



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 10:44 PM UTC

PDB ID : 9Y6U / pdb_00009y6u
EMDB ID : EMD-72631
Title : Cryo-EM Structure of Gp77 within the In Vitro Reconstituted RAZR:GP77 Complex
Authors : Yifei, L.; Zhang, T.; Laub, M.; Ghanbarpour, A.
Deposited on : 2025-09-09
Resolution : 3.10 Å(reported)
Based on initial model : .

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

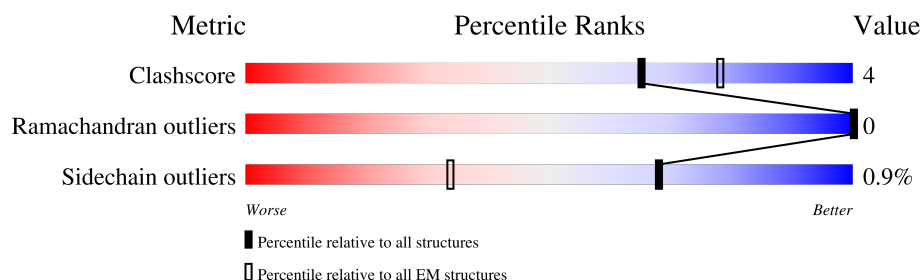
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



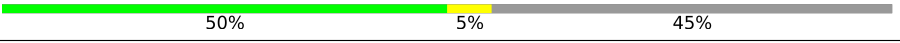
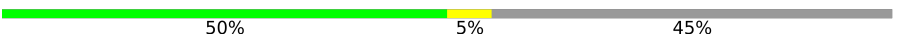
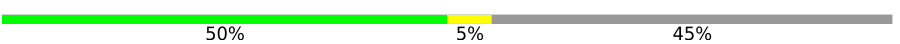
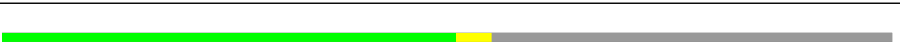
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	IA	227	50% 5% 45%
1	IB	227	50% 5% 45%
1	IC	227	50% 5% 45%
1	ID	227	49% 6% 45%
1	IE	227	49% 6% 45%
1	IF	227	51% . 45%
1	IG	227	50% 5% 45%
1	IH	227	51% . 45%
1	II	227	51% . 45%

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Mol	Chain	Length	Quality of chain
1	IJ	227	
1	IK	227	
1	IL	227	
1	IM	227	
1	IN	227	
1	IO	227	
1	IP	227	
1	IQ	227	
1	IR	227	
1	IS	227	
1	IT	227	
1	IU	227	
1	IV	227	
1	IW	227	
1	IX	227	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 47328 atoms, of which 23664 are hydrogens and 0 are deuteriums.

In the tables below, 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 Gp77.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	IA	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IB	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IC	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	ID	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IE	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IF	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IG	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IH	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	II	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IJ	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IK	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IL	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IM	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IN	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IO	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IP	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IQ	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	IR	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IS	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IT	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IU	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IV	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IW	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		
1	IX	125	Total	C	H	N	O	S	0	0
			1972	623	986	172	186	5		

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IA	218	GLY	-	expression tag	UNP A0AAE8YXX1
IA	219	SER	-	expression tag	UNP A0AAE8YXX1
IA	220	SER	-	expression tag	UNP A0AAE8YXX1
IA	221	GLY	-	expression tag	UNP A0AAE8YXX1
IA	222	HIS	-	expression tag	UNP A0AAE8YXX1
IA	223	HIS	-	expression tag	UNP A0AAE8YXX1
IA	224	HIS	-	expression tag	UNP A0AAE8YXX1
IA	225	HIS	-	expression tag	UNP A0AAE8YXX1
IA	226	HIS	-	expression tag	UNP A0AAE8YXX1
IA	227	HIS	-	expression tag	UNP A0AAE8YXX1
IB	218	GLY	-	expression tag	UNP A0AAE8YXX1
IB	219	SER	-	expression tag	UNP A0AAE8YXX1
IB	220	SER	-	expression tag	UNP A0AAE8YXX1
IB	221	GLY	-	expression tag	UNP A0AAE8YXX1
IB	222	HIS	-	expression tag	UNP A0AAE8YXX1
IB	223	HIS	-	expression tag	UNP A0AAE8YXX1
IB	224	HIS	-	expression tag	UNP A0AAE8YXX1
IB	225	HIS	-	expression tag	UNP A0AAE8YXX1
IB	226	HIS	-	expression tag	UNP A0AAE8YXX1
IB	227	HIS	-	expression tag	UNP A0AAE8YXX1
IC	218	GLY	-	expression tag	UNP A0AAE8YXX1
IC	219	SER	-	expression tag	UNP A0AAE8YXX1
IC	220	SER	-	expression tag	UNP A0AAE8YXX1
IC	221	GLY	-	expression tag	UNP A0AAE8YXX1
IC	222	HIS	-	expression tag	UNP A0AAE8YXX1

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Chain	Residue	Modelled	Actual	Comment	Reference
IC	223	HIS	-	expression tag	UNP A0AAE8YXX1
IC	224	HIS	-	expression tag	UNP A0AAE8YXX1
IC	225	HIS	-	expression tag	UNP A0AAE8YXX1
IC	226	HIS	-	expression tag	UNP A0AAE8YXX1
IC	227	HIS	-	expression tag	UNP A0AAE8YXX1
ID	218	GLY	-	expression tag	UNP A0AAE8YXX1
ID	219	SER	-	expression tag	UNP A0AAE8YXX1
ID	220	SER	-	expression tag	UNP A0AAE8YXX1
ID	221	GLY	-	expression tag	UNP A0AAE8YXX1
ID	222	HIS	-	expression tag	UNP A0AAE8YXX1
ID	223	HIS	-	expression tag	UNP A0AAE8YXX1
ID	224	HIS	-	expression tag	UNP A0AAE8YXX1
ID	225	HIS	-	expression tag	UNP A0AAE8YXX1
ID	226	HIS	-	expression tag	UNP A0AAE8YXX1
ID	227	HIS	-	expression tag	UNP A0AAE8YXX1
IE	218	GLY	-	expression tag	UNP A0AAE8YXX1
IE	219	SER	-	expression tag	UNP A0AAE8YXX1
IE	220	SER	-	expression tag	UNP A0AAE8YXX1
IE	221	GLY	-	expression tag	UNP A0AAE8YXX1
IE	222	HIS	-	expression tag	UNP A0AAE8YXX1
IE	223	HIS	-	expression tag	UNP A0AAE8YXX1
IE	224	HIS	-	expression tag	UNP A0AAE8YXX1
IE	225	HIS	-	expression tag	UNP A0AAE8YXX1
IE	226	HIS	-	expression tag	UNP A0AAE8YXX1
IE	227	HIS	-	expression tag	UNP A0AAE8YXX1
IF	218	GLY	-	expression tag	UNP A0AAE8YXX1
IF	219	SER	-	expression tag	UNP A0AAE8YXX1
IF	220	SER	-	expression tag	UNP A0AAE8YXX1
IF	221	GLY	-	expression tag	UNP A0AAE8YXX1
IF	222	HIS	-	expression tag	UNP A0AAE8YXX1
IF	223	HIS	-	expression tag	UNP A0AAE8YXX1
IF	224	HIS	-	expression tag	UNP A0AAE8YXX1
IF	225	HIS	-	expression tag	UNP A0AAE8YXX1
IF	226	HIS	-	expression tag	UNP A0AAE8YXX1
IF	227	HIS	-	expression tag	UNP A0AAE8YXX1
IG	218	GLY	-	expression tag	UNP A0AAE8YXX1
IG	219	SER	-	expression tag	UNP A0AAE8YXX1
IG	220	SER	-	expression tag	UNP A0AAE8YXX1
IG	221	GLY	-	expression tag	UNP A0AAE8YXX1
IG	222	HIS	-	expression tag	UNP A0AAE8YXX1
IG	223	HIS	-	expression tag	UNP A0AAE8YXX1
IG	224	HIS	-	expression tag	UNP A0AAE8YXX1

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Chain	Residue	Modelled	Actual	Comment	Reference
IG	225	HIS	-	expression tag	UNP A0AAE8YXX1
IG	226	HIS	-	expression tag	UNP A0AAE8YXX1
IG	227	HIS	-	expression tag	UNP A0AAE8YXX1
IH	218	GLY	-	expression tag	UNP A0AAE8YXX1
IH	219	SER	-	expression tag	UNP A0AAE8YXX1
IH	220	SER	-	expression tag	UNP A0AAE8YXX1
IH	221	GLY	-	expression tag	UNP A0AAE8YXX1
IH	222	HIS	-	expression tag	UNP A0AAE8YXX1
IH	223	HIS	-	expression tag	UNP A0AAE8YXX1
IH	224	HIS	-	expression tag	UNP A0AAE8YXX1
IH	225	HIS	-	expression tag	UNP A0AAE8YXX1
IH	226	HIS	-	expression tag	UNP A0AAE8YXX1
IH	227	HIS	-	expression tag	UNP A0AAE8YXX1
II	218	GLY	-	expression tag	UNP A0AAE8YXX1
II	219	SER	-	expression tag	UNP A0AAE8YXX1
II	220	SER	-	expression tag	UNP A0AAE8YXX1
II	221	GLY	-	expression tag	UNP A0AAE8YXX1
II	222	HIS	-	expression tag	UNP A0AAE8YXX1
II	223	HIS	-	expression tag	UNP A0AAE8YXX1
II	224	HIS	-	expression tag	UNP A0AAE8YXX1
II	225	HIS	-	expression tag	UNP A0AAE8YXX1
II	226	HIS	-	expression tag	UNP A0AAE8YXX1
II	227	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	218	GLY	-	expression tag	UNP A0AAE8YXX1
IJ	219	SER	-	expression tag	UNP A0AAE8YXX1
IJ	220	SER	-	expression tag	UNP A0AAE8YXX1
IJ	221	GLY	-	expression tag	UNP A0AAE8YXX1
IJ	222	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	223	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	224	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	225	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	226	HIS	-	expression tag	UNP A0AAE8YXX1
IJ	227	HIS	-	expression tag	UNP A0AAE8YXX1
IK	218	GLY	-	expression tag	UNP A0AAE8YXX1
IK	219	SER	-	expression tag	UNP A0AAE8YXX1
IK	220	SER	-	expression tag	UNP A0AAE8YXX1
IK	221	GLY	-	expression tag	UNP A0AAE8YXX1
IK	222	HIS	-	expression tag	UNP A0AAE8YXX1
IK	223	HIS	-	expression tag	UNP A0AAE8YXX1
IK	224	HIS	-	expression tag	UNP A0AAE8YXX1
IK	225	HIS	-	expression tag	UNP A0AAE8YXX1
IK	226	HIS	-	expression tag	UNP A0AAE8YXX1

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Chain	Residue	Modelled	Actual	Comment	Reference
IK	227	HIS	-	expression tag	UNP A0AAE8YXX1
IL	218	GLY	-	expression tag	UNP A0AAE8YXX1
IL	219	SER	-	expression tag	UNP A0AAE8YXX1
IL	220	SER	-	expression tag	UNP A0AAE8YXX1
IL	221	GLY	-	expression tag	UNP A0AAE8YXX1
IL	222	HIS	-	expression tag	UNP A0AAE8YXX1
IL	223	HIS	-	expression tag	UNP A0AAE8YXX1
IL	224	HIS	-	expression tag	UNP A0AAE8YXX1
IL	225	HIS	-	expression tag	UNP A0AAE8YXX1
IL	226	HIS	-	expression tag	UNP A0AAE8YXX1
IL	227	HIS	-	expression tag	UNP A0AAE8YXX1
IM	218	GLY	-	expression tag	UNP A0AAE8YXX1
IM	219	SER	-	expression tag	UNP A0AAE8YXX1
IM	220	SER	-	expression tag	UNP A0AAE8YXX1
IM	221	GLY	-	expression tag	UNP A0AAE8YXX1
IM	222	HIS	-	expression tag	UNP A0AAE8YXX1
IM	223	HIS	-	expression tag	UNP A0AAE8YXX1
IM	224	HIS	-	expression tag	UNP A0AAE8YXX1
IM	225	HIS	-	expression tag	UNP A0AAE8YXX1
IM	226	HIS	-	expression tag	UNP A0AAE8YXX1
IM	227	HIS	-	expression tag	UNP A0AAE8YXX1
IN	218	GLY	-	expression tag	UNP A0AAE8YXX1
IN	219	SER	-	expression tag	UNP A0AAE8YXX1
IN	220	SER	-	expression tag	UNP A0AAE8YXX1
IN	221	GLY	-	expression tag	UNP A0AAE8YXX1
IN	222	HIS	-	expression tag	UNP A0AAE8YXX1
IN	223	HIS	-	expression tag	UNP A0AAE8YXX1
IN	224	HIS	-	expression tag	UNP A0AAE8YXX1
IN	225	HIS	-	expression tag	UNP A0AAE8YXX1
IN	226	HIS	-	expression tag	UNP A0AAE8YXX1
IN	227	HIS	-	expression tag	UNP A0AAE8YXX1
IO	218	GLY	-	expression tag	UNP A0AAE8YXX1
IO	219	SER	-	expression tag	UNP A0AAE8YXX1
IO	220	SER	-	expression tag	UNP A0AAE8YXX1
IO	221	GLY	-	expression tag	UNP A0AAE8YXX1
IO	222	HIS	-	expression tag	UNP A0AAE8YXX1
IO	223	HIS	-	expression tag	UNP A0AAE8YXX1
IO	224	HIS	-	expression tag	UNP A0AAE8YXX1
IO	225	HIS	-	expression tag	UNP A0AAE8YXX1
IO	226	HIS	-	expression tag	UNP A0AAE8YXX1
IO	227	HIS	-	expression tag	UNP A0AAE8YXX1
IP	218	GLY	-	expression tag	UNP A0AAE8YXX1

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Chain	Residue	Modelled	Actual	Comment	Reference
IP	219	SER	-	expression tag	UNP A0AAE8YXX1
IP	220	SER	-	expression tag	UNP A0AAE8YXX1
IP	221	GLY	-	expression tag	UNP A0AAE8YXX1
IP	222	HIS	-	expression tag	UNP A0AAE8YXX1
IP	223	HIS	-	expression tag	UNP A0AAE8YXX1
IP	224	HIS	-	expression tag	UNP A0AAE8YXX1
IP	225	HIS	-	expression tag	UNP A0AAE8YXX1
IP	226	HIS	-	expression tag	UNP A0AAE8YXX1
IP	227	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	218	GLY	-	expression tag	UNP A0AAE8YXX1
IQ	219	SER	-	expression tag	UNP A0AAE8YXX1
IQ	220	SER	-	expression tag	UNP A0AAE8YXX1
IQ	221	GLY	-	expression tag	UNP A0AAE8YXX1
IQ	222	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	223	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	224	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	225	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	226	HIS	-	expression tag	UNP A0AAE8YXX1
IQ	227	HIS	-	expression tag	UNP A0AAE8YXX1
IR	218	GLY	-	expression tag	UNP A0AAE8YXX1
IR	219	SER	-	expression tag	UNP A0AAE8YXX1
IR	220	SER	-	expression tag	UNP A0AAE8YXX1
IR	221	GLY	-	expression tag	UNP A0AAE8YXX1
IR	222	HIS	-	expression tag	UNP A0AAE8YXX1
IR	223	HIS	-	expression tag	UNP A0AAE8YXX1
IR	224	HIS	-	expression tag	UNP A0AAE8YXX1
IR	225	HIS	-	expression tag	UNP A0AAE8YXX1
IR	226	HIS	-	expression tag	UNP A0AAE8YXX1
IR	227	HIS	-	expression tag	UNP A0AAE8YXX1
IS	218	GLY	-	expression tag	UNP A0AAE8YXX1
IS	219	SER	-	expression tag	UNP A0AAE8YXX1
IS	220	SER	-	expression tag	UNP A0AAE8YXX1
IS	221	GLY	-	expression tag	UNP A0AAE8YXX1
IS	222	HIS	-	expression tag	UNP A0AAE8YXX1
IS	223	HIS	-	expression tag	UNP A0AAE8YXX1
IS	224	HIS	-	expression tag	UNP A0AAE8YXX1
IS	225	HIS	-	expression tag	UNP A0AAE8YXX1
IS	226	HIS	-	expression tag	UNP A0AAE8YXX1
IS	227	HIS	-	expression tag	UNP A0AAE8YXX1
IT	218	GLY	-	expression tag	UNP A0AAE8YXX1
IT	219	SER	-	expression tag	UNP A0AAE8YXX1
IT	220	SER	-	expression tag	UNP A0AAE8YXX1

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Chain	Residue	Modelled	Actual	Comment	Reference
IT	221	GLY	-	expression tag	UNP A0AAE8YXX1
IT	222	HIS	-	expression tag	UNP A0AAE8YXX1
IT	223	HIS	-	expression tag	UNP A0AAE8YXX1
IT	224	HIS	-	expression tag	UNP A0AAE8YXX1
IT	225	HIS	-	expression tag	UNP A0AAE8YXX1
IT	226	HIS	-	expression tag	UNP A0AAE8YXX1
IT	227	HIS	-	expression tag	UNP A0AAE8YXX1
IU	218	GLY	-	expression tag	UNP A0AAE8YXX1
IU	219	SER	-	expression tag	UNP A0AAE8YXX1
IU	220	SER	-	expression tag	UNP A0AAE8YXX1
IU	221	GLY	-	expression tag	UNP A0AAE8YXX1
IU	222	HIS	-	expression tag	UNP A0AAE8YXX1
IU	223	HIS	-	expression tag	UNP A0AAE8YXX1
IU	224	HIS	-	expression tag	UNP A0AAE8YXX1
IU	225	HIS	-	expression tag	UNP A0AAE8YXX1
IU	226	HIS	-	expression tag	UNP A0AAE8YXX1
IU	227	HIS	-	expression tag	UNP A0AAE8YXX1
IV	218	GLY	-	expression tag	UNP A0AAE8YXX1
IV	219	SER	-	expression tag	UNP A0AAE8YXX1
IV	220	SER	-	expression tag	UNP A0AAE8YXX1
IV	221	GLY	-	expression tag	UNP A0AAE8YXX1
IV	222	HIS	-	expression tag	UNP A0AAE8YXX1
IV	223	HIS	-	expression tag	UNP A0AAE8YXX1
IV	224	HIS	-	expression tag	UNP A0AAE8YXX1
IV	225	HIS	-	expression tag	UNP A0AAE8YXX1
IV	226	HIS	-	expression tag	UNP A0AAE8YXX1
IV	227	HIS	-	expression tag	UNP A0AAE8YXX1
IW	218	GLY	-	expression tag	UNP A0AAE8YXX1
IW	219	SER	-	expression tag	UNP A0AAE8YXX1
IW	220	SER	-	expression tag	UNP A0AAE8YXX1
IW	221	GLY	-	expression tag	UNP A0AAE8YXX1
IW	222	HIS	-	expression tag	UNP A0AAE8YXX1
IW	223	HIS	-	expression tag	UNP A0AAE8YXX1
IW	224	HIS	-	expression tag	UNP A0AAE8YXX1
IW	225	HIS	-	expression tag	UNP A0AAE8YXX1
IW	226	HIS	-	expression tag	UNP A0AAE8YXX1
IW	227	HIS	-	expression tag	UNP A0AAE8YXX1
IX	218	GLY	-	expression tag	UNP A0AAE8YXX1
IX	219	SER	-	expression tag	UNP A0AAE8YXX1
IX	220	SER	-	expression tag	UNP A0AAE8YXX1
IX	221	GLY	-	expression tag	UNP A0AAE8YXX1
IX	222	HIS	-	expression tag	UNP A0AAE8YXX1

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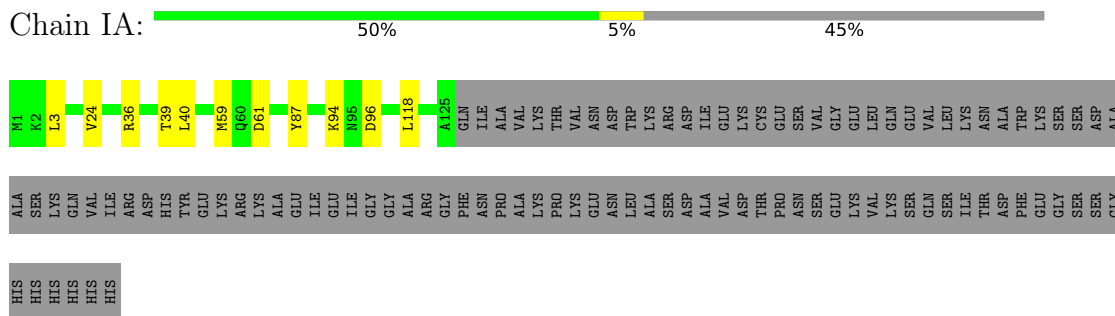
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Chain	Residue	Modelled	Actual	Comment	Reference
IX	223	HIS	-	expression tag	UNP A0AAE8YXX1
IX	224	HIS	-	expression tag	UNP A0AAE8YXX1
IX	225	HIS	-	expression tag	UNP A0AAE8YXX1
IX	226	HIS	-	expression tag	UNP A0AAE8YXX1
IX	227	HIS	-	expression tag	UNP A0AAE8YXX1

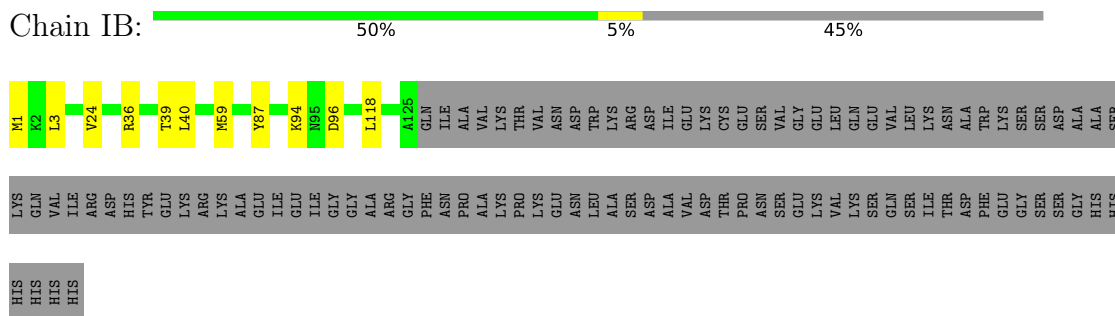
3 Residue-property plots

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. 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. 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.

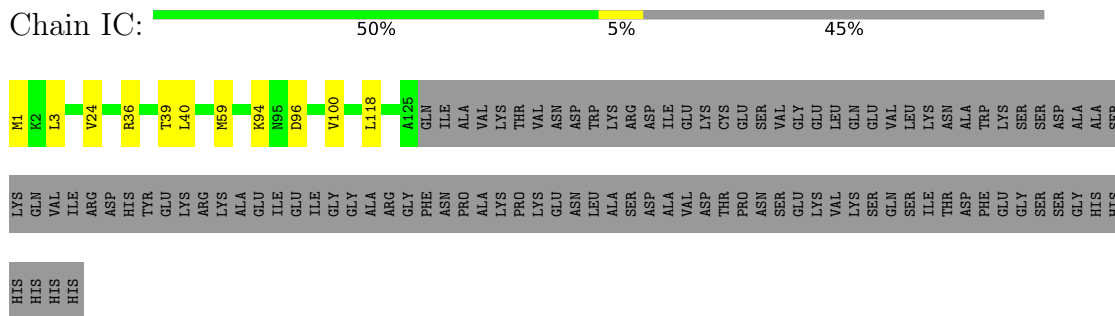
- Molecule 1: Gp77



- Molecule 1: Gp77

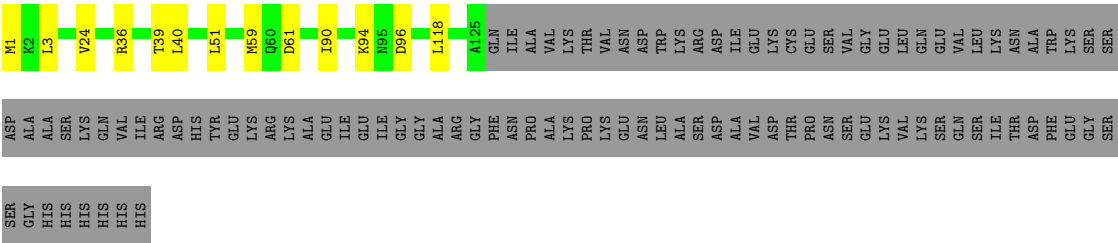


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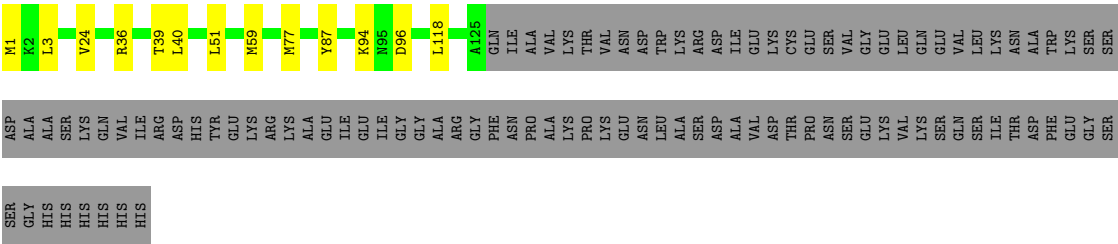


- Molecule 1: Gp77

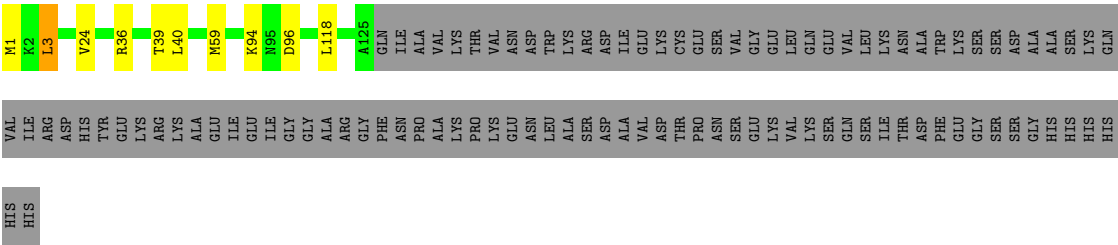




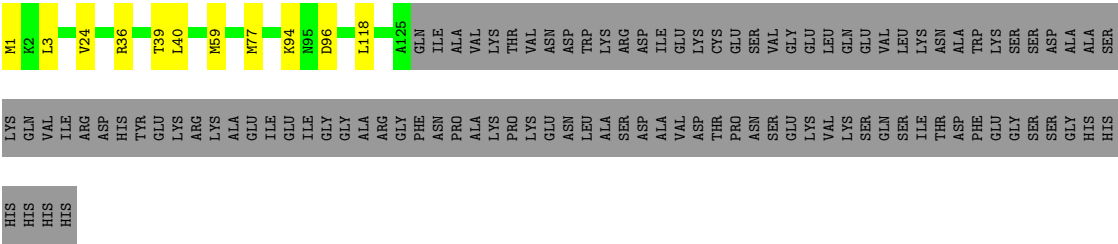
• Molecule 1: Gp77



• Molecule 1: Gp77



• Molecule 1: Gp77



• Molecule 1: Gp77



VAL	ILE	ARG	ASP	HIS	TYR	GLU	LYS	ARG	LYS	ALA	GLU	ILE	GLU	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	LYS	PRO	LYS	GLU	ASN	LEU	ALA	SER	ASP	ALA	VAL	ASP	THR	PRO	ASN	SER	GLU	LYS	VAL	LYS	SER	GLN	ILE	ILE	THR	THR	ASP	PHE	GLY	SER	SER	GLY	HIS	HIS	HIS	HIS
HIS	HIS																																																										

● Molecule 1: Gp77



HIS	M1	K2	L3	V24	R36	T39	L40	M59	K94	N95	D96	L118	A125	GLN	ILE	ALA	VAL	LYS	THR	VAL	ASN	ASP	TRP	LYS	ARG	ASP	ASP	ILE	GLU	LYS	CYS	GLU	SER	VAL	GLY	GLU	LEU	VAL	GLN	GLU	VAL	LEU	LYS	ILE	THR	ASN	ALA	TRP	LYS	SER	SER	ASP	ALA	ALA	SER	LYS	HIS
	VAL	ARG	ASP	HIS	TYR	GLU	LYS	ARG	LYS	ALA	ILE	GLU	ILE	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	LYS	PRO	LYS	GLU	ASN	ASN	LEU	ALA	SER	THR	ASN	SER	GLU	LYS	VAL	LYS	SER	GLN	SER	ILE	THR	ASP	PHE	GLU	GLY	SER	SER	GLY	ALA	HIS	HIS	HIS				

● Molecule 1: Gp77



HIS HIS HIS HIS	M1	K2	L3	V24	R36	T39	L40	M59	M77	K94	N95	D96	L118	A125	GLN	ILE	ALA	VAL	LYS	THR	VAL	ASN	ASP	TRP	LYS	ARG	ASP	ASP	ILE	VAL	GLU	LYS	CYS	GLU	SER	VAL	GLY	LYS	GLU	LEU	VAL	GLN	GLU	VAL	LEU	LYS	ASN	ALA	TRP	LYS	SER	SER	ASP	ALA	ALA	SER	LYS	HIS
	GLN	VAL	ILE	ARG	ASP	HIS	TYR	GLU	LYS	LYS	ARG	LYS	ALA	GLU	ILE	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	VAL	LYS	PRO	LYS	THR	VAL	ASN	GLU	LEU	ALA	SER	ASP	ASP	ILE	VAL	ASP	THR	PRO	ASN	SER	VAL	GLY	LYS	GLY	SER	SER	GLY	HIS					
	VAL	ILE	ARG	ASP	HIS	TYR	GLU	LYS	LYS	ARG	LYS	ALA	GLU	ILE	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	VAL	LYS	PRO	LYS	THR	VAL	ASN	GLU	LEU	ALA	SER	ASP	ASP	ILE	VAL	ASP	THR	PRO	ASN	SER	VAL	GLY	LYS	GLY	SER	SER	GLY	HIS						
	ILE	ARG	ASP	HIS	TYR	GLU	LYS	LYS	ARG	LYS	ALA	GLU	ILE	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	VAL	LYS	PRO	LYS	THR	VAL	ASN	GLU	LEU	ALA	SER	ASP	ASP	ILE	VAL	ASP	THR	PRO	ASN	SER	VAL	GLY	LYS	GLY	SER	SER	GLY	HIS							

● Molecule 1: Gp77



HIS HIS HIS HIS	M1	K2	L3	V24	R36	T39	L40	L51	M59	K94	N95	D96	L118	A125	GLN	ILE	ALA	VAL	LYS	THR	VAL	ASN	ASP	TRP	LYS	ARG	SER	ASP	ASP	ILE	VAL	GLU	LYS	CYS	GLU	SER	VAL	GLY	GLU	LEU	GLN	GLU	VAL	LEU	LYS	ASN	ALA	TRP	LYS	SER	SER	ASP	ALA	ALA	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
	LYS	GLN	VAL	ILE	ARG	ASP	HIS	TYR	GLU	LYS	ARG	LYS	ALA	ALA	GLU	ILE	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	VAL	LYS	PRO	LYS	LYS	THR	VAL	ASN	SER	SER	GLY	GLU	LEU	ALA	SER	THR	ILE	LYS	LEU	VAL	LYS	SER	GLN	VAL	GLY	GLU	GLY	SER	SER	ASP	GLY	ALA	ALA	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												

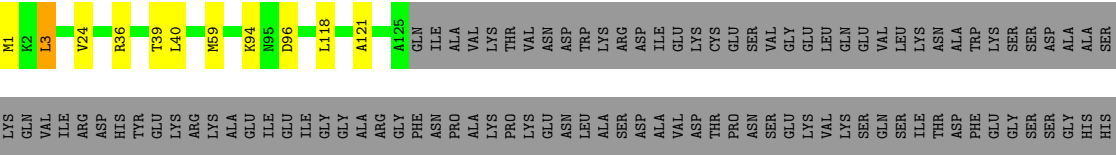
● Molecule 1: Gp77



M1	K2	L3	V24	R36	T39	L40	M59	M77	K94	N95	D96	L118	A125	GLN	ILE	ALA	VAL	LYS	THR	VAL	ASN	ASP	TRP	LYS	ARG	SER	ASP	ASP	ILE	GLU	LYS	CYS	GLU	SER	VAL	GLY	GLU	LEU	GLN	GLU	VAL	LEU	LYS	ASN	ALA	TRP	LYS	SER	SER	ASP	ALA	ALA	SER	LYS	HIS	HIS																
LYS	GLN	VAL	ILE	ARG	ASP	HIS	TYR	GLU	LYS	ARG	LYS	ALA	GLU	ILE	ILE	ILE	GLY	GLY	ALA	ARG	GLY	PHE	ASN	PRO	ALA	VAL	LYS	LYS	THR	VAL	ASN	GLU	LEU	ALA	SER	ASP	ASP	ILE	VAL	ASP	THR	PRO	ASN	SER	VAL	GLY	LYS	THR	PHE	GLU	SER	SER	ASP	GLY	HIS	HIS																
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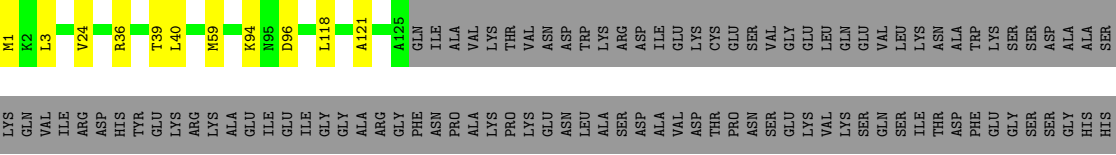
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• Molecule 1: Gp77



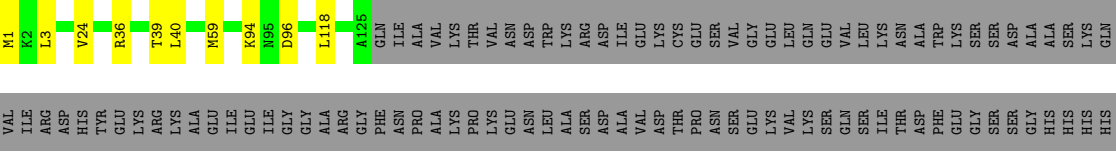
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• Molecule 1: Gp77



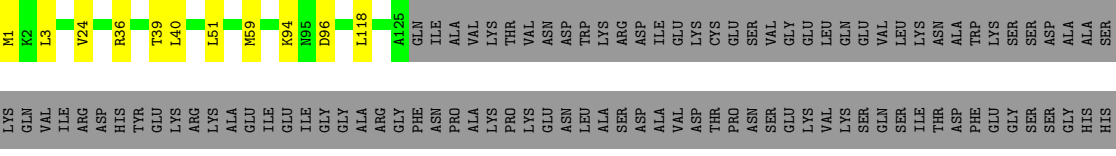
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• Molecule 1: Gp77



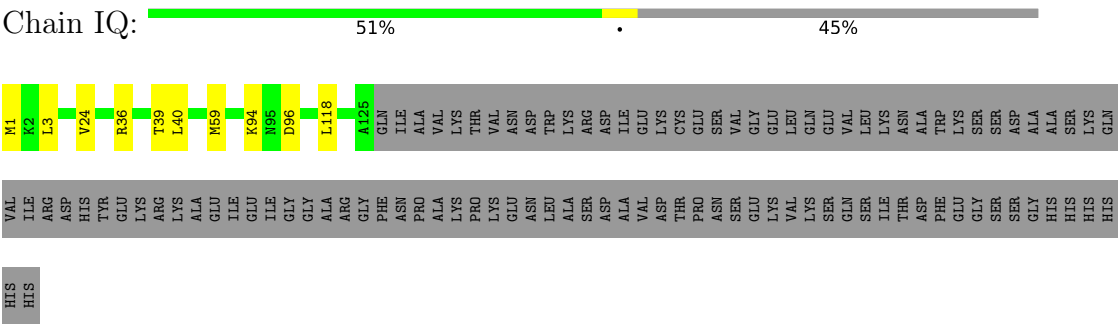
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• Molecule 1: Gp77

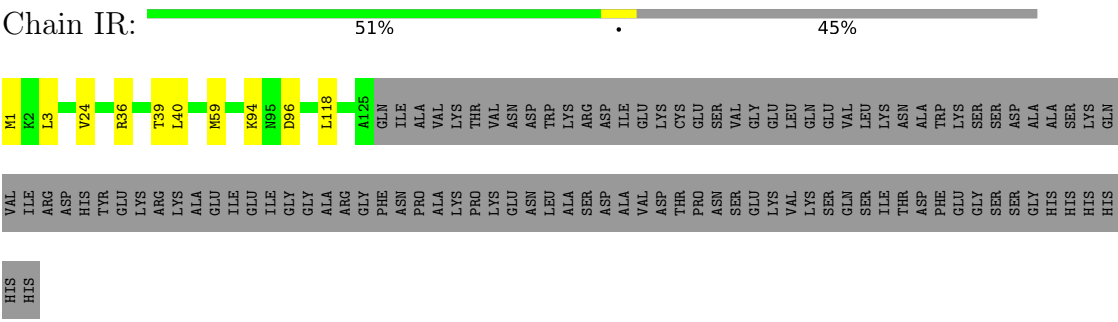


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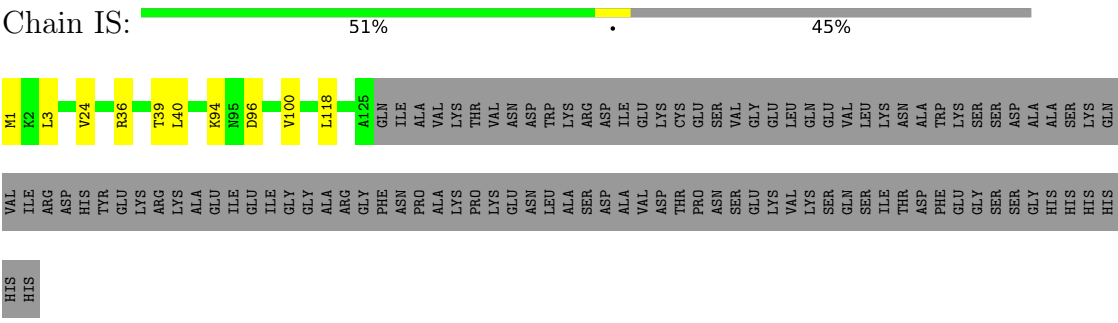
• Molecule 1: Gp77



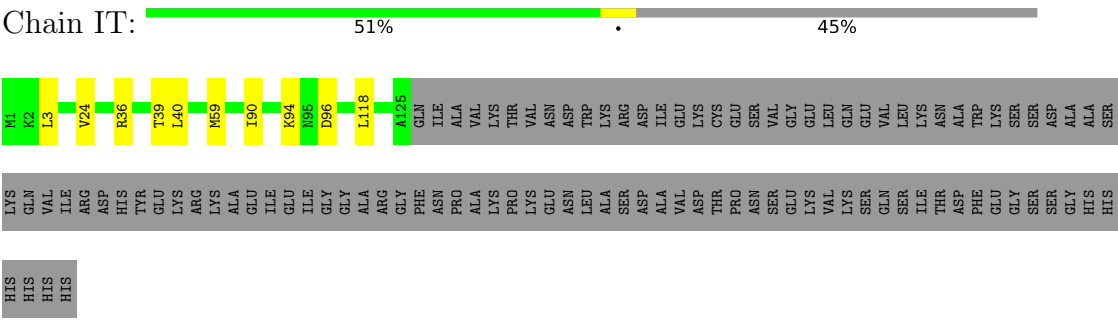
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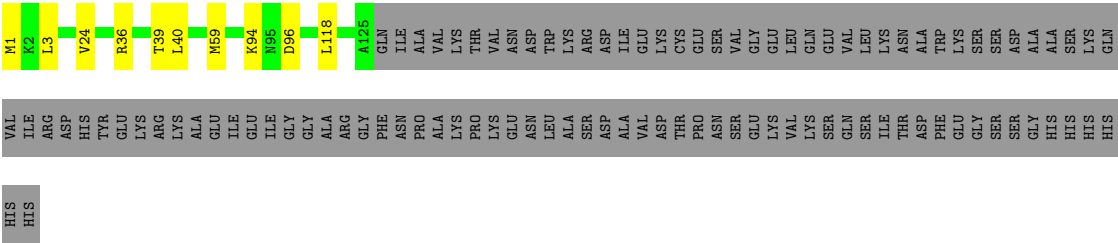
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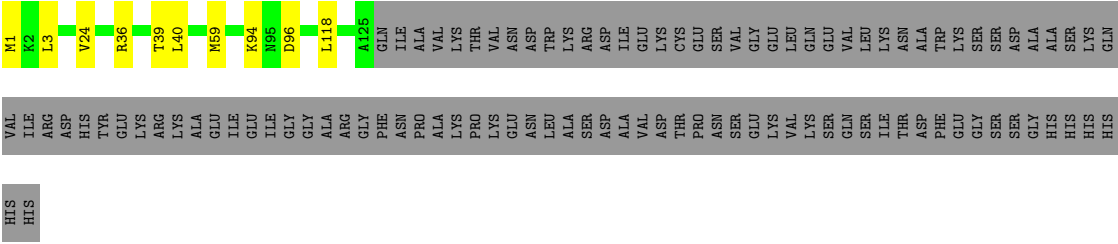
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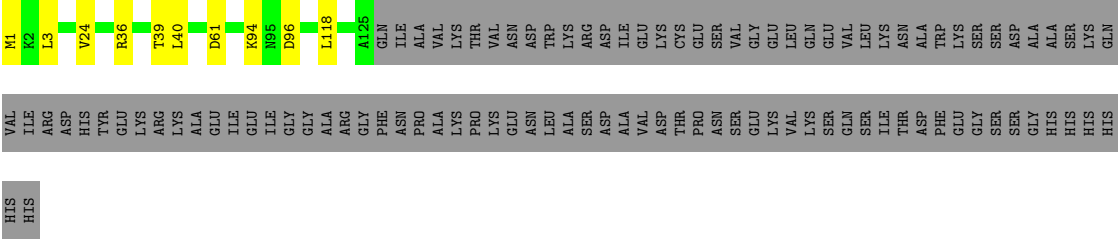
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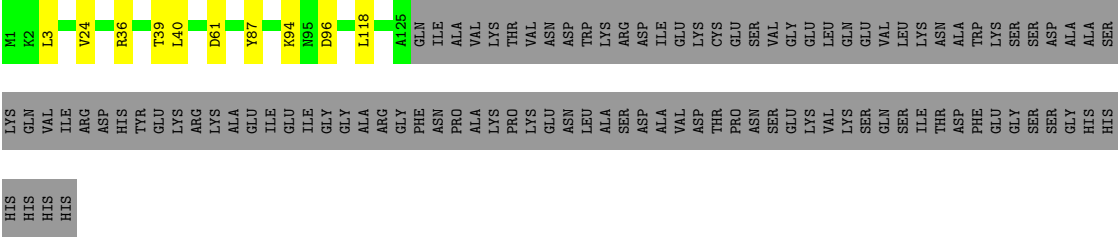
• Molecule 1: Gp77



• Molecule 1: Gp77



• Molecule 1: Gp77



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28191	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.18	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor

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	IA	0.12	0/1004	0.27	0/1355
1	IB	0.12	0/1004	0.28	0/1355
1	IC	0.12	0/1004	0.28	0/1355
1	ID	0.12	0/1004	0.27	0/1355
1	IE	0.12	0/1004	0.28	0/1355
1	IF	0.12	0/1004	0.27	0/1355
1	IG	0.12	0/1004	0.27	0/1355
1	IH	0.12	0/1004	0.28	0/1355
1	II	0.12	0/1004	0.28	0/1355
1	IJ	0.12	0/1004	0.27	0/1355
1	IK	0.12	0/1004	0.28	0/1355
1	IL	0.12	0/1004	0.28	0/1355
1	IM	0.12	0/1004	0.27	0/1355
1	IN	0.12	0/1004	0.28	0/1355
1	IO	0.12	0/1004	0.27	0/1355
1	IP	0.12	0/1004	0.27	0/1355
1	IQ	0.12	0/1004	0.28	0/1355
1	IR	0.12	0/1004	0.28	0/1355
1	IS	0.12	0/1004	0.27	0/1355
1	IT	0.12	0/1004	0.28	0/1355
1	IU	0.12	0/1004	0.27	0/1355
1	IV	0.12	0/1004	0.27	0/1355
1	IW	0.12	0/1004	0.27	0/1355
1	IX	0.12	0/1004	0.27	0/1355
All	All	0.12	0/24096	0.27	0/32520

There are no bond length outliers.

There are no bond angle outliers.

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	IA	986	986	986	9	0
1	IB	986	986	986	9	0
1	IC	986	986	986	9	0
1	ID	986	986	986	11	0
1	IE	986	986	986	11	0
1	IF	986	986	986	9	0
1	IG	986	986	986	9	0
1	IH	986	986	986	10	0
1	II	986	986	986	9	0
1	IJ	986	986	986	10	0
1	IK	986	986	986	12	0
1	IL	986	986	986	12	0
1	IM	986	986	986	13	0
1	IN	986	986	986	11	0
1	IO	986	986	986	10	0
1	IP	986	986	986	10	0
1	IQ	986	986	986	8	0
1	IR	986	986	986	8	0
1	IS	986	986	986	8	0
1	IT	986	986	986	8	0
1	IU	986	986	986	8	0
1	IV	986	986	986	8	0
1	IW	986	986	986	8	0
1	IX	986	986	986	8	0
All	All	23664	23664	23664	188	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 4.

All (188) 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:IL:59:MET:SD	1:IM:1:MET:HE1	2.31	0.70
1:IJ:59:MET:SD	1:IK:1:MET:HE1	2.37	0.64
1:IH:59:MET:SD	1:II:1:MET:HE1	2.38	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IN:59:MET:SD	1:IO:1:MET:HE1	2.39	0.63
1:IM:59:MET:SD	1:IN:1:MET:HE1	2.40	0.60
1:IO:59:MET:SD	1:IP:1:MET:HE1	2.41	0.60
1:IG:59:MET:SD	1:IH:1:MET:HE1	2.43	0.58
1:IF:59:MET:SD	1:IG:1:MET:HE1	2.45	0.57
1:IK:59:MET:SD	1:IL:1:MET:HE1	2.44	0.57
1:II:59:MET:SD	1:IJ:1:MET:HE1	2.45	0.56
1:IA:24:VAL:HG21	1:IA:36:ARG:CZ	2.36	0.56
1:IP:24:VAL:HG21	1:IP:36:ARG:CZ	2.36	0.56
1:IT:24:VAL:HG21	1:IT:36:ARG:CZ	2.36	0.56
1:IV:24:VAL:HG21	1:IV:36:ARG:CZ	2.36	0.56
1:IR:24:VAL:HG21	1:IR:36:ARG:CZ	2.36	0.56
1:IX:24:VAL:HG21	1:IX:36:ARG:CZ	2.36	0.56
1:IB:24:VAL:HG21	1:IB:36:ARG:CZ	2.36	0.56
1:ID:24:VAL:HG21	1:ID:36:ARG:CZ	2.36	0.56
1:IS:24:VAL:HG21	1:IS:36:ARG:CZ	2.36	0.56
1:IE:24:VAL:HG21	1:IE:36:ARG:CZ	2.36	0.56
1:IG:24:VAL:HG21	1:IG:36:ARG:CZ	2.36	0.56
1:IL:24:VAL:HG21	1:IL:36:ARG:CZ	2.36	0.56
1:IN:24:VAL:HG21	1:IN:36:ARG:CZ	2.36	0.56
1:IF:24:VAL:HG21	1:IF:36:ARG:CZ	2.36	0.56
1:IJ:24:VAL:HG21	1:IJ:36:ARG:CZ	2.36	0.56
1:IW:24:VAL:HG21	1:IW:36:ARG:CZ	2.36	0.56
1:IC:24:VAL:HG21	1:IC:36:ARG:CZ	2.36	0.55
1:IH:24:VAL:HG21	1:IH:36:ARG:CZ	2.36	0.55
1:II:24:VAL:HG21	1:II:36:ARG:CZ	2.36	0.55
1:IQ:24:VAL:HG21	1:IQ:36:ARG:CZ	2.36	0.55
1:IU:24:VAL:HG21	1:IU:36:ARG:CZ	2.36	0.55
1:IE:59:MET:SD	1:IF:1:MET:HE1	2.47	0.55
1:IK:24:VAL:HG21	1:IK:36:ARG:CZ	2.36	0.55
1:IO:24:VAL:HG21	1:IO:36:ARG:CZ	2.36	0.55
1:IM:24:VAL:HG21	1:IM:36:ARG:CZ	2.36	0.55
1:IN:39:THR:HG23	1:IN:40:LEU:HD12	1.92	0.52
1:IQ:39:THR:HG23	1:IQ:40:LEU:HD12	1.92	0.52
1:IR:39:THR:HG23	1:IR:40:LEU:HD12	1.92	0.52
1:IS:39:THR:HG23	1:IS:40:LEU:HD12	1.92	0.52
1:IM:39:THR:HG23	1:IM:40:LEU:HD12	1.92	0.52
1:IO:39:THR:HG23	1:IO:40:LEU:HD12	1.92	0.52
1:IP:39:THR:HG23	1:IP:40:LEU:HD12	1.92	0.52
1:IT:39:THR:HG23	1:IT:40:LEU:HD12	1.92	0.52
1:IU:39:THR:HG23	1:IU:40:LEU:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IV:39:THR:HG23	1:IV:40:LEU:HD12	1.92	0.52
1:IL:39:THR:HG23	1:IL:40:LEU:HD12	1.92	0.52
1:IW:39:THR:HG23	1:IW:40:LEU:HD12	1.92	0.52
1:IK:39:THR:HG23	1:IK:40:LEU:HD12	1.92	0.52
1:IL:59:MET:SD	1:IM:1:MET:CE	2.97	0.52
1:IJ:39:THR:HG23	1:IJ:40:LEU:HD12	1.92	0.51
1:IX:39:THR:HG23	1:IX:40:LEU:HD12	1.92	0.51
1:II:39:THR:HG23	1:II:40:LEU:HD12	1.92	0.51
1:IP:59:MET:SD	1:IQ:1:MET:HE1	2.51	0.51
1:IA:39:THR:HG23	1:IA:40:LEU:HD12	1.92	0.51
1:IG:39:THR:HG23	1:IG:40:LEU:HD12	1.92	0.51
1:IF:39:THR:HG23	1:IF:40:LEU:HD12	1.92	0.51
1:IH:39:THR:HG23	1:IH:40:LEU:HD12	1.92	0.51
1:IC:39:THR:HG23	1:IC:40:LEU:HD12	1.92	0.51
1:ID:39:THR:HG23	1:ID:40:LEU:HD12	1.92	0.51
1:IE:39:THR:HG23	1:IE:40:LEU:HD12	1.92	0.51
1:IB:39:THR:HG23	1:IB:40:LEU:HD12	1.92	0.51
1:IQ:59:MET:SD	1:IR:1:MET:HE1	2.50	0.50
1:IM:39:THR:HG23	1:IM:40:LEU:CD1	2.43	0.49
1:IP:39:THR:HG23	1:IP:40:LEU:CD1	2.43	0.49
1:IW:39:THR:HG23	1:IW:40:LEU:CD1	2.43	0.49
1:IU:39:THR:HG23	1:IU:40:LEU:CD1	2.43	0.49
1:IK:39:THR:HG23	1:IK:40:LEU:CD1	2.43	0.49
1:IO:39:THR:HG23	1:IO:40:LEU:CD1	2.43	0.49
1:IQ:39:THR:HG23	1:IQ:40:LEU:CD1	2.43	0.49
1:IT:59:MET:SD	1:IU:1:MET:HE1	2.53	0.49
1:IV:39:THR:HG23	1:IV:40:LEU:CD1	2.43	0.49
1:IB:39:THR:HG23	1:IB:40:LEU:CD1	2.43	0.48
1:IN:39:THR:HG23	1:IN:40:LEU:CD1	2.43	0.48
1:IR:39:THR:HG23	1:IR:40:LEU:CD1	2.43	0.48
1:IX:39:THR:HG23	1:IX:40:LEU:CD1	2.43	0.48
1:IJ:39:THR:HG23	1:IJ:40:LEU:CD1	2.43	0.48
1:IH:39:THR:HG23	1:IH:40:LEU:CD1	2.43	0.48
1:IE:39:THR:HG23	1:IE:40:LEU:CD1	2.43	0.48
1:IL:77:MET:CE	1:IM:3:LEU:HD21	2.44	0.48
1:IS:39:THR:HG23	1:IS:40:LEU:CD1	2.43	0.48
1:IT:39:THR:HG23	1:IT:40:LEU:CD1	2.43	0.48
1:ID:59:MET:SD	1:IE:1:MET:HE1	2.54	0.48
1:IC:39:THR:HG23	1:IC:40:LEU:CD1	2.43	0.48
1:II:39:THR:HG23	1:II:40:LEU:CD1	2.43	0.47
1:IA:39:THR:HG23	1:IA:40:LEU:CD1	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IL:39:THR:HG23	1:IL:40:LEU:CD1	2.43	0.47
1:IB:59:MET:SD	1:IC:1:MET:HE1	2.54	0.47
1:ID:39:THR:HG23	1:ID:40:LEU:CD1	2.43	0.47
1:IF:39:THR:HG23	1:IF:40:LEU:CD1	2.43	0.47
1:IG:39:THR:HG23	1:IG:40:LEU:CD1	2.43	0.47
1:IH:59:MET:SD	1:II:1:MET:CE	3.04	0.46
1:IR:59:MET:SD	1:IS:1:MET:HE1	2.55	0.46
1:IS:100:VAL:HG11	1:IT:90:ILE:HD12	1.97	0.46
1:IJ:77:MET:CE	1:IK:3:LEU:HD21	2.46	0.46
1:IJ:59:MET:SD	1:IK:1:MET:CE	3.04	0.45
1:IJ:24:VAL:HG22	1:IJ:118:LEU:HD23	1.99	0.45
1:IH:24:VAL:HG22	1:IH:118:LEU:HD23	2.00	0.44
1:IO:24:VAL:HG22	1:IO:118:LEU:HD23	2.00	0.44
1:IQ:24:VAL:HG22	1:IQ:118:LEU:HD23	2.00	0.44
1:IR:24:VAL:HG22	1:IR:118:LEU:HD23	1.99	0.44
1:IM:24:VAL:HG22	1:IM:118:LEU:HD23	2.00	0.44
1:IE:24:VAL:HG22	1:IE:118:LEU:HD23	2.00	0.44
1:IF:24:VAL:HG22	1:IF:118:LEU:HD23	2.00	0.44
1:IG:24:VAL:HG22	1:IG:118:LEU:HD23	2.00	0.44
1:II:24:VAL:HG22	1:II:118:LEU:HD23	1.99	0.44
1:IK:24:VAL:HG22	1:IK:118:LEU:HD23	2.00	0.44
1:IL:24:VAL:HG22	1:IL:118:LEU:HD23	2.00	0.44
1:IP:24:VAL:HG22	1:IP:118:LEU:HD23	2.00	0.44
1:IT:24:VAL:HG22	1:IT:118:LEU:HD23	2.00	0.44
1:IN:24:VAL:HG22	1:IN:118:LEU:HD23	2.00	0.44
1:IC:24:VAL:HG22	1:IC:118:LEU:HD23	1.99	0.44
1:IU:24:VAL:HG22	1:IU:118:LEU:HD23	2.00	0.44
1:IW:24:VAL:HG22	1:IW:118:LEU:HD23	1.99	0.44
1:IA:24:VAL:HG22	1:IA:118:LEU:HD23	2.00	0.44
1:ID:24:VAL:HG22	1:ID:118:LEU:HD23	1.99	0.44
1:IS:24:VAL:HG22	1:IS:118:LEU:HD23	2.00	0.44
1:IV:24:VAL:HG22	1:IV:118:LEU:HD23	2.00	0.44
1:IA:61:ASP:OD1	1:IB:87:TYR:O	2.36	0.44
1:IX:24:VAL:HG22	1:IX:118:LEU:HD23	1.99	0.43
1:IB:24:VAL:HG22	1:IB:118:LEU:HD23	2.00	0.43
1:IM:59:MET:SD	1:IN:1:MET:CE	3.05	0.43
1:IO:59:MET:SD	1:IP:1:MET:CE	3.06	0.43
1:IJ:24:VAL:CG2	1:IJ:118:LEU:HD23	2.50	0.42
1:IO:24:VAL:CG2	1:IO:118:LEU:HD23	2.50	0.42
1:IU:59:MET:SD	1:IV:1:MET:HE1	2.59	0.42
1:IH:94:LYS:HE2	1:IH:96:ASP:OD1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IN:94:LYS:HE2	1:IN:96:ASP:OD1	2.20	0.42
1:IQ:94:LYS:HE2	1:IQ:96:ASP:OD1	2.20	0.42
1:IU:94:LYS:HE2	1:IU:96:ASP:OD1	2.20	0.42
1:II:94:LYS:HE2	1:II:96:ASP:OD1	2.20	0.42
1:IK:94:LYS:HE2	1:IK:96:ASP:OD1	2.20	0.42
1:IL:40:LEU:HD11	1:IM:121:ALA:HB3	2.02	0.42
1:IM:24:VAL:CG2	1:IM:118:LEU:HD23	2.50	0.42
1:IT:94:LYS:HE2	1:IT:96:ASP:OD1	2.20	0.42
1:IV:94:LYS:HE2	1:IV:96:ASP:OD1	2.20	0.42
1:IQ:24:VAL:CG2	1:IQ:118:LEU:HD23	2.50	0.42
1:IC:94:LYS:HE2	1:IC:96:ASP:OD1	2.20	0.42
1:IL:24:VAL:CG2	1:IL:118:LEU:HD23	2.50	0.42
1:IO:94:LYS:HE2	1:IO:96:ASP:OD1	2.20	0.42
1:IG:94:LYS:HE2	1:IG:96:ASP:OD1	2.20	0.42
1:IH:24:VAL:CG2	1:IH:118:LEU:HD23	2.50	0.42
1:IM:94:LYS:HE2	1:IM:96:ASP:OD1	2.20	0.42
1:IP:94:LYS:HE2	1:IP:96:ASP:OD1	2.20	0.42
1:IR:24:VAL:CG2	1:IR:118:LEU:HD23	2.50	0.42
1:IT:24:VAL:CG2	1:IT:118:LEU:HD23	2.50	0.42
1:IB:94:LYS:HE2	1:IB:96:ASP:OD1	2.20	0.42
1:IL:94:LYS:HE2	1:IL:96:ASP:OD1	2.20	0.42
1:IW:94:LYS:HE2	1:IW:96:ASP:OD1	2.20	0.42
1:ID:94:LYS:HE2	1:ID:96:ASP:OD1	2.20	0.42
1:IG:24:VAL:CG2	1:IG:118:LEU:HD23	2.50	0.42
1:II:24:VAL:CG2	1:II:118:LEU:HD23	2.49	0.42
1:IJ:94:LYS:HE2	1:IJ:96:ASP:OD1	2.20	0.42
1:IN:24:VAL:CG2	1:IN:118:LEU:HD23	2.50	0.42
1:IP:24:VAL:CG2	1:IP:118:LEU:HD23	2.50	0.42
1:IK:24:VAL:CG2	1:IK:118:LEU:HD23	2.50	0.42
1:IS:94:LYS:HE2	1:IS:96:ASP:OD1	2.20	0.42
1:IR:94:LYS:HE2	1:IR:96:ASP:OD1	2.20	0.41
1:IA:59:MET:SD	1:IB:1:MET:HE1	2.60	0.41
1:IA:94:LYS:HE2	1:IA:96:ASP:OD1	2.20	0.41
1:IE:24:VAL:CG2	1:IE:118:LEU:HD23	2.50	0.41
1:IG:77:MET:CE	1:IH:3:LEU:HD21	2.49	0.41
1:IW:24:VAL:CG2	1:IW:118:LEU:HD23	2.50	0.41
1:ID:51:LEU:HD23	1:ID:51:LEU:HA	1.96	0.41
1:IF:94:LYS:HE2	1:IF:96:ASP:OD1	2.20	0.41
1:IK:51:LEU:HD23	1:IK:51:LEU:HA	1.96	0.41
1:IV:24:VAL:CG2	1:IV:118:LEU:HD23	2.50	0.41
1:IC:59:MET:SD	1:ID:1:MET:HE1	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IN:59:MET:SD	1:IO:1:MET:CE	3.07	0.41
1:IS:24:VAL:CG2	1:IS:118:LEU:HD23	2.50	0.41
1:IX:24:VAL:CG2	1:IX:118:LEU:HD23	2.50	0.41
1:IB:24:VAL:CG2	1:IB:118:LEU:HD23	2.50	0.41
1:IC:100:VAL:HG11	1:ID:90:ILE:HD12	2.02	0.41
1:IU:24:VAL:CG2	1:IU:118:LEU:HD23	2.50	0.41
1:IE:94:LYS:HE2	1:IE:96:ASP:OD1	2.20	0.41
1:IX:94:LYS:HE2	1:IX:96:ASP:OD1	2.20	0.41
1:ID:24:VAL:CG2	1:ID:118:LEU:HD23	2.50	0.41
1:IE:51:LEU:HD23	1:IE:51:LEU:HA	1.96	0.41
1:IF:24:VAL:CG2	1:IF:118:LEU:HD23	2.50	0.41
1:IA:24:VAL:CG2	1:IA:118:LEU:HD23	2.50	0.41
1:IA:87:TYR:O	1:IX:61:ASP:OD1	2.39	0.41
1:IC:24:VAL:CG2	1:IC:118:LEU:HD23	2.50	0.41
1:IM:40:LEU:HD11	1:IN:121:ALA:HB3	2.03	0.41
1:IW:61:ASP:OD1	1:IX:87:TYR:O	2.39	0.41
1:IV:59:MET:SD	1:IW:1:MET:HE1	2.61	0.40
1:IE:77:MET:CE	1:IF:3:LEU:HD21	2.51	0.40
1:IP:51:LEU:HD23	1:IP:51:LEU:HA	1.96	0.40
1:ID:61:ASP:OD1	1:IE:87:TYR:O	2.40	0.40
1:IK:59:MET:SD	1:IL:1:MET:CE	3.09	0.40

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 PDB entries followed by that with respect to all EM entries.

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	IA	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IB	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IC	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	ID	123/227 (54%)	122 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	IE	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IF	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IG	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IH	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	II	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IJ	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IK	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IL	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IM	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IN	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IO	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IP	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IQ	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IR	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IS	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IT	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IU	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IV	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IW	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
1	IX	123/227 (54%)	122 (99%)	1 (1%)	0	100	100
All	All	2952/5448 (54%)	2928 (99%)	24 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	IA	107/194 (55%)	106 (99%)	1 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IB	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IC	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	ID	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IE	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IF	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IG	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IH	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	II	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IJ	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IK	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IL	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IM	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IN	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IO	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IP	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IQ	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IR	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IS	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IT	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IU	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IV	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IW	107/194 (55%)	106 (99%)	1 (1%)	70	80
1	IX	107/194 (55%)	106 (99%)	1 (1%)	70	80
All	All	2568/4656 (55%)	2544 (99%)	24 (1%)	68	80

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	IA	3	LEU
1	IB	3	LEU
1	IC	3	LEU
1	ID	3	LEU
1	IE	3	LEU
1	IF	3	LEU

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Mol	Chain	Res	Type
1	IG	3	LEU
1	IH	3	LEU
1	II	3	LEU
1	IJ	3	LEU
1	IK	3	LEU
1	IL	3	LEU
1	IM	3	LEU
1	IN	3	LEU
1	IO	3	LEU
1	IP	3	LEU
1	IQ	3	LEU
1	IR	3	LEU
1	IS	3	LEU
1	IT	3	LEU
1	IU	3	LEU
1	IV	3	LEU
1	IW	3	LEU
1	IX	3	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-72631. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.