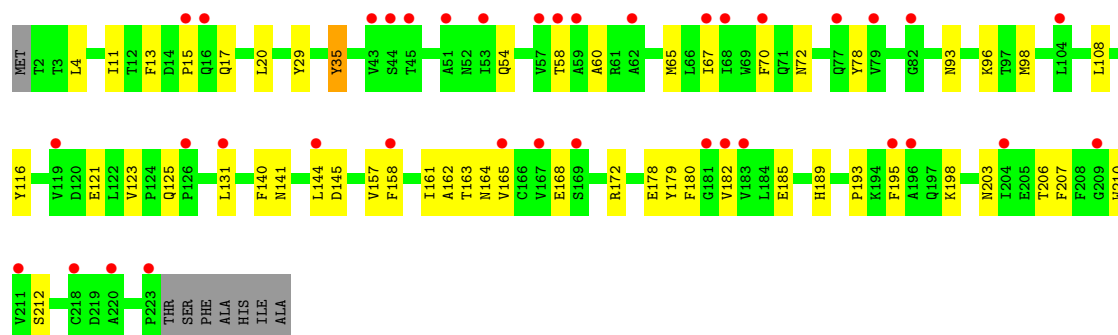
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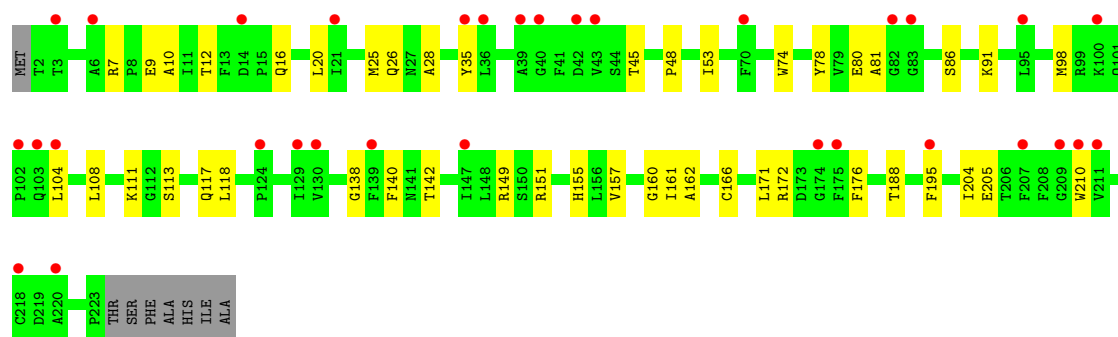
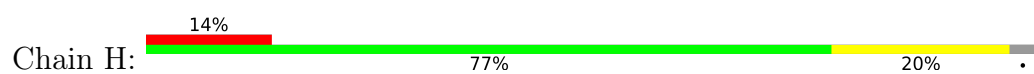
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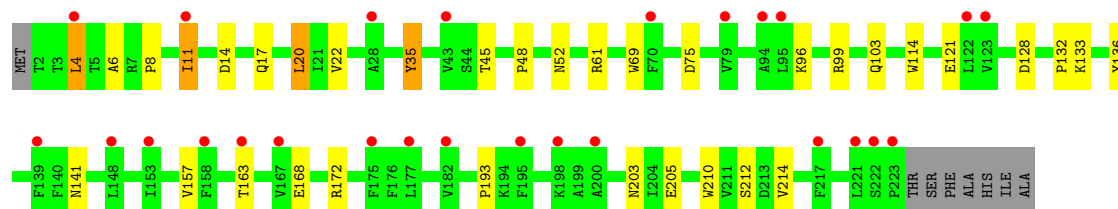
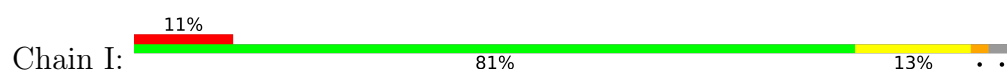
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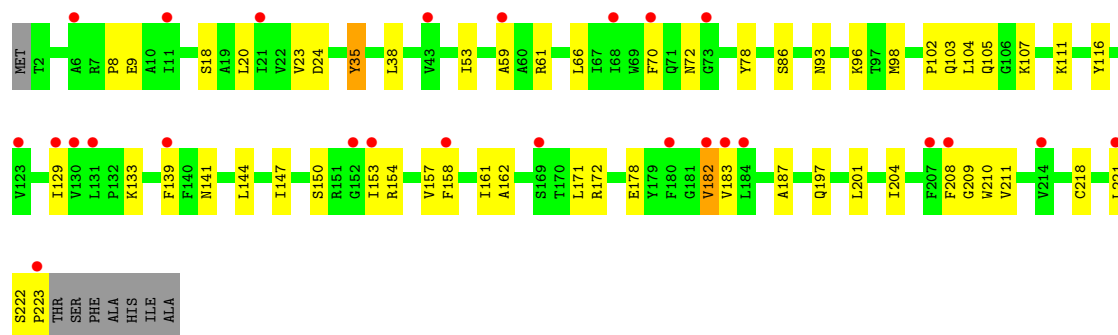
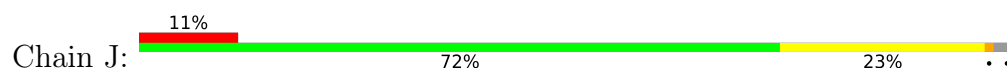
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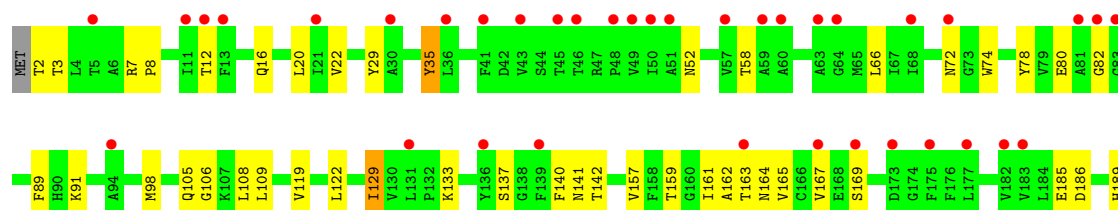
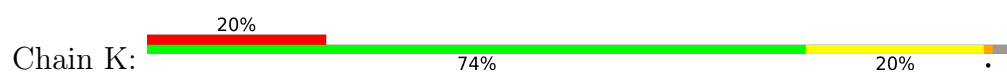
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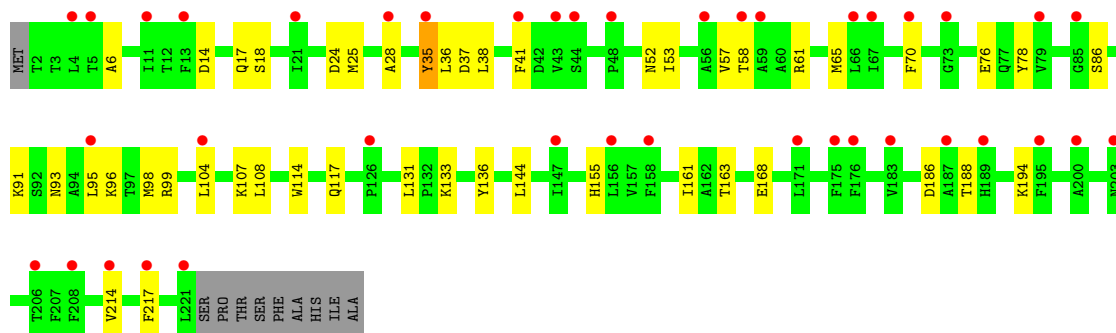
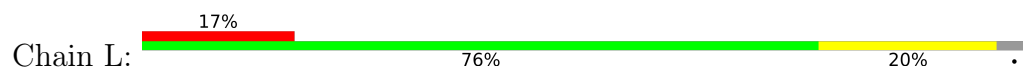


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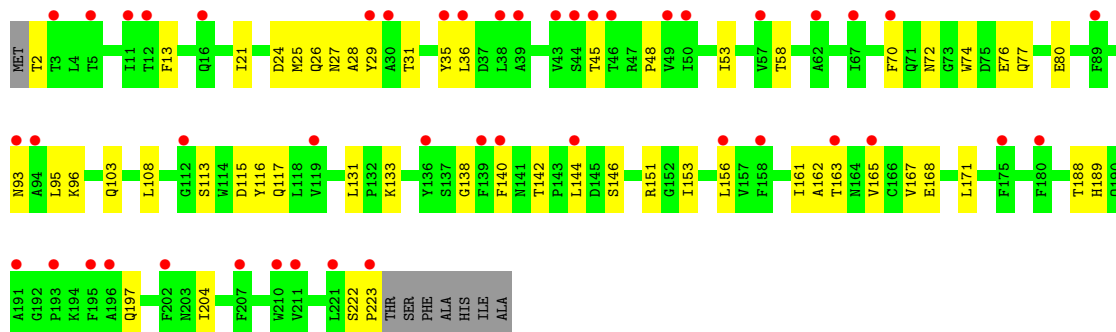
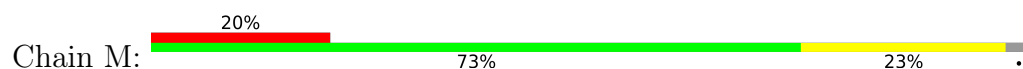




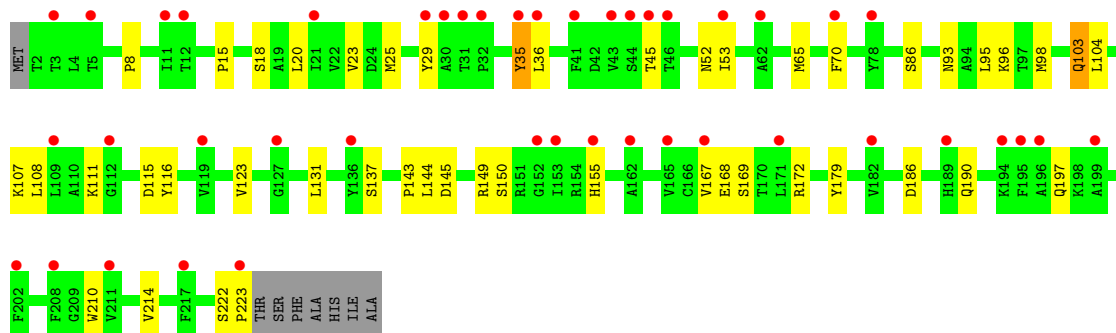
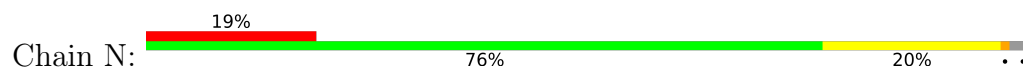
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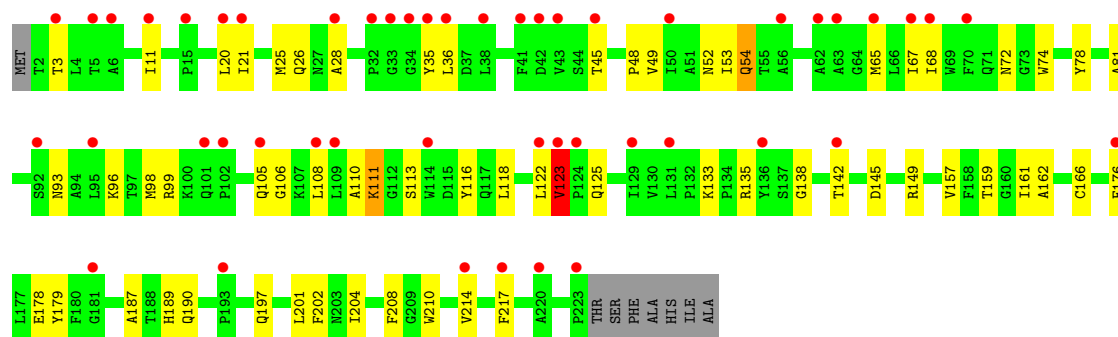


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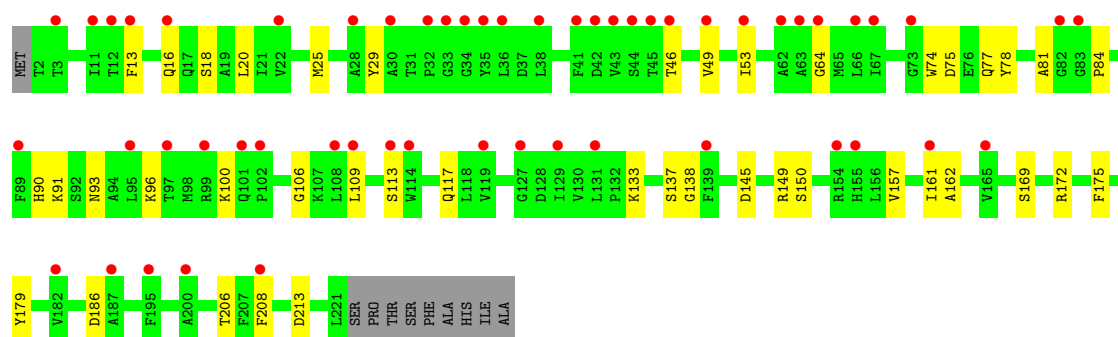
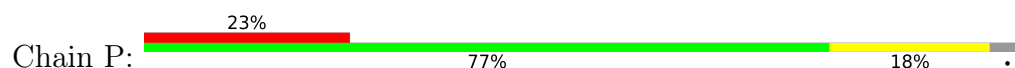


• Molecule 1: Ureidoacrylate amidohydrolase RutB





● Molecule 1: Ureidoacrylate amidohydrolase RutB



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	121.59Å 110.89Å 128.71Å 90.00° 99.13° 90.00°	Depositor
Resolution (Å)	47.67 – 1.90 47.67 – 1.90	Depositor EDS
% Data completeness (in resolution range)	81.3 (47.67-1.90) 85.6 (47.67-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.95 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.13-2998	Depositor
R, R_{free}	0.263 , 0.318 0.265 , 0.317	Depositor DCC
R_{free} test set	11083 reflections (4.17%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.561	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	28516	wwPDB-VP
Average B, all atoms (Å ²)	30.0	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 38.57 % 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 3.6160e-04. 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

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	0.40	0/1753	0.62	0/2392
1	B	0.42	0/1760	0.64	0/2401
1	C	0.44	0/1760	0.68	0/2401
1	D	0.44	0/1746	0.63	0/2381
1	E	0.38	0/1748	0.59	0/2386
1	F	0.37	0/1738	0.60	0/2371
1	G	0.41	0/1756	0.62	0/2397
1	H	0.39	0/1760	0.60	0/2401
1	I	0.42	0/1753	0.64	0/2392
1	J	0.41	0/1741	0.62	0/2379
1	K	0.42	0/1736	0.66	0/2369
1	L	0.41	1/1746 (0.1%)	0.60	0/2381
1	M	0.37	0/1758	0.59	0/2398
1	N	0.41	0/1756	0.61	0/2396
1	O	0.36	0/1760	0.58	1/2401 (0.0%)
1	P	0.34	0/1727	0.56	0/2359
All	All	0.40	1/27998 (0.0%)	0.62	1/38205 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	6	ALA	C-N	-5.35	1.22	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	123	VAL	O-C-N	-5.21	115.16	121.10

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	1709	0	1668	36	0
1	B	1715	0	1675	35	1
1	C	1715	0	1675	37	0
1	D	1702	0	1663	28	0
1	E	1703	0	1659	28	0
1	F	1694	0	1653	32	0
1	G	1711	0	1664	40	0
1	H	1715	0	1675	35	0
1	I	1708	0	1662	25	0
1	J	1696	0	1632	42	1
1	K	1692	0	1648	40	0
1	L	1702	0	1663	28	1
1	M	1713	0	1670	40	0
1	N	1711	0	1669	29	0
1	O	1715	0	1675	45	0
1	P	1683	0	1627	23	1
2	A	95	0	0	1	0
2	B	87	0	0	5	0
2	C	96	0	0	5	0
2	D	81	0	0	7	0
2	E	78	0	0	6	0
2	F	70	0	0	1	0
2	G	78	0	0	4	0
2	H	81	0	0	7	0
2	I	93	0	0	5	0
2	J	84	0	0	5	0
2	K	71	0	0	6	0
2	L	82	0	0	3	0
2	M	68	0	0	3	0
2	N	48	0	0	1	0
2	O	62	0	0	4	0
2	P	58	0	0	1	0
All	All	28516	0	26578	510	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 9.

The worst 5 of 510 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:J:72:ASN:HD22	1:J:133:LYS:NZ	1.57	1.03
1:J:72:ASN:ND2	1:J:133:LYS:HZ2	1.57	1.01
1:K:98:MET:HE3	1:K:105:GLN:HA	1.52	0.92
1:M:163:THR:HG22	1:M:188:THR:HB	1.53	0.90
1:I:172:ARG:NH2	2:I:301:HOH:O	2.11	0.82

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:J:209:GLY:O	1:P:91:LYS:NZ[2_656]	2.04	0.16
1:B:105:GLN:O	1:L:107:LYS:NZ[2_556]	2.11	0.09

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	220/230 (96%)	214 (97%)	6 (3%)	0	100	100
1	B	220/230 (96%)	211 (96%)	9 (4%)	0	100	100
1	C	220/230 (96%)	213 (97%)	6 (3%)	1 (0%)	24	16
1	D	218/230 (95%)	211 (97%)	7 (3%)	0	100	100
1	E	220/230 (96%)	213 (97%)	7 (3%)	0	100	100
1	F	218/230 (95%)	210 (96%)	8 (4%)	0	100	100
1	G	220/230 (96%)	212 (96%)	7 (3%)	1 (0%)	24	16
1	H	220/230 (96%)	210 (96%)	10 (4%)	0	100	100
1	I	220/230 (96%)	211 (96%)	9 (4%)	0	100	100
1	J	220/230 (96%)	213 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	218/230 (95%)	205 (94%)	12 (6%)	1 (0%)	24	16
1	L	218/230 (95%)	210 (96%)	8 (4%)	0	100	100
1	M	220/230 (96%)	212 (96%)	7 (3%)	1 (0%)	24	16
1	N	220/230 (96%)	211 (96%)	9 (4%)	0	100	100
1	O	220/230 (96%)	211 (96%)	9 (4%)	0	100	100
1	P	218/230 (95%)	210 (96%)	8 (4%)	0	100	100
All	All	3510/3680 (95%)	3377 (96%)	129 (4%)	4 (0%)	48	40

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	35	TYR
1	K	165	VAL
1	G	165	VAL
1	M	165	VAL

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	180/188 (96%)	177 (98%)	3 (2%)	53	52
1	B	181/188 (96%)	179 (99%)	2 (1%)	65	67
1	C	181/188 (96%)	179 (99%)	2 (1%)	65	67
1	D	179/188 (95%)	176 (98%)	3 (2%)	53	52
1	E	178/188 (95%)	175 (98%)	3 (2%)	53	52
1	F	177/188 (94%)	175 (99%)	2 (1%)	65	67
1	G	180/188 (96%)	178 (99%)	2 (1%)	65	67
1	H	181/188 (96%)	180 (99%)	1 (1%)	78	81
1	I	179/188 (95%)	174 (97%)	5 (3%)	38	32
1	J	176/188 (94%)	174 (99%)	2 (1%)	65	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	176/188 (94%)	171 (97%)	5 (3%)	38	32
1	L	179/188 (95%)	177 (99%)	2 (1%)	65	67
1	M	180/188 (96%)	177 (98%)	3 (2%)	53	52
1	N	180/188 (96%)	174 (97%)	6 (3%)	33	26
1	O	181/188 (96%)	177 (98%)	4 (2%)	45	42
1	P	174/188 (93%)	172 (99%)	2 (1%)	65	67
All	All	2862/3008 (95%)	2815 (98%)	47 (2%)	55	54

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	141	ASN
1	N	20	LEU
1	K	211	VAL
1	M	58	THR
1	N	45	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	125	GLN
1	N	141	ASN
1	M	141	ASN
1	N	27	ASN
1	O	103	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	222/230 (96%)	1.16	21 (9%)	14 14	21, 27, 36, 44	0
1	B	222/230 (96%)	1.14	21 (9%)	14 14	18, 27, 36, 44	0
1	C	222/230 (96%)	1.23	26 (11%)	9 10	19, 28, 37, 53	0
1	D	220/230 (95%)	1.29	32 (14%)	6 6	19, 28, 37, 48	0
1	E	222/230 (96%)	1.40	41 (18%)	3 3	18, 31, 44, 57	0
1	F	220/230 (95%)	1.27	32 (14%)	6 6	21, 30, 40, 46	0
1	G	222/230 (96%)	1.39	37 (16%)	4 4	20, 30, 39, 48	0
1	H	222/230 (96%)	1.29	32 (14%)	6 6	19, 29, 41, 51	0
1	I	222/230 (96%)	1.10	26 (11%)	9 10	19, 27, 37, 47	0
1	J	222/230 (96%)	1.19	26 (11%)	9 10	19, 28, 36, 42	0
1	K	220/230 (95%)	1.43	47 (21%)	2 2	21, 30, 41, 46	0
1	L	220/230 (95%)	1.41	40 (18%)	3 3	21, 31, 40, 48	0
1	M	222/230 (96%)	1.50	46 (20%)	2 2	21, 34, 46, 55	0
1	N	222/230 (96%)	1.47	43 (19%)	3 3	21, 34, 49, 62	0
1	O	222/230 (96%)	1.48	48 (21%)	2 2	20, 32, 48, 61	0
1	P	220/230 (95%)	1.50	54 (24%)	2 1	21, 33, 48, 62	0
All	All	3542/3680 (96%)	1.33	572 (16%)	4 4	18, 29, 43, 62	0

The worst 5 of 572 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	LEU	4.8
1	N	223	PRO	4.5
1	N	43	VAL	4.4
1	K	167	VAL	4.3
1	G	82	GLY	4.3

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.