



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2017 – 07:05 PM EDT

PDB ID : 5C6H
Title : Mcl-1 complexed with Mule
Authors : Song, T.; Wang, Z.; Ji, F.; Chai, G.; Liu, Y.; Li, X.; Li, Z.; Fan, Y.; Zhang, Z.
Deposited on : unknown
Resolution : 2.05 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
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-20030345

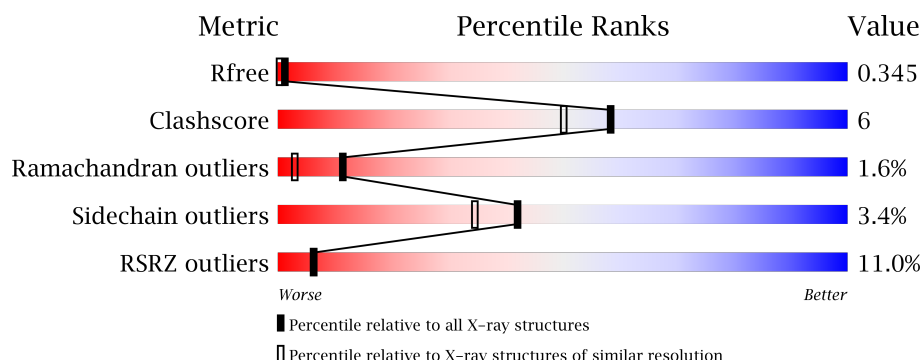
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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	157	<div> <div>20%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>..</div> </div> </div>
1	C	157	<div> <div>13%</div> <div> <div></div> <div>86%</div> <div>11%</div> <div>..</div> </div> </div>
1	E	157	<div> <div>10%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>...</div> </div> </div>
1	G	157	<div> <div>10%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>..</div> </div> </div>
1	I	157	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>17%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	K	157	
1	M	157	
1	O	157	
1	Q	157	
1	S	157	
1	U	157	
1	W	157	
2	B	26	
2	D	26	
2	F	26	
2	H	26	
2	J	26	
2	L	26	
2	N	26	
2	P	26	
2	R	26	
2	T	26	
2	V	26	
2	X	26	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17481 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 Induced myeloid leukemia cell differentiation protein Mcl-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	155	Total	C	N	O	S	0	0	0
			1251	784	228	235	4			
1	C	155	Total	C	N	O	S	0	0	0
			1251	784	228	235	4			
1	E	154	Total	C	N	O	S	0	0	0
			1242	779	227	232	4			
1	G	154	Total	C	N	O	S	0	0	0
			1242	779	227	232	4			
1	I	155	Total	C	N	O	S	0	0	0
			1251	784	228	235	4			
1	K	153	Total	C	N	O	S	0	0	0
			1234	773	226	231	4			
1	M	155	Total	C	N	O	S	0	0	0
			1251	784	228	235	4			
1	O	155	Total	C	N	O	S	0	0	0
			1251	784	228	235	4			
1	Q	154	Total	C	N	O	S	0	0	0
			1242	779	227	232	4			
1	S	154	Total	C	N	O	S	0	0	0
			1241	779	227	231	4			
1	U	151	Total	C	N	O	S	0	0	0
			1217	764	224	225	4			
1	W	153	Total	C	N	O	S	0	0	0
			1231	772	226	229	4			

- Molecule 2 is a protein called Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	25	Total	C	N	O	S	0	0	0
			198	121	33	42	2			
2	D	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			
2	H	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			
2	J	24	Total	C	N	O	S	0	0	0
			192	118	32	40	2			
2	L	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			
2	N	26	Total	C	N	O	S	0	0	0
			204	125	34	43	2			
2	P	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			
2	R	24	Total	C	N	O	S	0	0	0
			192	118	32	40	2			
2	T	26	Total	C	N	O	S	0	0	0
			206	127	34	43	2			
2	V	23	Total	C	N	O	S	0	0	0
			185	113	31	39	2			
2	X	25	Total	C	N	O	S	0	0	0
			198	121	33	42	2			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	1	Total	O	0	0
			1	1		
3	C	11	Total	O	0	0
			11	11		
3	D	1	Total	O	0	0
			1	1		
3	E	1	Total	O	0	0
			1	1		
3	G	12	Total	O	0	0
			12	12		
3	H	1	Total	O	0	0
			1	1		
3	I	10	Total	O	0	0
			10	10		
3	J	2	Total	O	0	0
			2	2		

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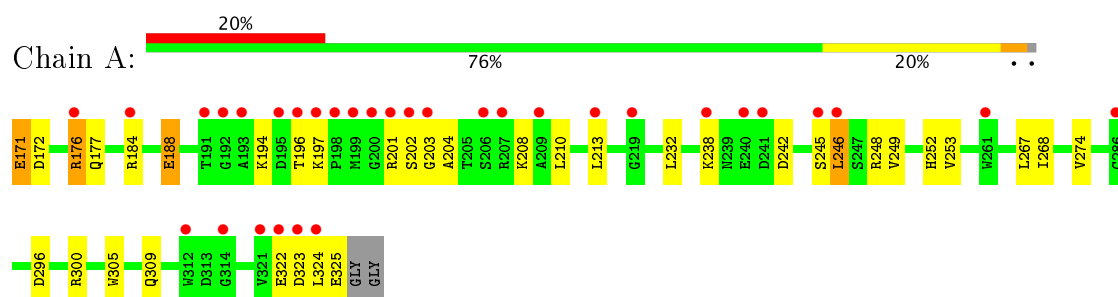
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	K	7	Total 7	O 7	0	0
3	L	1	Total 1	O 1	0	0
3	M	20	Total 20	O 20	0	0
3	N	4	Total 4	O 4	0	0
3	O	33	Total 33	O 33	0	0
3	P	6	Total 6	O 6	0	0
3	Q	14	Total 14	O 14	0	0
3	R	5	Total 5	O 5	0	0
3	S	12	Total 12	O 12	0	0
3	T	7	Total 7	O 7	0	0
3	U	9	Total 9	O 9	0	0
3	V	2	Total 2	O 2	0	0
3	W	5	Total 5	O 5	0	0
3	X	2	Total 2	O 2	0	0

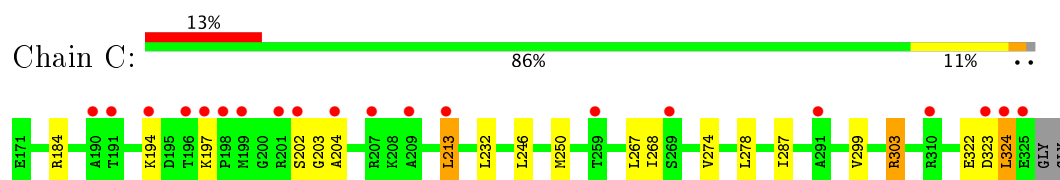
3 Residue-property plots [i](#)

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.

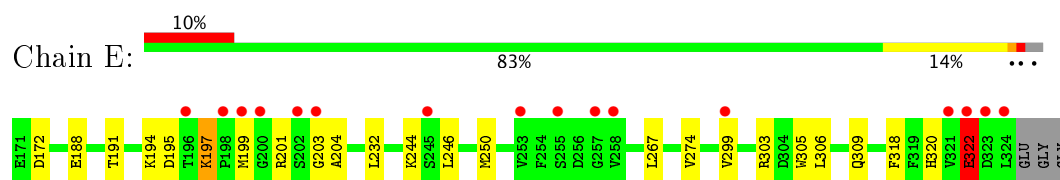
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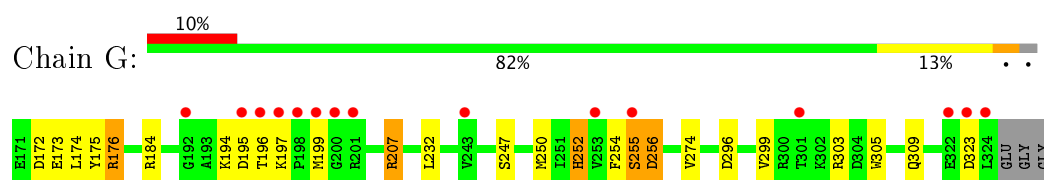
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



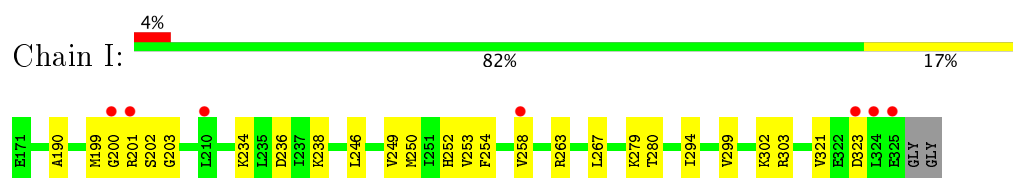
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



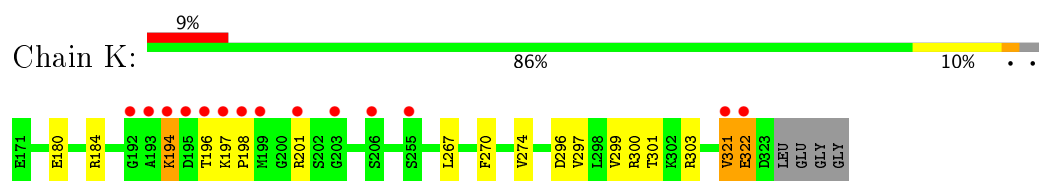
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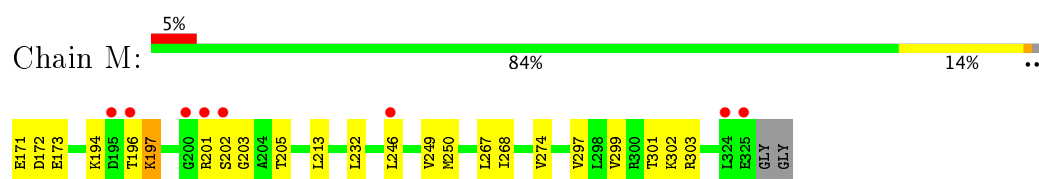
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



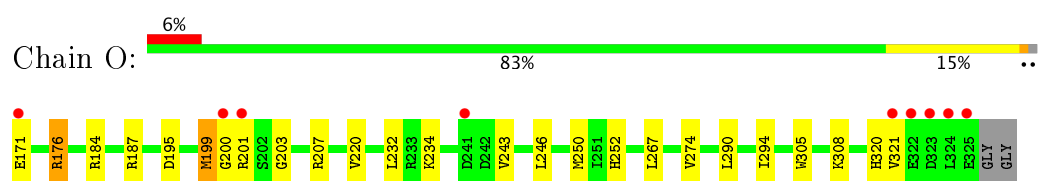
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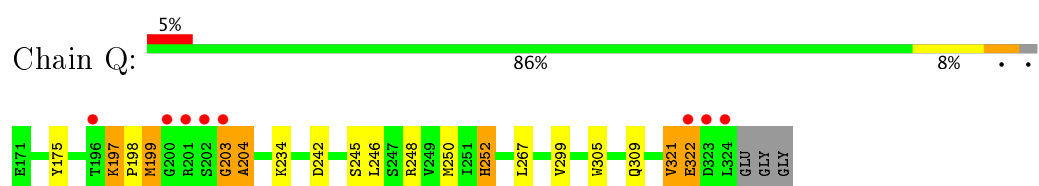
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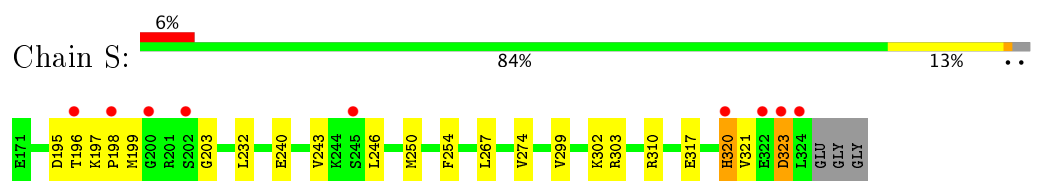
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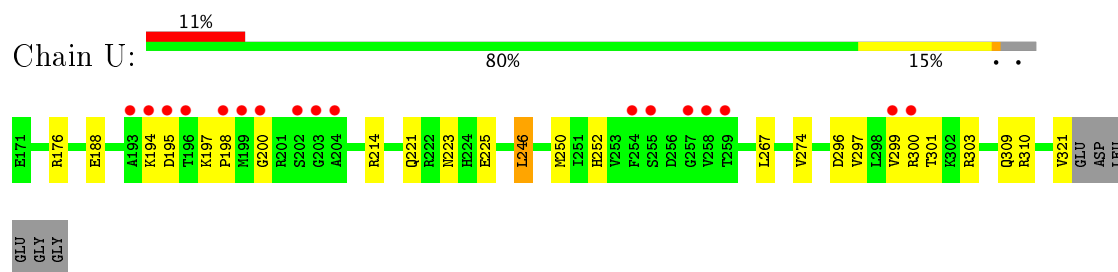
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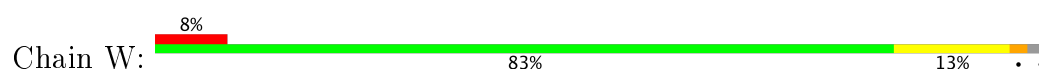
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

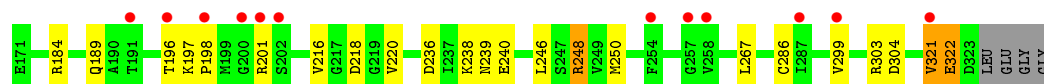


- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

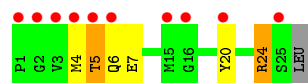
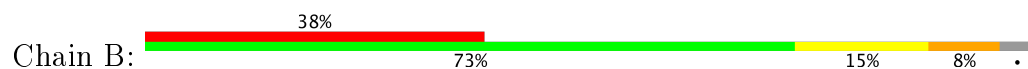


- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

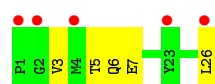
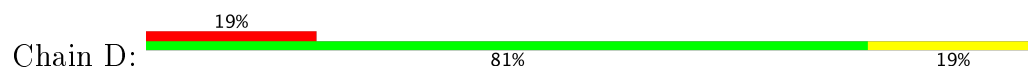




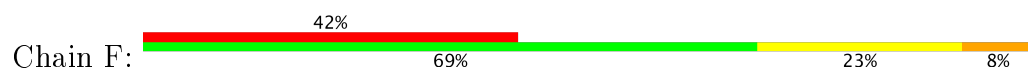
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



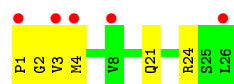
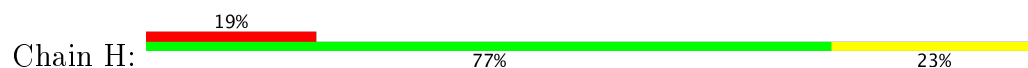
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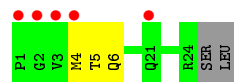
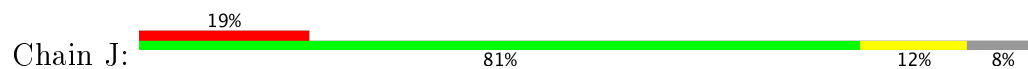
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



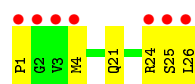
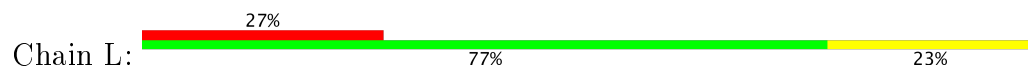
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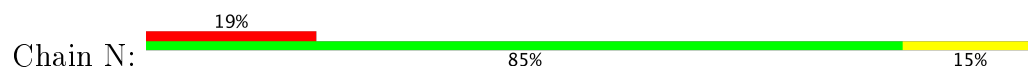
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1

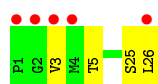


- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1

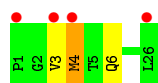
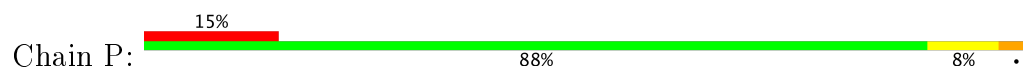


- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1





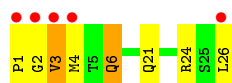
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



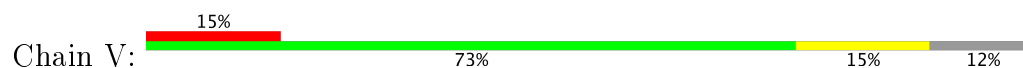
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



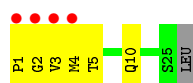
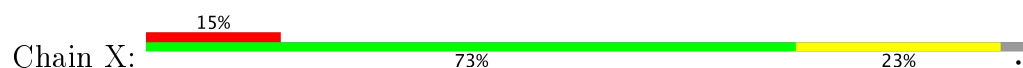
- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



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- Molecule 2: Mule BH3 peptide from E3 ubiquitin-protein ligase HUWE1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	31.79Å 114.24Å 135.98Å 90.12° 92.32° 90.01°	Depositor
Resolution (Å)	35.45 – 2.05 45.29 – 2.05	Depositor EDS
% Data completeness (in resolution range)	95.6 (35.45-2.05) 95.9 (45.29-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.8.2 _1309	Depositor
R, R_{free}	0.295 , 0.346 0.293 , 0.345	Depositor DCC
R_{free} test set	5765 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l 0.299 for -h,k,-l 0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17481	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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 78.04 % 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 7.5113e-07. 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

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	0.22	0/1271	0.41	0/1709
1	C	0.22	0/1271	0.37	0/1709
1	E	0.34	0/1262	0.42	0/1697
1	G	0.21	0/1262	0.40	0/1697
1	I	0.39	0/1271	0.40	0/1709
1	K	0.22	0/1254	0.38	0/1686
1	M	0.23	0/1271	0.39	0/1709
1	O	0.25	0/1271	0.41	0/1709
1	Q	0.23	0/1262	0.40	0/1697
1	S	0.23	0/1261	0.41	0/1695
1	U	0.30	0/1237	0.45	2/1663 (0.1%)
1	W	0.21	0/1251	0.36	0/1682
2	B	0.21	0/200	0.37	0/268
2	D	0.20	0/208	0.37	0/279
2	F	0.20	0/208	0.41	0/279
2	H	0.20	0/208	0.36	0/279
2	J	0.21	0/194	0.40	0/260
2	L	0.20	0/208	0.35	0/279
2	N	0.20	0/206	0.35	0/276
2	P	0.23	0/208	0.41	0/279
2	R	0.20	0/194	0.34	0/260
2	T	0.22	0/208	0.36	0/279
2	V	0.22	0/186	0.36	0/249
2	X	0.23	0/200	0.47	0/268
All	All	0.25	0/17572	0.40	2/23617 (0.0%)

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	O	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	310	ARG	NE-CZ-NH2	-7.67	116.47	120.30
1	U	310	ARG	NE-CZ-NH1	6.05	123.33	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	320	HIS	Peptide

5.2 Too-close contacts [i](#)

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	1251	0	1253	19	0
1	C	1251	0	1253	11	0
1	E	1242	0	1247	15	0
1	G	1242	0	1247	16	0
1	I	1251	0	1253	13	0
1	K	1234	0	1236	10	0
1	M	1251	0	1253	13	0
1	O	1251	0	1253	17	0
1	Q	1242	0	1247	15	0
1	S	1241	0	1247	11	0
1	U	1217	0	1226	13	0
1	W	1231	0	1228	13	0
2	B	198	0	186	4	0
2	D	206	0	197	3	0
2	F	206	0	197	5	0
2	H	206	0	197	2	0
2	J	192	0	181	2	0
2	L	206	0	197	3	0
2	N	204	0	190	2	0
2	P	206	0	197	2	0
2	R	192	0	181	3	0
2	T	206	0	197	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	V	185	0	171	1	0
2	X	198	0	186	3	0
3	A	6	0	0	0	0
3	B	1	0	0	0	0
3	C	11	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	G	12	0	0	0	0
3	H	1	0	0	0	0
3	I	10	0	0	0	0
3	J	2	0	0	0	0
3	K	7	0	0	0	0
3	L	1	0	0	0	0
3	M	20	0	0	0	0
3	N	4	0	0	0	0
3	O	33	0	0	1	0
3	P	6	0	0	0	0
3	Q	14	0	0	0	0
3	R	5	0	0	0	0
3	S	12	0	0	0	0
3	T	7	0	0	0	0
3	U	9	0	0	0	0
3	V	2	0	0	0	0
3	W	5	0	0	0	0
3	X	2	0	0	0	0
All	All	17481	0	17220	190	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 6.

The worst 5 of 190 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:C:250:MET:HG2	1:C:267:LEU:HD11	1.40	1.03
1:I:250:MET:HG2	1:I:267:LEU:HD11	1.52	0.92
1:U:250:MET:HG2	1:U:267:LEU:HD11	1.67	0.77
1:A:253:VAL:HG21	1:A:267:LEU:HD21	1.68	0.75
1:E:188:GLU:HB2	1:E:194:LYS:HA	1.67	0.74

There are no symmetry-related clashes.

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	153/157 (98%)	141 (92%)	11 (7%)	1 (1%)	25	14
1	C	153/157 (98%)	141 (92%)	9 (6%)	3 (2%)	9	2
1	E	152/157 (97%)	144 (95%)	6 (4%)	2 (1%)	14	5
1	G	152/157 (97%)	142 (93%)	7 (5%)	3 (2%)	9	2
1	I	153/157 (98%)	148 (97%)	2 (1%)	3 (2%)	9	2
1	K	151/157 (96%)	142 (94%)	8 (5%)	1 (1%)	25	14
1	M	153/157 (98%)	142 (93%)	9 (6%)	2 (1%)	14	5
1	O	153/157 (98%)	148 (97%)	4 (3%)	1 (1%)	25	14
1	Q	152/157 (97%)	146 (96%)	2 (1%)	4 (3%)	6	1
1	S	152/157 (97%)	146 (96%)	5 (3%)	1 (1%)	25	14
1	U	149/157 (95%)	144 (97%)	5 (3%)	0	100	100
1	W	151/157 (96%)	144 (95%)	5 (3%)	2 (1%)	14	5
2	B	23/26 (88%)	19 (83%)	2 (9%)	2 (9%)	1	0
2	D	24/26 (92%)	22 (92%)	2 (8%)	0	100	100
2	F	24/26 (92%)	22 (92%)	1 (4%)	1 (4%)	3	0
2	H	24/26 (92%)	22 (92%)	1 (4%)	1 (4%)	3	0
2	J	22/26 (85%)	20 (91%)	2 (9%)	0	100	100
2	L	24/26 (92%)	22 (92%)	1 (4%)	1 (4%)	3	0
2	N	24/26 (92%)	23 (96%)	0	1 (4%)	3	0
2	P	24/26 (92%)	22 (92%)	1 (4%)	1 (4%)	3	0
2	R	22/26 (85%)	22 (100%)	0	0	100	100
2	T	24/26 (92%)	22 (92%)	1 (4%)	1 (4%)	3	0
2	V	21/26 (81%)	19 (90%)	1 (5%)	1 (5%)	2	0
2	X	23/26 (88%)	21 (91%)	1 (4%)	1 (4%)	3	0
All	All	2103/2196 (96%)	1984 (94%)	86 (4%)	33 (2%)	11	3

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	323	ASP
1	M	197	LYS
2	N	3	VAL
1	Q	204	ALA
2	B	5	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	136/136 (100%)	127 (93%)	9 (7%)	19	10
1	C	136/136 (100%)	133 (98%)	3 (2%)	57	51
1	E	135/136 (99%)	131 (97%)	4 (3%)	46	39
1	G	135/136 (99%)	131 (97%)	4 (3%)	46	39
1	I	136/136 (100%)	133 (98%)	3 (2%)	57	51
1	K	134/136 (98%)	130 (97%)	4 (3%)	46	39
1	M	136/136 (100%)	133 (98%)	3 (2%)	57	51
1	O	136/136 (100%)	131 (96%)	5 (4%)	39	31
1	Q	135/136 (99%)	132 (98%)	3 (2%)	57	51
1	S	135/136 (99%)	133 (98%)	2 (2%)	70	68
1	U	132/136 (97%)	127 (96%)	5 (4%)	38	30
1	W	132/136 (97%)	129 (98%)	3 (2%)	56	49
2	B	22/23 (96%)	21 (96%)	1 (4%)	32	23
2	D	23/23 (100%)	22 (96%)	1 (4%)	33	25
2	F	23/23 (100%)	20 (87%)	3 (13%)	5	1
2	H	23/23 (100%)	22 (96%)	1 (4%)	33	25
2	J	21/23 (91%)	20 (95%)	1 (5%)	30	21
2	L	23/23 (100%)	23 (100%)	0	100	100
2	N	22/23 (96%)	22 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	23/23 (100%)	22 (96%)	1 (4%)	33	25
2	R	21/23 (91%)	18 (86%)	3 (14%)	4	1
2	T	23/23 (100%)	21 (91%)	2 (9%)	12	5
2	V	20/23 (87%)	19 (95%)	1 (5%)	28	19
2	X	22/23 (96%)	20 (91%)	2 (9%)	11	4
All	All	1884/1908 (99%)	1820 (97%)	64 (3%)	42	34

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	323	ASP
1	M	194	LYS
1	W	196	THR
2	J	5	THR
1	K	321	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	282	ASN

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 ⓘ

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	155/157 (98%)	1.41	32 (20%) 1 1	16, 31, 62, 79	0
1	C	155/157 (98%)	1.20	20 (12%) 4 3	15, 29, 60, 79	0
1	E	154/157 (98%)	0.95	16 (10%) 7 7	10, 26, 59, 72	0
1	G	154/157 (98%)	0.78	15 (9%) 8 9	9, 24, 51, 67	0
1	I	155/157 (98%)	0.53	7 (4%) 34 37	9, 24, 45, 69	0
1	K	153/157 (97%)	0.60	14 (9%) 10 11	10, 23, 57, 76	0
1	M	155/157 (98%)	0.29	8 (5%) 28 30	7, 16, 46, 71	0
1	O	155/157 (98%)	0.37	9 (5%) 24 26	6, 15, 40, 78	0
1	Q	154/157 (98%)	0.47	8 (5%) 28 30	9, 20, 51, 70	0
1	S	154/157 (98%)	0.53	9 (5%) 24 26	7, 19, 52, 73	0
1	U	151/157 (96%)	0.66	17 (11%) 6 6	9, 23, 54, 70	0
1	W	153/157 (97%)	0.73	12 (7%) 14 15	9, 24, 48, 66	0
2	B	25/26 (96%)	1.99	10 (40%) 0 0	21, 29, 69, 78	0
2	D	26/26 (100%)	1.50	5 (19%) 1 1	17, 28, 60, 72	0
2	F	26/26 (100%)	3.00	11 (42%) 0 0	17, 34, 73, 82	0
2	H	26/26 (100%)	1.39	5 (19%) 1 1	14, 26, 61, 66	0
2	J	24/26 (92%)	1.27	5 (20%) 1 1	16, 26, 62, 70	0
2	L	26/26 (100%)	1.95	7 (26%) 1 0	14, 29, 74, 79	0
2	N	26/26 (100%)	1.21	5 (19%) 1 1	8, 17, 77, 88	0
2	P	26/26 (100%)	0.79	4 (15%) 2 2	7, 13, 56, 62	0
2	R	24/26 (92%)	1.42	5 (20%) 1 1	13, 23, 58, 72	0
2	T	26/26 (100%)	0.98	5 (19%) 1 1	8, 21, 60, 71	0
2	V	23/26 (88%)	1.11	4 (17%) 2 1	16, 28, 49, 66	0
2	X	25/26 (96%)	1.38	4 (16%) 2 2	17, 25, 68, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	2151/2196 (97%)	0.82	237 (11%) 6 6	6, 24, 59, 88	0

The worst 5 of 237 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	324	LEU	20.4
2	L	26	LEU	12.9
1	E	324	LEU	12.4
2	F	1	PRO	12.4
2	R	1	PRO	10.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.