



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 03:27 pm BST

PDB ID : 4H56  
Title : Crystal structure of the Clostridium perfringens NetB toxin in the membrane inserted form  
Authors : Savva, C.G.; Fernandes da Costa, S.P.; Bokori-Brown, M.; Naylor, C.; Cole, A.R.; Moss, D.S.; Titball, R.W.; Basak, A.K.  
Deposited on : 2012-09-18  
Resolution : 3.90 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](mailto: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.

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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

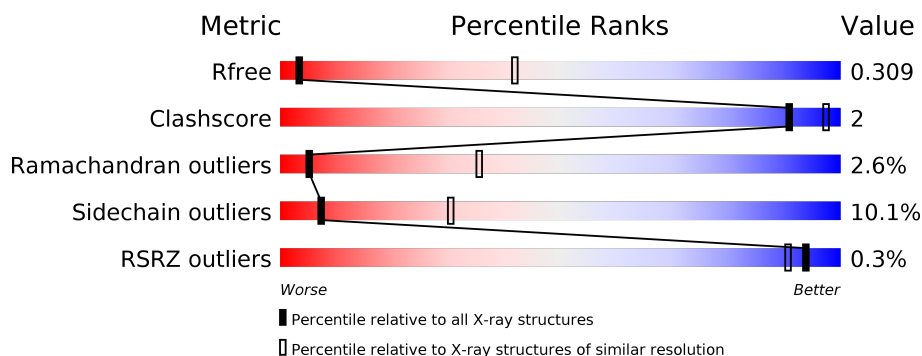
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.90 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))
$R_{free}$	130704	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)

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  $\geq 3$ , 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	296	<div> <div style="width: 78%;"></div> <div style="width: 11%;"></div> <div style="width: 10%;"></div> </div> <div>78% 11% • 10%</div>
1	B	296	<div> <div style="width: 78%;"></div> <div style="width: 11%;"></div> <div style="width: 10%;"></div> </div> <div>78% 11% • 10%</div>
1	C	296	<div> <div style="width: 79%;"></div> <div style="width: 10%;"></div> <div style="width: 10%;"></div> </div> <div>79% 10% • 10%</div>
1	D	296	<div> <div style="width: 79%;"></div> <div style="width: 10%;"></div> <div style="width: 10%;"></div> </div> <div>79% 10% • 10%</div>
1	E	296	<div> <div style="width: 80%;"></div> <div style="width: 9%;"></div> <div style="width: 10%;"></div> </div> <div>80% 9% • 10%</div>
1	F	296	<div> <div style="width: 77%;"></div> <div style="width: 11%;"></div> <div style="width: 10%;"></div> </div> <div>77% 11% • 10%</div>

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Mol	Chain	Length	Quality of chain
1	G	296	<div><div>%</div><div><div></div><div>78%</div><div>11%</div><div>•</div><div>10%</div></div></div>
1	H	296	<div><div></div><div>78%</div><div>11%</div><div>•</div><div>10%</div></div>
1	I	296	<div><div></div><div>79%</div><div>10%</div><div>•</div><div>10%</div></div>
1	J	296	<div><div></div><div>78%</div><div>11%</div><div>•</div><div>10%</div></div>
1	K	296	<div><div></div><div>78%</div><div>11%</div><div>•</div><div>10%</div></div>
1	L	296	<div><div></div><div>77%</div><div>12%</div><div>•</div><div>10%</div></div>
1	M	296	<div><div></div><div>78%</div><div>11%</div><div>•</div><div>10%</div></div>
1	N	296	<div><div></div><div>77%</div><div>12%</div><div>•</div><div>10%</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 27963 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 Necrotic enteritis toxin B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			1984	1239	335	406	4			
1	B	267	Total	C	N	O	S	0	0	0
			1977	1236	328	409	4			
1	C	267	Total	C	N	O	S	0	0	0
			1996	1247	337	409	3			
1	D	267	Total	C	N	O	S	0	0	0
			1988	1249	331	405	3			
1	E	267	Total	C	N	O	S	0	0	0
			1966	1232	331	399	4			
1	F	267	Total	C	N	O	S	0	0	0
			1983	1238	330	412	3			
1	G	267	Total	C	N	O	S	0	0	0
			1995	1252	331	408	4			
1	H	267	Total	C	N	O	S	0	0	0
			1996	1249	335	408	4			
1	I	267	Total	C	N	O	S	0	0	0
			2008	1259	336	410	3			
1	J	267	Total	C	N	O	S	0	0	0
			2009	1262	336	407	4			
1	K	267	Total	C	N	O	S	0	0	0
			2013	1267	334	408	4			
1	L	267	Total	C	N	O	S	0	0	0
			2023	1270	336	413	4			
1	M	267	Total	C	N	O	S	0	0	0
			2005	1259	332	410	4			
1	N	267	Total	C	N	O	S	0	0	0
			2020	1265	337	414	4			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
A	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
A	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
B	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
B	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
B	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
B	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
C	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
C	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
C	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
C	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
D	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
D	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
D	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
D	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
E	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
E	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
E	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
E	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
F	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
F	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
F	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
F	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
G	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
G	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
G	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
G	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
H	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
H	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
H	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
H	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
I	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
I	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
I	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
I	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
J	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
J	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
J	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
J	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
K	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
K	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
K	-1	MET	-	EXPRESSION TAG	UNP A8ULG6

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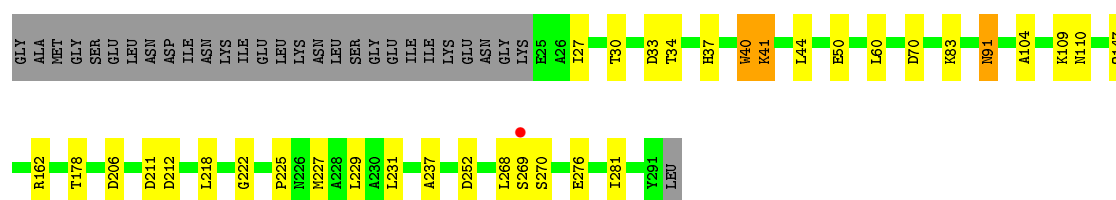
Chain	Residue	Modelled	Actual	Comment	Reference
K	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
L	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
L	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
L	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
L	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
M	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
M	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
M	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
M	0	GLY	-	EXPRESSION TAG	UNP A8ULG6
N	-3	GLY	-	EXPRESSION TAG	UNP A8ULG6
N	-2	ALA	-	EXPRESSION TAG	UNP A8ULG6
N	-1	MET	-	EXPRESSION TAG	UNP A8ULG6
N	0	GLY	-	EXPRESSION TAG	UNP A8ULG6

### 3 Residue-property plots


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

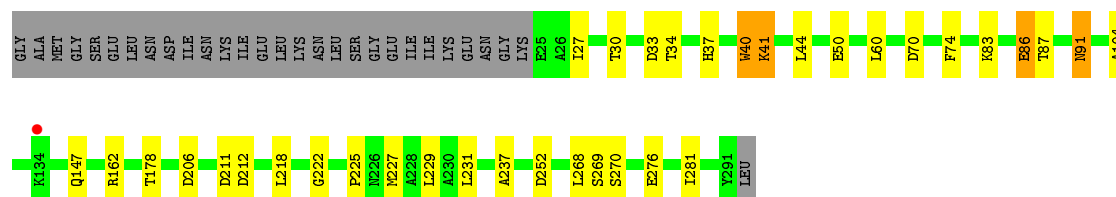
#### • Molecule 1: Necrotic enteritis toxin B

Chain A: 




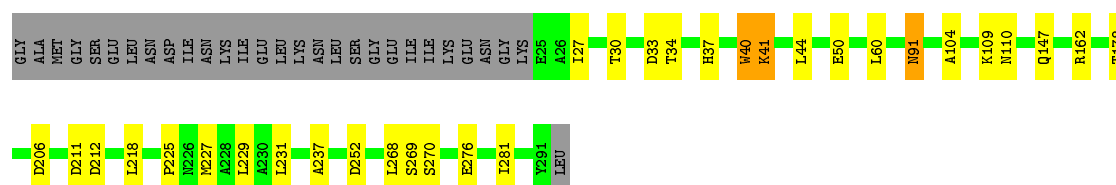
#### • Molecule 1: Necrotic enteritis toxin B

Chain B: 




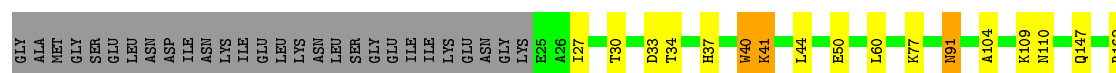
#### • Molecule 1: Necrotic enteritis toxin B

Chain C: 



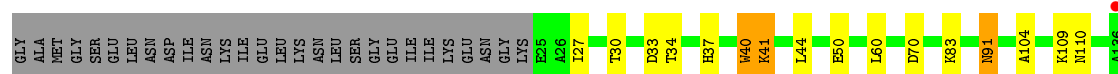
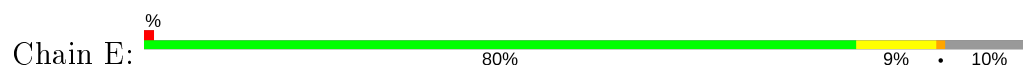
#### • Molecule 1: Necrotic enteritis toxin B

Chain D: 

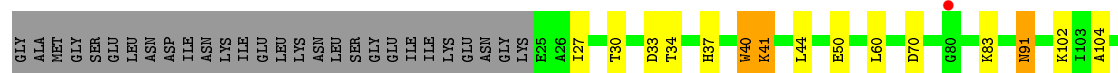
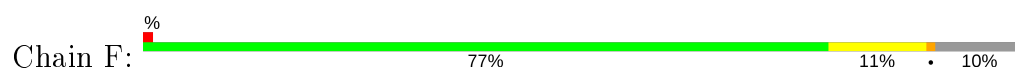




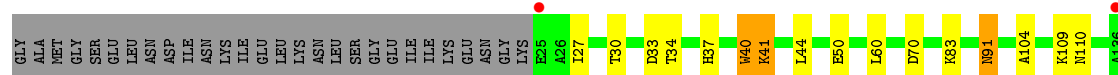
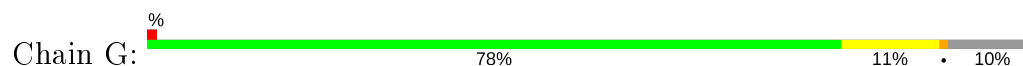
- Molecule 1: Necrotic enteritis toxin B



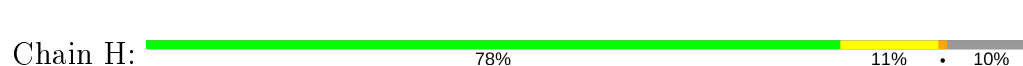
- Molecule 1: Necrotic enteritis toxin B



- Molecule 1: Necrotic enteritis toxin B



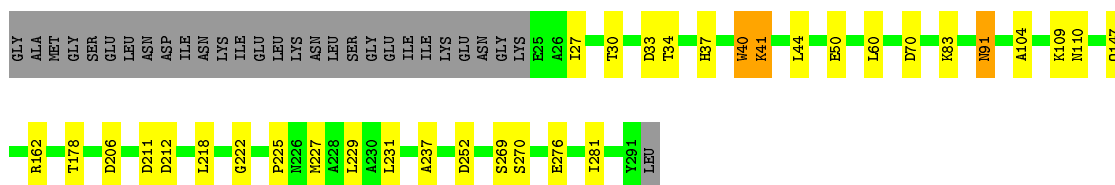
- Molecule 1: Necrotic enteritis toxin B



- Molecule 1: Necrotic enteritis toxin B

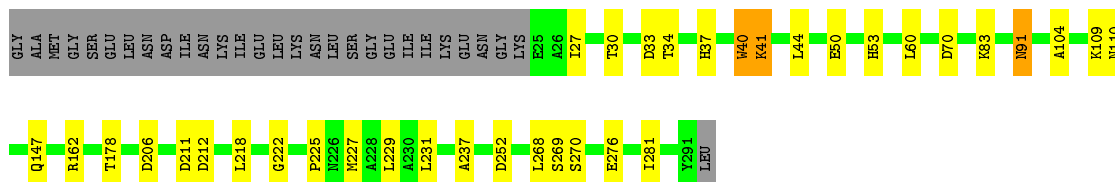






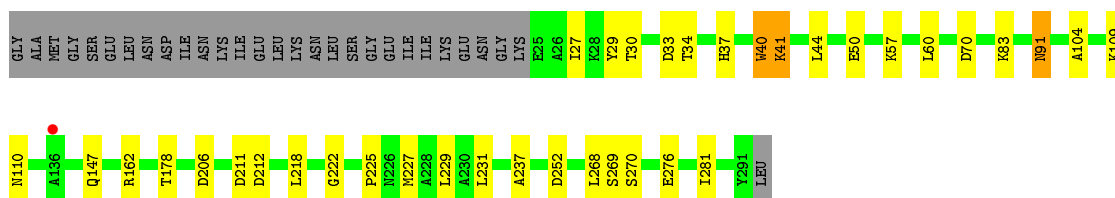
- Molecule 1: Necrotic enteritis toxin B

Chain J: 78% 11% 10%



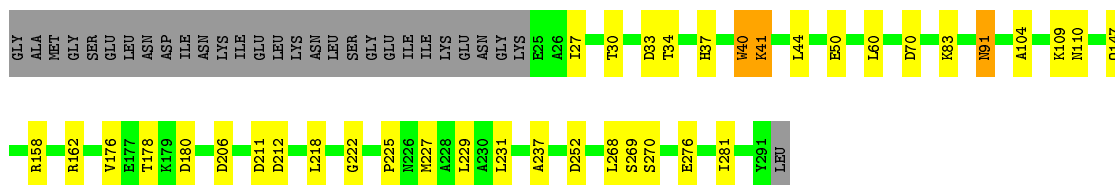
- Molecule 1: Necrotic enteritis toxin B

Chain K: 78% 11% 10%



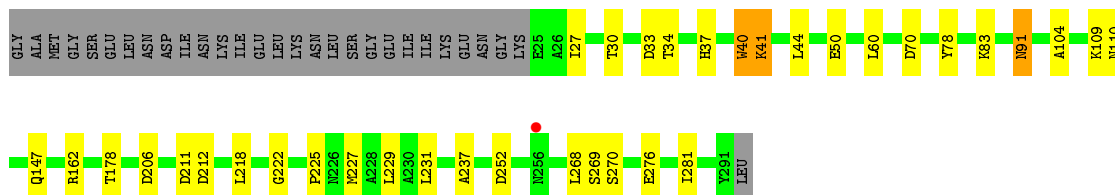
- Molecule 1: Necrotic enteritis toxin B

Chain L: 77% 12% 10%



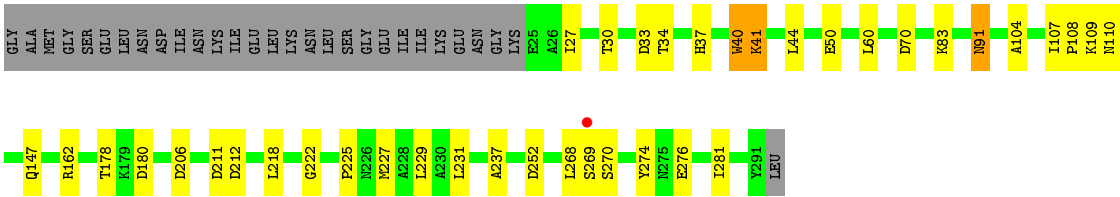
- Molecule 1: Necrotic enteritis toxin B

Chain M: 78% 11% 10%



- Molecule 1: Necrotic enteritis toxin B

Chain N: 77% 12% 10%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	313.23Å 168.04Å 160.46Å 90.00° 109.42° 90.00°	Depositor
Resolution (Å)	27.70 – 3.90 27.71 – 3.90	Depositor EDS
% Data completeness (in resolution range)	89.6 (27.70-3.90) 97.5 (27.71-3.90)	Depositor EDS
$R_{merge}$	0.34	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.44 (at 3.85Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.284 , 0.309 0.284 , 0.309	Depositor DCC
$R_{free}$ test set	3514 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.7	Xtrriage
Anisotropy	1.037	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 61.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	27963	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.23	0/2025	0.46	0/2763
1	B	0.23	0/2019	0.47	0/2761
1	C	0.23	0/2039	0.47	0/2785
1	D	0.23	0/2033	0.46	0/2779
1	E	0.23	0/2009	0.46	0/2747
1	F	0.24	0/2025	0.47	0/2767
1	G	0.23	0/2040	0.46	0/2788
1	H	0.23	0/2040	0.47	0/2786
1	I	0.24	0/2053	0.46	0/2802
1	J	0.23	0/2053	0.46	0/2798
1	K	0.23	0/2058	0.46	0/2805
1	L	0.24	0/2068	0.48	1/2820 (0.0%)
1	M	0.24	0/2051	0.47	0/2803
1	N	0.23	0/2064	0.47	1/2815 (0.0%)
All	All	0.23	0/28577	0.47	2/39019 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	180	ASP	CB-CG-OD2	5.22	123.00	118.30
1	N	180	ASP	CB-CG-OD2	5.17	122.95	118.30

There are no chirality outliers.

There are no planarity outliers.

### 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	1984	0	1765	7	0
1	B	1977	0	1728	8	0
1	C	1996	0	1765	5	0
1	D	1988	0	1748	6	0
1	E	1966	0	1721	7	0
1	F	1983	0	1737	8	0
1	G	1995	0	1754	7	0
1	H	1996	0	1760	8	0
1	I	2008	0	1781	7	0
1	J	2009	0	1804	9	0
1	K	2013	0	1809	9	0
1	L	2023	0	1815	9	0
1	M	2005	0	1765	7	0
1	N	2020	0	1809	9	0
All	All	27963	0	24761	90	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 2.

The worst 5 of 90 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:F:183:ASN:OD1	1:G:213:ARG:NE	2.24	0.70
1:F:176:VAL:O	1:F:183:ASN:ND2	2.27	0.68
1:C:110:ASN:ND2	1:D:222:GLY:O	2.35	0.60
1:B:74:PHE:HB3	1:N:274:TYR:CG	2.39	0.57
1:M:110:ASN:ND2	1:N:222:GLY:O	2.40	0.54

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	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	B	265/296 (90%)	236 (89%)	22 (8%)	7 (3%)	5	35
1	C	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	D	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	E	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	F	265/296 (90%)	236 (89%)	22 (8%)	7 (3%)	5	35
1	G	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	H	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	I	265/296 (90%)	237 (89%)	21 (8%)	7 (3%)	5	35
1	J	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	K	265/296 (90%)	236 (89%)	22 (8%)	7 (3%)	5	35
1	L	265/296 (90%)	236 (89%)	22 (8%)	7 (3%)	5	35
1	M	265/296 (90%)	235 (89%)	23 (9%)	7 (3%)	5	35
1	N	265/296 (90%)	236 (89%)	22 (8%)	7 (3%)	5	35
All	All	3710/4144 (90%)	3297 (89%)	315 (8%)	98 (3%)	5	35

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	269	SER
1	B	41	LYS
1	B	269	SER
1	C	41	LYS

### 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	197/258 (76%)	177 (90%)	20 (10%)	7	30
1	B	194/258 (75%)	174 (90%)	20 (10%)	7	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	198/258 (77%)	178 (90%)	20 (10%)	7	30
1	D	195/258 (76%)	175 (90%)	20 (10%)	7	30
1	E	190/258 (74%)	174 (92%)	16 (8%)	11	39
1	F	196/258 (76%)	173 (88%)	23 (12%)	5	26
1	G	197/258 (76%)	177 (90%)	20 (10%)	7	30
1	H	197/258 (76%)	177 (90%)	20 (10%)	7	30
1	I	200/258 (78%)	181 (90%)	19 (10%)	8	33
1	J	201/258 (78%)	181 (90%)	20 (10%)	7	30
1	K	202/258 (78%)	181 (90%)	21 (10%)	7	29
1	L	205/258 (80%)	185 (90%)	20 (10%)	8	31
1	M	199/258 (77%)	178 (89%)	21 (11%)	6	29
1	N	205/258 (80%)	185 (90%)	20 (10%)	8	31
All	All	2776/3612 (77%)	2496 (90%)	280 (10%)	7	30

5 of 280 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	147	GLN
1	H	270	SER
1	M	276	GLU
1	G	218	LEU
1	H	50	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	53	HIS
1	M	53	HIS

### 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 [i](#)

There are no carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	267/296 (90%)	-0.25	1 (0%) 92 87	3, 61, 120, 283	0
1	B	267/296 (90%)	-0.16	1 (0%) 92 87	23, 70, 128, 261	0
1	C	267/296 (90%)	-0.15	0 100 100	13, 78, 135, 315	0
1	D	267/296 (90%)	-0.03	0 100 100	28, 89, 137, 213	0
1	E	267/296 (90%)	0.04	4 (1%) 73 64	36, 91, 155, 249	0
1	F	267/296 (90%)	0.02	2 (0%) 87 82	18, 84, 140, 260	0
1	G	267/296 (90%)	-0.09	2 (0%) 87 82	18, 70, 131, 170	0
1	H	267/296 (90%)	-0.23	0 100 100	21, 67, 124, 284	0
1	I	267/296 (90%)	-0.13	0 100 100	15, 69, 117, 180	0
1	J	267/296 (90%)	-0.26	0 100 100	6, 67, 114, 214	0
1	K	267/296 (90%)	-0.25	1 (0%) 92 87	3, 59, 117, 239	0
1	L	267/296 (90%)	-0.28	0 100 100	2, 56, 108, 168	0
1	M	267/296 (90%)	-0.24	1 (0%) 92 87	9, 59, 114, 292	0
1	N	267/296 (90%)	-0.18	1 (0%) 92 87	4, 70, 126, 227	0
All	All	3738/4144 (90%)	-0.16	13 (0%) 94 90	2, 71, 132, 315	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	136	ALA	3.9
1	F	80	GLY	3.0
1	E	136	ALA	2.8
1	F	262	TRP	2.8
1	E	269	SER	2.6

## 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 carbohydrates 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.