



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 12, 2026 – 10:59 PM JST

PDB ID : 9UE8 / pdb_00009ue8
Title : Crystal structure of MPXV A35R in complex with a neutralizing antibody BA345
Authors : Sun, D.; Zhang, N.; Guo, Y.
Deposited on : 2025-04-08
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

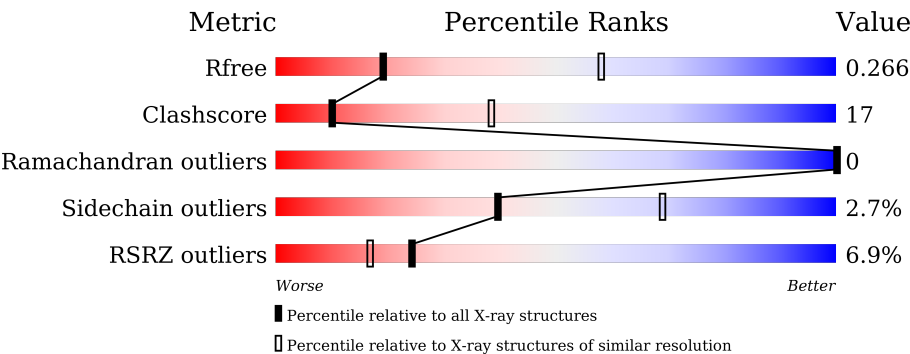
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.48.1

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	164625	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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	221	<div><div>3%</div><div>59%</div><div>39%</div><div>.</div></div>
1	E	221	<div><div>7%</div><div>73%</div><div>24%</div><div>.</div></div>
1	I	221	<div><div>5%</div><div>59%</div><div>41%</div><div>.</div></div>
1	M	221	<div><div>4%</div><div>65%</div><div>31%</div><div>.</div></div>
1	Q	221	<div><div>4%</div><div>71%</div><div>28%</div><div>.</div></div>
1	U	221	<div><div>10%</div><div>62%</div><div>38%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
2	B	215	
2	F	215	
2	J	215	
2	N	215	
2	R	215	
2	V	215	
3	C	152	
3	D	152	
3	G	152	
3	H	152	
3	K	152	
3	L	152	
3	O	152	
3	P	152	
3	S	152	
3	T	152	
3	W	152	
3	X	152	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27654 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 345 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			
1	E	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			
1	I	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			
1	M	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			
1	Q	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			
1	U	221	Total	C	N	O	S	0	0	0
			1632	1030	274	323	5			

- Molecule 2 is a protein called 345 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			
2	F	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			
2	J	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			
2	N	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			
2	R	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			
2	V	215	Total	C	N	O	S	0	0	0
			1649	1028	282	334	5			

- Molecule 3 is a protein called Protein OPG161.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	D	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	G	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	H	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	K	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	L	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	O	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	P	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	S	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	T	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	W	84	Total 664	C 412	N 103	O 145	S 4	0	0	0
3	X	84	Total 664	C 412	N 103	O 145	S 4	0	0	0

There are 336 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	85	GLY	-	expression tag	UNP A0A7H0DND2
C	86	SER	-	expression tag	UNP A0A7H0DND2
C	87	GLY	-	expression tag	UNP A0A7H0DND2
C	88	LEU	-	expression tag	UNP A0A7H0DND2
C	89	ASN	-	expression tag	UNP A0A7H0DND2
C	90	ASP	-	expression tag	UNP A0A7H0DND2
C	91	ILE	-	expression tag	UNP A0A7H0DND2
C	92	PHE	-	expression tag	UNP A0A7H0DND2
C	93	GLU	-	expression tag	UNP A0A7H0DND2
C	94	ALA	-	expression tag	UNP A0A7H0DND2
C	95	GLN	-	expression tag	UNP A0A7H0DND2
C	96	LYS	-	expression tag	UNP A0A7H0DND2
C	97	ILE	-	expression tag	UNP A0A7H0DND2
C	98	GLU	-	expression tag	UNP A0A7H0DND2
C	99	TRP	-	expression tag	UNP A0A7H0DND2
C	100	HIS	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	101	GLU	-	expression tag	UNP A0A7H0DND2
C	102	ALA	-	expression tag	UNP A0A7H0DND2
C	103	ALA	-	expression tag	UNP A0A7H0DND2
C	104	ALA	-	expression tag	UNP A0A7H0DND2
C	105	HIS	-	expression tag	UNP A0A7H0DND2
C	106	HIS	-	expression tag	UNP A0A7H0DND2
C	107	HIS	-	expression tag	UNP A0A7H0DND2
C	108	HIS	-	expression tag	UNP A0A7H0DND2
C	109	HIS	-	expression tag	UNP A0A7H0DND2
C	110	HIS	-	expression tag	UNP A0A7H0DND2
C	111	HIS	-	expression tag	UNP A0A7H0DND2
C	112	HIS	-	expression tag	UNP A0A7H0DND2
D	85	GLY	-	expression tag	UNP A0A7H0DND2
D	86	SER	-	expression tag	UNP A0A7H0DND2
D	87	GLY	-	expression tag	UNP A0A7H0DND2
D	88	LEU	-	expression tag	UNP A0A7H0DND2
D	89	ASN	-	expression tag	UNP A0A7H0DND2
D	90	ASP	-	expression tag	UNP A0A7H0DND2
D	91	ILE	-	expression tag	UNP A0A7H0DND2
D	92	PHE	-	expression tag	UNP A0A7H0DND2
D	93	GLU	-	expression tag	UNP A0A7H0DND2
D	94	ALA	-	expression tag	UNP A0A7H0DND2
D	95	GLN	-	expression tag	UNP A0A7H0DND2
D	96	LYS	-	expression tag	UNP A0A7H0DND2
D	97	ILE	-	expression tag	UNP A0A7H0DND2
D	98	GLU	-	expression tag	UNP A0A7H0DND2
D	99	TRP	-	expression tag	UNP A0A7H0DND2
D	100	HIS	-	expression tag	UNP A0A7H0DND2
D	101	GLU	-	expression tag	UNP A0A7H0DND2
D	102	ALA	-	expression tag	UNP A0A7H0DND2
D	103	ALA	-	expression tag	UNP A0A7H0DND2
D	104	ALA	-	expression tag	UNP A0A7H0DND2
D	105	HIS	-	expression tag	UNP A0A7H0DND2
D	106	HIS	-	expression tag	UNP A0A7H0DND2
D	107	HIS	-	expression tag	UNP A0A7H0DND2
D	108	HIS	-	expression tag	UNP A0A7H0DND2
D	109	HIS	-	expression tag	UNP A0A7H0DND2
D	110	HIS	-	expression tag	UNP A0A7H0DND2
D	111	HIS	-	expression tag	UNP A0A7H0DND2
D	112	HIS	-	expression tag	UNP A0A7H0DND2
G	85	GLY	-	expression tag	UNP A0A7H0DND2
G	86	SER	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	87	GLY	-	expression tag	UNP A0A7H0DND2
G	88	LEU	-	expression tag	UNP A0A7H0DND2
G	89	ASN	-	expression tag	UNP A0A7H0DND2
G	90	ASP	-	expression tag	UNP A0A7H0DND2
G	91	ILE	-	expression tag	UNP A0A7H0DND2
G	92	PHE	-	expression tag	UNP A0A7H0DND2
G	93	GLU	-	expression tag	UNP A0A7H0DND2
G	94	ALA	-	expression tag	UNP A0A7H0DND2
G	95	GLN	-	expression tag	UNP A0A7H0DND2
G	96	LYS	-	expression tag	UNP A0A7H0DND2
G	97	ILE	-	expression tag	UNP A0A7H0DND2
G	98	GLU	-	expression tag	UNP A0A7H0DND2
G	99	TRP	-	expression tag	UNP A0A7H0DND2
G	100	HIS	-	expression tag	UNP A0A7H0DND2
G	101	GLU	-	expression tag	UNP A0A7H0DND2
G	102	ALA	-	expression tag	UNP A0A7H0DND2
G	103	ALA	-	expression tag	UNP A0A7H0DND2
G	104	ALA	-	expression tag	UNP A0A7H0DND2
G	105	HIS	-	expression tag	UNP A0A7H0DND2
G	106	HIS	-	expression tag	UNP A0A7H0DND2
G	107	HIS	-	expression tag	UNP A0A7H0DND2
G	108	HIS	-	expression tag	UNP A0A7H0DND2
G	109	HIS	-	expression tag	UNP A0A7H0DND2
G	110	HIS	-	expression tag	UNP A0A7H0DND2
G	111	HIS	-	expression tag	UNP A0A7H0DND2
G	112	HIS	-	expression tag	UNP A0A7H0DND2
H	85	GLY	-	expression tag	UNP A0A7H0DND2
H	86	SER	-	expression tag	UNP A0A7H0DND2
H	87	GLY	-	expression tag	UNP A0A7H0DND2
H	88	LEU	-	expression tag	UNP A0A7H0DND2
H	89	ASN	-	expression tag	UNP A0A7H0DND2
H	90	ASP	-	expression tag	UNP A0A7H0DND2
H	91	ILE	-	expression tag	UNP A0A7H0DND2
H	92	PHE	-	expression tag	UNP A0A7H0DND2
H	93	GLU	-	expression tag	UNP A0A7H0DND2
H	94	ALA	-	expression tag	UNP A0A7H0DND2
H	95	GLN	-	expression tag	UNP A0A7H0DND2
H	96	LYS	-	expression tag	UNP A0A7H0DND2
H	97	ILE	-	expression tag	UNP A0A7H0DND2
H	98	GLU	-	expression tag	UNP A0A7H0DND2
H	99	TRP	-	expression tag	UNP A0A7H0DND2
H	100	HIS	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
H	101	GLU	-	expression tag	UNP A0A7H0DND2
H	102	ALA	-	expression tag	UNP A0A7H0DND2
H	103	ALA	-	expression tag	UNP A0A7H0DND2
H	104	ALA	-	expression tag	UNP A0A7H0DND2
H	105	HIS	-	expression tag	UNP A0A7H0DND2
H	106	HIS	-	expression tag	UNP A0A7H0DND2
H	107	HIS	-	expression tag	UNP A0A7H0DND2
H	108	HIS	-	expression tag	UNP A0A7H0DND2
H	109	HIS	-	expression tag	UNP A0A7H0DND2
H	110	HIS	-	expression tag	UNP A0A7H0DND2
H	111	HIS	-	expression tag	UNP A0A7H0DND2
H	112	HIS	-	expression tag	UNP A0A7H0DND2
K	85	GLY	-	expression tag	UNP A0A7H0DND2
K	86	SER	-	expression tag	UNP A0A7H0DND2
K	87	GLY	-	expression tag	UNP A0A7H0DND2
K	88	LEU	-	expression tag	UNP A0A7H0DND2
K	89	ASN	-	expression tag	UNP A0A7H0DND2
K	90	ASP	-	expression tag	UNP A0A7H0DND2
K	91	ILE	-	expression tag	UNP A0A7H0DND2
K	92	PHE	-	expression tag	UNP A0A7H0DND2
K	93	GLU	-	expression tag	UNP A0A7H0DND2
K	94	ALA	-	expression tag	UNP A0A7H0DND2
K	95	GLN	-	expression tag	UNP A0A7H0DND2
K	96	LYS	-	expression tag	UNP A0A7H0DND2
K	97	ILE	-	expression tag	UNP A0A7H0DND2
K	98	GLU	-	expression tag	UNP A0A7H0DND2
K	99	TRP	-	expression tag	UNP A0A7H0DND2
K	100	HIS	-	expression tag	UNP A0A7H0DND2
K	101	GLU	-	expression tag	UNP A0A7H0DND2
K	102	ALA	-	expression tag	UNP A0A7H0DND2
K	103	ALA	-	expression tag	UNP A0A7H0DND2
K	104	ALA	-	expression tag	UNP A0A7H0DND2
K	105	HIS	-	expression tag	UNP A0A7H0DND2
K	106	HIS	-	expression tag	UNP A0A7H0DND2
K	107	HIS	-	expression tag	UNP A0A7H0DND2
K	108	HIS	-	expression tag	UNP A0A7H0DND2
K	109	HIS	-	expression tag	UNP A0A7H0DND2
K	110	HIS	-	expression tag	UNP A0A7H0DND2
K	111	HIS	-	expression tag	UNP A0A7H0DND2
K	112	HIS	-	expression tag	UNP A0A7H0DND2
L	85	GLY	-	expression tag	UNP A0A7H0DND2
L	86	SER	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
L	87	GLY	-	expression tag	UNP A0A7H0DND2
L	88	LEU	-	expression tag	UNP A0A7H0DND2
L	89	ASN	-	expression tag	UNP A0A7H0DND2
L	90	ASP	-	expression tag	UNP A0A7H0DND2
L	91	ILE	-	expression tag	UNP A0A7H0DND2
L	92	PHE	-	expression tag	UNP A0A7H0DND2
L	93	GLU	-	expression tag	UNP A0A7H0DND2
L	94	ALA	-	expression tag	UNP A0A7H0DND2
L	95	GLN	-	expression tag	UNP A0A7H0DND2
L	96	LYS	-	expression tag	UNP A0A7H0DND2
L	97	ILE	-	expression tag	UNP A0A7H0DND2
L	98	GLU	-	expression tag	UNP A0A7H0DND2
L	99	TRP	-	expression tag	UNP A0A7H0DND2
L	100	HIS	-	expression tag	UNP A0A7H0DND2
L	101	GLU	-	expression tag	UNP A0A7H0DND2
L	102	ALA	-	expression tag	UNP A0A7H0DND2
L	103	ALA	-	expression tag	UNP A0A7H0DND2
L	104	ALA	-	expression tag	UNP A0A7H0DND2
L	105	HIS	-	expression tag	UNP A0A7H0DND2
L	106	HIS	-	expression tag	UNP A0A7H0DND2
L	107	HIS	-	expression tag	UNP A0A7H0DND2
L	108	HIS	-	expression tag	UNP A0A7H0DND2
L	109	HIS	-	expression tag	UNP A0A7H0DND2
L	110	HIS	-	expression tag	UNP A0A7H0DND2
L	111	HIS	-	expression tag	UNP A0A7H0DND2
L	112	HIS	-	expression tag	UNP A0A7H0DND2
O	85	GLY	-	expression tag	UNP A0A7H0DND2
O	86	SER	-	expression tag	UNP A0A7H0DND2
O	87	GLY	-	expression tag	UNP A0A7H0DND2
O	88	LEU	-	expression tag	UNP A0A7H0DND2
O	89	ASN	-	expression tag	UNP A0A7H0DND2
O	90	ASP	-	expression tag	UNP A0A7H0DND2
O	91	ILE	-	expression tag	UNP A0A7H0DND2
O	92	PHE	-	expression tag	UNP A0A7H0DND2
O	93	GLU	-	expression tag	UNP A0A7H0DND2
O	94	ALA	-	expression tag	UNP A0A7H0DND2
O	95	GLN	-	expression tag	UNP A0A7H0DND2
O	96	LYS	-	expression tag	UNP A0A7H0DND2
O	97	ILE	-	expression tag	UNP A0A7H0DND2
O	98	GLU	-	expression tag	UNP A0A7H0DND2
O	99	TRP	-	expression tag	UNP A0A7H0DND2
O	100	HIS	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
O	101	GLU	-	expression tag	UNP A0A7H0DND2
O	102	ALA	-	expression tag	UNP A0A7H0DND2
O	103	ALA	-	expression tag	UNP A0A7H0DND2
O	104	ALA	-	expression tag	UNP A0A7H0DND2
O	105	HIS	-	expression tag	UNP A0A7H0DND2
O	106	HIS	-	expression tag	UNP A0A7H0DND2
O	107	HIS	-	expression tag	UNP A0A7H0DND2
O	108	HIS	-	expression tag	UNP A0A7H0DND2
O	109	HIS	-	expression tag	UNP A0A7H0DND2
O	110	HIS	-	expression tag	UNP A0A7H0DND2
O	111	HIS	-	expression tag	UNP A0A7H0DND2
O	112	HIS	-	expression tag	UNP A0A7H0DND2
P	85	GLY	-	expression tag	UNP A0A7H0DND2
P	86	SER	-	expression tag	UNP A0A7H0DND2
P	87	GLY	-	expression tag	UNP A0A7H0DND2
P	88	LEU	-	expression tag	UNP A0A7H0DND2
P	89	ASN	-	expression tag	UNP A0A7H0DND2
P	90	ASP	-	expression tag	UNP A0A7H0DND2
P	91	ILE	-	expression tag	UNP A0A7H0DND2
P	92	PHE	-	expression tag	UNP A0A7H0DND2
P	93	GLU	-	expression tag	UNP A0A7H0DND2
P	94	ALA	-	expression tag	UNP A0A7H0DND2
P	95	GLN	-	expression tag	UNP A0A7H0DND2
P	96	LYS	-	expression tag	UNP A0A7H0DND2
P	97	ILE	-	expression tag	UNP A0A7H0DND2
P	98	GLU	-	expression tag	UNP A0A7H0DND2
P	99	TRP	-	expression tag	UNP A0A7H0DND2
P	100	HIS	-	expression tag	UNP A0A7H0DND2
P	101	GLU	-	expression tag	UNP A0A7H0DND2
P	102	ALA	-	expression tag	UNP A0A7H0DND2
P	103	ALA	-	expression tag	UNP A0A7H0DND2
P	104	ALA	-	expression tag	UNP A0A7H0DND2
P	105	HIS	-	expression tag	UNP A0A7H0DND2
P	106	HIS	-	expression tag	UNP A0A7H0DND2
P	107	HIS	-	expression tag	UNP A0A7H0DND2
P	108	HIS	-	expression tag	UNP A0A7H0DND2
P	109	HIS	-	expression tag	UNP A0A7H0DND2
P	110	HIS	-	expression tag	UNP A0A7H0DND2
P	111	HIS	-	expression tag	UNP A0A7H0DND2
P	112	HIS	-	expression tag	UNP A0A7H0DND2
S	85	GLY	-	expression tag	UNP A0A7H0DND2
S	86	SER	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
S	87	GLY	-	expression tag	UNP A0A7H0DND2
S	88	LEU	-	expression tag	UNP A0A7H0DND2
S	89	ASN	-	expression tag	UNP A0A7H0DND2
S	90	ASP	-	expression tag	UNP A0A7H0DND2
S	91	ILE	-	expression tag	UNP A0A7H0DND2
S	92	PHE	-	expression tag	UNP A0A7H0DND2
S	93	GLU	-	expression tag	UNP A0A7H0DND2
S	94	ALA	-	expression tag	UNP A0A7H0DND2
S	95	GLN	-	expression tag	UNP A0A7H0DND2
S	96	LYS	-	expression tag	UNP A0A7H0DND2
S	97	ILE	-	expression tag	UNP A0A7H0DND2
S	98	GLU	-	expression tag	UNP A0A7H0DND2
S	99	TRP	-	expression tag	UNP A0A7H0DND2
S	100	HIS	-	expression tag	UNP A0A7H0DND2
S	101	GLU	-	expression tag	UNP A0A7H0DND2
S	102	ALA	-	expression tag	UNP A0A7H0DND2
S	103	ALA	-	expression tag	UNP A0A7H0DND2
S	104	ALA	-	expression tag	UNP A0A7H0DND2
S	105	HIS	-	expression tag	UNP A0A7H0DND2
S	106	HIS	-	expression tag	UNP A0A7H0DND2
S	107	HIS	-	expression tag	UNP A0A7H0DND2
S	108	HIS	-	expression tag	UNP A0A7H0DND2
S	109	HIS	-	expression tag	UNP A0A7H0DND2
S	110	HIS	-	expression tag	UNP A0A7H0DND2
S	111	HIS	-	expression tag	UNP A0A7H0DND2
S	112	HIS	-	expression tag	UNP A0A7H0DND2
T	85	GLY	-	expression tag	UNP A0A7H0DND2
T	86	SER	-	expression tag	UNP A0A7H0DND2
T	87	GLY	-	expression tag	UNP A0A7H0DND2
T	88	LEU	-	expression tag	UNP A0A7H0DND2
T	89	ASN	-	expression tag	UNP A0A7H0DND2
T	90	ASP	-	expression tag	UNP A0A7H0DND2
T	91	ILE	-	expression tag	UNP A0A7H0DND2
T	92	PHE	-	expression tag	UNP A0A7H0DND2
T	93	GLU	-	expression tag	UNP A0A7H0DND2
T	94	ALA	-	expression tag	UNP A0A7H0DND2
T	95	GLN	-	expression tag	UNP A0A7H0DND2
T	96	LYS	-	expression tag	UNP A0A7H0DND2
T	97	ILE	-	expression tag	UNP A0A7H0DND2
T	98	GLU	-	expression tag	UNP A0A7H0DND2
T	99	TRP	-	expression tag	UNP A0A7H0DND2
T	100	HIS	-	expression tag	UNP A0A7H0DND2

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Chain	Residue	Modelled	Actual	Comment	Reference
T	101	GLU	-	expression tag	UNP A0A7H0DND2
T	102	ALA	-	expression tag	UNP A0A7H0DND2
T	103	ALA	-	expression tag	UNP A0A7H0DND2
T	104	ALA	-	expression tag	UNP A0A7H0DND2
T	105	HIS	-	expression tag	UNP A0A7H0DND2
T	106	HIS	-	expression tag	UNP A0A7H0DND2
T	107	HIS	-	expression tag	UNP A0A7H0DND2
T	108	HIS	-	expression tag	UNP A0A7H0DND2
T	109	HIS	-	expression tag	UNP A0A7H0DND2
T	110	HIS	-	expression tag	UNP A0A7H0DND2
T	111	HIS	-	expression tag	UNP A0A7H0DND2
T	112	HIS	-	expression tag	UNP A0A7H0DND2
W	85	GLY	-	expression tag	UNP A0A7H0DND2
W	86	SER	-	expression tag	UNP A0A7H0DND2
W	87	GLY	-	expression tag	UNP A0A7H0DND2
W	88	LEU	-	expression tag	UNP A0A7H0DND2
W	89	ASN	-	expression tag	UNP A0A7H0DND2
W	90	ASP	-	expression tag	UNP A0A7H0DND2
W	91	ILE	-	expression tag	UNP A0A7H0DND2
W	92	PHE	-	expression tag	UNP A0A7H0DND2
W	93	GLU	-	expression tag	UNP A0A7H0DND2
W	94	ALA	-	expression tag	UNP A0A7H0DND2
W	95	GLN	-	expression tag	UNP A0A7H0DND2
W	96	LYS	-	expression tag	UNP A0A7H0DND2
W	97	ILE	-	expression tag	UNP A0A7H0DND2
W	98	GLU	-	expression tag	UNP A0A7H0DND2
W	99	TRP	-	expression tag	UNP A0A7H0DND2
W	100	HIS	-	expression tag	UNP A0A7H0DND2
W	101	GLU	-	expression tag	UNP A0A7H0DND2
W	102	ALA	-	expression tag	UNP A0A7H0DND2
W	103	ALA	-	expression tag	UNP A0A7H0DND2
W	104	ALA	-	expression tag	UNP A0A7H0DND2
W	105	HIS	-	expression tag	UNP A0A7H0DND2
W	106	HIS	-	expression tag	UNP A0A7H0DND2
W	107	HIS	-	expression tag	UNP A0A7H0DND2
W	108	HIS	-	expression tag	UNP A0A7H0DND2
W	109	HIS	-	expression tag	UNP A0A7H0DND2
W	110	HIS	-	expression tag	UNP A0A7H0DND2
W	111	HIS	-	expression tag	UNP A0A7H0DND2
W	112	HIS	-	expression tag	UNP A0A7H0DND2
X	85	GLY	-	expression tag	UNP A0A7H0DND2
X	86	SER	-	expression tag	UNP A0A7H0DND2

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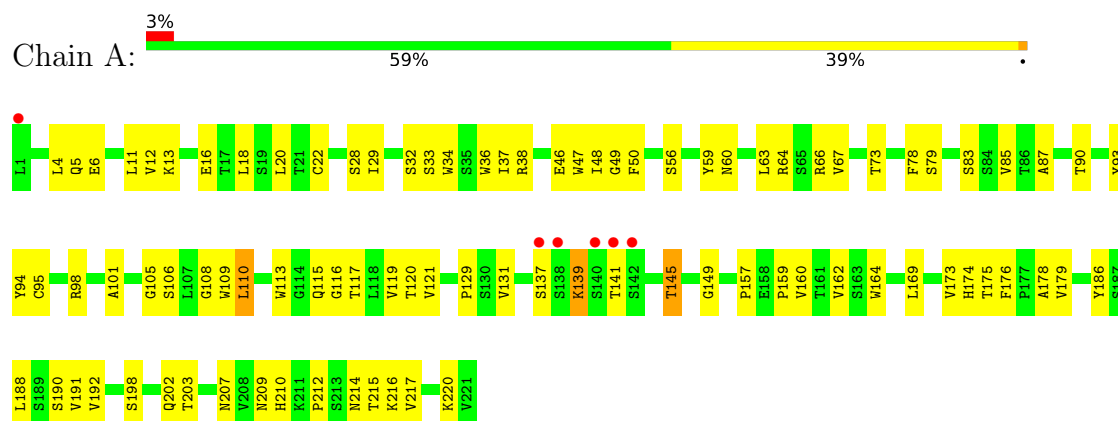
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Chain	Residue	Modelled	Actual	Comment	Reference
X	87	GLY	-	expression tag	UNP A0A7H0DND2
X	88	LEU	-	expression tag	UNP A0A7H0DND2
X	89	ASN	-	expression tag	UNP A0A7H0DND2
X	90	ASP	-	expression tag	UNP A0A7H0DND2
X	91	ILE	-	expression tag	UNP A0A7H0DND2
X	92	PHE	-	expression tag	UNP A0A7H0DND2
X	93	GLU	-	expression tag	UNP A0A7H0DND2
X	94	ALA	-	expression tag	UNP A0A7H0DND2
X	95	GLN	-	expression tag	UNP A0A7H0DND2
X	96	LYS	-	expression tag	UNP A0A7H0DND2
X	97	ILE	-	expression tag	UNP A0A7H0DND2
X	98	GLU	-	expression tag	UNP A0A7H0DND2
X	99	TRP	-	expression tag	UNP A0A7H0DND2
X	100	HIS	-	expression tag	UNP A0A7H0DND2
X	101	GLU	-	expression tag	UNP A0A7H0DND2
X	102	ALA	-	expression tag	UNP A0A7H0DND2
X	103	ALA	-	expression tag	UNP A0A7H0DND2
X	104	ALA	-	expression tag	UNP A0A7H0DND2
X	105	HIS	-	expression tag	UNP A0A7H0DND2
X	106	HIS	-	expression tag	UNP A0A7H0DND2
X	107	HIS	-	expression tag	UNP A0A7H0DND2
X	108	HIS	-	expression tag	UNP A0A7H0DND2
X	109	HIS	-	expression tag	UNP A0A7H0DND2
X	110	HIS	-	expression tag	UNP A0A7H0DND2
X	111	HIS	-	expression tag	UNP A0A7H0DND2
X	112	HIS	-	expression tag	UNP A0A7H0DND2

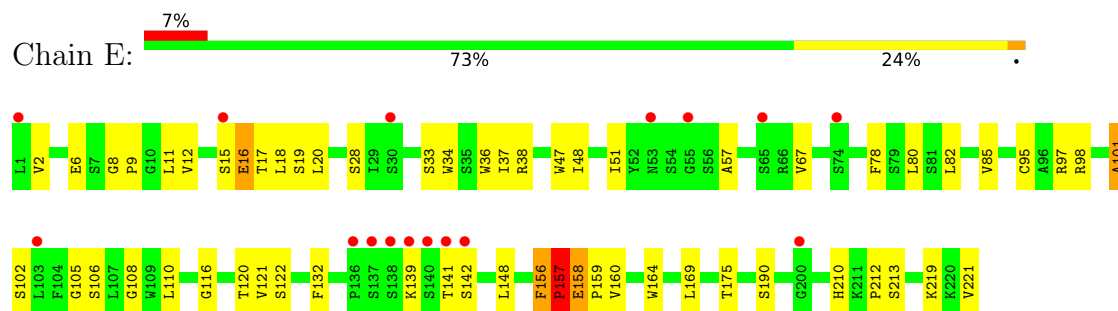
3 Residue-property plots [i](#)

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

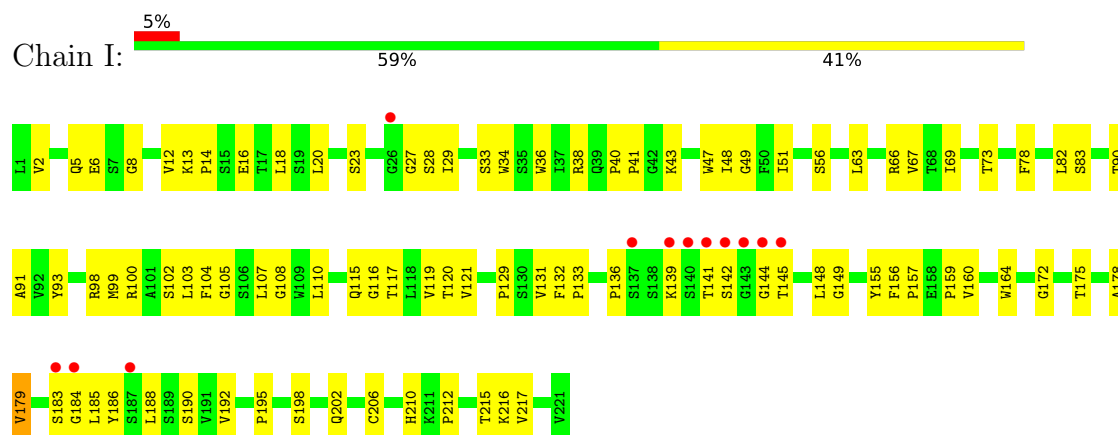
• Molecule 1: 345 Heavy Chain

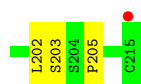


• Molecule 1: 345 Heavy Chain



• Molecule 1: 345 Heavy Chain

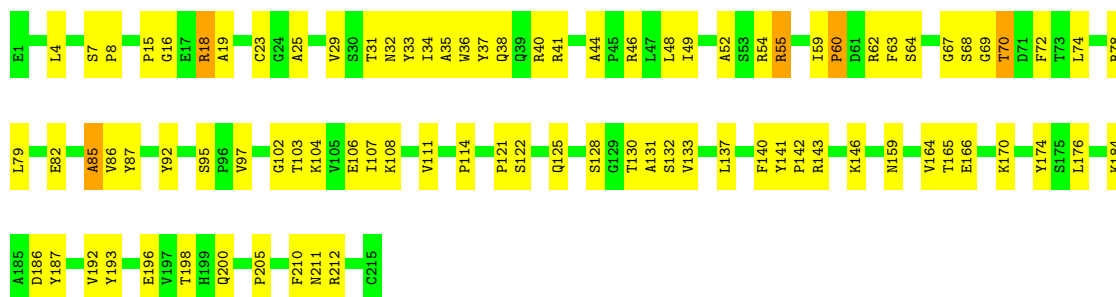




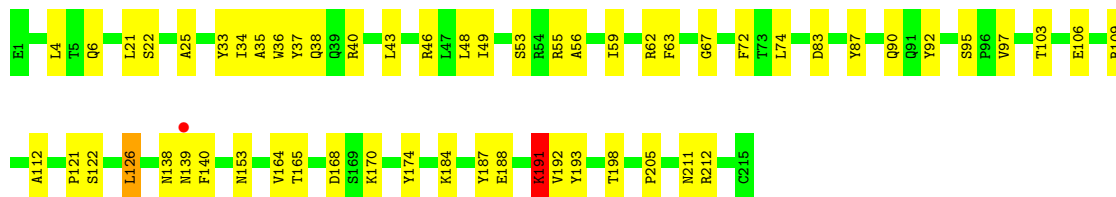
• Molecule 2: 345 Light Chain



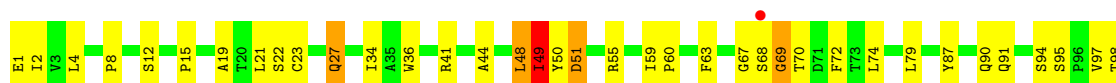
• Molecule 2: 345 Light Chain



• Molecule 2: 345 Light Chain



• Molecule 2: 345 Light Chain

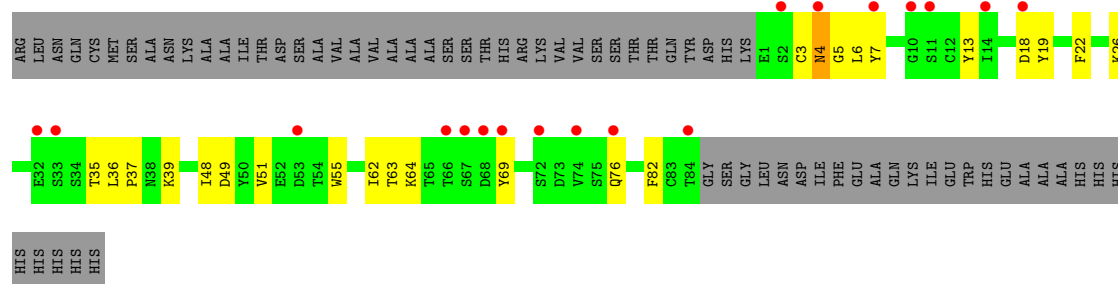
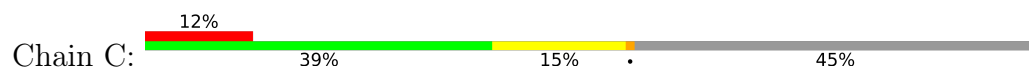




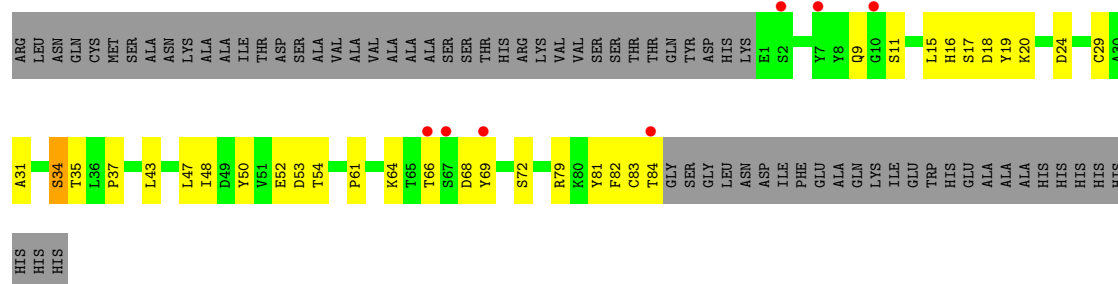
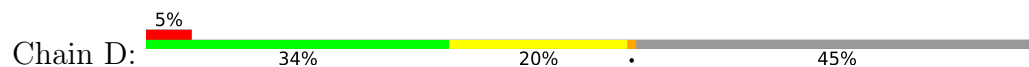
• Molecule 2: 345 Light Chain



• Molecule 3: Protein OPG161



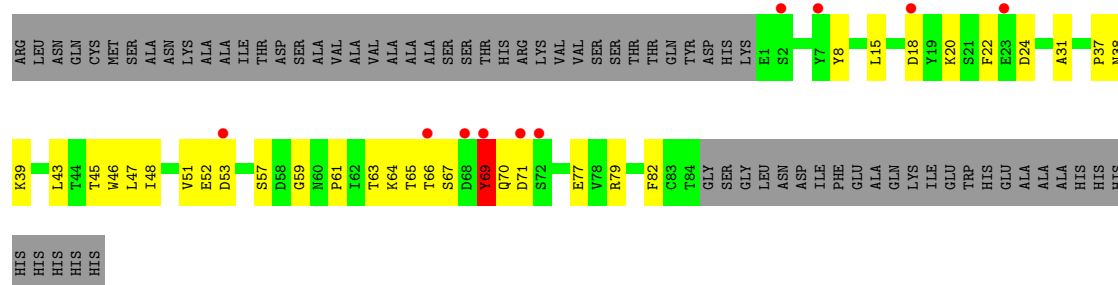
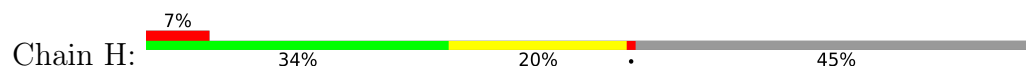
• Molecule 3: Protein OPG161



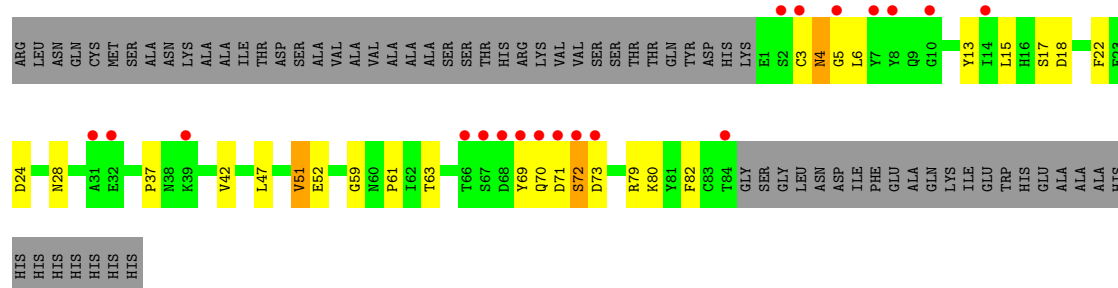
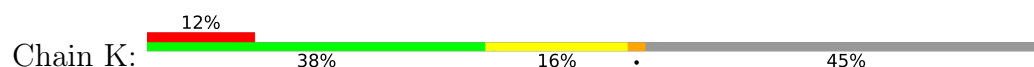
• Molecule 3: Protein OPG161



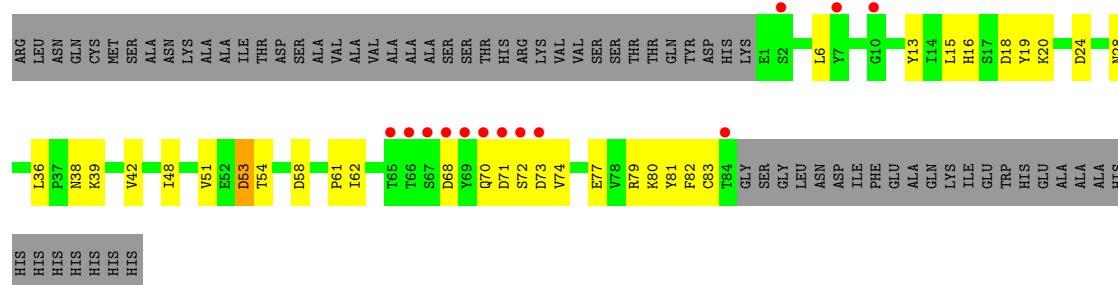
- Molecule 3: Protein OPG161



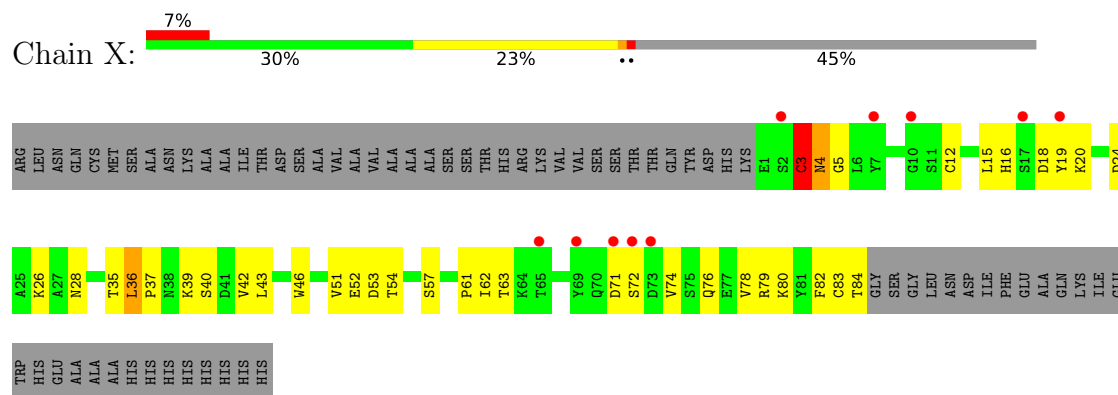
- Molecule 3: Protein OPG161



- Molecule 3: Protein OPG161



- Molecule 3: Protein OPG161



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	113.06Å 126.07Å 350.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.48 – 3.20 49.48 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.48-3.20) 99.5 (49.48-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.202 , 0.267 0.213 , 0.266	Depositor DCC
R_{free} test set	2000 reflections (2.39%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.653	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	27654	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.57 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5143e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.60	0/1672	0.98	5/2283 (0.2%)
1	E	0.84	1/1672 (0.1%)	1.09	10/2283 (0.4%)
1	I	0.69	0/1672	1.05	8/2283 (0.4%)
1	M	0.93	1/1672 (0.1%)	1.49	18/2283 (0.8%)
1	Q	0.55	0/1672	0.84	4/2283 (0.2%)
1	U	0.69	1/1672 (0.1%)	0.93	6/2283 (0.3%)
2	B	0.70	0/1683	0.92	3/2284 (0.1%)
2	F	0.72	0/1683	1.05	12/2284 (0.5%)
2	J	0.73	0/1683	0.94	7/2284 (0.3%)
2	N	0.67	0/1683	0.98	9/2284 (0.4%)
2	R	0.59	0/1683	0.91	6/2284 (0.3%)
2	V	0.64	0/1683	0.87	4/2284 (0.2%)
3	C	0.53	0/679	1.31	3/924 (0.3%)
3	D	0.42	0/679	0.74	3/924 (0.3%)
3	G	0.47	0/679	0.81	1/924 (0.1%)
3	H	0.52	0/679	0.85	3/924 (0.3%)
3	K	0.55	0/679	1.59	8/924 (0.9%)
3	L	0.61	0/679	1.17	5/924 (0.5%)
3	O	0.53	0/679	1.14	6/924 (0.6%)
3	P	0.43	0/679	0.75	3/924 (0.3%)
3	S	0.65	0/679	0.98	5/924 (0.5%)
3	T	0.70	0/679	0.95	1/924 (0.1%)
3	W	0.64	0/679	1.08	3/924 (0.3%)
3	X	0.57	0/679	1.33	5/924 (0.5%)
All	All	0.66	3/28278 (0.0%)	1.04	138/38490 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
2	F	0	1
2	J	0	2
3	L	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	159	PRO	N-CD	26.84	1.85	1.47
1	E	157	PRO	N-CD	21.53	1.77	1.47
1	U	12	VAL	C-N	5.45	1.44	1.33

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	158	GLU	CB-CA-C	-28.92	68.49	108.68
3	K	72	SER	N-CA-C	-25.36	71.58	108.60
1	M	159	PRO	N-CA-CB	-24.04	76.16	102.60
3	C	4	ASN	N-CA-C	-23.33	74.27	110.42
3	K	4	ASN	N-CA-C	-21.73	75.89	109.79

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	PRO	Peptide
2	B	203	SER	Peptide
2	F	203	SER	Peptide
2	J	18	ARG	Sidechain
2	J	55	ARG	Sidechain

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1632	0	1621	67	0
1	E	1632	0	1621	49	0
1	I	1632	0	1621	70	0
1	M	1632	0	1621	62	1
1	Q	1632	0	1621	56	0
1	U	1632	0	1621	79	0
2	B	1649	0	1604	59	0
2	F	1649	0	1604	52	0
2	J	1649	0	1604	67	0
2	N	1649	0	1604	39	0
2	R	1649	0	1604	62	1
2	V	1649	0	1604	48	0
3	C	664	0	599	16	8
3	D	664	0	599	32	0
3	G	664	0	599	21	0
3	H	664	0	599	23	0
3	K	664	0	599	18	0
3	L	664	0	599	25	0
3	O	664	0	599	26	0
3	P	664	0	599	19	0
3	S	664	0	599	43	0
3	T	664	0	599	36	0
3	W	664	0	599	36	8
3	X	664	0	599	36	0
All	All	27654	0	26538	919	9

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 17.

The worst 5 of 919 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:E:157:PRO:N	1:E:157:PRO:CD	1.77	1.40
1:M:159:PRO:CD	1:M:159:PRO:N	1.85	1.32
1:U:140:SER:O	2:V:117:PHE:CD1	1.90	1.25
1:E:156:PHE:O	1:E:156:PHE:CD1	2.05	1.10
3:K:3:CYS:SG	3:K:4:ASN:O	2.09	1.09

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes

the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:76:GLN:OE1	3:W:76:GLN:NE2[1_455]	1.07	1.13
3:C:76:GLN:CD	3:W:76:GLN:OE1[1_455]	1.38	0.82
3:C:76:GLN:NE2	3:W:76:GLN:OE1[1_455]	1.41	0.79
3:C:76:GLN:CD	3:W:76:GLN:CD[1_455]	1.51	0.69
3:C:76:GLN:CD	3:W:76:GLN:NE2[1_455]	1.61	0.59

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	219/221 (99%)	207 (94%)	12 (6%)	0	100	100
1	E	219/221 (99%)	207 (94%)	12 (6%)	0	100	100
1	I	219/221 (99%)	204 (93%)	15 (7%)	0	100	100
1	M	219/221 (99%)	209 (95%)	10 (5%)	0	100	100
1	Q	219/221 (99%)	210 (96%)	9 (4%)	0	100	100
1	U	219/221 (99%)	211 (96%)	8 (4%)	0	100	100
2	B	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
2	F	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
2	J	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
2	N	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
2	R	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
2	V	213/215 (99%)	209 (98%)	4 (2%)	0	100	100
3	C	82/152 (54%)	74 (90%)	8 (10%)	0	100	100
3	D	82/152 (54%)	73 (89%)	9 (11%)	0	100	100
3	G	82/152 (54%)	77 (94%)	5 (6%)	0	100	100
3	H	82/152 (54%)	75 (92%)	7 (8%)	0	100	100
3	K	82/152 (54%)	79 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	L	82/152 (54%)	77 (94%)	5 (6%)	0	100	100
3	O	82/152 (54%)	77 (94%)	5 (6%)	0	100	100
3	P	82/152 (54%)	78 (95%)	4 (5%)	0	100	100
3	S	82/152 (54%)	78 (95%)	4 (5%)	0	100	100
3	T	82/152 (54%)	74 (90%)	8 (10%)	0	100	100
3	W	82/152 (54%)	74 (90%)	8 (10%)	0	100	100
3	X	82/152 (54%)	75 (92%)	7 (8%)	0	100	100
All	All	3576/4440 (80%)	3398 (95%)	178 (5%)	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 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	189/189 (100%)	186 (98%)	3 (2%)	58	79
1	E	189/189 (100%)	185 (98%)	4 (2%)	48	74
1	I	189/189 (100%)	185 (98%)	4 (2%)	48	74
1	M	189/189 (100%)	182 (96%)	7 (4%)	29	62
1	Q	189/189 (100%)	186 (98%)	3 (2%)	58	79
1	U	189/189 (100%)	180 (95%)	9 (5%)	21	55
2	B	185/185 (100%)	183 (99%)	2 (1%)	70	86
2	F	185/185 (100%)	178 (96%)	7 (4%)	28	60
2	J	185/185 (100%)	182 (98%)	3 (2%)	58	79
2	N	185/185 (100%)	183 (99%)	2 (1%)	70	86
2	R	185/185 (100%)	181 (98%)	4 (2%)	47	73
2	V	185/185 (100%)	179 (97%)	6 (3%)	34	65
3	C	76/130 (58%)	74 (97%)	2 (3%)	41	70
3	D	76/130 (58%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	76/130 (58%)	75 (99%)	1 (1%)	65	83
3	H	76/130 (58%)	71 (93%)	5 (7%)	14	45
3	K	76/130 (58%)	73 (96%)	3 (4%)	27	60
3	L	76/130 (58%)	74 (97%)	2 (3%)	41	70
3	O	76/130 (58%)	73 (96%)	3 (4%)	27	60
3	P	76/130 (58%)	76 (100%)	0	100	100
3	S	76/130 (58%)	71 (93%)	5 (7%)	14	45
3	T	76/130 (58%)	73 (96%)	3 (4%)	27	60
3	W	76/130 (58%)	71 (93%)	5 (7%)	14	45
3	X	76/130 (58%)	73 (96%)	3 (4%)	27	60
All	All	3156/3804 (83%)	3070 (97%)	86 (3%)	40	69

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	S	68	ASP
1	U	196	SER
3	S	75	SER
1	U	100	ARG
2	V	191	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	T	16	HIS
3	W	76	GLN
3	X	60	ASN
1	U	76	ASN
1	M	76	ASN

5.3.3 RNA ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	221/221 (100%)	-0.12	6 (2%) 56 40	17, 34, 62, 99	0
1	E	221/221 (100%)	0.12	16 (7%) 23 16	17, 35, 71, 105	0
1	I	221/221 (100%)	-0.12	12 (5%) 32 22	15, 26, 49, 112	0
1	M	221/221 (100%)	-0.13	8 (3%) 46 32	14, 27, 49, 107	0
1	Q	221/221 (100%)	0.30	9 (4%) 42 28	26, 48, 74, 110	0
1	U	221/221 (100%)	0.66	21 (9%) 15 10	27, 50, 82, 117	0
2	B	215/215 (100%)	-0.35	3 (1%) 73 58	12, 25, 44, 67	0
2	F	215/215 (100%)	-0.26	4 (1%) 66 50	12, 25, 46, 74	0
2	J	215/215 (100%)	-0.40	0 100 100	11, 23, 44, 72	0
2	N	215/215 (100%)	-0.38	1 (0%) 87 78	11, 22, 44, 69	0
2	R	215/215 (100%)	-0.19	1 (0%) 87 78	22, 34, 52, 77	0
2	V	215/215 (100%)	-0.14	2 (0%) 81 68	20, 34, 54, 86	0
3	C	84/152 (55%)	1.15	18 (21%) 3 2	40, 65, 119, 135	0
3	D	84/152 (55%)	0.86	7 (8%) 19 13	49, 66, 100, 108	0
3	G	84/152 (55%)	1.45	18 (21%) 3 2	48, 78, 126, 135	0
3	H	84/152 (55%)	1.03	10 (11%) 10 7	49, 70, 109, 113	0
3	K	84/152 (55%)	1.16	19 (22%) 3 2	41, 69, 107, 124	0
3	L	84/152 (55%)	0.94	13 (15%) 6 4	30, 58, 95, 106	0
3	O	84/152 (55%)	1.07	16 (19%) 4 3	38, 69, 104, 111	0
3	P	84/152 (55%)	0.69	8 (9%) 15 10	31, 63, 97, 105	0
3	S	84/152 (55%)	0.88	15 (17%) 4 4	32, 51, 104, 109	0
3	T	84/152 (55%)	1.15	19 (22%) 3 2	31, 54, 91, 122	0
3	W	84/152 (55%)	0.86	15 (17%) 4 4	30, 50, 108, 126	0
3	X	84/152 (55%)	0.61	10 (11%) 10 7	34, 53, 90, 107	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3624/4440 (81%)	0.22	251 (6%) 24 17	11, 38, 90, 135	0

The worst 5 of 251 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	140	SER	7.7
1	U	125	SER	6.5
1	U	140	SER	6.5
1	U	141	THR	5.9
3	L	70	GLN	5.8

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.