



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 06:06 am BST

PDB ID : 4ZWT
Title : Crystal Structure of the Bacteriophage T4 recombination mediator protein
UvsY, Lattice Type IV
Authors : Gajewski, S.; White, S.W.
Deposited on : 2015-05-19
Resolution : 4.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

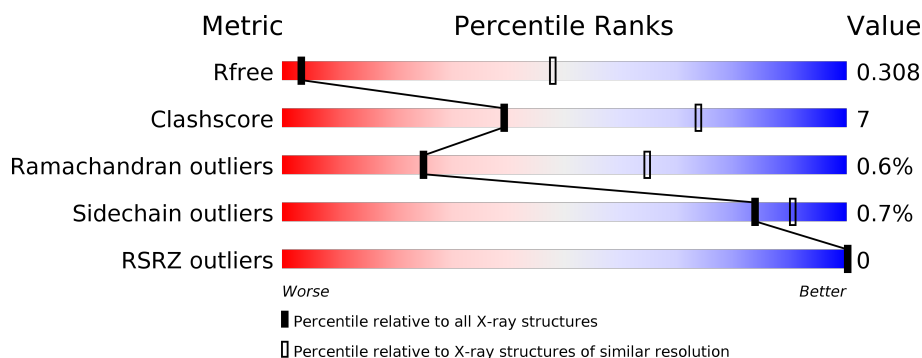
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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}	130704	1005 (4.62-3.78)
Clashscore	141614	1044 (4.60-3.80)
Ramachandran outliers	138981	1000 (4.60-3.80)
Sidechain outliers	138945	1007 (4.62-3.78)
RSRZ outliers	127900	1063 (4.70-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	157	<div> <div style="width: 65%;"></div> <div style="width: 10%;"></div> <div style="width: 23%;"></div> </div>
1	B	157	<div> <div style="width: 72%;"></div> <div style="width: 7%;"></div> <div style="width: 20%;"></div> </div>
1	C	157	<div> <div style="width: 74%;"></div> <div style="width: 10%;"></div> <div style="width: 15%;"></div> </div>
1	D	157	<div> <div style="width: 66%;"></div> <div style="width: 14%;"></div> <div style="width: 18%;"></div> </div>
1	E	157	<div> <div style="width: 68%;"></div> <div style="width: 12%;"></div> <div style="width: 20%;"></div> </div>
1	F	157	<div> <div style="width: 74%;"></div> <div style="width: 6%;"></div> <div style="width: 20%;"></div> </div>

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Mol	Chain	Length	Quality of chain
1	G	157	
1	H	157	
1	I	157	
1	J	157	
1	K	157	
1	L	157	
1	M	157	
1	N	157	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 11717 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 Recombination protein uvsY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	121	Total	C	N	O	S	0	0	0
			798	496	135	166	1			
1	B	126	Total	C	N	O	S	0	0	0
			826	513	143	169	1			
1	C	134	Total	C	N	O	S	0	0	0
			848	528	145	174	1			
1	D	128	Total	C	N	O	S	0	0	0
			833	519	142	171	1			
1	E	126	Total	C	N	O	S	0	0	0
			837	519	145	172	1			
1	F	125	Total	C	N	O	S	0	0	0
			812	501	140	170	1			
1	G	127	Total	C	N	O	S	0	0	0
			866	551	143	170	2			
1	H	127	Total	C	N	O	S	0	0	0
			838	522	144	171	1			
1	I	128	Total	C	N	O	S	0	0	0
			843	522	146	174	1			
1	J	135	Total	C	N	O	S	0	0	0
			886	550	154	181	1			
1	K	128	Total	C	N	O	S	0	0	0
			847	525	147	174	1			
1	L	126	Total	C	N	O	S	0	0	0
			825	514	145	165	1			
1	M	123	Total	C	N	O	S	0	0	0
			811	501	141	168	1			
1	N	125	Total	C	N	O	S	0	0	0
			847	535	146	163	3			

There are 322 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP P04537
A	-17	SER	-	expression tag	UNP P04537
A	-16	SER	-	expression tag	UNP P04537
A	-15	HIS	-	expression tag	UNP P04537
A	-14	HIS	-	expression tag	UNP P04537
A	-13	HIS	-	expression tag	UNP P04537
A	-12	HIS	-	expression tag	UNP P04537
A	-11	HIS	-	expression tag	UNP P04537
A	-10	HIS	-	expression tag	UNP P04537
A	-9	SER	-	expression tag	UNP P04537
A	-8	SER	-	expression tag	UNP P04537
A	-7	GLY	-	expression tag	UNP P04537
A	-6	LEU	-	expression tag	UNP P04537
A	-5	VAL	-	expression tag	UNP P04537
A	-4	PRO	-	expression tag	UNP P04537
A	-3	ARG	-	expression tag	UNP P04537
A	-2	GLY	-	expression tag	UNP P04537
A	-1	SER	-	expression tag	UNP P04537
A	0	HIS	-	expression tag	UNP P04537
A	79	ALA	GLU	engineered mutation	UNP P04537
A	80	ALA	LYS	engineered mutation	UNP P04537
A	81	ALA	SER	engineered mutation	UNP P04537
B	-19	MET	-	expression tag	UNP P04537
B	-18	GLY	-	expression tag	UNP P04537
B	-17	SER	-	expression tag	UNP P04537
B	-16	SER	-	expression tag	UNP P04537
B	-15	HIS	-	expression tag	UNP P04537
B	-14	HIS	-	expression tag	UNP P04537
B	-13	HIS	-	expression tag	UNP P04537
B	-12	HIS	-	expression tag	UNP P04537
B	-11	HIS	-	expression tag	UNP P04537
B	-10	HIS	-	expression tag	UNP P04537
B	-9	SER	-	expression tag	UNP P04537
B	-8	SER	-	expression tag	UNP P04537
B	-7	GLY	-	expression tag	UNP P04537
B	-6	LEU	-	expression tag	UNP P04537
B	-5	VAL	-	expression tag	UNP P04537
B	-4	PRO	-	expression tag	UNP P04537
B	-3	ARG	-	expression tag	UNP P04537
B	-2	GLY	-	expression tag	UNP P04537
B	-1	SER	-	expression tag	UNP P04537
B	0	HIS	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
B	79	ALA	GLU	engineered mutation	UNP P04537
B	80	ALA	LYS	engineered mutation	UNP P04537
B	81	ALA	SER	engineered mutation	UNP P04537
C	-19	MET	-	expression tag	UNP P04537
C	-18	GLY	-	expression tag	UNP P04537
C	-17	SER	-	expression tag	UNP P04537
C	-16	SER	-	expression tag	UNP P04537
C	-15	HIS	-	expression tag	UNP P04537
C	-14	HIS	-	expression tag	UNP P04537
C	-13	HIS	-	expression tag	UNP P04537
C	-12	HIS	-	expression tag	UNP P04537
C	-11	HIS	-	expression tag	UNP P04537
C	-10	HIS	-	expression tag	UNP P04537
C	-9	SER	-	expression tag	UNP P04537
C	-8	SER	-	expression tag	UNP P04537
C	-7	GLY	-	expression tag	UNP P04537
C	-6	LEU	-	expression tag	UNP P04537
C	-5	VAL	-	expression tag	UNP P04537
C	-4	PRO	-	expression tag	UNP P04537
C	-3	ARG	-	expression tag	UNP P04537
C	-2	GLY	-	expression tag	UNP P04537
C	-1	SER	-	expression tag	UNP P04537
C	0	HIS	-	expression tag	UNP P04537
C	79	ALA	GLU	engineered mutation	UNP P04537
C	80	ALA	LYS	engineered mutation	UNP P04537
C	81	ALA	SER	engineered mutation	UNP P04537
D	-19	MET	-	expression tag	UNP P04537
D	-18	GLY	-	expression tag	UNP P04537
D	-17	SER	-	expression tag	UNP P04537
D	-16	SER	-	expression tag	UNP P04537
D	-15	HIS	-	expression tag	UNP P04537
D	-14	HIS	-	expression tag	UNP P04537
D	-13	HIS	-	expression tag	UNP P04537
D	-12	HIS	-	expression tag	UNP P04537
D	-11	HIS	-	expression tag	UNP P04537
D	-10	HIS	-	expression tag	UNP P04537
D	-9	SER	-	expression tag	UNP P04537
D	-8	SER	-	expression tag	UNP P04537
D	-7	GLY	-	expression tag	UNP P04537
D	-6	LEU	-	expression tag	UNP P04537
D	-5	VAL	-	expression tag	UNP P04537
D	-4	PRO	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	ARG	-	expression tag	UNP P04537
D	-2	GLY	-	expression tag	UNP P04537
D	-1	SER	-	expression tag	UNP P04537
D	0	HIS	-	expression tag	UNP P04537
D	79	ALA	GLU	engineered mutation	UNP P04537
D	80	ALA	LYS	engineered mutation	UNP P04537
D	81	ALA	SER	engineered mutation	UNP P04537
E	-19	MET	-	expression tag	UNP P04537
E	-18	GLY	-	expression tag	UNP P04537
E	-17	SER	-	expression tag	UNP P04537
E	-16	SER	-	expression tag	UNP P04537
E	-15	HIS	-	expression tag	UNP P04537
E	-14	HIS	-	expression tag	UNP P04537
E	-13	HIS	-	expression tag	UNP P04537
E	-12	HIS	-	expression tag	UNP P04537
E	-11	HIS	-	expression tag	UNP P04537
E	-10	HIS	-	expression tag	UNP P04537
E	-9	SER	-	expression tag	UNP P04537
E	-8	SER	-	expression tag	UNP P04537
E	-7	GLY	-	expression tag	UNP P04537
E	-6	LEU	-	expression tag	UNP P04537
E	-5	VAL	-	expression tag	UNP P04537
E	-4	PRO	-	expression tag	UNP P04537
E	-3	ARG	-	expression tag	UNP P04537
E	-2	GLY	-	expression tag	UNP P04537
E	-1	SER	-	expression tag	UNP P04537
E	0	HIS	-	expression tag	UNP P04537
E	79	ALA	GLU	engineered mutation	UNP P04537
E	80	ALA	LYS	engineered mutation	UNP P04537
E	81	ALA	SER	engineered mutation	UNP P04537
F	-19	MET	-	expression tag	UNP P04537
F	-18	GLY	-	expression tag	UNP P04537
F	-17	SER	-	expression tag	UNP P04537
F	-16	SER	-	expression tag	UNP P04537
F	-15	HIS	-	expression tag	UNP P04537
F	-14	HIS	-	expression tag	UNP P04537
F	-13	HIS	-	expression tag	UNP P04537
F	-12	HIS	-	expression tag	UNP P04537
F	-11	HIS	-	expression tag	UNP P04537
F	-10	HIS	-	expression tag	UNP P04537
F	-9	SER	-	expression tag	UNP P04537
F	-8	SER	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-7	GLY	-	expression tag	UNP P04537
F	-6	LEU	-	expression tag	UNP P04537
F	-5	VAL	-	expression tag	UNP P04537
F	-4	PRO	-	expression tag	UNP P04537
F	-3	ARG	-	expression tag	UNP P04537
F	-2	GLY	-	expression tag	UNP P04537
F	-1	SER	-	expression tag	UNP P04537
F	0	HIS	-	expression tag	UNP P04537
F	79	ALA	GLU	engineered mutation	UNP P04537
F	80	ALA	LYS	engineered mutation	UNP P04537
F	81	ALA	SER	engineered mutation	UNP P04537
G	-19	MET	-	expression tag	UNP P04537
G	-18	GLY	-	expression tag	UNP P04537
G	-17	SER	-	expression tag	UNP P04537
G	-16	SER	-	expression tag	UNP P04537
G	-15	HIS	-	expression tag	UNP P04537
G	-14	HIS	-	expression tag	UNP P04537
G	-13	HIS	-	expression tag	UNP P04537
G	-12	HIS	-	expression tag	UNP P04537
G	-11	HIS	-	expression tag	UNP P04537
G	-10	HIS	-	expression tag	UNP P04537
G	-9	SER	-	expression tag	UNP P04537
G	-8	SER	-	expression tag	UNP P04537
G	-7	GLY	-	expression tag	UNP P04537
G	-6	LEU	-	expression tag	UNP P04537
G	-5	VAL	-	expression tag	UNP P04537
G	-4	PRO	-	expression tag	UNP P04537
G	-3	ARG	-	expression tag	UNP P04537
G	-2	GLY	-	expression tag	UNP P04537
G	-1	SER	-	expression tag	UNP P04537
G	0	HIS	-	expression tag	UNP P04537
G	79	ALA	GLU	engineered mutation	UNP P04537
G	80	ALA	LYS	engineered mutation	UNP P04537
G	81	ALA	SER	engineered mutation	UNP P04537
H	-19	MET	-	expression tag	UNP P04537
H	-18	GLY	-	expression tag	UNP P04537
H	-17	SER	-	expression tag	UNP P04537
H	-16	SER	-	expression tag	UNP P04537
H	-15	HIS	-	expression tag	UNP P04537
H	-14	HIS	-	expression tag	UNP P04537
H	-13	HIS	-	expression tag	UNP P04537
H	-12	HIS	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-11	HIS	-	expression tag	UNP P04537
H	-10	HIS	-	expression tag	UNP P04537
H	-9	SER	-	expression tag	UNP P04537
H	-8	SER	-	expression tag	UNP P04537
H	-7	GLY	-	expression tag	UNP P04537
H	-6	LEU	-	expression tag	UNP P04537
H	-5	VAL	-	expression tag	UNP P04537
H	-4	PRO	-	expression tag	UNP P04537
H	-3	ARG	-	expression tag	UNP P04537
H	-2	GLY	-	expression tag	UNP P04537
H	-1	SER	-	expression tag	UNP P04537
H	0	HIS	-	expression tag	UNP P04537
H	79	ALA	GLU	engineered mutation	UNP P04537
H	80	ALA	LYS	engineered mutation	UNP P04537
H	81	ALA	SER	engineered mutation	UNP P04537
I	-19	MET	-	expression tag	UNP P04537
I	-18	GLY	-	expression tag	UNP P04537
I	-17	SER	-	expression tag	UNP P04537
I	-16	SER	-	expression tag	UNP P04537
I	-15	HIS	-	expression tag	UNP P04537
I	-14	HIS	-	expression tag	UNP P04537
I	-13	HIS	-	expression tag	UNP P04537
I	-12	HIS	-	expression tag	UNP P04537
I	-11	HIS	-	expression tag	UNP P04537
I	-10	HIS	-	expression tag	UNP P04537
I	-9	SER	-	expression tag	UNP P04537
I	-8	SER	-	expression tag	UNP P04537
I	-7	GLY	-	expression tag	UNP P04537
I	-6	LEU	-	expression tag	UNP P04537
I	-5	VAL	-	expression tag	UNP P04537
I	-4	PRO	-	expression tag	UNP P04537
I	-3	ARG	-	expression tag	UNP P04537
I	-2	GLY	-	expression tag	UNP P04537
I	-1	SER	-	expression tag	UNP P04537
I	0	HIS	-	expression tag	UNP P04537
I	79	ALA	GLU	engineered mutation	UNP P04537
I	80	ALA	LYS	engineered mutation	UNP P04537
I	81	ALA	SER	engineered mutation	UNP P04537
J	-19	MET	-	expression tag	UNP P04537
J	-18	GLY	-	expression tag	UNP P04537
J	-17	SER	-	expression tag	UNP P04537
J	-16	SER	-	expression tag	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-15	HIS	-	expression tag	UNP P04537
J	-14	HIS	-	expression tag	UNP P04537
J	-13	HIS	-	expression tag	UNP P04537
J	-12	HIS	-	expression tag	UNP P04537
J	-11	HIS	-	expression tag	UNP P04537
J	-10	HIS	-	expression tag	UNP P04537
J	-9	SER	-	expression tag	UNP P04537
J	-8	SER	-	expression tag	UNP P04537
J	-7	GLY	-	expression tag	UNP P04537
J	-6	LEU	-	expression tag	UNP P04537
J	-5	VAL	-	expression tag	UNP P04537
J	-4	PRO	-	expression tag	UNP P04537
J	-3	ARG	-	expression tag	UNP P04537
J	-2	GLY	-	expression tag	UNP P04537
J	-1	SER	-	expression tag	UNP P04537
J	0	HIS	-	expression tag	UNP P04537
J	79	ALA	GLU	engineered mutation	UNP P04537
J	80	ALA	LYS	engineered mutation	UNP P04537
J	81	ALA	SER	engineered mutation	UNP P04537
K	-19	MET	-	expression tag	UNP P04537
K	-18	GLY	-	expression tag	UNP P04537
K	-17	SER	-	expression tag	UNP P04537
K	-16	SER	-	expression tag	UNP P04537
K	-15	HIS	-	expression tag	UNP P04537
K	-14	HIS	-	expression tag	UNP P04537
K	-13	HIS	-	expression tag	UNP P04537
K	-12	HIS	-	expression tag	UNP P04537
K	-11	HIS	-	expression tag	UNP P04537
K	-10	HIS	-	expression tag	UNP P04537
K	-9	SER	-	expression tag	UNP P04537
K	-8	SER	-	expression tag	UNP P04537
K	-7	GLY	-	expression tag	UNP P04537
K	-6	LEU	-	expression tag	UNP P04537
K	-5	VAL	-	expression tag	UNP P04537
K	-4	PRO	-	expression tag	UNP P04537
K	-3	ARG	-	expression tag	UNP P04537
K	-2	GLY	-	expression tag	UNP P04537
K	-1	SER	-	expression tag	UNP P04537
K	0	HIS	-	expression tag	UNP P04537
K	79	ALA	GLU	engineered mutation	UNP P04537
K	80	ALA	LYS	engineered mutation	UNP P04537
K	81	ALA	SER	engineered mutation	UNP P04537

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-19	MET	-	expression tag	UNP P04537
L	-18	GLY	-	expression tag	UNP P04537
L	-17	SER	-	expression tag	UNP P04537
L	-16	SER	-	expression tag	UNP P04537
L	-15	HIS	-	expression tag	UNP P04537
L	-14	HIS	-	expression tag	UNP P04537
L	-13	HIS	-	expression tag	UNP P04537
L	-12	HIS	-	expression tag	UNP P04537
L	-11	HIS	-	expression tag	UNP P04537
L	-10	HIS	-	expression tag	UNP P04537
L	-9	SER	-	expression tag	UNP P04537
L	-8	SER	-	expression tag	UNP P04537
L	-7	GLY	-	expression tag	UNP P04537
L	-6	LEU	-	expression tag	UNP P04537
L	-5	VAL	-	expression tag	UNP P04537
L	-4	PRO	-	expression tag	UNP P04537
L	-3	ARG	-	expression tag	UNP P04537
L	-2	GLY	-	expression tag	UNP P04537
L	-1	SER	-	expression tag	UNP P04537
L	0	HIS	-	expression tag	UNP P04537
L	79	ALA	GLU	engineered mutation	UNP P04537
L	80	ALA	LYS	engineered mutation	UNP P04537
L	81	ALA	SER	engineered mutation	UNP P04537
M	-19	MET	-	expression tag	UNP P04537
M	-18	GLY	-	expression tag	UNP P04537
M	-17	SER	-	expression tag	UNP P04537
M	-16	SER	-	expression tag	UNP P04537
M	-15	HIS	-	expression tag	UNP P04537
M	-14	HIS	-	expression tag	UNP P04537
M	-13	HIS	-	expression tag	UNP P04537
M	-12	HIS	-	expression tag	UNP P04537
M	-11	HIS	-	expression tag	UNP P04537
M	-10	HIS	-	expression tag	UNP P04537
M	-9	SER	-	expression tag	UNP P04537
M	-8	SER	-	expression tag	UNP P04537
M	-7	GLY	-	expression tag	UNP P04537
M	-6	LEU	-	expression tag	UNP P04537
M	-5	VAL	-	expression tag	UNP P04537
M	-4	PRO	-	expression tag	UNP P04537
M	-3	ARG	-	expression tag	UNP P04537
M	-2	GLY	-	expression tag	UNP P04537
M	-1	SER	-	expression tag	UNP P04537

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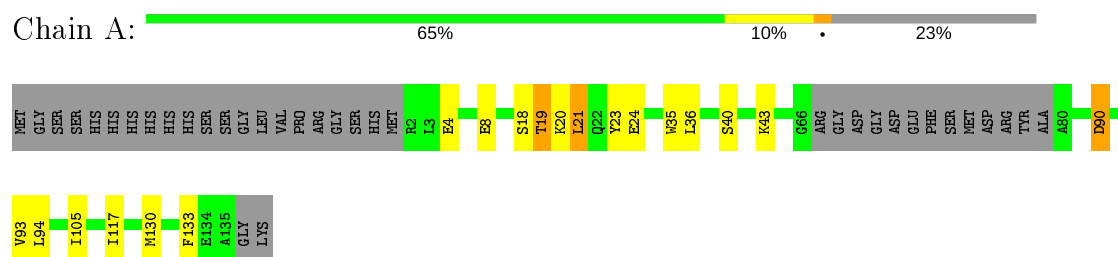
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Chain	Residue	Modelled	Actual	Comment	Reference
M	0	HIS	-	expression tag	UNP P04537
M	79	ALA	GLU	engineered mutation	UNP P04537
M	80	ALA	LYS	engineered mutation	UNP P04537
M	81	ALA	SER	engineered mutation	UNP P04537
N	-19	MET	-	expression tag	UNP P04537
N	-18	GLY	-	expression tag	UNP P04537
N	-17	SER	-	expression tag	UNP P04537
N	-16	SER	-	expression tag	UNP P04537
N	-15	HIS	-	expression tag	UNP P04537
N	-14	HIS	-	expression tag	UNP P04537
N	-13	HIS	-	expression tag	UNP P04537
N	-12	HIS	-	expression tag	UNP P04537
N	-11	HIS	-	expression tag	UNP P04537
N	-10	HIS	-	expression tag	UNP P04537
N	-9	SER	-	expression tag	UNP P04537
N	-8	SER	-	expression tag	UNP P04537
N	-7	GLY	-	expression tag	UNP P04537
N	-6	LEU	-	expression tag	UNP P04537
N	-5	VAL	-	expression tag	UNP P04537
N	-4	PRO	-	expression tag	UNP P04537
N	-3	ARG	-	expression tag	UNP P04537
N	-2	GLY	-	expression tag	UNP P04537
N	-1	SER	-	expression tag	UNP P04537
N	0	HIS	-	expression tag	UNP P04537
N	79	ALA	GLU	engineered mutation	UNP P04537
N	80	ALA	LYS	engineered mutation	UNP P04537
N	81	ALA	SER	engineered mutation	UNP P04537

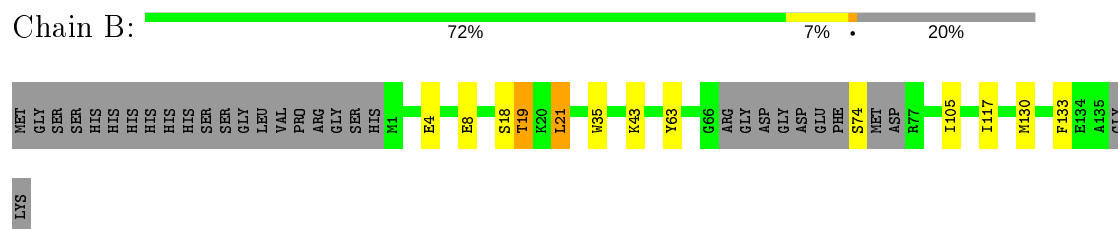
3 Residue-property plots [i](#)

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

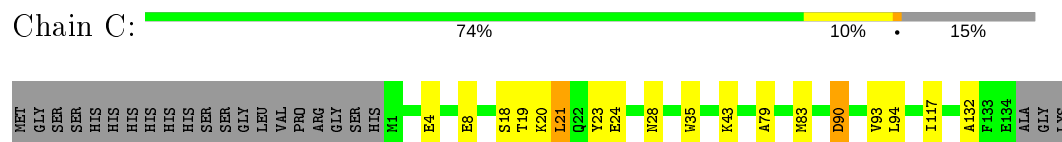
- Molecule 1: Recombination protein uvsY



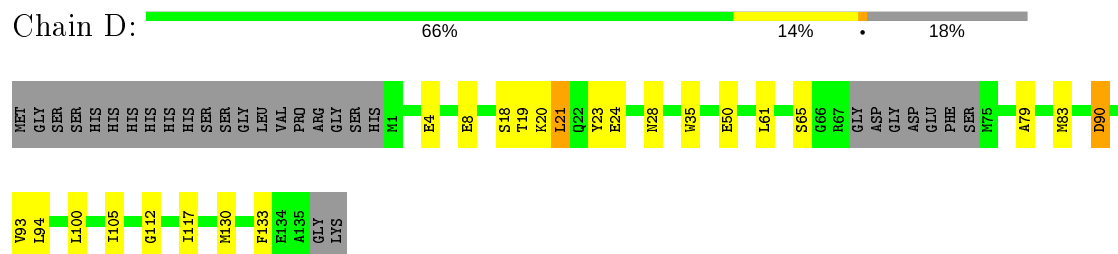
- Molecule 1: Recombination protein uvsY



- Molecule 1: Recombination protein uvsY

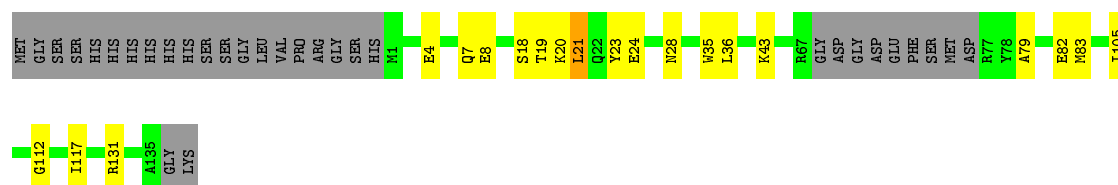


- Molecule 1: Recombination protein uvsY



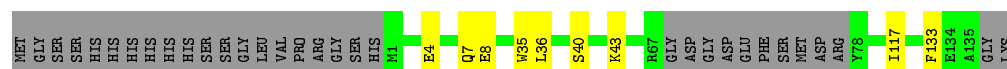
- Molecule 1: Recombination protein uvsY

Chain E: 



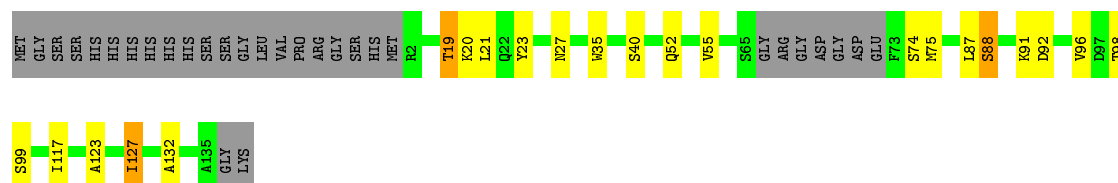
- Molecule 1: Recombination protein uvsY

Chain F: 



- Molecule 1: Recombination protein uvsY

Chain G: 



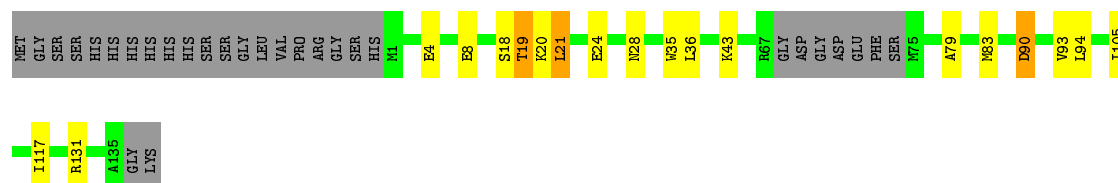
- Molecule 1: Recombination protein uvsY

Chain H: 



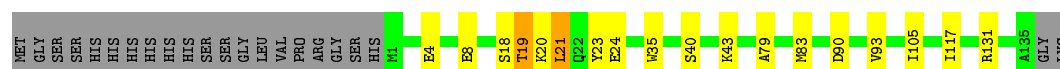
- Molecule 1: Recombination protein uvsY

Chain I: 

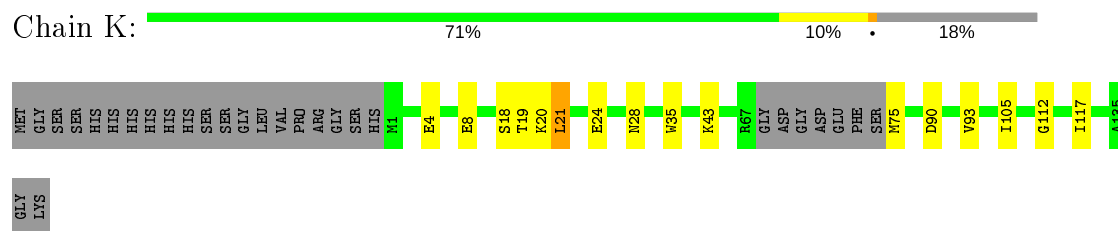


- Molecule 1: Recombination protein uvsY

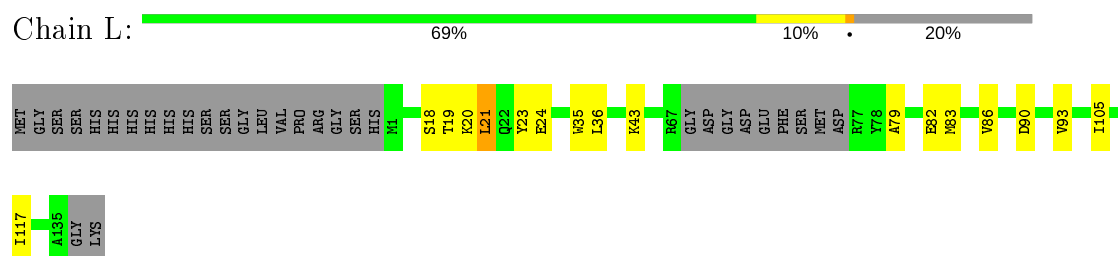
Chain J: 



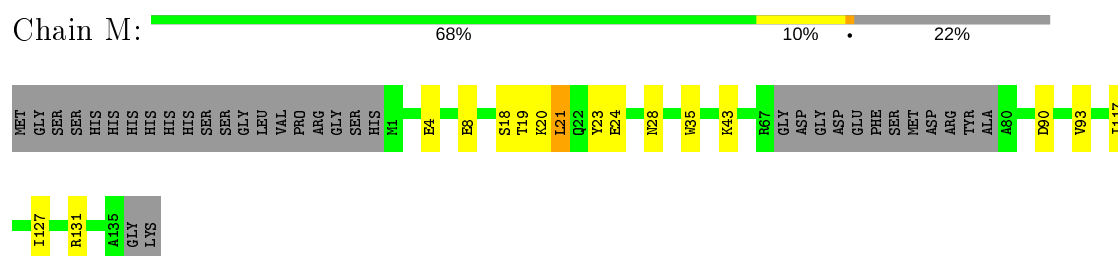
- Molecule 1: Recombination protein uvsY



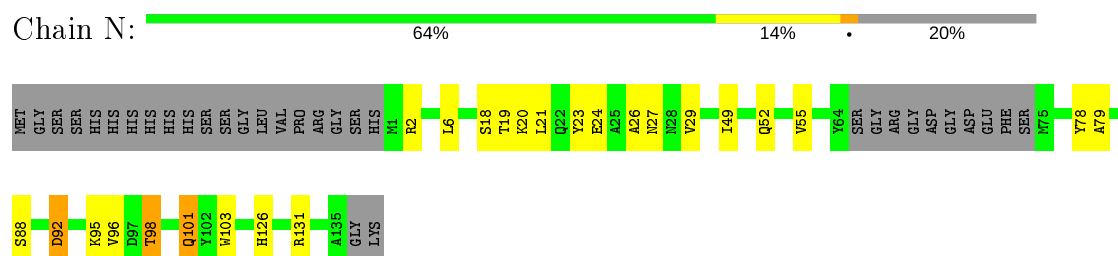
- Molecule 1: Recombination protein uvsY



- Molecule 1: Recombination protein uvsY



- Molecule 1: Recombination protein uvsY



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	184.38Å 184.38Å 615.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.62 – 4.20 49.62 – 4.01	Depositor EDS
% Data completeness (in resolution range)	64.7 (49.62-4.20) 57.0 (49.62-4.01)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 4.00Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.274 , 0.308 0.282 , 0.308	Depositor DCC
R_{free} test set	1281 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	128.6	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 174.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	11717	wwPDB-VP
Average B, all atoms (Å ²)	140.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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	0.43	0/807	0.71	1/1107 (0.1%)
1	B	0.42	0/834	0.68	2/1142 (0.2%)
1	C	0.41	0/858	0.73	1/1180 (0.1%)
1	D	0.43	0/842	0.75	1/1156 (0.1%)
1	E	0.40	0/846	0.70	1/1158 (0.1%)
1	F	0.36	0/820	0.52	0/1125
1	G	0.44	0/878	0.82	3/1202 (0.2%)
1	H	0.38	0/848	0.63	0/1163
1	I	0.44	0/852	0.74	2/1168 (0.2%)
1	J	0.42	0/897	0.73	1/1229 (0.1%)
1	K	0.42	0/856	0.71	1/1172 (0.1%)
1	L	0.42	0/834	0.73	1/1143 (0.1%)
1	M	0.43	0/819	0.69	1/1122 (0.1%)
1	N	0.43	0/858	0.81	1/1173 (0.1%)
All	All	0.42	0/11849	0.72	16/16240 (0.1%)

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
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	G	0	1
1	I	0	1
1	J	0	1
1	K	0	2
1	L	0	1
1	M	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	1
All	All	0	13

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	21	LEU	N-CA-C	-6.89	92.40	111.00
1	D	21	LEU	N-CA-C	-6.85	92.51	111.00
1	C	21	LEU	N-CA-C	-6.83	92.55	111.00
1	G	21	LEU	N-CA-C	-6.49	93.48	111.00
1	B	21	LEU	N-CA-C	-6.44	93.61	111.00
1	A	21	LEU	N-CA-C	-6.41	93.70	111.00
1	N	21	LEU	N-CA-C	-6.40	93.72	111.00
1	L	21	LEU	N-CA-C	-6.37	93.80	111.00
1	K	21	LEU	N-CA-C	-6.27	94.07	111.00
1	J	21	LEU	N-CA-C	-6.27	94.08	111.00
1	M	21	LEU	N-CA-C	-6.26	94.08	111.00
1	I	21	LEU	N-CA-C	-6.18	94.30	111.00
1	G	127	ILE	CG1-CB-CG2	-5.59	99.10	111.40
1	I	20	LYS	N-CA-C	-5.30	96.68	111.00
1	G	19	THR	C-N-CA	-5.26	108.55	121.70
1	B	19	THR	C-N-CA	-5.02	109.14	121.70

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	19	THR	Mainchain
1	B	19	THR	Mainchain
1	C	19	THR	Mainchain
1	D	19	THR	Mainchain
1	E	19	THR	Mainchain
1	G	19	THR	Mainchain
1	I	19	THR	Mainchain
1	J	19	THR	Mainchain
1	K	19	THR	Mainchain
1	K	75	MET	Mainchain
1	L	19	THR	Mainchain
1	M	19	THR	Mainchain
1	N	19	THR	Mainchain

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	798	0	625	15	0
1	B	826	0	649	10	0
1	C	848	0	642	12	0
1	D	833	0	652	15	0
1	E	837	0	669	17	0
1	F	812	0	629	7	0
1	G	866	0	719	10	0
1	H	838	0	659	9	0
1	I	843	0	662	15	0
1	J	886	0	697	14	0
1	K	847	0	673	10	0
1	L	825	0	656	12	0
1	M	811	0	642	12	0
1	N	847	0	705	15	0
All	All	11717	0	9279	155	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 7.

All (155) 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:K:35:TRP:CD1	1:K:117:ILE:HD11	2.29	0.67
1:A:90:ASP:OD2	1:A:93:VAL:N	2.17	0.64
1:J:79:ALA:O	1:J:83:MET:N	2.31	0.63
1:K:105:ILE:HG23	1:L:43:LYS:HD2	1.81	0.62
1:B:63:TYR:O	1:B:74:SER:N	2.33	0.61
1:H:35:TRP:HD1	1:H:117:ILE:HD11	1.66	0.61
1:A:90:ASP:HB3	1:A:93:VAL:HB	1.82	0.61
1:I:35:TRP:CD1	1:I:117:ILE:HD11	2.36	0.60
1:C:90:ASP:O	1:C:94:LEU:N	2.23	0.60
1:I:90:ASP:HB3	1:I:93:VAL:HB	1.84	0.59
1:J:35:TRP:HD1	1:J:117:ILE:HD11	1.66	0.59
1:E:35:TRP:CD1	1:E:117:ILE:HD11	2.38	0.59
1:L:79:ALA:O	1:L:83:MET:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:105:ILE:HG23	1:F:43:LYS:HD2	1.84	0.58
1:L:35:TRP:CD1	1:L:117:ILE:HD11	2.38	0.58
1:I:105:ILE:HG23	1:J:43:LYS:HD2	1.84	0.57
1:F:35:TRP:CD1	1:F:117:ILE:HD11	2.38	0.57
1:D:35:TRP:CD1	1:D:117:ILE:HD11	2.39	0.57
1:L:105:ILE:HG23	1:M:43:LYS:HD2	1.87	0.57
1:C:35:TRP:CD1	1:C:117:ILE:HD11	2.39	0.57
1:D:18:SER:HA	1:D:21:LEU:HD13	1.86	0.57
1:A:18:SER:O	1:A:21:LEU:HB2	2.05	0.57
1:I:79:ALA:O	1:I:83:MET:N	2.38	0.57
1:E:112:GLY:HA3	1:F:36:LEU:HD21	1.86	0.56
1:B:35:TRP:CD1	1:B:117:ILE:HD11	2.41	0.55
1:G:35:TRP:CD1	1:G:117:ILE:HD11	2.41	0.55
1:J:18:SER:HB3	1:J:131:ARG:HH21	1.71	0.55
1:F:4:GLU:O	1:F:8:GLU:HG3	2.07	0.55
1:A:18:SER:HA	1:A:21:LEU:HD13	1.88	0.55
1:I:4:GLU:O	1:I:8:GLU:HG3	2.07	0.55
1:N:95:LYS:O	1:N:98:THR:HG22	2.07	0.55
1:A:35:TRP:CD1	1:A:117:ILE:HD11	2.41	0.54
1:H:112:GLY:HA3	1:I:36:LEU:HD21	1.90	0.54
1:I:18:SER:O	1:I:21:LEU:HB2	2.07	0.54
1:N:49:ILE:HG22	1:N:96:VAL:HG13	1.90	0.54
1:B:4:GLU:O	1:B:8:GLU:HG3	2.07	0.54
1:N:18:SER:HB3	1:N:131:ARG:NH2	2.22	0.54
1:M:4:GLU:O	1:M:8:GLU:HG3	2.07	0.54
1:E:79:ALA:O	1:E:83:MET:N	2.41	0.53
1:K:18:SER:HA	1:K:21:LEU:HD13	1.89	0.53
1:C:18:SER:O	1:C:21:LEU:HB2	2.08	0.53
1:I:18:SER:HB3	1:I:131:ARG:HH21	1.73	0.53
1:A:105:ILE:HG23	1:B:43:LYS:HD2	1.89	0.53
1:K:18:SER:O	1:K:21:LEU:HB2	2.08	0.53
1:B:105:ILE:HG23	1:C:43:LYS:HD2	1.89	0.53
1:B:130:MET:O	1:B:133:PHE:HB3	2.09	0.53
1:E:18:SER:O	1:E:21:LEU:HB2	2.09	0.53
1:J:4:GLU:O	1:J:8:GLU:HG3	2.09	0.53
1:C:79:ALA:O	1:C:83:MET:N	2.42	0.53
1:D:18:SER:O	1:D:21:LEU:HB2	2.09	0.52
1:C:4:GLU:O	1:C:8:GLU:HG3	2.09	0.52
1:D:24:GLU:O	1:D:28:ASN:N	2.41	0.52
1:E:18:SER:HA	1:E:21:LEU:HD13	1.91	0.52
1:M:21:LEU:HD22	1:M:131:ARG:CZ	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:35:TRP:CD1	1:M:117:ILE:HD11	2.44	0.52
1:N:20:LYS:CB	1:N:23:TYR:HB3	2.40	0.52
1:A:4:GLU:O	1:A:8:GLU:HG3	2.09	0.51
1:E:4:GLU:O	1:E:8:GLU:HG3	2.10	0.51
1:H:105:ILE:HG23	1:I:43:LYS:HD2	1.93	0.51
1:E:20:LYS:CB	1:E:23:TYR:HB3	2.40	0.51
1:K:4:GLU:O	1:K:8:GLU:HG3	2.10	0.51
1:H:4:GLU:O	1:H:8:GLU:HG3	2.11	0.51
1:D:4:GLU:O	1:D:8:GLU:HG3	2.10	0.51
1:H:90:ASP:O	1:H:94:LEU:N	2.24	0.51
1:I:18:SER:HA	1:I:21:LEU:HD13	1.93	0.51
1:L:20:LYS:O	1:L:24:GLU:N	2.27	0.51
1:N:49:ILE:CG2	1:N:96:VAL:HG13	2.41	0.51
1:D:61:LEU:O	1:D:65:SER:N	2.38	0.50
1:G:20:LYS:CB	1:G:23:TYR:HB3	2.42	0.50
1:A:20:LYS:O	1:A:24:GLU:N	2.27	0.50
1:A:130:MET:O	1:A:133:PHE:HB3	2.09	0.50
1:K:20:LYS:O	1:K:24:GLU:N	2.27	0.50
1:J:18:SER:O	1:J:21:LEU:HB2	2.11	0.50
1:N:52:GLN:O	1:N:55:VAL:HG12	2.12	0.50
1:J:35:TRP:CD1	1:J:117:ILE:HD11	2.45	0.49
1:L:18:SER:O	1:L:21:LEU:HB2	2.11	0.49
1:F:7:GLN:HE21	1:G:40:SER:HB2	1.78	0.49
1:M:20:LYS:O	1:M:24:GLU:N	2.25	0.49
1:C:24:GLU:O	1:C:28:ASN:N	2.42	0.49
1:G:52:GLN:O	1:G:55:VAL:HG12	2.13	0.49
1:N:49:ILE:HG13	1:N:103:TRP:HZ3	1.77	0.49
1:A:90:ASP:O	1:A:94:LEU:N	2.27	0.48
1:D:79:ALA:O	1:D:83:MET:N	2.47	0.48
1:C:18:SER:HA	1:C:21:LEU:HD13	1.95	0.48
1:D:112:GLY:HA3	1:E:36:LEU:HD21	1.95	0.47
1:N:49:ILE:HG13	1:N:103:TRP:CZ3	2.49	0.47
1:E:24:GLU:O	1:E:28:ASN:N	2.47	0.47
1:J:105:ILE:HG23	1:K:43:LYS:HD2	1.95	0.47
1:H:35:TRP:CE3	1:H:35:TRP:HA	2.50	0.47
1:B:18:SER:O	1:B:21:LEU:HB2	2.14	0.47
1:N:26:ALA:O	1:N:29:VAL:HG12	2.15	0.46
1:E:7:GLN:NE2	1:F:40:SER:OG	2.41	0.46
1:G:92:ASP:O	1:G:96:VAL:HG23	2.15	0.46
1:D:20:LYS:CB	1:D:23:TYR:HB3	2.46	0.46
1:N:92:ASP:O	1:N:96:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:ASP:O	1:D:94:LEU:N	2.26	0.46
1:J:90:ASP:HB3	1:J:93:VAL:HB	1.98	0.46
1:M:24:GLU:O	1:M:28:ASN:N	2.49	0.46
1:G:123:ALA:O	1:G:127:ILE:HD13	2.15	0.45
1:N:18:SER:HB3	1:N:131:ARG:HH21	1.80	0.45
1:N:20:LYS:O	1:N:24:GLU:N	2.38	0.45
1:G:96:VAL:O	1:G:99:SER:HB3	2.17	0.45
1:C:35:TRP:HD1	1:C:117:ILE:HD11	1.80	0.45
1:H:90:ASP:CB	1:H:93:VAL:HB	2.47	0.45
1:L:18:SER:HA	1:L:21:LEU:HD13	1.99	0.45
1:E:18:SER:HB3	1:E:131:ARG:HH21	1.81	0.44
1:E:35:TRP:HD1	1:E:117:ILE:HD11	1.81	0.44
1:A:40:SER:O	1:A:43:LYS:HG2	2.17	0.44
1:M:18:SER:C	1:M:131:ARG:HH22	2.19	0.44
1:J:20:LYS:O	1:J:24:GLU:N	2.28	0.44
1:D:90:ASP:CB	1:D:93:VAL:HB	2.47	0.44
1:K:24:GLU:O	1:K:28:ASN:N	2.51	0.44
1:L:90:ASP:HB3	1:L:93:VAL:HB	2.00	0.44
1:N:2:ARG:O	1:N:6:LEU:HD13	2.18	0.44
1:A:36:LEU:HD12	1:A:36:LEU:HA	1.92	0.43
1:I:19:THR:C	1:I:21:LEU:H	2.21	0.43
1:I:90:ASP:O	1:I:94:LEU:N	2.29	0.43
1:K:90:ASP:HB3	1:K:93:VAL:HB	2.00	0.43
1:D:130:MET:O	1:D:133:PHE:HB3	2.19	0.43
1:A:20:LYS:CB	1:A:23:TYR:HB3	2.49	0.43
1:A:90:ASP:OD2	1:A:93:VAL:HG23	2.19	0.42
1:C:90:ASP:CB	1:C:93:VAL:HB	2.49	0.42
1:I:35:TRP:HD1	1:I:117:ILE:HD11	1.81	0.42
1:E:18:SER:O	1:E:131:ARG:NH2	2.50	0.42
1:C:20:LYS:CB	1:C:23:TYR:HB3	2.50	0.42
1:E:79:ALA:HB3	1:E:82:GLU:CB	2.50	0.42
1:M:18:SER:HB3	1:M:131:ARG:HH21	1.84	0.42
1:M:90:ASP:HB3	1:M:93:VAL:HB	2.02	0.42
1:E:4:GLU:H	1:E:4:GLU:CD	2.23	0.41
1:G:87:LEU:O	1:G:88:SER:C	2.58	0.41
1:N:78:TYR:O	1:N:79:ALA:HB3	2.19	0.41
1:I:24:GLU:O	1:I:28:ASN:N	2.49	0.41
1:M:18:SER:O	1:M:21:LEU:HB2	2.21	0.41
1:B:18:SER:HA	1:B:21:LEU:HD13	2.03	0.41
1:L:20:LYS:CB	1:L:23:TYR:HB3	2.50	0.41
1:L:79:ALA:HB3	1:L:82:GLU:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:82:GLU:O	1:L:86:VAL:HG23	2.21	0.41
1:D:50:GLU:HG3	1:D:100:LEU:HD21	2.03	0.41
1:M:20:LYS:CB	1:M:23:TYR:HB3	2.51	0.41
1:A:19:THR:C	1:A:21:LEU:H	2.24	0.41
1:D:4:GLU:CD	1:D:4:GLU:H	2.25	0.41
1:B:4:GLU:H	1:B:4:GLU:CD	2.24	0.41
1:F:133:PHE:CE1	1:G:132:ALA:HA	2.55	0.40
1:J:19:THR:C	1:J:21:LEU:H	2.24	0.40
1:G:91:LYS:HA	1:N:101:GLN:OE1	2.21	0.40
1:H:35:TRP:CD1	1:H:117:ILE:HD11	2.51	0.40
1:J:20:LYS:CB	1:J:23:TYR:HB3	2.52	0.40
1:J:40:SER:O	1:J:43:LYS:HG2	2.21	0.40
1:M:127:ILE:O	1:M:131:ARG:HG3	2.21	0.40
1:B:133:PHE:CE1	1:C:132:ALA:HA	2.57	0.40
1:H:50:GLU:HG3	1:H:100:LEU:HD21	2.02	0.40
1:I:4:GLU:CD	1:I:4:GLU:H	2.24	0.40
1:J:18:SER:HA	1:J:21:LEU:HD13	2.03	0.40
1:D:105:ILE:HG23	1:E:43:LYS:HD2	2.04	0.40
1:K:112:GLY:HA3	1:L:36:LEU:HD21	2.02	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	117/157 (74%)	116 (99%)	0	1 (1%)	17	56
1	B	121/157 (77%)	120 (99%)	1 (1%)	0	100	100
1	C	132/157 (84%)	130 (98%)	1 (1%)	1 (1%)	19	60
1	D	124/157 (79%)	123 (99%)	0	1 (1%)	19	60
1	E	122/157 (78%)	122 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	121/157 (77%)	121 (100%)	0	0	100	100
1	G	123/157 (78%)	118 (96%)	2 (2%)	3 (2%)	6	36
1	H	123/157 (78%)	122 (99%)	0	1 (1%)	19	60
1	I	124/157 (79%)	122 (98%)	1 (1%)	1 (1%)	19	60
1	J	133/157 (85%)	129 (97%)	4 (3%)	0	100	100
1	K	124/157 (79%)	124 (100%)	0	0	100	100
1	L	122/157 (78%)	122 (100%)	0	0	100	100
1	M	119/157 (76%)	118 (99%)	1 (1%)	0	100	100
1	N	121/157 (77%)	117 (97%)	2 (2%)	2 (2%)	9	44
All	All	1726/2198 (78%)	1704 (99%)	12 (1%)	10 (1%)	25	65

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	74	SER
1	G	75	MET
1	N	92	ASP
1	C	90	ASP
1	G	88	SER
1	A	90	ASP
1	D	90	ASP
1	H	90	ASP
1	I	90	ASP
1	N	88	SER

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	59/133 (44%)	59 (100%)	0	100	100
1	B	59/133 (44%)	59 (100%)	0	100	100
1	C	56/133 (42%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	59/133 (44%)	59 (100%)	0	100	100
1	E	62/133 (47%)	62 (100%)	0	100	100
1	F	58/133 (44%)	58 (100%)	0	100	100
1	G	68/133 (51%)	66 (97%)	2 (3%)	42	64
1	H	60/133 (45%)	60 (100%)	0	100	100
1	I	61/133 (46%)	61 (100%)	0	100	100
1	J	63/133 (47%)	63 (100%)	0	100	100
1	K	62/133 (47%)	62 (100%)	0	100	100
1	L	58/133 (44%)	58 (100%)	0	100	100
1	M	60/133 (45%)	60 (100%)	0	100	100
1	N	65/133 (49%)	61 (94%)	4 (6%)	18	46
All	All	850/1862 (46%)	844 (99%)	6 (1%)	84	90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	27	ASN
1	G	98	THR
1	N	27	ASN
1	N	98	THR
1	N	101	GLN
1	N	126	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	22	GLN
1	F	7	GLN
1	G	27	ASN
1	I	22	GLN
1	N	27	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	121/157 (77%)	-0.53	0 100 100	147, 180, 217, 231	0
1	B	126/157 (80%)	-0.59	0 100 100	114, 148, 204, 230	0
1	C	134/157 (85%)	-0.63	0 100 100	99, 134, 184, 199	0
1	D	128/157 (81%)	-0.53	0 100 100	89, 134, 195, 216	0
1	E	126/157 (80%)	-0.66	0 100 100	92, 140, 206, 218	0
1	F	125/157 (79%)	-0.58	0 100 100	111, 151, 201, 221	0
1	G	127/157 (80%)	-0.51	0 100 100	133, 178, 223, 241	0
1	H	127/157 (80%)	-0.65	0 100 100	93, 127, 175, 207	0
1	I	128/157 (81%)	-0.58	0 100 100	78, 111, 150, 182	0
1	J	135/157 (85%)	-0.64	0 100 100	68, 104, 149, 179	0
1	K	128/157 (81%)	-0.62	0 100 100	68, 109, 169, 186	0
1	L	126/157 (80%)	-0.62	0 100 100	78, 117, 177, 192	0
1	M	123/157 (78%)	-0.53	0 100 100	100, 135, 171, 193	0
1	N	125/157 (79%)	-0.56	0 100 100	100, 132, 216, 261	0
All	All	1779/2198 (80%)	-0.59	0 100 100	68, 136, 202, 261	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.