



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:37 AM UTC

PDB ID : 7YNY / pdb_00007yny
Title : Crystal structure of baculovirus LEF-3 from Helicoverpa armigera nucleopolyhedrovirus
Authors : Yin, J.; Li, Z.; Cao, S.
Deposited on : 2022-08-01
Resolution : 3.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

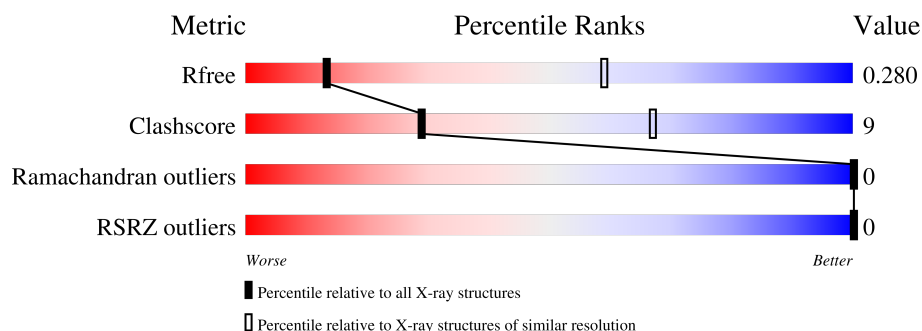
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.51 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	1025 (3.56-3.48)
Clashscore	190562	1079 (3.56-3.48)
Ramachandran outliers	187476	1052 (3.56-3.48)
RSRZ outliers	180081	1024 (3.56-3.48)

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	413	
1	B	413	
1	C	413	
1	D	413	
1	E	413	
1	F	413	

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Mol	Chain	Length	Quality of chain
1	G	413	 66% 14% 20%
1	H	413	 63% 16% 21%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 21644 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 Lef3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	0	0
			2726	1728	444	542	12			
1	B	332	Total	C	N	O	S	0	0	0
			2726	1728	444	542	12			
1	C	325	Total	C	N	O	S	0	0	0
			2669	1694	437	527	11			
1	D	325	Total	C	N	O	S	0	0	0
			2669	1694	437	527	11			
1	E	332	Total	C	N	O	S	0	0	0
			2726	1728	444	542	12			
1	F	332	Total	C	N	O	S	0	0	0
			2726	1728	444	542	12			
1	G	332	Total	C	N	O	S	0	0	0
			2726	1728	444	542	12			
1	H	327	Total	C	N	O	S	0	0	0
			2676	1695	438	531	12			

There are 272 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	initiating methionine	UNP Q91BW6
A	-32	GLY	-	expression tag	UNP Q91BW6
A	-31	SER	-	expression tag	UNP Q91BW6
A	-30	SER	-	expression tag	UNP Q91BW6
A	-29	HIS	-	expression tag	UNP Q91BW6
A	-28	HIS	-	expression tag	UNP Q91BW6
A	-27	HIS	-	expression tag	UNP Q91BW6
A	-26	HIS	-	expression tag	UNP Q91BW6
A	-25	HIS	-	expression tag	UNP Q91BW6
A	-24	HIS	-	expression tag	UNP Q91BW6
A	-23	SER	-	expression tag	UNP Q91BW6
A	-22	SER	-	expression tag	UNP Q91BW6
A	-21	GLY	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	LEU	-	expression tag	UNP Q91BW6
A	-19	VAL	-	expression tag	UNP Q91BW6
A	-18	PRO	-	expression tag	UNP Q91BW6
A	-17	ARG	-	expression tag	UNP Q91BW6
A	-16	GLY	-	expression tag	UNP Q91BW6
A	-15	SER	-	expression tag	UNP Q91BW6
A	-14	HIS	-	expression tag	UNP Q91BW6
A	-13	MET	-	expression tag	UNP Q91BW6
A	-12	ALA	-	expression tag	UNP Q91BW6
A	-11	SER	-	expression tag	UNP Q91BW6
A	-10	MET	-	expression tag	UNP Q91BW6
A	-9	THR	-	expression tag	UNP Q91BW6
A	-8	GLY	-	expression tag	UNP Q91BW6
A	-7	GLY	-	expression tag	UNP Q91BW6
A	-6	GLN	-	expression tag	UNP Q91BW6
A	-5	GLN	-	expression tag	UNP Q91BW6
A	-4	MET	-	expression tag	UNP Q91BW6
A	-3	GLY	-	expression tag	UNP Q91BW6
A	-2	ARG	-	expression tag	UNP Q91BW6
A	-1	GLY	-	expression tag	UNP Q91BW6
A	0	SER	-	expression tag	UNP Q91BW6
B	-33	MET	-	initiating methionine	UNP Q91BW6
B	-32	GLY	-	expression tag	UNP Q91BW6
B	-31	SER	-	expression tag	UNP Q91BW6
B	-30	SER	-	expression tag	UNP Q91BW6
B	-29	HIS	-	expression tag	UNP Q91BW6
B	-28	HIS	-	expression tag	UNP Q91BW6
B	-27	HIS	-	expression tag	UNP Q91BW6
B	-26	HIS	-	expression tag	UNP Q91BW6
B	-25	HIS	-	expression tag	UNP Q91BW6
B	-24	HIS	-	expression tag	UNP Q91BW6
B	-23	SER	-	expression tag	UNP Q91BW6
B	-22	SER	-	expression tag	UNP Q91BW6
B	-21	GLY	-	expression tag	UNP Q91BW6
B	-20	LEU	-	expression tag	UNP Q91BW6
B	-19	VAL	-	expression tag	UNP Q91BW6
B	-18	PRO	-	expression tag	UNP Q91BW6
B	-17	ARG	-	expression tag	UNP Q91BW6
B	-16	GLY	-	expression tag	UNP Q91BW6
B	-15	SER	-	expression tag	UNP Q91BW6
B	-14	HIS	-	expression tag	UNP Q91BW6
B	-13	MET	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	ALA	-	expression tag	UNP Q91BW6
B	-11	SER	-	expression tag	UNP Q91BW6
B	-10	MET	-	expression tag	UNP Q91BW6
B	-9	THR	-	expression tag	UNP Q91BW6
B	-8	GLY	-	expression tag	UNP Q91BW6
B	-7	GLY	-	expression tag	UNP Q91BW6
B	-6	GLN	-	expression tag	UNP Q91BW6
B	-5	GLN	-	expression tag	UNP Q91BW6
B	-4	MET	-	expression tag	UNP Q91BW6
B	-3	GLY	-	expression tag	UNP Q91BW6
B	-2	ARG	-	expression tag	UNP Q91BW6
B	-1	GLY	-	expression tag	UNP Q91BW6
B	0	SER	-	expression tag	UNP Q91BW6
C	-33	MET	-	initiating methionine	UNP Q91BW6
C	-32	GLY	-	expression tag	UNP Q91BW6
C	-31	SER	-	expression tag	UNP Q91BW6
C	-30	SER	-	expression tag	UNP Q91BW6
C	-29	HIS	-	expression tag	UNP Q91BW6
C	-28	HIS	-	expression tag	UNP Q91BW6
C	-27	HIS	-	expression tag	UNP Q91BW6
C	-26	HIS	-	expression tag	UNP Q91BW6
C	-25	HIS	-	expression tag	UNP Q91BW6
C	-24	HIS	-	expression tag	UNP Q91BW6
C	-23	SER	-	expression tag	UNP Q91BW6
C	-22	SER	-	expression tag	UNP Q91BW6
C	-21	GLY	-	expression tag	UNP Q91BW6
C	-20	LEU	-	expression tag	UNP Q91BW6
C	-19	VAL	-	expression tag	UNP Q91BW6
C	-18	PRO	-	expression tag	UNP Q91BW6
C	-17	ARG	-	expression tag	UNP Q91BW6
C	-16	GLY	-	expression tag	UNP Q91BW6
C	-15	SER	-	expression tag	UNP Q91BW6
C	-14	HIS	-	expression tag	UNP Q91BW6
C	-13	MET	-	expression tag	UNP Q91BW6
C	-12	ALA	-	expression tag	UNP Q91BW6
C	-11	SER	-	expression tag	UNP Q91BW6
C	-10	MET	-	expression tag	UNP Q91BW6
C	-9	THR	-	expression tag	UNP Q91BW6
C	-8	GLY	-	expression tag	UNP Q91BW6
C	-7	GLY	-	expression tag	UNP Q91BW6
C	-6	GLN	-	expression tag	UNP Q91BW6
C	-5	GLN	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	MET	-	expression tag	UNP Q91BW6
C	-3	GLY	-	expression tag	UNP Q91BW6
C	-2	ARG	-	expression tag	UNP Q91BW6
C	-1	GLY	-	expression tag	UNP Q91BW6
C	0	SER	-	expression tag	UNP Q91BW6
D	-33	MET	-	initiating methionine	UNP Q91BW6
D	-32	GLY	-	expression tag	UNP Q91BW6
D	-31	SER	-	expression tag	UNP Q91BW6
D	-30	SER	-	expression tag	UNP Q91BW6
D	-29	HIS	-	expression tag	UNP Q91BW6
D	-28	HIS	-	expression tag	UNP Q91BW6
D	-27	HIS	-	expression tag	UNP Q91BW6
D	-26	HIS	-	expression tag	UNP Q91BW6
D	-25	HIS	-	expression tag	UNP Q91BW6
D	-24	HIS	-	expression tag	UNP Q91BW6
D	-23	SER	-	expression tag	UNP Q91BW6
D	-22	SER	-	expression tag	UNP Q91BW6
D	-21	GLY	-	expression tag	UNP Q91BW6
D	-20	LEU	-	expression tag	UNP Q91BW6
D	-19	VAL	-	expression tag	UNP Q91BW6
D	-18	PRO	-	expression tag	UNP Q91BW6
D	-17	ARG	-	expression tag	UNP Q91BW6
D	-16	GLY	-	expression tag	UNP Q91BW6
D	-15	SER	-	expression tag	UNP Q91BW6
D	-14	HIS	-	expression tag	UNP Q91BW6
D	-13	MET	-	expression tag	UNP Q91BW6
D	-12	ALA	-	expression tag	UNP Q91BW6
D	-11	SER	-	expression tag	UNP Q91BW6
D	-10	MET	-	expression tag	UNP Q91BW6
D	-9	THR	-	expression tag	UNP Q91BW6
D	-8	GLY	-	expression tag	UNP Q91BW6
D	-7	GLY	-	expression tag	UNP Q91BW6
D	-6	GLN	-	expression tag	UNP Q91BW6
D	-5	GLN	-	expression tag	UNP Q91BW6
D	-4	MET	-	expression tag	UNP Q91BW6
D	-3	GLY	-	expression tag	UNP Q91BW6
D	-2	ARG	-	expression tag	UNP Q91BW6
D	-1	GLY	-	expression tag	UNP Q91BW6
D	0	SER	-	expression tag	UNP Q91BW6
E	-33	MET	-	initiating methionine	UNP Q91BW6
E	-32	GLY	-	expression tag	UNP Q91BW6
E	-31	SER	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-30	SER	-	expression tag	UNP Q91BW6
E	-29	HIS	-	expression tag	UNP Q91BW6
E	-28	HIS	-	expression tag	UNP Q91BW6
E	-27	HIS	-	expression tag	UNP Q91BW6
E	-26	HIS	-	expression tag	UNP Q91BW6
E	-25	HIS	-	expression tag	UNP Q91BW6
E	-24	HIS	-	expression tag	UNP Q91BW6
E	-23	SER	-	expression tag	UNP Q91BW6
E	-22	SER	-	expression tag	UNP Q91BW6
E	-21	GLY	-	expression tag	UNP Q91BW6
E	-20	LEU	-	expression tag	UNP Q91BW6
E	-19	VAL	-	expression tag	UNP Q91BW6
E	-18	PRO	-	expression tag	UNP Q91BW6
E	-17	ARG	-	expression tag	UNP Q91BW6
E	-16	GLY	-	expression tag	UNP Q91BW6
E	-15	SER	-	expression tag	UNP Q91BW6
E	-14	HIS	-	expression tag	UNP Q91BW6
E	-13	MET	-	expression tag	UNP Q91BW6
E	-12	ALA	-	expression tag	UNP Q91BW6
E	-11	SER	-	expression tag	UNP Q91BW6
E	-10	MET	-	expression tag	UNP Q91BW6
E	-9	THR	-	expression tag	UNP Q91BW6
E	-8	GLY	-	expression tag	UNP Q91BW6
E	-7	GLY	-	expression tag	UNP Q91BW6
E	-6	GLN	-	expression tag	UNP Q91BW6
E	-5	GLN	-	expression tag	UNP Q91BW6
E	-4	MET	-	expression tag	UNP Q91BW6
E	-3	GLY	-	expression tag	UNP Q91BW6
E	-2	ARG	-	expression tag	UNP Q91BW6
E	-1	GLY	-	expression tag	UNP Q91BW6
E	0	SER	-	expression tag	UNP Q91BW6
F	-33	MET	-	initiating methionine	UNP Q91BW6
F	-32	GLY	-	expression tag	UNP Q91BW6
F	-31	SER	-	expression tag	UNP Q91BW6
F	-30	SER	-	expression tag	UNP Q91BW6
F	-29	HIS	-	expression tag	UNP Q91BW6
F	-28	HIS	-	expression tag	UNP Q91BW6
F	-27	HIS	-	expression tag	UNP Q91BW6
F	-26	HIS	-	expression tag	UNP Q91BW6
F	-25	HIS	-	expression tag	UNP Q91BW6
F	-24	HIS	-	expression tag	UNP Q91BW6
F	-23	SER	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-22	SER	-	expression tag	UNP Q91BW6
F	-21	GLY	-	expression tag	UNP Q91BW6
F	-20	LEU	-	expression tag	UNP Q91BW6
F	-19	VAL	-	expression tag	UNP Q91BW6
F	-18	PRO	-	expression tag	UNP Q91BW6
F	-17	ARG	-	expression tag	UNP Q91BW6
F	-16	GLY	-	expression tag	UNP Q91BW6
F	-15	SER	-	expression tag	UNP Q91BW6
F	-14	HIS	-	expression tag	UNP Q91BW6
F	-13	MET	-	expression tag	UNP Q91BW6
F	-12	ALA	-	expression tag	UNP Q91BW6
F	-11	SER	-	expression tag	UNP Q91BW6
F	-10	MET	-	expression tag	UNP Q91BW6
F	-9	THR	-	expression tag	UNP Q91BW6
F	-8	GLY	-	expression tag	UNP Q91BW6
F	-7	GLY	-	expression tag	UNP Q91BW6
F	-6	GLN	-	expression tag	UNP Q91BW6
F	-5	GLN	-	expression tag	UNP Q91BW6
F	-4	MET	-	expression tag	UNP Q91BW6
F	-3	GLY	-	expression tag	UNP Q91BW6
F	-2	ARG	-	expression tag	UNP Q91BW6
F	-1	GLY	-	expression tag	UNP Q91BW6
F	0	SER	-	expression tag	UNP Q91BW6
G	-33	MET	-	initiating methionine	UNP Q91BW6
G	-32	GLY	-	expression tag	UNP Q91BW6
G	-31	SER	-	expression tag	UNP Q91BW6
G	-30	SER	-	expression tag	UNP Q91BW6
G	-29	HIS	-	expression tag	UNP Q91BW6
G	-28	HIS	-	expression tag	UNP Q91BW6
G	-27	HIS	-	expression tag	UNP Q91BW6
G	-26	HIS	-	expression tag	UNP Q91BW6
G	-25	HIS	-	expression tag	UNP Q91BW6
G	-24	HIS	-	expression tag	UNP Q91BW6
G	-23	SER	-	expression tag	UNP Q91BW6
G	-22	SER	-	expression tag	UNP Q91BW6
G	-21	GLY	-	expression tag	UNP Q91BW6
G	-20	LEU	-	expression tag	UNP Q91BW6
G	-19	VAL	-	expression tag	UNP Q91BW6
G	-18	PRO	-	expression tag	UNP Q91BW6
G	-17	ARG	-	expression tag	UNP Q91BW6
G	-16	GLY	-	expression tag	UNP Q91BW6
G	-15	SER	-	expression tag	UNP Q91BW6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-14	HIS	-	expression tag	UNP Q91BW6
G	-13	MET	-	expression tag	UNP Q91BW6
G	-12	ALA	-	expression tag	UNP Q91BW6
G	-11	SER	-	expression tag	UNP Q91BW6
G	-10	MET	-	expression tag	UNP Q91BW6
G	-9	THR	-	expression tag	UNP Q91BW6
G	-8	GLY	-	expression tag	UNP Q91BW6
G	-7	GLY	-	expression tag	UNP Q91BW6
G	-6	GLN	-	expression tag	UNP Q91BW6
G	-5	GLN	-	expression tag	UNP Q91BW6
G	-4	MET	-	expression tag	UNP Q91BW6
G	-3	GLY	-	expression tag	UNP Q91BW6
G	-2	ARG	-	expression tag	UNP Q91BW6
G	-1	GLY	-	expression tag	UNP Q91BW6
G	0	SER	-	expression tag	UNP Q91BW6
H	-33	MET	-	initiating methionine	UNP Q91BW6
H	-32	GLY	-	expression tag	UNP Q91BW6
H	-31	SER	-	expression tag	UNP Q91BW6
H	-30	SER	-	expression tag	UNP Q91BW6
H	-29	HIS	-	expression tag	UNP Q91BW6
H	-28	HIS	-	expression tag	UNP Q91BW6
H	-27	HIS	-	expression tag	UNP Q91BW6
H	-26	HIS	-	expression tag	UNP Q91BW6
H	-25	HIS	-	expression tag	UNP Q91BW6
H	-24	HIS	-	expression tag	UNP Q91BW6
H	-23	SER	-	expression tag	UNP Q91BW6
H	-22	SER	-	expression tag	UNP Q91BW6
H	-21	GLY	-	expression tag	UNP Q91BW6
H	-20	LEU	-	expression tag	UNP Q91BW6
H	-19	VAL	-	expression tag	UNP Q91BW6
H	-18	PRO	-	expression tag	UNP Q91BW6
H	-17	ARG	-	expression tag	UNP Q91BW6
H	-16	GLY	-	expression tag	UNP Q91BW6
H	-15	SER	-	expression tag	UNP Q91BW6
H	-14	HIS	-	expression tag	UNP Q91BW6
H	-13	MET	-	expression tag	UNP Q91BW6
H	-12	ALA	-	expression tag	UNP Q91BW6
H	-11	SER	-	expression tag	UNP Q91BW6
H	-10	MET	-	expression tag	UNP Q91BW6
H	-9	THR	-	expression tag	UNP Q91BW6
H	-8	GLY	-	expression tag	UNP Q91BW6
H	-7	GLY	-	expression tag	UNP Q91BW6

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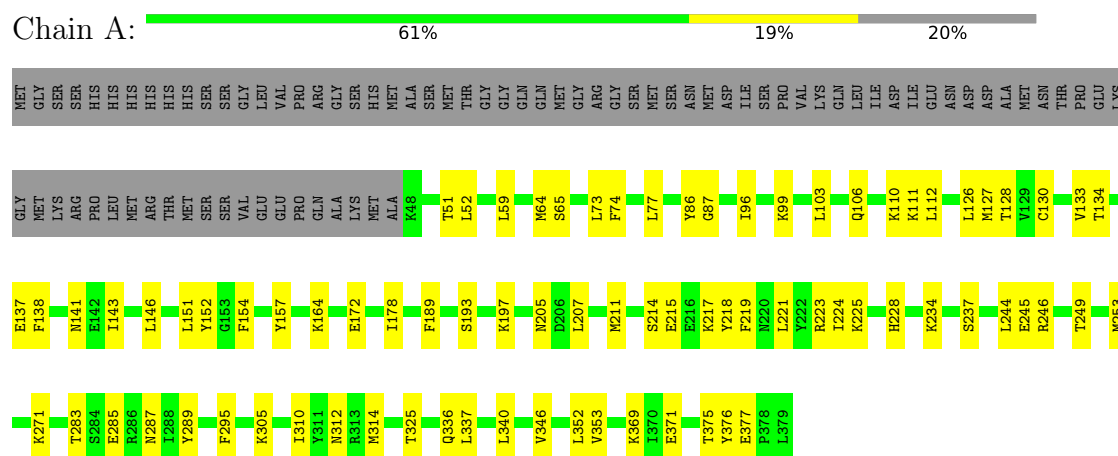
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Chain	Residue	Modelled	Actual	Comment	Reference
H	-6	GLN	-	expression tag	UNP Q91BW6
H	-5	GLN	-	expression tag	UNP Q91BW6
H	-4	MET	-	expression tag	UNP Q91BW6
H	-3	GLY	-	expression tag	UNP Q91BW6
H	-2	ARG	-	expression tag	UNP Q91BW6
H	-1	GLY	-	expression tag	UNP Q91BW6
H	0	SER	-	expression tag	UNP Q91BW6

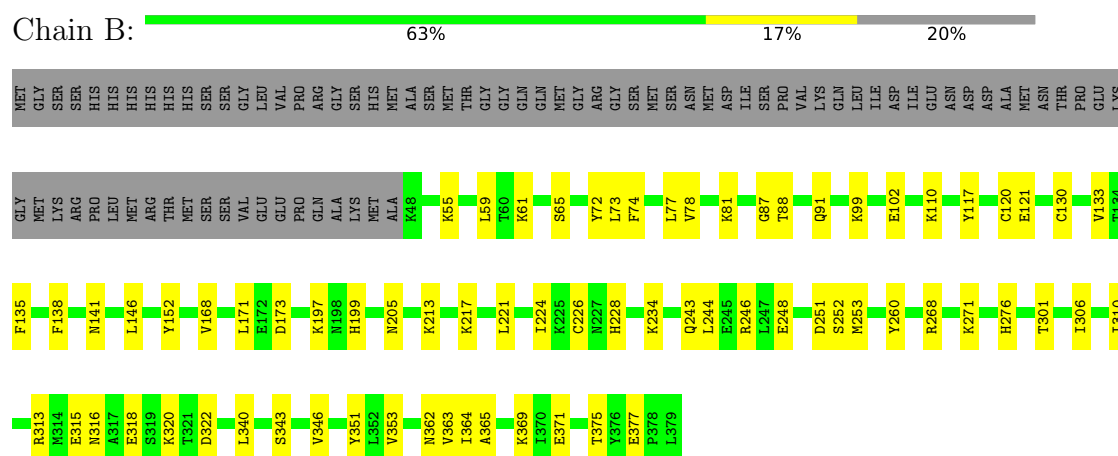
3 Residue-property plots

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.

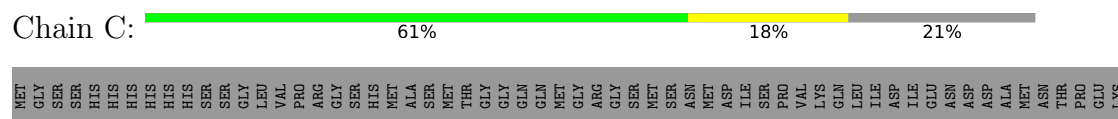
• Molecule 1: Lef3

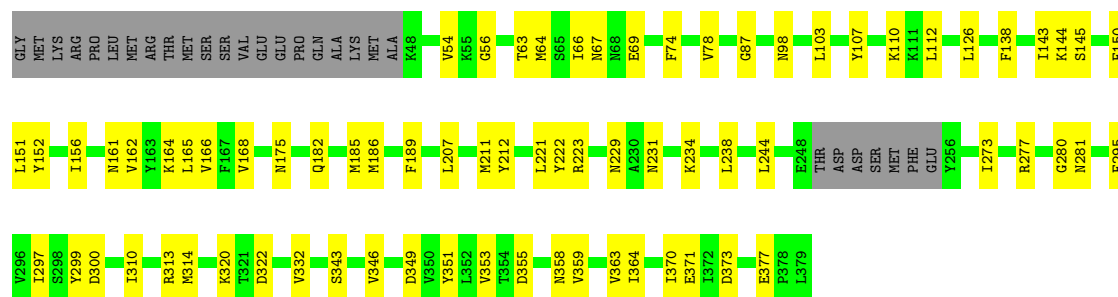


• Molecule 1: Lef3



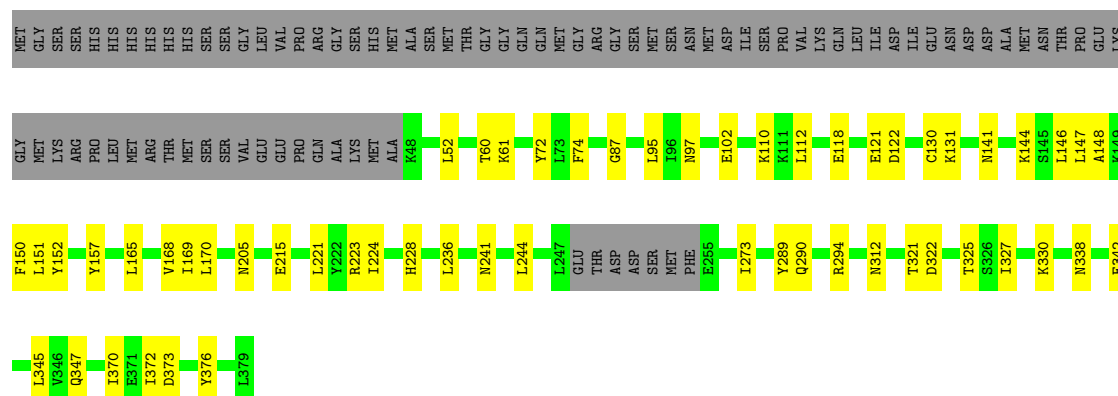
• Molecule 1: Lef3





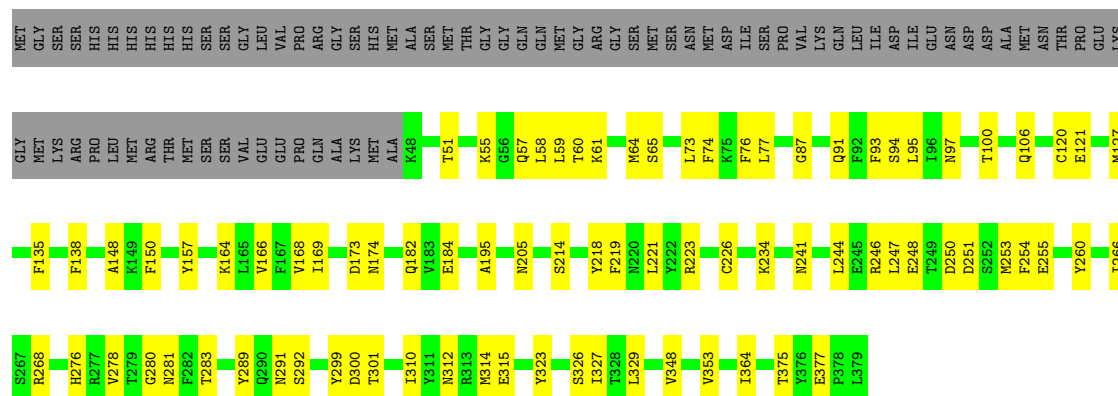
• Molecule 1: Lef3

Chain D: 65% 14% 21%



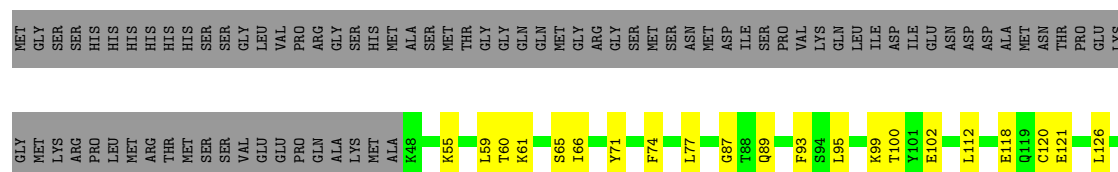
• Molecule 1: Lef3

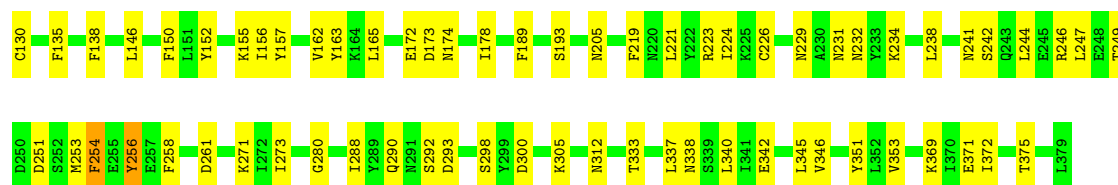
Chain E: 60% 20% 20%



• Molecule 1: Lef3

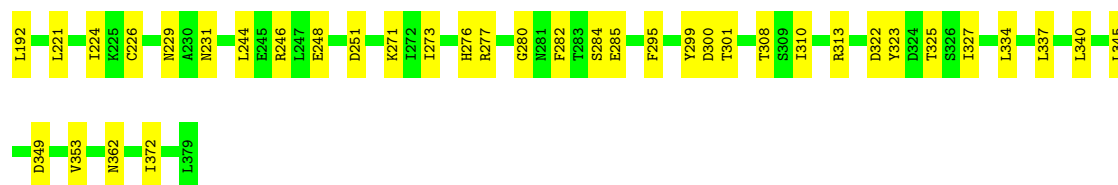
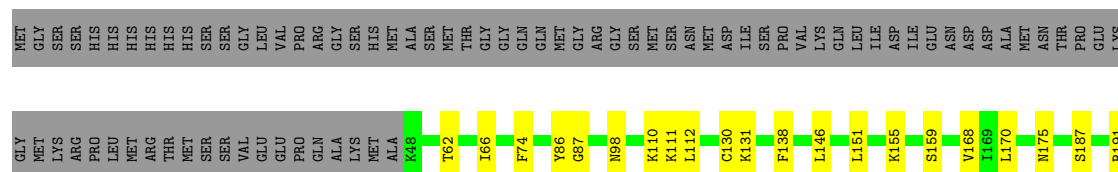
Chain F: 60% 20% 20%





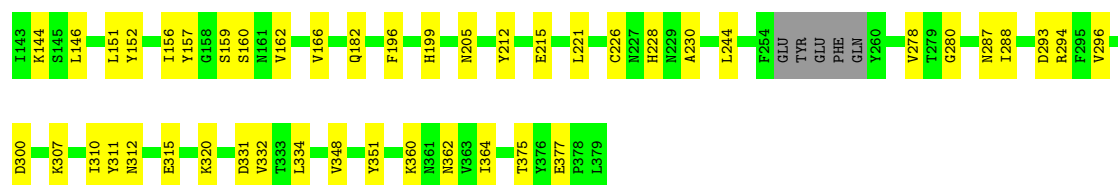
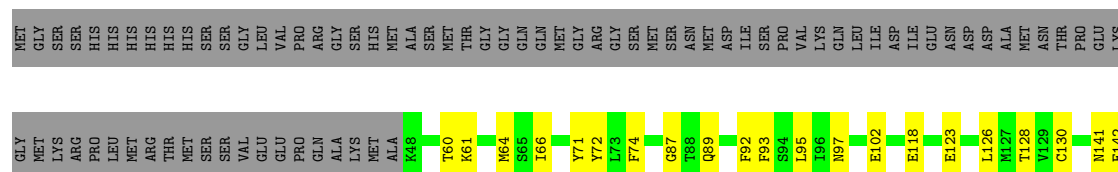
• Molecule 1: Lef3

Chain G: 66% 14% 20%



• Molecule 1: Lef3

Chain H: 63% 16% 21%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	250.06Å 117.74Å 128.47Å 90.00° 108.12° 90.00°	Depositor
Resolution (Å)	48.52 – 3.51 48.52 – 3.51	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.52-3.51) 99.2 (48.52-3.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.236 , 0.287 (Not available) , 0.280	Depositor DCC
R_{free} test set	2202 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	133.3	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 93.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	21644	wwPDB-VP
Average B, all atoms (Å ²)	137.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

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	0.15	0/2770	0.40	0/3735
1	B	0.13	0/2770	0.41	0/3735
1	C	0.13	0/2711	0.39	0/3654
1	D	0.13	0/2711	0.37	0/3654
1	E	0.16	0/2770	0.43	0/3735
1	F	0.15	0/2770	0.47	3/3735 (0.1%)
1	G	0.12	0/2770	0.39	0/3735
1	H	0.21	0/2717	0.47	3/3662 (0.1%)
All	All	0.15	0/21989	0.42	6/29645 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	256	TYR	N-CA-C	7.58	120.10	110.24
1	H	287	ASN	CA-C-N	-6.25	115.44	123.19
1	H	287	ASN	C-N-CA	-6.25	115.44	123.19
1	H	230	ALA	N-CA-C	-5.57	105.30	111.71
1	F	254	PHE	CA-C-N	-5.02	111.79	121.58
1	F	254	PHE	C-N-CA	-5.02	111.79	121.58

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	2726	0	2686	66	0
1	B	2726	0	2686	54	0
1	C	2669	0	2641	57	0
1	D	2669	0	2641	40	0
1	E	2726	0	2686	56	0
1	F	2726	0	2686	64	0
1	G	2726	0	2686	39	0
1	H	2676	0	2647	43	0
All	All	21644	0	21359	372	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 9.

All (372) 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:99:LYS:HZ3	1:F:121:GLU:HA	1.29	0.96
1:A:287:ASN:ND2	1:A:289:TYR:CE1	2.51	0.79
1:C:166:VAL:HG11	1:C:182:GLN:HE21	1.52	0.75
1:C:151:LEU:HD11	1:C:168:VAL:HG23	1.71	0.73
1:H:205:ASN:HD21	1:H:375:THR:HA	1.56	0.70
1:A:287:ASN:ND2	1:A:289:TYR:CZ	2.60	0.70
1:B:346:VAL:HG12	1:B:371:GLU:HG2	1.74	0.68
1:E:60:THR:HG22	1:H:64:MET:HB3	1.74	0.68
1:C:314:MET:O	1:D:141:ASN:ND2	2.26	0.68
1:A:346:VAL:HG12	1:A:371:GLU:HG2	1.76	0.67
1:C:98:ASN:ND2	1:F:65:SER:O	2.25	0.67
1:G:295:PHE:HB2	1:G:310:ILE:HG22	1.76	0.67
1:G:221:LEU:HD22	1:G:244:LEU:HD22	1.76	0.67
1:A:59:LEU:HD11	1:A:77:LEU:HD13	1.77	0.66
1:D:221:LEU:HB3	1:D:224:ILE:HG13	1.79	0.65
1:B:59:LEU:HD11	1:B:77:LEU:HD13	1.79	0.65
1:B:221:LEU:HB3	1:B:224:ILE:HG13	1.79	0.65
1:H:280:GLY:H	1:H:300:ASP:HB2	1.62	0.65
1:A:221:LEU:HB3	1:A:224:ILE:HG13	1.78	0.64
1:C:175:ASN:HA	1:E:283:THR:HG21	1.79	0.64
1:G:273:ILE:HG12	1:G:353:VAL:HG22	1.79	0.64
1:F:205:ASN:HD21	1:F:375:THR:HA	1.62	0.64
1:E:74:PHE:HE2	1:E:87:GLY:HA3	1.63	0.63
1:C:161:ASN:ND2	1:C:189:PHE:H	1.97	0.63
1:C:346:VAL:HG12	1:C:371:GLU:HG2	1.81	0.62
1:F:99:LYS:NZ	1:F:121:GLU:HA	2.11	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:LYS:NZ	1:B:121:GLU:HG2	2.14	0.62
1:A:337:LEU:HD21	1:A:369:LYS:HD2	1.81	0.61
1:D:322:ASP:HA	1:D:325:THR:HG22	1.82	0.61
1:F:247:LEU:HD21	1:F:253:MET:HG2	1.82	0.61
1:H:152:TYR:HB2	1:H:351:TYR:HE1	1.64	0.61
1:A:221:LEU:HD22	1:A:244:LEU:HD22	1.81	0.61
1:E:314:MET:HE3	1:E:315:GLU:H	1.65	0.61
1:F:157:TYR:HE1	1:F:312:ASN:HA	1.64	0.60
1:D:74:PHE:HE2	1:D:87:GLY:HA3	1.67	0.60
1:E:214:SER:OG	1:E:246:ARG:NH1	2.35	0.60
1:C:222:TYR:HB3	1:C:223:ARG:HE	1.67	0.59
1:E:51:THR:HG22	1:E:106:GLN:HA	1.83	0.59
1:E:127:MET:HG3	1:E:223:ARG:HH21	1.68	0.59
1:A:130:CYS:H	1:A:146:LEU:HA	1.67	0.59
1:B:251:ASP:OD1	1:B:252:SER:N	2.35	0.59
1:B:320:LYS:HD3	1:B:322:ASP:HB2	1.84	0.59
1:G:221:LEU:HB3	1:G:224:ILE:HG13	1.84	0.59
1:A:295:PHE:HB2	1:A:310:ILE:HG22	1.84	0.58
1:D:121:GLU:HG3	1:D:122:ASP:H	1.68	0.58
1:A:340:LEU:HB3	1:A:346:VAL:HG22	1.85	0.58
1:B:74:PHE:HE2	1:B:87:GLY:HA3	1.68	0.58
1:F:223:ARG:NH1	1:F:241:ASN:O	2.34	0.58
1:E:278:VAL:HB	1:E:348:VAL:HB	1.84	0.58
1:F:61:LYS:NZ	1:F:95:LEU:O	2.29	0.58
1:B:353:VAL:HG23	1:B:365:ALA:HB2	1.86	0.58
1:H:294:ARG:NH1	1:H:311:TYR:OH	2.37	0.58
1:C:353:VAL:HB	1:C:363:VAL:HG23	1.86	0.58
1:C:161:ASN:OD1	1:C:189:PHE:HB2	2.03	0.58
1:A:249:THR:HA	1:A:253:MET:SD	2.44	0.57
1:F:89:GLN:HG2	1:F:93:PHE:CZ	2.39	0.57
1:G:74:PHE:HE2	1:G:87:GLY:HA3	1.68	0.57
1:B:88:THR:HG23	1:B:91:GLN:H	1.69	0.57
1:C:295:PHE:HB2	1:C:310:ILE:HG22	1.87	0.57
1:D:61:LYS:NZ	1:D:95:LEU:O	2.36	0.57
1:B:310:ILE:HB	1:B:364:ILE:HB	1.85	0.57
1:F:371:GLU:OE1	1:F:375:THR:OG1	2.23	0.57
1:H:296:VAL:HG13	1:H:307:LYS:HE2	1.86	0.57
1:B:268:ARG:HG3	1:B:271:LYS:HB2	1.86	0.57
1:C:277:ARG:NE	1:C:349:ASP:OD1	2.31	0.57
1:F:346:VAL:HG21	1:F:369:LYS:HD2	1.87	0.57
1:A:64:MET:HB3	1:D:60:THR:HG22	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:LYS:HD3	1:A:245:GLU:HG3	1.88	0.56
1:A:271:LYS:HE3	1:A:353:VAL:HG12	1.87	0.56
1:A:305:LYS:HZ3	1:G:175:ASN:HB3	1.69	0.56
1:C:110:LYS:HD3	1:E:377:GLU:HB2	1.87	0.56
1:E:280:GLY:HA3	1:E:300:ASP:HB2	1.87	0.56
1:H:166:VAL:HG11	1:H:182:GLN:HE21	1.70	0.56
1:F:156:ILE:HD12	1:F:156:ILE:H	1.70	0.56
1:F:258:PHE:CE2	1:F:261:ASP:HB3	2.41	0.56
1:G:322:ASP:HA	1:G:325:THR:HG22	1.87	0.56
1:F:155:LYS:HG3	1:F:162:VAL:O	2.06	0.56
1:F:221:LEU:HD22	1:F:244:LEU:HD22	1.86	0.56
1:E:59:LEU:HD11	1:E:77:LEU:HB2	1.86	0.56
1:E:289:TYR:O	1:F:174:ASN:ND2	2.37	0.56
1:G:323:TYR:O	1:G:327:ILE:HG12	2.05	0.56
1:G:271:LYS:HE3	1:G:353:VAL:HG12	1.87	0.56
1:A:74:PHE:HE2	1:A:87:GLY:HA3	1.71	0.55
1:G:280:GLY:HA3	1:G:300:ASP:HB2	1.89	0.55
1:A:205:ASN:HD21	1:A:375:THR:HA	1.71	0.55
1:F:288:ILE:HG12	1:G:285:GLU:HG3	1.88	0.55
1:B:102:GLU:HB2	1:B:120:CYS:SG	2.47	0.55
1:E:205:ASN:HD21	1:E:375:THR:HA	1.72	0.55
1:F:172:GLU:HB2	1:F:178:ILE:HG12	1.88	0.55
1:A:285:GLU:HG3	1:H:288:ILE:CG1	2.38	0.54
1:G:313:ARG:HE	1:H:228:HIS:HB3	1.72	0.54
1:H:159:SER:HA	1:H:315:GLU:HB2	1.88	0.54
1:C:182:GLN:NE2	1:C:273:ILE:HB	2.22	0.54
1:B:377:GLU:HG3	1:D:110:LYS:HD3	1.88	0.54
1:C:221:LEU:HD22	1:C:244:LEU:HD22	1.89	0.54
1:A:151:LEU:HB3	1:A:152:TYR:CD1	2.43	0.53
1:A:73:LEU:HD13	1:C:332:VAL:HG21	1.89	0.53
1:F:74:PHE:HE2	1:F:87:GLY:HA3	1.73	0.53
1:A:51:THR:HG22	1:A:106:GLN:HA	1.90	0.53
1:C:98:ASN:OD1	1:D:321:THR:OG1	2.21	0.53
1:C:144:LYS:NZ	1:C:145:SER:O	2.41	0.53
1:A:127:MET:SD	1:A:223:ARG:NH2	2.81	0.53
1:B:205:ASN:HD21	1:B:375:THR:HA	1.73	0.53
1:C:161:ASN:HD21	1:C:189:PHE:H	1.56	0.53
1:C:164:LYS:HZ3	1:C:186:MET:HE2	1.73	0.53
1:D:151:LEU:O	1:D:215:GLU:HA	2.09	0.53
1:A:314:MET:O	1:B:141:ASN:ND2	2.43	0.52
1:E:221:LEU:HD22	1:E:244:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:337:LEU:HD23	1:G:340:LEU:HD12	1.91	0.52
1:C:185:MET:SD	1:C:238:LEU:HD22	2.49	0.52
1:H:74:PHE:HE2	1:H:87:GLY:HA3	1.74	0.52
1:H:160:SER:N	1:H:315:GLU:OE1	2.33	0.52
1:A:141:ASN:HB2	1:B:316:ASN:H	1.74	0.52
1:E:268:ARG:HH21	1:E:353:VAL:HG21	1.73	0.52
1:F:229:ASN:HB2	1:F:231:ASN:O	2.10	0.52
1:F:333:THR:O	1:F:337:LEU:HG	2.10	0.52
1:F:338:ASN:O	1:F:342:GLU:HG2	2.10	0.52
1:A:285:GLU:HG3	1:H:288:ILE:HG13	1.91	0.52
1:C:164:LYS:NZ	1:C:186:MET:HE2	2.24	0.51
1:G:246:ARG:HG2	1:G:248:GLU:HG2	1.91	0.51
1:B:133:VAL:HG23	1:B:171:LEU:HD23	1.93	0.51
1:B:99:LYS:HZ3	1:B:121:GLU:HG2	1.76	0.51
1:F:253:MET:HE3	1:F:254:PHE:CD1	2.44	0.51
1:E:93:PHE:HE1	1:H:93:PHE:HE1	1.56	0.51
1:F:271:LYS:HE3	1:F:353:VAL:HG12	1.92	0.51
1:G:276:HIS:HB3	1:G:301:THR:HG21	1.93	0.51
1:B:213:LYS:O	1:B:246:ARG:NH2	2.43	0.51
1:D:72:TYR:O	1:D:87:GLY:N	2.44	0.51
1:F:138:PHE:CD1	1:F:226:CYS:HB3	2.46	0.51
1:B:221:LEU:HD22	1:B:244:LEU:HD22	1.92	0.51
1:G:345:LEU:O	1:G:372:ILE:HG23	2.11	0.51
1:A:305:LYS:NZ	1:G:175:ASN:HB3	2.25	0.50
1:A:205:ASN:OD1	1:A:376:TYR:HD2	1.95	0.50
1:F:273:ILE:HG12	1:F:353:VAL:HG22	1.93	0.50
1:C:74:PHE:HE2	1:C:87:GLY:HA3	1.76	0.50
1:C:56:GLY:HA3	1:C:78:VAL:HG22	1.94	0.50
1:B:130:CYS:O	1:B:146:LEU:HB2	2.11	0.50
1:D:150:PHE:CZ	1:D:165:LEU:HD22	2.46	0.50
1:F:130:CYS:H	1:F:146:LEU:HA	1.76	0.50
1:G:138:PHE:CD1	1:G:226:CYS:HB3	2.47	0.50
1:A:154:PHE:CZ	1:A:164:LYS:HD2	2.46	0.49
1:D:327:ILE:HD13	1:D:330:LYS:HD2	1.95	0.49
1:H:310:ILE:HB	1:H:364:ILE:HB	1.94	0.49
1:F:221:LEU:HB3	1:F:224:ILE:HG13	1.94	0.49
1:H:278:VAL:HB	1:H:348:VAL:HB	1.94	0.49
1:B:61:LYS:O	1:G:62:THR:HA	2.13	0.49
1:B:138:PHE:CD1	1:B:226:CYS:HB3	2.48	0.49
1:H:221:LEU:HD22	1:H:244:LEU:HD22	1.95	0.49
1:H:331:ASP:HA	1:H:334:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:102:GLU:HB3	1:D:118:GLU:HB2	1.94	0.48
1:F:298:SER:OG	1:F:305:LYS:HE3	2.13	0.48
1:A:157:TYR:HE1	1:A:312:ASN:HA	1.79	0.48
1:A:189:PHE:O	1:A:193:SER:OG	2.27	0.48
1:A:228:HIS:HD2	1:A:234:LYS:HE3	1.78	0.48
1:A:336:GLN:NE2	1:G:112:LEU:HB2	2.28	0.48
1:B:199:HIS:CE1	1:B:246:ARG:HD3	2.48	0.48
1:B:353:VAL:HB	1:B:363:VAL:HG23	1.94	0.48
1:D:151:LEU:HB3	1:D:152:TYR:CD1	2.48	0.48
1:A:287:ASN:CG	1:A:289:TYR:CZ	2.91	0.48
1:B:88:THR:HG22	1:B:91:GLN:HG3	1.94	0.48
1:E:310:ILE:HD12	1:E:364:ILE:HB	1.95	0.48
1:C:54:VAL:HG23	1:C:103:LEU:HB2	1.96	0.48
1:E:65:SER:HB2	1:H:97:ASN:HB2	1.95	0.48
1:B:152:TYR:HB2	1:B:351:TYR:HE1	1.79	0.48
1:B:340:LEU:HB3	1:B:346:VAL:HG22	1.96	0.48
1:F:152:TYR:HB3	1:F:351:TYR:CE1	2.48	0.48
1:C:373:ASP:OD1	1:C:373:ASP:N	2.46	0.48
1:H:212:TYR:HA	1:H:215:GLU:HG3	1.97	0.47
1:A:228:HIS:O	1:B:313:ARG:NH2	2.34	0.47
1:F:150:PHE:HE2	1:F:165:LEU:HB3	1.78	0.47
1:F:126:LEU:HA	1:F:126:LEU:HD23	1.80	0.47
1:G:98:ASN:HB3	1:H:320:LYS:HD2	1.96	0.47
1:E:276:HIS:HB3	1:E:301:THR:HG21	1.97	0.47
1:C:138:PHE:CD1	1:C:234:LYS:HB3	2.50	0.47
1:C:152:TYR:HB3	1:C:351:TYR:CE1	2.49	0.47
1:C:161:ASN:HD21	1:C:189:PHE:HB3	1.80	0.47
1:C:182:GLN:HE22	1:C:273:ILE:HB	1.78	0.47
1:A:151:LEU:O	1:A:215:GLU:HG3	2.14	0.47
1:D:221:LEU:HD22	1:D:244:LEU:HD22	1.96	0.46
1:F:300:ASP:OD1	1:F:305:LYS:HD3	2.14	0.46
1:B:78:VAL:O	1:B:81:LYS:HB2	2.15	0.46
1:E:60:THR:HG21	1:H:64:MET:HE2	1.97	0.46
1:F:135:PHE:CE2	1:F:173:ASP:HA	2.49	0.46
1:D:131:LYS:O	1:D:170:LEU:HB2	2.15	0.46
1:C:355:ASP:HB3	1:C:358:ASN:O	2.16	0.46
1:E:55:LYS:NZ	1:E:120:CYS:HB2	2.31	0.46
1:A:126:LEU:C	1:A:128:THR:H	2.23	0.46
1:F:238:LEU:HD11	1:F:244:LEU:HD21	1.97	0.46
1:H:196:PHE:HB3	1:H:199:HIS:HB2	1.97	0.46
1:A:283:THR:HG21	1:G:175:ASN:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:VAL:HG12	1:B:260:TYR:HD1	1.80	0.46
1:B:217:LYS:HZ3	1:B:246:ARG:HE	1.64	0.46
1:G:86:TYR:CD2	1:G:111:LYS:HB3	2.51	0.46
1:E:138:PHE:CD1	1:E:226:CYS:HB3	2.50	0.46
1:G:130:CYS:H	1:G:146:LEU:HA	1.80	0.46
1:A:207:LEU:O	1:A:211:MET:HG3	2.15	0.46
1:A:134:THR:OG1	1:A:137:GLU:HG3	2.16	0.45
1:A:218:TYR:CD2	1:A:253:MET:HE3	2.51	0.45
1:B:306:ILE:HG23	1:B:362:ASN:HD22	1.81	0.45
1:F:59:LEU:HD11	1:F:77:LEU:HD13	1.98	0.45
1:B:248:GLU:O	1:B:248:GLU:HG3	2.16	0.45
1:C:156:ILE:HD12	1:C:162:VAL:HG12	1.98	0.45
1:E:234:LYS:HB3	1:E:266:ILE:HD12	1.98	0.45
1:A:287:ASN:CG	1:A:289:TYR:CE1	2.94	0.45
1:B:72:TYR:C	1:B:73:LEU:HD12	2.41	0.45
1:B:110:LYS:HD3	1:H:377:GLU:HG3	1.98	0.45
1:C:313:ARG:NH2	1:D:228:HIS:O	2.37	0.45
1:F:293:ASP:CG	1:F:312:ASN:HD22	2.24	0.45
1:C:112:LEU:HD23	1:C:112:LEU:HA	1.87	0.45
1:E:135:PHE:HE2	1:E:174:ASN:H	1.63	0.45
1:C:320:LYS:HG3	1:C:322:ASP:H	1.81	0.45
1:D:347:GLN:HB2	1:D:370:ILE:HB	1.98	0.45
1:E:91:GLN:HA	1:E:94:SER:HB2	1.98	0.45
1:A:52:LEU:HD21	1:C:343:SER:HB3	1.98	0.45
1:A:112:LEU:HD23	1:A:112:LEU:HA	1.88	0.45
1:A:225:LYS:HB3	1:A:237:SER:OG	2.17	0.45
1:A:340:LEU:CB	1:A:346:VAL:HG22	2.46	0.45
1:E:157:TYR:HE1	1:E:312:ASN:HA	1.81	0.45
1:G:151:LEU:HD21	1:G:168:VAL:HG23	1.99	0.45
1:C:63:THR:HG23	1:F:61:LYS:HG3	1.99	0.45
1:E:254:PHE:CE1	1:E:255:GLU:HG2	2.52	0.45
1:H:288:ILE:HG22	1:H:293:ASP:OD1	2.17	0.45
1:C:64:MET:HB3	1:F:60:THR:HG22	1.98	0.44
1:E:173:ASP:OD2	1:F:290:GLN:NE2	2.49	0.44
1:B:228:HIS:HD2	1:B:234:LYS:HG2	1.81	0.44
1:B:276:HIS:HB3	1:B:301:THR:HG21	1.99	0.44
1:E:251:ASP:C	1:E:253:MET:N	2.74	0.44
1:G:229:ASN:HB2	1:G:231:ASN:O	2.17	0.44
1:D:205:ASN:OD1	1:D:376:TYR:N	2.49	0.44
1:E:214:SER:HB3	1:E:219:PHE:CE2	2.53	0.44
1:F:219:PHE:CE1	1:F:246:ARG:HG2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:ARG:O	1:F:242:SER:OG	2.32	0.44
1:H:142:GLU:OE2	1:H:144:LYS:HD3	2.18	0.44
1:B:369:LYS:HE2	1:B:377:GLU:HB3	1.98	0.44
1:C:229:ASN:HB2	1:C:231:ASN:O	2.17	0.44
1:E:323:TYR:O	1:E:327:ILE:HG12	2.17	0.44
1:F:102:GLU:N	1:F:118:GLU:O	2.51	0.44
1:D:131:LYS:HG2	1:D:147:LEU:HD23	1.99	0.44
1:H:151:LEU:HD12	1:H:166:VAL:HG12	2.00	0.44
1:A:377:GLU:HB2	1:G:110:LYS:HD2	1.99	0.43
1:D:150:PHE:HZ	1:D:165:LEU:HD22	1.83	0.43
1:F:189:PHE:O	1:F:193:SER:OG	2.36	0.43
1:A:218:TYR:CE2	1:A:253:MET:HE3	2.53	0.43
1:A:295:PHE:HB2	1:A:310:ILE:CG2	2.48	0.43
1:D:224:ILE:HG22	1:D:236:LEU:HD22	2.01	0.43
1:E:223:ARG:HD2	1:E:241:ASN:O	2.18	0.43
1:F:340:LEU:HB3	1:F:346:VAL:HG22	2.01	0.43
1:E:168:VAL:HG11	1:E:260:TYR:O	2.17	0.43
1:E:246:ARG:HB2	1:E:248:GLU:HG2	2.00	0.43
1:F:288:ILE:HG13	1:F:288:ILE:O	2.17	0.43
1:H:102:GLU:HB3	1:H:118:GLU:HB2	2.01	0.43
1:B:55:LYS:HB2	1:B:102:GLU:HG2	1.99	0.43
1:C:281:ASN:O	1:C:299:TYR:HA	2.18	0.43
1:D:289:TYR:HD2	1:D:294:ARG:HG3	1.84	0.43
1:D:289:TYR:CD2	1:D:294:ARG:HG3	2.54	0.43
1:E:64:MET:HE3	1:E:73:LEU:HD12	2.01	0.43
1:G:277:ARG:NE	1:G:349:ASP:OD1	2.46	0.43
1:C:74:PHE:CE2	1:C:87:GLY:HA3	2.53	0.43
1:C:280:GLY:HA3	1:C:300:ASP:HB2	2.01	0.43
1:D:345:LEU:O	1:D:372:ILE:HG23	2.18	0.43
1:H:126:LEU:C	1:H:128:THR:H	2.26	0.43
1:H:360:LYS:O	1:H:362:ASN:N	2.51	0.43
1:C:63:THR:CG2	1:F:61:LYS:HG3	2.48	0.43
1:D:372:ILE:HG13	1:D:373:ASP:N	2.34	0.43
1:E:164:LYS:NZ	1:E:184:GLU:OE2	2.51	0.43
1:E:268:ARG:HE	1:E:353:VAL:HG11	1.83	0.43
1:F:280:GLY:H	1:F:300:ASP:HB2	1.84	0.43
1:G:308:THR:OG1	1:G:362:ASN:HB3	2.19	0.43
1:H:61:LYS:HG2	1:H:74:PHE:HD1	1.84	0.43
1:H:123:GLU:HG2	1:H:123:GLU:O	2.18	0.43
1:H:130:CYS:H	1:H:146:LEU:HA	1.84	0.43
1:H:157:TYR:HE1	1:H:312:ASN:HA	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LYS:HZ2	1:A:246:ARG:HH21	1.67	0.43
1:F:55:LYS:HE3	1:F:100:THR:HG21	2.00	0.43
1:G:191:ARG:HA	1:G:191:ARG:HD3	1.88	0.43
1:H:89:GLN:HG2	1:H:93:PHE:HE2	1.83	0.43
1:A:141:ASN:ND2	1:B:315:GLU:HA	2.34	0.43
1:C:150:PHE:HE2	1:C:165:LEU:HB3	1.84	0.43
1:D:112:LEU:HD23	1:D:112:LEU:HA	1.91	0.43
1:F:219:PHE:CZ	1:F:246:ARG:HG2	2.54	0.43
1:A:151:LEU:HD23	1:A:151:LEU:HA	1.85	0.42
1:B:141:ASN:HA	1:B:226:CYS:O	2.19	0.42
1:E:100:THR:HB	1:E:121:GLU:HA	2.01	0.42
1:A:143:ILE:HG12	1:A:225:LYS:HB2	2.01	0.42
1:B:99:LYS:HD2	1:B:99:LYS:HA	1.82	0.42
1:D:130:CYS:SG	1:D:144:LYS:NZ	2.92	0.42
1:G:284:SER:HB3	1:G:334:LEU:HB3	2.01	0.42
1:A:133:VAL:HG21	1:A:138:PHE:HE2	1.85	0.42
1:C:156:ILE:HD12	1:C:162:VAL:CG1	2.49	0.42
1:A:214:SER:HB3	1:A:219:PHE:CE2	2.55	0.42
1:B:251:ASP:C	1:B:253:MET:H	2.27	0.42
1:E:148:ALA:HB2	1:E:169:ILE:HG22	2.00	0.42
1:F:135:PHE:CD2	1:F:173:ASP:HA	2.54	0.42
1:F:256:TYR:C	1:F:258:PHE:N	2.77	0.42
1:A:65:SER:HB3	1:D:97:ASN:HB2	2.01	0.42
1:A:96:ILE:HG13	1:A:99:LYS:HG3	2.00	0.42
1:A:110:LYS:HD3	1:C:377:GLU:HB2	2.00	0.42
1:B:228:HIS:CD2	1:B:234:LYS:HE2	2.55	0.42
1:D:151:LEU:HD11	1:D:168:VAL:HG23	2.00	0.42
1:D:152:TYR:HE2	1:D:273:ILE:HG22	1.84	0.42
1:E:166:VAL:HG11	1:E:182:GLN:HE21	1.85	0.42
1:F:249:THR:HB	1:F:251:ASP:OD1	2.19	0.42
1:F:346:VAL:HG12	1:F:371:GLU:HG2	2.01	0.42
1:H:66:ILE:HD12	1:H:71:TYR:CE2	2.55	0.42
1:A:217:LYS:NZ	1:A:246:ARG:HH21	2.17	0.42
1:B:65:SER:HB3	1:G:98:ASN:HD22	1.85	0.42
1:F:100:THR:HB	1:F:120:CYS:O	2.20	0.42
1:H:156:ILE:HD12	1:H:162:VAL:HG12	2.02	0.42
1:A:86:TYR:CD2	1:A:111:LYS:HB3	2.55	0.42
1:B:135:PHE:HE2	1:B:173:ASP:HB3	1.83	0.42
1:B:251:ASP:O	1:B:253:MET:N	2.51	0.42
1:C:175:ASN:HD22	1:D:290:GLN:HG2	1.84	0.42
1:D:74:PHE:CE2	1:D:87:GLY:HA3	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:130:CYS:H	1:D:146:LEU:HA	1.85	0.42
1:E:281:ASN:O	1:E:299:TYR:HA	2.19	0.42
1:F:66:ILE:HD12	1:F:71:TYR:CE2	2.55	0.42
1:F:163:TYR:HE2	1:F:189:PHE:HB2	1.85	0.42
1:D:157:TYR:HE1	1:D:312:ASN:HA	1.84	0.42
1:E:195:ALA:O	1:E:244:LEU:N	2.51	0.42
1:B:197:LYS:HD2	1:B:243:GLN:OE1	2.20	0.42
1:B:343:SER:OG	1:D:52:LEU:HD11	2.20	0.42
1:D:338:ASN:O	1:D:342:GLU:HG2	2.20	0.42
1:E:135:PHE:CE1	1:F:292:SER:HA	2.55	0.42
1:F:135:PHE:CE1	1:F:234:LYS:NZ	2.88	0.42
1:G:131:LYS:O	1:G:170:LEU:HB2	2.20	0.42
1:A:134:THR:HA	1:A:172:GLU:O	2.20	0.41
1:C:212:TYR:CE1	1:C:370:ILE:HD11	2.55	0.41
1:G:187:SER:HB3	1:G:192:LEU:HG	2.01	0.41
1:E:326:SER:O	1:E:329:LEU:HB3	2.19	0.41
1:G:251:ASP:OD1	1:G:251:ASP:N	2.53	0.41
1:H:72:TYR:HD1	1:H:92:PHE:CD1	2.38	0.41
1:D:148:ALA:HB2	1:D:169:ILE:HG22	2.02	0.41
1:E:74:PHE:CE2	1:E:87:GLY:HA3	2.50	0.41
1:B:217:LYS:HZ3	1:B:246:ARG:NE	2.18	0.41
1:F:345:LEU:O	1:F:372:ILE:HG23	2.20	0.41
1:C:66:ILE:HG22	1:C:67:ASN:OD1	2.21	0.41
1:E:57:GLN:O	1:E:76:PHE:HA	2.20	0.41
1:E:59:LEU:CD1	1:E:77:LEU:HB2	2.51	0.41
1:A:103:LEU:HD23	1:A:103:LEU:HA	1.89	0.41
1:A:285:GLU:HG3	1:H:288:ILE:HG12	2.01	0.41
1:C:126:LEU:HD21	1:C:143:ILE:HG22	2.03	0.41
1:E:58:LEU:HD23	1:E:97:ASN:HA	2.03	0.41
1:E:291:ASN:OD1	1:E:292:SER:N	2.53	0.41
1:C:67:ASN:O	1:C:69:GLU:HG3	2.21	0.41
1:C:107:TYR:CZ	1:C:110:LYS:HA	2.56	0.41
1:C:207:LEU:HG	1:C:211:MET:HE2	2.02	0.41
1:C:297:ILE:HD13	1:C:364:ILE:HD12	2.03	0.41
1:A:325:THR:O	1:G:66:ILE:HD11	2.21	0.41
1:C:64:MET:HE2	1:F:60:THR:HG21	2.03	0.41
1:C:359:VAL:HG12	1:C:359:VAL:O	2.21	0.41
1:E:247:LEU:HG	1:E:250:ASP:OD2	2.20	0.41
1:F:112:LEU:HD23	1:F:112:LEU:HA	1.87	0.41
1:F:231:ASN:O	1:F:232:ASN:C	2.63	0.41
1:H:141:ASN:HA	1:H:226:CYS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:138:PHE:CG	1:G:226:CYS:HB3	2.55	0.41
1:A:172:GLU:HB2	1:A:178:ILE:HG12	2.02	0.40
1:A:287:ASN:ND2	1:A:289:TYR:OH	2.54	0.40
1:B:73:LEU:HD22	1:H:332:VAL:HG21	2.03	0.40
1:E:150:PHE:HB2	1:E:219:PHE:CD2	2.57	0.40
1:G:155:LYS:HE2	1:G:159:SER:O	2.21	0.40
1:C:110:LYS:HE2	1:E:375:THR:HG21	2.03	0.40
1:E:255:GLU:H	1:E:255:GLU:HG3	1.69	0.40
1:F:126:LEU:HD22	1:F:223:ARG:HG2	2.02	0.40
1:B:318:GLU:H	1:B:320:LYS:NZ	2.19	0.40
1:E:61:LYS:NZ	1:E:95:LEU:O	2.50	0.40
1:E:64:MET:HB3	1:H:60:THR:HG22	2.03	0.40
1:E:218:TYR:O	1:E:247:LEU:N	2.52	0.40
1:G:282:PHE:CD2	1:G:299:TYR:HB3	2.56	0.40
1:A:352:LEU:HD12	1:A:352:LEU:HA	1.90	0.40
1:B:91:GLN:HG2	1:B:117:TYR:CE1	2.56	0.40
1:D:223:ARG:HD3	1:D:241:ASN:O	2.21	0.40
1:H:61:LYS:NZ	1:H:95:LEU:O	2.54	0.40

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	232/413 (56%)	218 (94%)	14 (6%)	0	100	100
1	B	330/413 (80%)	312 (94%)	18 (6%)	0	100	100
1	C	321/413 (78%)	309 (96%)	12 (4%)	0	100	100
1	D	321/413 (78%)	301 (94%)	20 (6%)	0	100	100
1	E	330/413 (80%)	309 (94%)	21 (6%)	0	100	100
1	F	330/413 (80%)	311 (94%)	19 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	330/413 (80%)	311 (94%)	19 (6%)	0	100	100
1	H	323/413 (78%)	309 (96%)	14 (4%)	0	100	100
All	All	2517/3304 (76%)	2380 (95%)	137 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

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 [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	332/413 (80%)	-0.57	0 100 100	89, 126, 160, 182	0
1	B	332/413 (80%)	-0.55	0 100 100	101, 138, 176, 195	0
1	C	325/413 (78%)	-0.58	0 100 100	89, 123, 159, 190	0
1	D	325/413 (78%)	-0.54	0 100 100	94, 132, 164, 187	0
1	E	332/413 (80%)	-0.55	0 100 100	86, 129, 172, 198	0
1	F	332/413 (80%)	-0.57	0 100 100	102, 136, 170, 198	0
1	G	332/413 (80%)	-0.60	0 100 100	105, 139, 180, 213	0
1	H	327/413 (79%)	-0.55	0 100 100	129, 158, 184, 212	0
All	All	2637/3304 (79%)	-0.56	0 100 100	86, 136, 175, 213	0

There are no RSRZ outliers to report.

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.