



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:26 AM UTC

PDB ID : 4ZK7 / pdb_00004zk7
Title : Crystal structure of rescued two-component self-assembling tetrahedral cage T33-31
Authors : Liu, Y.; Cascio, D.; Sawaya, M.R.; Bale, J.; Collazo, M.J.; Park, R.; King, N.; Baker, D.; Yeates, T.
Deposited on : 2015-04-30
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

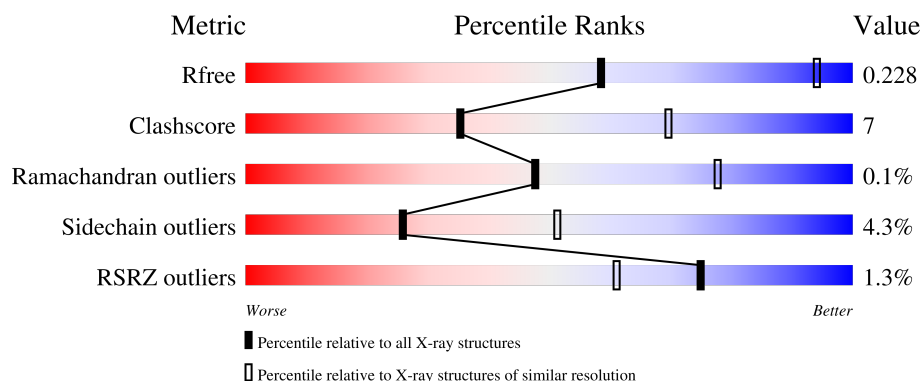
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	130	0% 70% 18% • 10%
1	B	130	3% 68% 20% • 10%
1	C	130	2% 69% 19% • 10%
1	D	130	2% 72% 18% • 10%
1	E	130	3% 71% 17% • 10%

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Mol	Chain	Length	Quality of chain
1	F	130	 69% 19% • 10%
1	G	130	 72% 16% • 10%
1	H	130	 73% 15% • 10%
1	I	130	 73% 15% • 10%
1	J	130	 72% 15% • 10%
1	K	130	 72% 17% • 10%
1	L	130	 70% 17% • 10%
2	M	111	 78% 13% • 7%
2	N	111	 71% 19% • 7%
2	O	111	 73% 17% • 7%
2	P	111	 73% 19% • 7%
2	Q	111	 70% 23% 5% •
2	R	111	 71% 20% • 7%
2	S	111	 68% 22% • • 7%
2	T	111	 71% 21% • 7%
2	U	111	 72% 20% • 7%
2	V	111	 68% 24% • 7%
2	W	111	 79% 13% • 7%
2	X	111	 72% 18% • 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20678 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 Chorismate mutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	B	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	C	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	D	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	E	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	F	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	G	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	H	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	I	117	Total	C	N	O	S	0	4	0
			909	582	163	161	3			
1	J	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	K	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			
1	L	117	Total	C	N	O	S	0	4	0
			913	584	164	162	3			

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ALA	GLU	engineered mutation	UNP Q5SJY4
A	20	LEU	HIS	engineered mutation	UNP Q5SJY4
A	21	ALA	GLN	engineered mutation	UNP Q5SJY4
A	24	ILE	ARG	engineered mutation	UNP Q5SJY4
A	64	LEU	GLN	engineered mutation	UNP Q5SJY4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	109	ASN	ARG	engineered mutation	UNP Q5SJY4
A	123	LEU	-	expression tag	UNP Q5SJY4
A	124	GLU	-	expression tag	UNP Q5SJY4
A	125	HIS	-	expression tag	UNP Q5SJY4
A	126	HIS	-	expression tag	UNP Q5SJY4
A	127	HIS	-	expression tag	UNP Q5SJY4
A	128	HIS	-	expression tag	UNP Q5SJY4
A	129	HIS	-	expression tag	UNP Q5SJY4
A	130	HIS	-	expression tag	UNP Q5SJY4
B	17	ALA	GLU	engineered mutation	UNP Q5SJY4
B	20	LEU	HIS	engineered mutation	UNP Q5SJY4
B	21	ALA	GLN	engineered mutation	UNP Q5SJY4
B	24	ILE	ARG	engineered mutation	UNP Q5SJY4
B	64	LEU	GLN	engineered mutation	UNP Q5SJY4
B	109	ASN	ARG	engineered mutation	UNP Q5SJY4
B	123	LEU	-	expression tag	UNP Q5SJY4
B	124	GLU	-	expression tag	UNP Q5SJY4
B	125	HIS	-	expression tag	UNP Q5SJY4
B	126	HIS	-	expression tag	UNP Q5SJY4
B	127	HIS	-	expression tag	UNP Q5SJY4
B	128	HIS	-	expression tag	UNP Q5SJY4
B	129	HIS	-	expression tag	UNP Q5SJY4
B	130	HIS	-	expression tag	UNP Q5SJY4
C	17	ALA	GLU	engineered mutation	UNP Q5SJY4
C	20	LEU	HIS	engineered mutation	UNP Q5SJY4
C	21	ALA	GLN	engineered mutation	UNP Q5SJY4
C	24	ILE	ARG	engineered mutation	UNP Q5SJY4
C	64	LEU	GLN	engineered mutation	UNP Q5SJY4
C	109	ASN	ARG	engineered mutation	UNP Q5SJY4
C	123	LEU	-	expression tag	UNP Q5SJY4
C	124	GLU	-	expression tag	UNP Q5SJY4
C	125	HIS	-	expression tag	UNP Q5SJY4
C	126	HIS	-	expression tag	UNP Q5SJY4
C	127	HIS	-	expression tag	UNP Q5SJY4
C	128	HIS	-	expression tag	UNP Q5SJY4
C	129	HIS	-	expression tag	UNP Q5SJY4
C	130	HIS	-	expression tag	UNP Q5SJY4
D	17	ALA	GLU	engineered mutation	UNP Q5SJY4
D	20	LEU	HIS	engineered mutation	UNP Q5SJY4
D	21	ALA	GLN	engineered mutation	UNP Q5SJY4
D	24	ILE	ARG	engineered mutation	UNP Q5SJY4
D	64	LEU	GLN	engineered mutation	UNP Q5SJY4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	109	ASN	ARG	engineered mutation	UNP Q5SJY4
D	123	LEU	-	expression tag	UNP Q5SJY4
D	124	GLU	-	expression tag	UNP Q5SJY4
D	125	HIS	-	expression tag	UNP Q5SJY4
D	126	HIS	-	expression tag	UNP Q5SJY4
D	127	HIS	-	expression tag	UNP Q5SJY4
D	128	HIS	-	expression tag	UNP Q5SJY4
D	129	HIS	-	expression tag	UNP Q5SJY4
D	130	HIS	-	expression tag	UNP Q5SJY4
E	17	ALA	GLU	engineered mutation	UNP Q5SJY4
E	20	LEU	HIS	engineered mutation	UNP Q5SJY4
E	21	ALA	GLN	engineered mutation	UNP Q5SJY4
E	24	ILE	ARG	engineered mutation	UNP Q5SJY4
E	64	LEU	GLN	engineered mutation	UNP Q5SJY4
E	109	ASN	ARG	engineered mutation	UNP Q5SJY4
E	123	LEU	-	expression tag	UNP Q5SJY4
E	124	GLU	-	expression tag	UNP Q5SJY4
E	125	HIS	-	expression tag	UNP Q5SJY4
E	126	HIS	-	expression tag	UNP Q5SJY4
E	127	HIS	-	expression tag	UNP Q5SJY4
E	128	HIS	-	expression tag	UNP Q5SJY4
E	129	HIS	-	expression tag	UNP Q5SJY4
E	130	HIS	-	expression tag	UNP Q5SJY4
F	17	ALA	GLU	engineered mutation	UNP Q5SJY4
F	20	LEU	HIS	engineered mutation	UNP Q5SJY4
F	21	ALA	GLN	engineered mutation	UNP Q5SJY4
F	24	ILE	ARG	engineered mutation	UNP Q5SJY4
F	64	LEU	GLN	engineered mutation	UNP Q5SJY4
F	109	ASN	ARG	engineered mutation	UNP Q5SJY4
F	123	LEU	-	expression tag	UNP Q5SJY4
F	124	GLU	-	expression tag	UNP Q5SJY4
F	125	HIS	-	expression tag	UNP Q5SJY4
F	126	HIS	-	expression tag	UNP Q5SJY4
F	127	HIS	-	expression tag	UNP Q5SJY4
F	128	HIS	-	expression tag	UNP Q5SJY4
F	129	HIS	-	expression tag	UNP Q5SJY4
F	130	HIS	-	expression tag	UNP Q5SJY4
G	17	ALA	GLU	engineered mutation	UNP Q5SJY4
G	20	LEU	HIS	engineered mutation	UNP Q5SJY4
G	21	ALA	GLN	engineered mutation	UNP Q5SJY4
G	24	ILE	ARG	engineered mutation	UNP Q5SJY4
G	64	LEU	GLN	engineered mutation	UNP Q5SJY4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	109	ASN	ARG	engineered mutation	UNP Q5SJY4
G	123	LEU	-	expression tag	UNP Q5SJY4
G	124	GLU	-	expression tag	UNP Q5SJY4
G	125	HIS	-	expression tag	UNP Q5SJY4
G	126	HIS	-	expression tag	UNP Q5SJY4
G	127	HIS	-	expression tag	UNP Q5SJY4
G	128	HIS	-	expression tag	UNP Q5SJY4
G	129	HIS	-	expression tag	UNP Q5SJY4
G	130	HIS	-	expression tag	UNP Q5SJY4
H	17	ALA	GLU	engineered mutation	UNP Q5SJY4
H	20	LEU	HIS	engineered mutation	UNP Q5SJY4
H	21	ALA	GLN	engineered mutation	UNP Q5SJY4
H	24	ILE	ARG	engineered mutation	UNP Q5SJY4
H	64	LEU	GLN	engineered mutation	UNP Q5SJY4
H	109	ASN	ARG	engineered mutation	UNP Q5SJY4
H	123	LEU	-	expression tag	UNP Q5SJY4
H	124	GLU	-	expression tag	UNP Q5SJY4
H	125	HIS	-	expression tag	UNP Q5SJY4
H	126	HIS	-	expression tag	UNP Q5SJY4
H	127	HIS	-	expression tag	UNP Q5SJY4
H	128	HIS	-	expression tag	UNP Q5SJY4
H	129	HIS	-	expression tag	UNP Q5SJY4
H	130	HIS	-	expression tag	UNP Q5SJY4
I	17	ALA	GLU	engineered mutation	UNP Q5SJY4
I	20	LEU	HIS	engineered mutation	UNP Q5SJY4
I	21	ALA	GLN	engineered mutation	UNP Q5SJY4
I	24	ILE	ARG	engineered mutation	UNP Q5SJY4
I	64	LEU	GLN	engineered mutation	UNP Q5SJY4
I	109	ASN	ARG	engineered mutation	UNP Q5SJY4
I	123	LEU	-	expression tag	UNP Q5SJY4
I	124	GLU	-	expression tag	UNP Q5SJY4
I	125	HIS	-	expression tag	UNP Q5SJY4
I	126	HIS	-	expression tag	UNP Q5SJY4
I	127	HIS	-	expression tag	UNP Q5SJY4
I	128	HIS	-	expression tag	UNP Q5SJY4
I	129	HIS	-	expression tag	UNP Q5SJY4
I	130	HIS	-	expression tag	UNP Q5SJY4
J	17	ALA	GLU	engineered mutation	UNP Q5SJY4
J	20	LEU	HIS	engineered mutation	UNP Q5SJY4
J	21	ALA	GLN	engineered mutation	UNP Q5SJY4
J	24	ILE	ARG	engineered mutation	UNP Q5SJY4
J	64	LEU	GLN	engineered mutation	UNP Q5SJY4

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Chain	Residue	Modelled	Actual	Comment	Reference
J	109	ASN	ARG	engineered mutation	UNP Q5SJY4
J	123	LEU	-	expression tag	UNP Q5SJY4
J	124	GLU	-	expression tag	UNP Q5SJY4
J	125	HIS	-	expression tag	UNP Q5SJY4
J	126	HIS	-	expression tag	UNP Q5SJY4
J	127	HIS	-	expression tag	UNP Q5SJY4
J	128	HIS	-	expression tag	UNP Q5SJY4
J	129	HIS	-	expression tag	UNP Q5SJY4
J	130	HIS	-	expression tag	UNP Q5SJY4
K	17	ALA	GLU	engineered mutation	UNP Q5SJY4
K	20	LEU	HIS	engineered mutation	UNP Q5SJY4
K	21	ALA	GLN	engineered mutation	UNP Q5SJY4
K	24	ILE	ARG	engineered mutation	UNP Q5SJY4
K	64	LEU	GLN	engineered mutation	UNP Q5SJY4
K	109	ASN	ARG	engineered mutation	UNP Q5SJY4
K	123	LEU	-	expression tag	UNP Q5SJY4
K	124	GLU	-	expression tag	UNP Q5SJY4
K	125	HIS	-	expression tag	UNP Q5SJY4
K	126	HIS	-	expression tag	UNP Q5SJY4
K	127	HIS	-	expression tag	UNP Q5SJY4
K	128	HIS	-	expression tag	UNP Q5SJY4
K	129	HIS	-	expression tag	UNP Q5SJY4
K	130	HIS	-	expression tag	UNP Q5SJY4
L	17	ALA	GLU	engineered mutation	UNP Q5SJY4
L	20	LEU	HIS	engineered mutation	UNP Q5SJY4
L	21	ALA	GLN	engineered mutation	UNP Q5SJY4
L	24	ILE	ARG	engineered mutation	UNP Q5SJY4
L	64	LEU	GLN	engineered mutation	UNP Q5SJY4
L	109	ASN	ARG	engineered mutation	UNP Q5SJY4
L	123	LEU	-	expression tag	UNP Q5SJY4
L	124	GLU	-	expression tag	UNP Q5SJY4
L	125	HIS	-	expression tag	UNP Q5SJY4
L	126	HIS	-	expression tag	UNP Q5SJY4
L	127	HIS	-	expression tag	UNP Q5SJY4
L	128	HIS	-	expression tag	UNP Q5SJY4
L	129	HIS	-	expression tag	UNP Q5SJY4
L	130	HIS	-	expression tag	UNP Q5SJY4

- Molecule 2 is a protein called Divalent-cation tolerance protein CutA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	O	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	P	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	Q	109	Total	C	N	O	S	0	0	0
			860	550	147	161	2			
2	R	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	S	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	T	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	U	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	V	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	W	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			
2	X	103	Total	C	N	O	S	0	0	0
			806	518	133	153	2			

There are 252 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	12	ALA	GLU	engineered mutation	UNP Q7SIA8
M	13	LEU	GLU	engineered mutation	UNP Q7SIA8
M	16	VAL	ARG	engineered mutation	UNP Q7SIA8
M	17	LYS	THR	engineered mutation	UNP Q7SIA8
M	20	HIS	LYS	engineered mutation	UNP Q7SIA8
M	43	GLU	TRP	engineered mutation	UNP Q7SIA8
M	44	GLU	GLN	engineered mutation	UNP Q7SIA8
M	46	SER	GLU	engineered mutation	UNP Q7SIA8
M	49	SER	GLU	engineered mutation	UNP Q7SIA8
M	51	HIS	GLN	engineered mutation	UNP Q7SIA8
M	62	ASP	HIS	engineered mutation	UNP Q7SIA8
M	73	GLU	ALA	engineered mutation	UNP Q7SIA8
M	78	GLU	THR	engineered mutation	UNP Q7SIA8
M	104	LEU	-	expression tag	UNP Q7SIA8
M	105	GLU	-	expression tag	UNP Q7SIA8
M	106	HIS	-	expression tag	UNP Q7SIA8
M	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
M	108	HIS	-	expression tag	UNP Q7SIA8
M	109	HIS	-	expression tag	UNP Q7SIA8
M	110	HIS	-	expression tag	UNP Q7SIA8
M	111	HIS	-	expression tag	UNP Q7SIA8
N	12	ALA	GLU	engineered mutation	UNP Q7SIA8
N	13	LEU	GLU	engineered mutation	UNP Q7SIA8
N	16	VAL	ARG	engineered mutation	UNP Q7SIA8
N	17	LYS	THR	engineered mutation	UNP Q7SIA8
N	20	HIS	LYS	engineered mutation	UNP Q7SIA8
N	43	GLU	TRP	engineered mutation	UNP Q7SIA8
N	44	GLU	GLN	engineered mutation	UNP Q7SIA8
N	46	SER	GLU	engineered mutation	UNP Q7SIA8
N	49	SER	GLU	engineered mutation	UNP Q7SIA8
N	51	HIS	GLN	engineered mutation	UNP Q7SIA8
N	62	ASP	HIS	engineered mutation	UNP Q7SIA8
N	73	GLU	ALA	engineered mutation	UNP Q7SIA8
N	78	GLU	THR	engineered mutation	UNP Q7SIA8
N	104	LEU	-	expression tag	UNP Q7SIA8
N	105	GLU	-	expression tag	UNP Q7SIA8
N	106	HIS	-	expression tag	UNP Q7SIA8
N	107	HIS	-	expression tag	UNP Q7SIA8
N	108	HIS	-	expression tag	UNP Q7SIA8
N	109	HIS	-	expression tag	UNP Q7SIA8
N	110	HIS	-	expression tag	UNP Q7SIA8
N	111	HIS	-	expression tag	UNP Q7SIA8
O	12	ALA	GLU	engineered mutation	UNP Q7SIA8
O	13	LEU	GLU	engineered mutation	UNP Q7SIA8
O	16	VAL	ARG	engineered mutation	UNP Q7SIA8
O	17	LYS	THR	engineered mutation	UNP Q7SIA8
O	20	HIS	LYS	engineered mutation	UNP Q7SIA8
O	43	GLU	TRP	engineered mutation	UNP Q7SIA8
O	44	GLU	GLN	engineered mutation	UNP Q7SIA8
O	46	SER	GLU	engineered mutation	UNP Q7SIA8
O	49	SER	GLU	engineered mutation	UNP Q7SIA8
O	51	HIS	GLN	engineered mutation	UNP Q7SIA8
O	62	ASP	HIS	engineered mutation	UNP Q7SIA8
O	73	GLU	ALA	engineered mutation	UNP Q7SIA8
O	78	GLU	THR	engineered mutation	UNP Q7SIA8
O	104	LEU	-	expression tag	UNP Q7SIA8
O	105	GLU	-	expression tag	UNP Q7SIA8
O	106	HIS	-	expression tag	UNP Q7SIA8
O	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
O	108	HIS	-	expression tag	UNP Q7SIA8
O	109	HIS	-	expression tag	UNP Q7SIA8
O	110	HIS	-	expression tag	UNP Q7SIA8
O	111	HIS	-	expression tag	UNP Q7SIA8
P	12	ALA	GLU	engineered mutation	UNP Q7SIA8
P	13	LEU	GLU	engineered mutation	UNP Q7SIA8
P	16	VAL	ARG	engineered mutation	UNP Q7SIA8
P	17	LYS	THR	engineered mutation	UNP Q7SIA8
P	20	HIS	LYS	engineered mutation	UNP Q7SIA8
P	43	GLU	TRP	engineered mutation	UNP Q7SIA8
P	44	GLU	GLN	engineered mutation	UNP Q7SIA8
P	46	SER	GLU	engineered mutation	UNP Q7SIA8
P	49	SER	GLU	engineered mutation	UNP Q7SIA8
P	51	HIS	GLN	engineered mutation	UNP Q7SIA8
P	62	ASP	HIS	engineered mutation	UNP Q7SIA8
P	73	GLU	ALA	engineered mutation	UNP Q7SIA8
P	78	GLU	THR	engineered mutation	UNP Q7SIA8
P	104	LEU	-	expression tag	UNP Q7SIA8
P	105	GLU	-	expression tag	UNP Q7SIA8
P	106	HIS	-	expression tag	UNP Q7SIA8
P	107	HIS	-	expression tag	UNP Q7SIA8
P	108	HIS	-	expression tag	UNP Q7SIA8
P	109	HIS	-	expression tag	UNP Q7SIA8
P	110	HIS	-	expression tag	UNP Q7SIA8
P	111	HIS	-	expression tag	UNP Q7SIA8
Q	12	ALA	GLU	engineered mutation	UNP Q7SIA8
Q	13	LEU	GLU	engineered mutation	UNP Q7SIA8
Q	16	VAL	ARG	engineered mutation	UNP Q7SIA8
Q	17	LYS	THR	engineered mutation	UNP Q7SIA8
Q	20	HIS	LYS	engineered mutation	UNP Q7SIA8
Q	43	GLU	TRP	engineered mutation	UNP Q7SIA8
Q	44	GLU	GLN	engineered mutation	UNP Q7SIA8
Q	46	SER	GLU	engineered mutation	UNP Q7SIA8
Q	49	SER	GLU	engineered mutation	UNP Q7SIA8
Q	51	HIS	GLN	engineered mutation	UNP Q7SIA8
Q	62	ASP	HIS	engineered mutation	UNP Q7SIA8
Q	73	GLU	ALA	engineered mutation	UNP Q7SIA8
Q	78	GLU	THR	engineered mutation	UNP Q7SIA8
Q	104	LEU	-	expression tag	UNP Q7SIA8
Q	105	GLU	-	expression tag	UNP Q7SIA8
Q	106	HIS	-	expression tag	UNP Q7SIA8
Q	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	108	HIS	-	expression tag	UNP Q7SIA8
Q	109	HIS	-	expression tag	UNP Q7SIA8
Q	110	HIS	-	expression tag	UNP Q7SIA8
Q	111	HIS	-	expression tag	UNP Q7SIA8
R	12	ALA	GLU	engineered mutation	UNP Q7SIA8
R	13	LEU	GLU	engineered mutation	UNP Q7SIA8
R	16	VAL	ARG	engineered mutation	UNP Q7SIA8
R	17	LYS	THR	engineered mutation	UNP Q7SIA8
R	20	HIS	LYS	engineered mutation	UNP Q7SIA8
R	43	GLU	TRP	engineered mutation	UNP Q7SIA8
R	44	GLU	GLN	engineered mutation	UNP Q7SIA8
R	46	SER	GLU	engineered mutation	UNP Q7SIA8
R	49	SER	GLU	engineered mutation	UNP Q7SIA8
R	51	HIS	GLN	engineered mutation	UNP Q7SIA8
R	62	ASP	HIS	engineered mutation	UNP Q7SIA8
R	73	GLU	ALA	engineered mutation	UNP Q7SIA8
R	78	GLU	THR	engineered mutation	UNP Q7SIA8
R	104	LEU	-	expression tag	UNP Q7SIA8
R	105	GLU	-	expression tag	UNP Q7SIA8
R	106	HIS	-	expression tag	UNP Q7SIA8
R	107	HIS	-	expression tag	UNP Q7SIA8
R	108	HIS	-	expression tag	UNP Q7SIA8
R	109	HIS	-	expression tag	UNP Q7SIA8
R	110	HIS	-	expression tag	UNP Q7SIA8
R	111	HIS	-	expression tag	UNP Q7SIA8
S	12	ALA	GLU	engineered mutation	UNP Q7SIA8
S	13	LEU	GLU	engineered mutation	UNP Q7SIA8
S	16	VAL	ARG	engineered mutation	UNP Q7SIA8
S	17	LYS	THR	engineered mutation	UNP Q7SIA8
S	20	HIS	LYS	engineered mutation	UNP Q7SIA8
S	43	GLU	TRP	engineered mutation	UNP Q7SIA8
S	44	GLU	GLN	engineered mutation	UNP Q7SIA8
S	46	SER	GLU	engineered mutation	UNP Q7SIA8
S	49	SER	GLU	engineered mutation	UNP Q7SIA8
S	51	HIS	GLN	engineered mutation	UNP Q7SIA8
S	62	ASP	HIS	engineered mutation	UNP Q7SIA8
S	73	GLU	ALA	engineered mutation	UNP Q7SIA8
S	78	GLU	THR	engineered mutation	UNP Q7SIA8
S	104	LEU	-	expression tag	UNP Q7SIA8
S	105	GLU	-	expression tag	UNP Q7SIA8
S	106	HIS	-	expression tag	UNP Q7SIA8
S	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
S	108	HIS	-	expression tag	UNP Q7SIA8
S	109	HIS	-	expression tag	UNP Q7SIA8
S	110	HIS	-	expression tag	UNP Q7SIA8
S	111	HIS	-	expression tag	UNP Q7SIA8
T	12	ALA	GLU	engineered mutation	UNP Q7SIA8
T	13	LEU	GLU	engineered mutation	UNP Q7SIA8
T	16	VAL	ARG	engineered mutation	UNP Q7SIA8
T	17	LYS	THR	engineered mutation	UNP Q7SIA8
T	20	HIS	LYS	engineered mutation	UNP Q7SIA8
T	43	GLU	TRP	engineered mutation	UNP Q7SIA8
T	44	GLU	GLN	engineered mutation	UNP Q7SIA8
T	46	SER	GLU	engineered mutation	UNP Q7SIA8
T	49	SER	GLU	engineered mutation	UNP Q7SIA8
T	51	HIS	GLN	engineered mutation	UNP Q7SIA8
T	62	ASP	HIS	engineered mutation	UNP Q7SIA8
T	73	GLU	ALA	engineered mutation	UNP Q7SIA8
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T	104	LEU	-	expression tag	UNP Q7SIA8
T	105	GLU	-	expression tag	UNP Q7SIA8
T	106	HIS	-	expression tag	UNP Q7SIA8
T	107	HIS	-	expression tag	UNP Q7SIA8
T	108	HIS	-	expression tag	UNP Q7SIA8
T	109	HIS	-	expression tag	UNP Q7SIA8
T	110	HIS	-	expression tag	UNP Q7SIA8
T	111	HIS	-	expression tag	UNP Q7SIA8
U	12	ALA	GLU	engineered mutation	UNP Q7SIA8
U	13	LEU	GLU	engineered mutation	UNP Q7SIA8
U	16	VAL	ARG	engineered mutation	UNP Q7SIA8
U	17	LYS	THR	engineered mutation	UNP Q7SIA8
U	20	HIS	LYS	engineered mutation	UNP Q7SIA8
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U	44	GLU	GLN	engineered mutation	UNP Q7SIA8
U	46	SER	GLU	engineered mutation	UNP Q7SIA8
U	49	SER	GLU	engineered mutation	UNP Q7SIA8
U	51	HIS	GLN	engineered mutation	UNP Q7SIA8
U	62	ASP	HIS	engineered mutation	UNP Q7SIA8
U	73	GLU	ALA	engineered mutation	UNP Q7SIA8
U	78	GLU	THR	engineered mutation	UNP Q7SIA8
U	104	LEU	-	expression tag	UNP Q7SIA8
U	105	GLU	-	expression tag	UNP Q7SIA8
U	106	HIS	-	expression tag	UNP Q7SIA8
U	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
U	108	HIS	-	expression tag	UNP Q7SIA8
U	109	HIS	-	expression tag	UNP Q7SIA8
U	110	HIS	-	expression tag	UNP Q7SIA8
U	111	HIS	-	expression tag	UNP Q7SIA8
V	12	ALA	GLU	engineered mutation	UNP Q7SIA8
V	13	LEU	GLU	engineered mutation	UNP Q7SIA8
V	16	VAL	ARG	engineered mutation	UNP Q7SIA8
V	17	LYS	THR	engineered mutation	UNP Q7SIA8
V	20	HIS	LYS	engineered mutation	UNP Q7SIA8
V	43	GLU	TRP	engineered mutation	UNP Q7SIA8
V	44	GLU	GLN	engineered mutation	UNP Q7SIA8
V	46	SER	GLU	engineered mutation	UNP Q7SIA8
V	49	SER	GLU	engineered mutation	UNP Q7SIA8
V	51	HIS	GLN	engineered mutation	UNP Q7SIA8
V	62	ASP	HIS	engineered mutation	UNP Q7SIA8
V	73	GLU	ALA	engineered mutation	UNP Q7SIA8
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V	105	GLU	-	expression tag	UNP Q7SIA8
V	106	HIS	-	expression tag	UNP Q7SIA8
V	107	HIS	-	expression tag	UNP Q7SIA8
V	108	HIS	-	expression tag	UNP Q7SIA8
V	109	HIS	-	expression tag	UNP Q7SIA8
V	110	HIS	-	expression tag	UNP Q7SIA8
V	111	HIS	-	expression tag	UNP Q7SIA8
W	12	ALA	GLU	engineered mutation	UNP Q7SIA8
W	13	LEU	GLU	engineered mutation	UNP Q7SIA8
W	16	VAL	ARG	engineered mutation	UNP Q7SIA8
W	17	LYS	THR	engineered mutation	UNP Q7SIA8
W	20	HIS	LYS	engineered mutation	UNP Q7SIA8
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W	46	SER	GLU	engineered mutation	UNP Q7SIA8
W	49	SER	GLU	engineered mutation	UNP Q7SIA8
W	51	HIS	GLN	engineered mutation	UNP Q7SIA8
W	62	ASP	HIS	engineered mutation	UNP Q7SIA8
W	73	GLU	ALA	engineered mutation	UNP Q7SIA8
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W	104	LEU	-	expression tag	UNP Q7SIA8
W	105	GLU	-	expression tag	UNP Q7SIA8
W	106	HIS	-	expression tag	UNP Q7SIA8
W	107	HIS	-	expression tag	UNP Q7SIA8

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Chain	Residue	Modelled	Actual	Comment	Reference
W	108	HIS	-	expression tag	UNP Q7SIA8
W	109	HIS	-	expression tag	UNP Q7SIA8
W	110	HIS	-	expression tag	UNP Q7SIA8
W	111	HIS	-	expression tag	UNP Q7SIA8
X	12	ALA	GLU	engineered mutation	UNP Q7SIA8
X	13	LEU	GLU	engineered mutation	UNP Q7SIA8
X	16	VAL	ARG	engineered mutation	UNP Q7SIA8
X	17	LYS	THR	engineered mutation	UNP Q7SIA8
X	20	HIS	LYS	engineered mutation	UNP Q7SIA8
X	43	GLU	TRP	engineered mutation	UNP Q7SIA8
X	44	GLU	GLN	engineered mutation	UNP Q7SIA8
X	46	SER	GLU	engineered mutation	UNP Q7SIA8
X	49	SER	GLU	engineered mutation	UNP Q7SIA8
X	51	HIS	GLN	engineered mutation	UNP Q7SIA8
X	62	ASP	HIS	engineered mutation	UNP Q7SIA8
X	73	GLU	ALA	engineered mutation	UNP Q7SIA8
X	78	GLU	THR	engineered mutation	UNP Q7SIA8
X	104	LEU	-	expression tag	UNP Q7SIA8
X	105	GLU	-	expression tag	UNP Q7SIA8
X	106	HIS	-	expression tag	UNP Q7SIA8
X	107	HIS	-	expression tag	UNP Q7SIA8
X	108	HIS	-	expression tag	UNP Q7SIA8
X	109	HIS	-	expression tag	UNP Q7SIA8
X	110	HIS	-	expression tag	UNP Q7SIA8
X	111	HIS	-	expression tag	UNP Q7SIA8

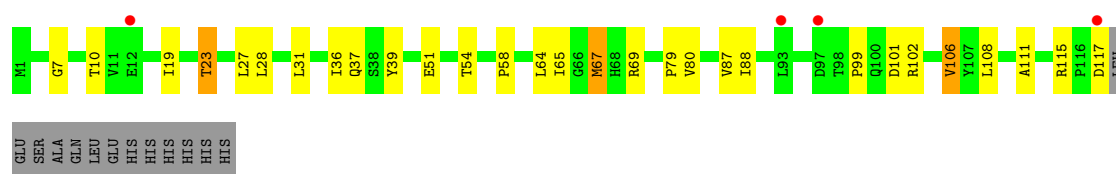
3 Residue-property plots [i](#)

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.

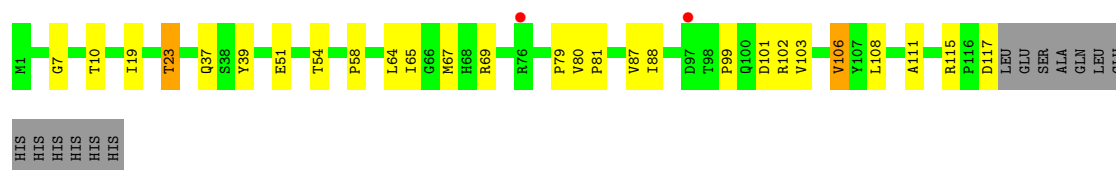
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- Molecule 1: Chorismate mutase



- Molecule 1: Chorismate mutase

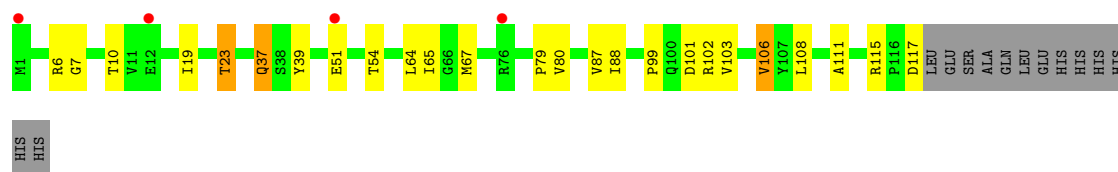


- Molecule 1: Chorismate mutase

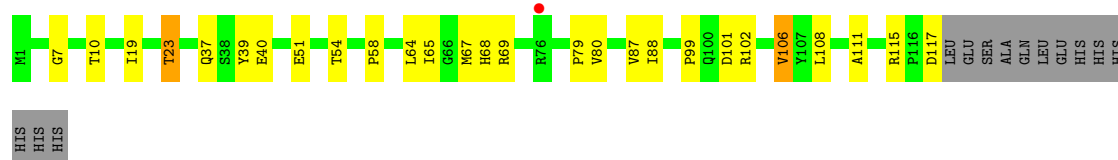


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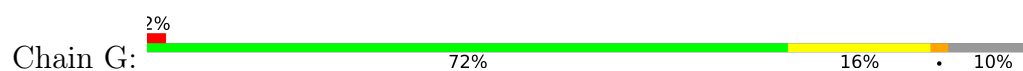




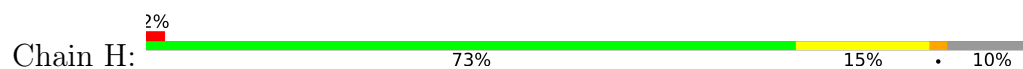
- Molecule 1: Chorismate mutase



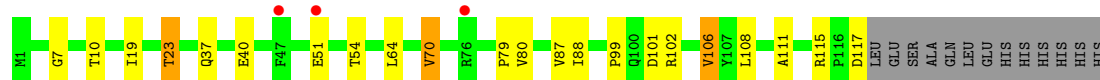
- Molecule 1: Chorismate mutase



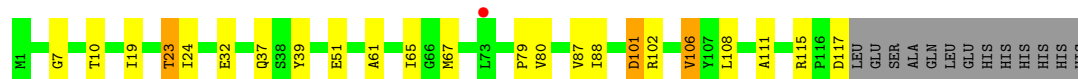
- Molecule 1: Chorismate mutase



- Molecule 1: Chorismate mutase

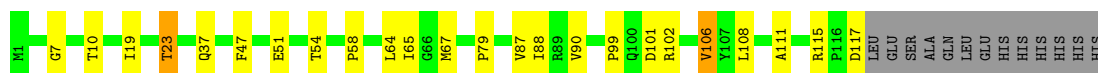


- Molecule 1: Chorismate mutase

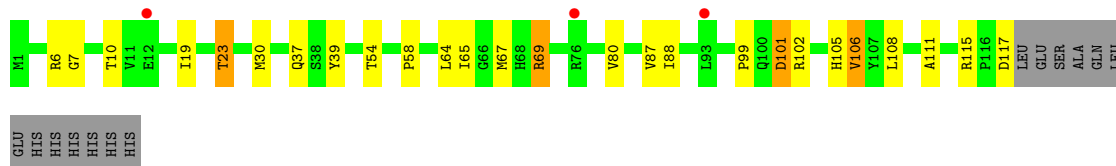


- Molecule 1: Chorismate mutase

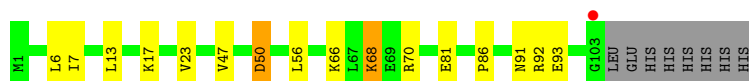
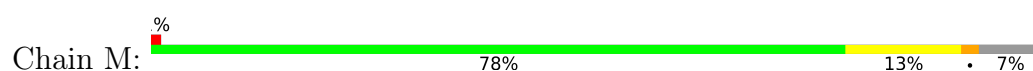




- Molecule 1: Chorismate mutase



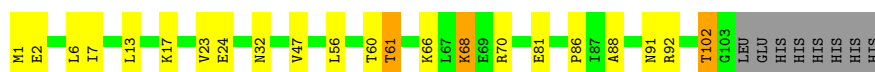
- Molecule 2: Divalent-cation tolerance protein CutA



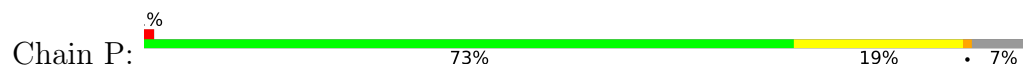
- Molecule 2: Divalent-cation tolerance protein CutA



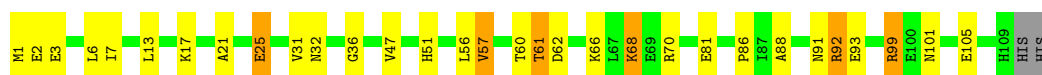
- Molecule 2: Divalent-cation tolerance protein CutA



- Molecule 2: Divalent-cation tolerance protein CutA



- Molecule 2: Divalent-cation tolerance protein CutA



- Molecule 2: Divalent-cation tolerance protein CutA

Chain R:  71% 20% 7%



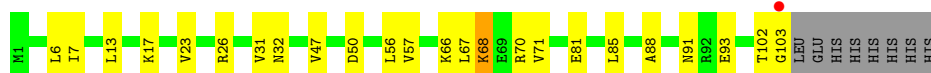
• Molecule 2: Divalent-cation tolerance protein CutA

Chain S:  68% 22% 7%



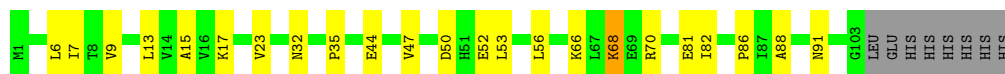
• Molecule 2: Divalent-cation tolerance protein CutA

Chain T:  71% 21% 7%



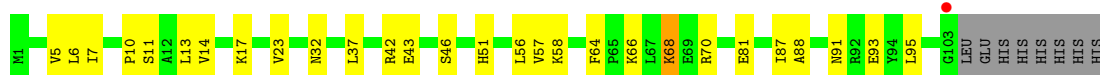
• Molecule 2: Divalent-cation tolerance protein CutA

Chain U:  72% 20% 7%



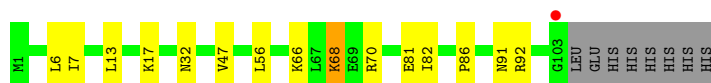
• Molecule 2: Divalent-cation tolerance protein CutA

Chain V:  68% 24% 7%



• Molecule 2: Divalent-cation tolerance protein CutA

Chain W:  79% 13% 7%



• Molecule 2: Divalent-cation tolerance protein CutA

Chain X:  72% 18% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	121.10Å 128.40Å 204.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.10 – 3.40 88.10 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (88.10-3.40) 99.1 (88.10-3.40)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 3.41Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.190 , 0.239 (Not available) , 0.228	Depositor DCC
R_{free} test set	2219 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	73.9	Xtriage
Anisotropy	0.798	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 87.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	20678	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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	0.93	1/948 (0.1%)	1.29	2/1293 (0.2%)
1	B	0.93	2/948 (0.2%)	1.26	1/1293 (0.1%)
1	C	0.85	0/948	1.25	1/1293 (0.1%)
1	D	0.95	0/948	1.28	2/1293 (0.2%)
1	E	0.87	0/948	1.27	3/1293 (0.2%)
1	F	0.89	0/948	1.26	2/1293 (0.2%)
1	G	0.93	0/948	1.24	1/1293 (0.1%)
1	H	0.94	0/948	1.27	1/1293 (0.1%)
1	I	0.92	0/944	1.29	3/1288 (0.2%)
1	J	0.98	0/948	1.29	5/1293 (0.4%)
1	K	0.91	0/948	1.30	1/1293 (0.1%)
1	L	0.93	0/948	1.26	2/1293 (0.2%)
2	M	0.78	0/820	1.31	3/1119 (0.3%)
2	N	0.82	0/820	1.36	0/1119
2	O	0.85	0/820	1.40	5/1119 (0.4%)
2	P	0.92	0/820	1.37	1/1119 (0.1%)
2	Q	0.94	1/878 (0.1%)	1.44	7/1198 (0.6%)
2	R	0.89	0/820	1.37	4/1119 (0.4%)
2	S	0.85	0/820	1.33	2/1119 (0.2%)
2	T	0.89	0/820	1.34	1/1119 (0.1%)
2	U	0.83	0/820	1.34	2/1119 (0.2%)
2	V	0.91	0/820	1.36	0/1119
2	W	0.92	0/820	1.35	2/1119 (0.2%)
2	X	0.85	0/820	1.31	2/1119 (0.2%)
All	All	0.90	4/21270 (0.0%)	1.31	53/29018 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	1	MET	SD-CE	5.30	1.92	1.79
1	B	27	LEU	CA-C	-5.30	1.45	1.52
1	A	108	LEU	C-N	5.11	1.38	1.33
1	B	67	MET	SD-CE	-5.09	1.66	1.79

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	91	ASN	CA-C-N	8.30	133.28	120.82
2	R	91	ASN	C-N-CA	8.30	133.28	120.82
1	D	106	VAL	N-CA-C	7.28	118.35	107.51
2	Q	105	GLU	CB-CG-CD	7.23	124.89	112.60
2	Q	105	GLU	N-CA-C	6.60	120.64	110.42
2	M	50	ASP	CA-CB-CG	6.47	119.07	112.60
2	S	78	GLU	CB-CG-CD	6.41	123.49	112.60
2	R	96	ASP	CA-CB-CG	6.15	118.75	112.60
2	Q	61	THR	CA-C-N	6.03	128.28	120.44
2	Q	61	THR	C-N-CA	6.03	128.28	120.44
2	X	50	ASP	CA-CB-CG	6.03	118.63	112.60
1	E	6	ARG	CA-C-N	5.89	126.64	121.58
1	E	6	ARG	C-N-CA	5.89	126.64	121.58
2	X	39	SER	N-CA-C	5.88	118.68	107.75
2	S	21	ALA	N-CA-C	5.86	117.36	110.97
2	R	96	ASP	N-CA-C	-5.81	104.85	111.07
1	B	106	VAL	N-CA-C	5.77	116.42	107.99
1	F	40	GLU	CB-CG-CD	5.76	122.39	112.60
2	U	50	ASP	N-CA-C	5.74	117.80	109.07
1	A	101	ASP	CA-CB-CG	-5.74	106.86	112.60
2	Q	101	ASN	N-CA-C	5.70	120.09	113.20
1	I	70	VAL	N-CA-CB	5.65	115.34	110.08
1	L	106	VAL	N-CA-C	5.63	116.20	107.99
1	A	106	VAL	N-CA-C	5.62	116.20	107.99
2	O	61	THR	CA-C-N	5.61	128.07	120.38
2	O	61	THR	C-N-CA	5.61	128.07	120.38
1	K	106	VAL	N-CA-C	5.51	116.04	107.99
1	J	106	VAL	N-CA-C	5.49	116.01	107.99
1	E	106	VAL	N-CA-C	5.47	115.98	107.99
1	G	106	VAL	N-CA-C	5.33	115.77	107.99
1	J	32[A]	GLU	CA-C-N	5.30	127.65	120.38
1	J	32[A]	GLU	C-N-CA	5.30	127.65	120.38
1	J	32[B]	GLU	CA-C-N	5.30	127.65	120.38
1	J	32[B]	GLU	C-N-CA	5.30	127.65	120.38
2	Q	92	ARG	CA-C-N	5.28	127.35	120.28
2	Q	92	ARG	C-N-CA	5.28	127.35	120.28
1	I	40	GLU	CB-CG-CD	5.27	121.56	112.60
1	D	106	VAL	N-CA-CB	-5.25	104.85	111.41
2	O	92	ARG	CA-C-N	5.24	127.30	120.28
2	O	92	ARG	C-N-CA	5.24	127.30	120.28
1	L	101	ASP	CA-CB-CG	-5.23	107.37	112.60
1	F	106	VAL	N-CA-C	5.20	115.58	107.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	106	VAL	N-CA-C	5.18	115.55	107.99
2	M	92	ARG	CA-C-N	5.14	127.17	120.28
2	M	92	ARG	C-N-CA	5.14	127.17	120.28
2	T	50	ASP	CA-CB-CG	5.14	117.74	112.60
2	W	92	ARG	CA-C-N	5.09	127.10	120.28
2	W	92	ARG	C-N-CA	5.09	127.10	120.28
1	I	106	VAL	N-CA-C	5.08	115.41	107.99
2	O	102	THR	CB-CA-C	5.08	118.85	109.71
2	U	44	GLU	CB-CG-CD	5.06	121.20	112.60
1	H	106	VAL	N-CA-C	5.05	115.37	107.99
2	P	50	ASP	CA-CB-CG	5.03	117.63	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	913	0	954	16	0
1	B	913	0	954	20	0
1	C	913	0	954	19	0
1	D	913	0	954	19	0
1	E	913	0	954	18	0
1	F	913	0	954	19	0
1	G	913	0	954	14	0
1	H	913	0	954	14	0
1	I	909	0	948	11	0
1	J	913	0	954	13	0
1	K	913	0	954	16	0
1	L	913	0	954	18	0
2	M	806	0	834	13	0
2	N	806	0	834	17	0
2	O	806	0	834	14	0
2	P	806	0	834	14	0
2	Q	860	0	870	16	0
2	R	806	0	834	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	S	806	0	834	16	0
2	T	806	0	834	16	0
2	U	806	0	834	15	0
2	V	806	0	834	23	0
2	W	806	0	834	11	0
2	X	806	0	834	13	0
All	All	20678	0	21486	313	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 (313) 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:D:13:GLU:HG2	2:V:51:HIS:CE1	2.12	0.84
1:D:106:VAL:HG12	1:D:108:LEU:HD21	1.63	0.78
1:B:64:LEU:HD22	2:R:17:LYS:HB2	1.66	0.77
1:E:19:ILE:O	1:E:23:THR:HG23	1.83	0.77
1:G:19:ILE:O	1:G:23:THR:HG23	1.88	0.74
1:A:19:ILE:O	1:A:23:THR:HG23	1.88	0.74
1:I:19:ILE:O	1:I:23:THR:HG23	1.90	0.71
1:C:19:ILE:O	1:C:23:THR:HG23	1.90	0.71
1:H:19:ILE:O	1:H:23:THR:HG23	1.89	0.71
1:D:106:VAL:CG1	1:D:108:LEU:HD21	2.20	0.71
1:B:28:LEU:HD21	1:B:65:ILE:HD12	1.73	0.70
1:K:19:ILE:O	1:K:23:THR:HG23	1.91	0.70
1:F:19:ILE:O	1:F:23:THR:HG23	1.93	0.68
1:J:19:ILE:O	1:J:23:THR:HG23	1.93	0.67
2:N:5:VAL:HG22	2:N:84:ALA:HB2	1.77	0.67
1:L:19:ILE:O	1:L:23:THR:HG23	1.94	0.67
1:G:69:ARG:NH2	1:H:103:VAL:O	2.28	0.67
1:D:12:GLU:HB2	2:V:51:HIS:CD2	2.32	0.65
1:B:19:ILE:O	1:B:23:THR:HG23	1.97	0.65
2:P:25:GLU:HB2	2:P:27:LEU:HD12	1.78	0.64
2:P:23:VAL:HG12	2:Q:47:VAL:HG22	1.80	0.64
1:L:30:MET:HA	1:L:106:VAL:HG21	1.80	0.63
2:V:10:PRO:HG2	2:V:14:VAL:HG21	1.80	0.63
2:V:11:SER:OG	2:V:14:VAL:HG23	1.99	0.63
2:Q:31:VAL:HG22	2:Q:57:VAL:HG13	1.79	0.63
1:H:99:PRO:HD2	1:H:102:ARG:HB2	1.81	0.63
1:L:65:ILE:HD11	1:L:67:MET:HE3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:90:GLY:O	2:R:92:ARG:HD3	1.99	0.62
1:G:99:PRO:HD2	1:G:102:ARG:HB2	1.81	0.62
2:S:25:GLU:HB3	2:S:27:LEU:HD12	1.81	0.62
1:A:64:LEU:HD22	2:U:17:LYS:HB2	1.81	0.61
2:S:68:LYS:HD3	2:U:91:ASN:HA	1.82	0.61
2:T:31:VAL:HG22	2:T:57:VAL:HG22	1.80	0.61
2:V:37:LEU:HD11	2:X:34:VAL:HG22	1.83	0.61
1:E:108:LEU:O	1:E:111:ALA:HB3	2.01	0.61
2:N:6:LEU:HD11	2:N:85:LEU:HD11	1.81	0.61
2:N:94:TYR:CE2	2:N:98:LEU:HD12	2.36	0.61
1:H:65:ILE:HD11	1:H:67:MET:HE3	1.82	0.60
2:P:88:ALA:HB2	2:Q:86:PRO:HD3	1.83	0.60
2:W:91:ASN:HA	2:X:68:LYS:HD3	1.82	0.60
1:J:65:ILE:HD11	1:J:67:MET:HE3	1.83	0.60
1:L:99:PRO:HD2	1:L:102:ARG:HB2	1.84	0.60
2:S:23:VAL:HG12	2:T:47:VAL:HG22	1.84	0.60
2:N:88:ALA:HB2	2:O:86:PRO:HD3	1.83	0.60
2:V:10:PRO:HD2	2:V:14:VAL:HG11	1.82	0.60
1:B:65:ILE:HD11	1:B:67:MET:HE3	1.83	0.59
2:M:86:PRO:HD3	2:O:88:ALA:HB2	1.84	0.59
1:K:7:GLY:HA2	1:K:106:VAL:O	2.03	0.59
1:D:9:ILE:HD12	1:D:108:LEU:HD12	1.85	0.59
1:I:99:PRO:HD2	1:I:102:ARG:HB2	1.85	0.59
1:A:62:ALA:HB1	1:A:67:MET:HE3	1.84	0.58
2:S:91:ASN:HA	2:T:68:LYS:HD3	1.84	0.58
1:A:108:LEU:O	1:A:111:ALA:HB3	2.04	0.58
1:A:99:PRO:HD2	1:A:102:ARG:HB2	1.85	0.58
1:I:10:THR:HG22	1:I:87:VAL:HG22	1.86	0.58
1:K:64:LEU:HD22	2:W:17:LYS:HB2	1.85	0.58
1:C:7:GLY:HA2	1:C:106:VAL:O	2.05	0.57
1:F:99:PRO:HD2	1:F:102:ARG:HB2	1.86	0.57
1:K:65:ILE:HD11	1:K:67:MET:HE3	1.85	0.57
1:C:10:THR:HG22	1:C:87:VAL:HG22	1.87	0.57
2:V:68:LYS:HD3	2:X:91:ASN:HA	1.86	0.57
2:S:86:PRO:HD3	2:U:88:ALA:HB2	1.87	0.57
1:B:99:PRO:HD2	1:B:102:ARG:HB2	1.87	0.56
2:N:102:THR:HG22	2:N:103:GLY:H	1.70	0.56
1:D:99:PRO:HD2	1:D:102:ARG:HB2	1.87	0.56
2:V:88:ALA:HB2	2:W:86:PRO:HD3	1.87	0.56
1:A:10:THR:HG22	1:A:87:VAL:HG22	1.88	0.56
1:H:10:THR:HG22	1:H:87:VAL:HG22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:47:PHE:CD1	1:K:90:VAL:HG22	2.42	0.55
1:J:7:GLY:HA2	1:J:106:VAL:O	2.06	0.55
1:C:99:PRO:HD2	1:C:102:ARG:HB2	1.87	0.55
1:E:65:ILE:HD11	1:E:67:MET:HE3	1.89	0.55
1:K:47:PHE:HD1	1:K:90:VAL:HG22	1.70	0.55
1:K:99:PRO:HD2	1:K:102:ARG:HB2	1.87	0.55
1:C:69:ARG:NH2	1:E:103:VAL:O	2.40	0.55
1:F:10:THR:HG22	1:F:87:VAL:HG22	1.89	0.55
1:E:10:THR:HG22	1:E:87:VAL:HG22	1.88	0.55
2:V:91:ASN:HA	2:W:68:LYS:HD3	1.88	0.55
1:C:65:ILE:HD11	1:C:67:MET:HE3	1.89	0.55
1:F:65:ILE:HD11	1:F:67:MET:HE3	1.87	0.55
1:F:108:LEU:O	1:F:111:ALA:HB3	2.07	0.55
1:A:54:THR:O	1:B:80:VAL:HA	2.08	0.54
1:B:7:GLY:HA2	1:B:106:VAL:O	2.07	0.54
2:U:35:PRO:HA	2:U:53:LEU:HG	1.90	0.54
1:E:54:THR:O	1:F:80:VAL:HA	2.08	0.54
2:P:59:THR:HG21	2:P:67:LEU:HD13	1.88	0.54
1:B:10:THR:HG22	1:B:87:VAL:HG22	1.89	0.54
2:Q:91:ASN:HA	2:R:68:LYS:HD3	1.90	0.54
1:J:10:THR:HG22	1:J:87:VAL:HG22	1.89	0.54
1:E:99:PRO:HD2	1:E:102:ARG:HB2	1.89	0.53
1:K:10:THR:HG22	1:K:87:VAL:HG22	1.88	0.53
1:G:108:LEU:O	1:G:111:ALA:HB3	2.08	0.53
2:S:66:LYS:H	2:S:66:LYS:HD2	1.73	0.53
2:T:26:ARG:HB3	2:T:103:GLY:H	1.73	0.53
2:T:66:LYS:H	2:T:66:LYS:HD2	1.73	0.53
1:B:108:LEU:O	1:B:111:ALA:HB3	2.08	0.53
1:H:108:LEU:O	1:H:111:ALA:HB3	2.09	0.52
2:T:91:ASN:HA	2:U:68:LYS:HD3	1.90	0.52
1:L:10:THR:HG22	1:L:87:VAL:HG22	1.90	0.52
1:C:103:VAL:O	1:F:69:ARG:NH2	2.43	0.52
1:D:9:ILE:HG13	1:D:108:LEU:HB2	1.90	0.52
1:E:23:THR:HG22	1:E:88:ILE:HD13	1.92	0.52
1:C:108:LEU:O	1:C:111:ALA:HB3	2.10	0.52
1:D:10:THR:HG22	1:D:87:VAL:HG22	1.91	0.52
1:L:30:MET:HA	1:L:106:VAL:CG2	2.39	0.52
1:D:99:PRO:HG2	1:D:102:ARG:HE	1.74	0.52
1:J:108:LEU:O	1:J:111:ALA:HB3	2.10	0.52
2:R:66:LYS:H	2:R:66:LYS:HD2	1.73	0.52
2:M:66:LYS:H	2:M:66:LYS:HD2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:66:LYS:H	2:U:66:LYS:HD2	1.74	0.51
2:W:66:LYS:H	2:W:66:LYS:HD2	1.75	0.51
2:P:86:PRO:HD3	2:R:88:ALA:HB2	1.92	0.51
2:Q:66:LYS:H	2:Q:66:LYS:HD2	1.76	0.51
2:S:21:ALA:O	2:S:25:GLU:HB2	2.11	0.51
1:E:7:GLY:HA2	1:E:106:VAL:O	2.11	0.51
1:G:10:THR:HG22	1:G:87:VAL:HG22	1.92	0.51
1:I:108:LEU:O	1:I:111:ALA:HB3	2.11	0.51
2:P:91:ASN:HA	2:Q:68:LYS:HD3	1.91	0.51
1:C:80:VAL:HA	1:F:54:THR:O	2.11	0.51
1:L:108:LEU:O	1:L:111:ALA:HB3	2.09	0.51
2:P:47:VAL:HG22	2:R:23:VAL:HG12	1.93	0.51
2:Q:88:ALA:HB2	2:R:86:PRO:HD3	1.93	0.51
2:N:91:ASN:HA	2:O:68:LYS:HD3	1.92	0.51
2:M:47:VAL:HG22	2:O:23:VAL:HG12	1.92	0.51
1:B:51:GLU:HG3	1:B:79:PRO:HB3	1.93	0.51
1:D:30:MET:HA	1:D:106:VAL:HG21	1.91	0.51
1:K:108:LEU:O	1:K:111:ALA:HB3	2.11	0.50
2:M:68:LYS:HD3	2:O:91:ASN:HA	1.93	0.50
1:D:106:VAL:HG12	1:D:108:LEU:CD2	2.38	0.50
2:P:66:LYS:H	2:P:66:LYS:HD2	1.77	0.50
2:V:66:LYS:H	2:V:66:LYS:HD2	1.74	0.50
2:N:66:LYS:H	2:N:66:LYS:HD2	1.75	0.50
1:D:108:LEU:O	1:D:111:ALA:HB3	2.11	0.50
2:O:66:LYS:H	2:O:66:LYS:HD2	1.75	0.50
2:X:9:VAL:HG21	2:X:15:ALA:HB2	1.93	0.50
1:G:65:ILE:HD11	1:G:67:MET:HE3	1.92	0.50
1:I:7:GLY:HA2	1:I:106:VAL:O	2.12	0.49
2:Q:6:LEU:HD23	2:Q:56:LEU:HD23	1.94	0.49
1:H:7:GLY:HA2	1:H:106:VAL:O	2.12	0.49
1:A:7:GLY:HA2	1:A:106:VAL:O	2.11	0.49
2:O:6:LEU:HD23	2:O:56:LEU:HD23	1.93	0.49
2:V:6:LEU:HD23	2:V:56:LEU:HD23	1.95	0.49
2:R:32:ASN:HB2	2:R:56:LEU:HB2	1.95	0.49
1:I:64:LEU:HD22	2:O:17:LYS:HB2	1.95	0.49
2:V:23:VAL:HG12	2:W:47:VAL:HG22	1.94	0.48
1:C:23:THR:HG21	1:C:58:PRO:HB3	1.96	0.48
1:K:54:THR:O	1:L:80:VAL:HA	2.13	0.48
2:O:2:GLU:H	2:O:2:GLU:CD	2.20	0.48
2:W:32:ASN:HB2	2:W:56:LEU:HB2	1.95	0.48
2:M:23:VAL:HG12	2:N:47:VAL:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:THR:O	1:D:80:VAL:HA	2.13	0.48
2:N:6:LEU:HD23	2:N:56:LEU:HD23	1.95	0.48
2:O:1:MET:HG2	2:O:60:THR:HB	1.96	0.48
1:D:65:ILE:HD11	1:D:67:MET:HE3	1.96	0.48
1:E:99:PRO:HG2	1:E:102:ARG:HE	1.79	0.48
1:F:99:PRO:HG2	1:F:102:ARG:HE	1.78	0.48
1:H:23:THR:HG22	1:H:88:ILE:HD13	1.95	0.48
1:F:23:THR:HG21	1:F:58:PRO:HB3	1.94	0.48
1:K:99:PRO:HG2	1:K:102:ARG:HE	1.79	0.48
2:O:32:ASN:HB2	2:O:56:LEU:HB2	1.96	0.48
2:Q:99:ARG:HE	2:Q:99:ARG:HB2	1.42	0.47
2:R:6:LEU:HD23	2:R:56:LEU:HD23	1.96	0.47
2:T:88:ALA:HB2	2:U:86:PRO:HD3	1.96	0.47
1:J:24:ILE:HG13	1:J:61:ALA:HB1	1.94	0.47
2:N:32:ASN:HB2	2:N:56:LEU:HB2	1.95	0.47
2:Q:91:ASN:HB2	2:R:82:ILE:HB	1.96	0.47
1:G:7:GLY:HA2	1:G:106:VAL:O	2.14	0.47
2:S:32:ASN:HB2	2:S:56:LEU:HB2	1.95	0.47
1:C:64:LEU:HD22	2:N:17:LYS:HB2	1.96	0.47
1:F:115:ARG:HE	1:F:117:ASP:CG	2.22	0.47
2:S:6:LEU:HD23	2:S:56:LEU:HD23	1.97	0.47
2:S:47:VAL:HG22	2:U:23:VAL:HG12	1.97	0.47
1:C:115:ARG:HE	1:C:117:ASP:CG	2.23	0.47
1:G:23:THR:HG22	1:G:88:ILE:HG21	1.96	0.47
1:H:115:ARG:HE	1:H:117:ASP:CG	2.22	0.47
1:L:115:ARG:HE	1:L:117:ASP:CG	2.22	0.47
2:N:23:VAL:HG12	2:O:47:VAL:HG22	1.97	0.47
2:R:31:VAL:HG22	2:R:57:VAL:HG13	1.96	0.47
2:Q:21:ALA:O	2:Q:25:GLU:HB2	2.15	0.47
1:B:39:TYR:CE1	1:B:67:MET:HE2	2.50	0.47
2:T:32:ASN:HB2	2:T:56:LEU:HB2	1.96	0.47
1:C:51:GLU:HG3	1:C:79:PRO:HB3	1.97	0.46
1:F:39:TYR:CE1	1:F:67:MET:HE2	2.50	0.46
1:L:6:ARG:O	1:L:105:HIS:HB3	2.14	0.46
2:X:6:LEU:HD23	2:X:56:LEU:HD23	1.97	0.46
1:D:24:ILE:HG13	1:D:61:ALA:HB1	1.97	0.46
2:P:68:LYS:HD3	2:R:91:ASN:HA	1.97	0.46
2:W:6:LEU:HD23	2:W:56:LEU:HD23	1.98	0.46
1:B:23:THR:HG21	1:B:58:PRO:HB3	1.97	0.46
1:J:39:TYR:CE1	1:J:67:MET:HE2	2.51	0.46
2:U:9:VAL:HG21	2:U:15:ALA:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:115:ARG:HE	1:J:117:ASP:CG	2.23	0.46
2:R:91:ASN:O	2:R:94:TYR:HB3	2.16	0.46
1:K:23:THR:HG22	1:K:88:ILE:HD13	1.97	0.45
1:L:64:LEU:HD22	2:M:17:LYS:HB2	1.98	0.45
1:E:64:LEU:HD22	2:V:17:LYS:HB2	1.98	0.45
1:L:7:GLY:HA2	1:L:106:VAL:O	2.16	0.45
2:M:6:LEU:HD23	2:M:56:LEU:HD23	1.98	0.45
1:B:31:LEU:HD22	1:B:36:ILE:HG21	1.97	0.45
1:K:115:ARG:HE	1:K:117:ASP:CG	2.24	0.45
2:N:7:ILE:HA	2:N:81:GLU:O	2.17	0.45
2:P:32:ASN:HB2	2:P:56:LEU:HB2	1.98	0.45
2:T:6:LEU:HD23	2:T:56:LEU:HD23	1.97	0.45
1:J:23:THR:HG22	1:J:88:ILE:HD13	1.99	0.45
2:X:65:PRO:HB2	2:X:66:LYS:HE3	1.98	0.45
1:A:23:THR:HG22	1:A:88:ILE:HD13	1.98	0.45
1:A:23:THR:HG21	1:A:58:PRO:HB3	1.97	0.45
2:Q:32:ASN:HB2	2:Q:56:LEU:HB2	1.98	0.45
1:B:23:THR:HG22	1:B:88:ILE:HD13	1.98	0.45
1:K:51:GLU:HG3	1:K:79:PRO:HB3	1.99	0.45
2:P:1:MET:SD	2:P:60:THR:HB	2.57	0.45
1:L:23:THR:HG21	1:L:58:PRO:HB3	1.99	0.44
1:F:7:GLY:HA2	1:F:106:VAL:O	2.17	0.44
2:O:7:ILE:HA	2:O:81:GLU:O	2.18	0.44
2:S:82:ILE:HB	2:U:91:ASN:HB2	2.00	0.44
2:V:42:ARG:NH2	2:X:24:GLU:HA	2.33	0.44
1:E:64:LEU:HD11	2:V:13:LEU:HD23	2.00	0.44
1:F:64:LEU:HD22	2:Q:17:LYS:HB2	1.99	0.44
1:J:115:ARG:HD2	1:J:115:ARG:HA	1.91	0.44
1:H:64:LEU:HD22	2:T:17:LYS:HB2	2.00	0.44
2:T:7:ILE:HA	2:T:81:GLU:O	2.18	0.44
2:Q:2:GLU:HA	2:Q:60:THR:HG22	2.00	0.44
1:D:61:ALA:HA	1:D:64:LEU:HD12	1.99	0.44
1:H:115:ARG:HD2	1:H:115:ARG:HA	1.89	0.44
2:Q:36:GLY:HA2	2:Q:51:HIS:HE1	1.82	0.44
1:I:115:ARG:HE	1:I:117:ASP:CG	2.24	0.44
1:G:23:THR:HG21	1:G:58:PRO:HB3	2.00	0.43
2:U:32:ASN:HB2	2:U:56:LEU:HB2	1.99	0.43
2:V:32:ASN:HB2	2:V:56:LEU:HB2	1.99	0.43
1:A:115:ARG:HE	1:A:117:ASP:CG	2.26	0.43
2:P:6:LEU:HD23	2:P:56:LEU:HD23	2.00	0.43
1:B:28:LEU:HD21	1:B:65:ILE:CD1	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ILE:HG13	1:A:61:ALA:HB1	2.01	0.43
1:C:54:THR:O	1:E:80:VAL:HA	2.19	0.43
1:E:115:ARG:HD2	1:E:115:ARG:HA	1.88	0.43
1:F:23:THR:HG22	1:F:88:ILE:HG21	2.00	0.43
1:I:23:THR:HG22	1:I:88:ILE:HD13	1.99	0.43
2:V:93:GLU:H	2:V:93:GLU:HG3	1.64	0.43
1:G:51:GLU:HG3	1:G:79:PRO:HB3	2.00	0.43
2:X:32:ASN:HB2	2:X:56:LEU:HB2	2.00	0.43
1:B:23:THR:HG22	1:B:88:ILE:HG21	2.01	0.43
1:C:39:TYR:CE1	1:C:67:MET:HE2	2.53	0.43
1:G:99:PRO:HG2	1:G:102:ARG:HE	1.84	0.43
1:J:101:ASP:HA	1:L:69:ARG:HD3	2.00	0.43
1:G:115:ARG:HE	1:G:117:ASP:CG	2.26	0.43
1:C:115:ARG:HD2	1:C:115:ARG:HA	1.93	0.43
1:E:39:TYR:CE1	1:E:67:MET:HE2	2.54	0.43
1:J:80:VAL:HA	1:L:54:THR:O	2.19	0.43
2:S:36:GLY:HA2	2:S:51:HIS:HE1	1.84	0.43
1:B:69:ARG:NH2	1:D:103:VAL:O	2.52	0.43
1:I:51:GLU:HG3	1:I:79:PRO:HB3	2.01	0.43
2:V:91:ASN:HB2	2:W:82:ILE:HB	2.01	0.43
2:X:7:ILE:HA	2:X:81:GLU:O	2.19	0.43
2:R:92:ARG:H	2:R:92:ARG:HG2	1.25	0.42
2:U:6:LEU:HD23	2:U:56:LEU:HD23	2.01	0.42
1:B:115:ARG:HE	1:B:117:ASP:CG	2.26	0.42
1:C:23:THR:HG22	1:C:88:ILE:HD13	2.00	0.42
1:D:51:GLU:HG3	1:D:79:PRO:HB3	2.01	0.42
2:M:7:ILE:HA	2:M:81:GLU:O	2.19	0.42
2:S:67:LEU:O	2:S:71:VAL:HG23	2.20	0.42
2:V:7:ILE:HA	2:V:81:GLU:O	2.18	0.42
1:A:23:THR:HG22	1:A:88:ILE:HG21	2.00	0.42
1:C:115:ARG:HH22	1:F:68:HIS:HB3	1.83	0.42
2:M:93:GLU:H	2:M:93:GLU:HG3	1.64	0.42
2:Q:7:ILE:HA	2:Q:81:GLU:O	2.19	0.42
2:R:2:GLU:OE1	2:R:99:ARG:NH1	2.52	0.42
2:S:24:GLU:C	2:S:26:ARG:H	2.27	0.42
2:U:7:ILE:HA	2:U:81:GLU:O	2.18	0.42
1:H:54:THR:O	1:I:80:VAL:HA	2.20	0.42
2:W:32:ASN:HB3	2:X:37:LEU:HD23	2.01	0.42
1:A:51:GLU:HG3	1:A:79:PRO:HB3	2.01	0.42
1:G:23:THR:OG1	1:G:61:ALA:HB3	2.20	0.42
1:L:23:THR:HG22	1:L:88:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:91:ASN:HB2	2:N:82:ILE:HB	2.01	0.42
1:C:81:PRO:HD3	1:F:54:THR:O	2.19	0.42
1:E:51:GLU:HG3	1:E:79:PRO:HB3	2.01	0.42
1:J:51:GLU:HG3	1:J:79:PRO:HB3	2.02	0.42
1:K:23:THR:HG22	1:K:88:ILE:HG21	2.00	0.42
2:T:67:LEU:O	2:T:71:VAL:HG23	2.19	0.42
1:K:23:THR:HG21	1:K:58:PRO:HB3	2.01	0.42
2:X:35:PRO:HA	2:X:53:LEU:HG	2.02	0.42
1:L:39:TYR:CE1	1:L:67:MET:HE2	2.54	0.42
2:T:93:GLU:H	2:T:93:GLU:HG3	1.63	0.42
1:F:51:GLU:HG3	1:F:79:PRO:HB3	2.02	0.42
2:V:64:PHE:CE2	2:V:68:LYS:HG3	2.54	0.42
1:A:63:ARG:HD3	1:B:115:ARG:NH1	2.35	0.42
2:V:32:ASN:OD1	2:V:58:LYS:NZ	2.38	0.42
1:D:115:ARG:HE	1:D:117:ASP:CG	2.27	0.41
2:M:93:GLU:HB2	2:N:79:VAL:HG13	2.02	0.41
2:R:7:ILE:HA	2:R:81:GLU:O	2.20	0.41
2:S:7:ILE:HA	2:S:81:GLU:O	2.20	0.41
1:H:39:TYR:CE1	1:H:67:MET:HE2	2.55	0.41
2:W:7:ILE:HA	2:W:81:GLU:O	2.20	0.41
1:E:37:GLN:H	1:E:37:GLN:HE21	1.68	0.41
2:P:7:ILE:HA	2:P:81:GLU:O	2.20	0.41
2:X:6:LEU:HD11	2:X:85:LEU:HD11	2.02	0.41
1:E:115:ARG:HE	1:E:117:ASP:CG	2.26	0.41
2:N:93:GLU:H	2:N:93:GLU:HG3	1.67	0.41
1:A:24:ILE:HG23	1:A:65:ILE:HG21	2.03	0.41
2:P:68:LYS:NZ	2:R:92:ARG:HE	2.18	0.41
2:T:6:LEU:HD11	2:T:85:LEU:HD11	2.03	0.41
2:V:87:ILE:HG21	2:V:95:LEU:HD21	2.03	0.41
1:H:23:THR:HG21	1:H:58:PRO:HB3	2.03	0.41
2:S:9:VAL:HG21	2:S:15:ALA:HB2	2.03	0.41
1:G:80:VAL:HA	1:I:54:THR:O	2.21	0.41
1:L:23:THR:HG22	1:L:88:ILE:HG21	2.02	0.41
2:X:64:PHE:CE2	2:X:68:LYS:HG3	2.55	0.41
1:F:23:THR:HG22	1:F:88:ILE:HD13	2.02	0.41
2:T:91:ASN:HB2	2:U:82:ILE:HB	2.02	0.41
2:M:91:ASN:HA	2:N:68:LYS:HD3	2.02	0.40
2:V:5:VAL:HB	2:V:57:VAL:HB	2.03	0.40
2:M:47:VAL:HG21	2:O:24:GLU:HA	2.04	0.40
2:T:23:VAL:HG12	2:U:47:VAL:HG22	2.03	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	119/130 (92%)	114 (96%)	5 (4%)	0	100	100
1	B	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	C	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	D	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	E	119/130 (92%)	115 (97%)	4 (3%)	0	100	100
1	F	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	G	119/130 (92%)	115 (97%)	4 (3%)	0	100	100
1	H	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	I	119/130 (92%)	112 (94%)	6 (5%)	1 (1%)	16	44
1	J	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	K	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
1	L	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
2	M	101/111 (91%)	100 (99%)	1 (1%)	0	100	100
2	N	101/111 (91%)	96 (95%)	5 (5%)	0	100	100
2	O	101/111 (91%)	101 (100%)	0	0	100	100
2	P	101/111 (91%)	101 (100%)	0	0	100	100
2	Q	107/111 (96%)	104 (97%)	3 (3%)	0	100	100
2	R	101/111 (91%)	100 (99%)	1 (1%)	0	100	100
2	S	101/111 (91%)	98 (97%)	1 (1%)	2 (2%)	6	25
2	T	101/111 (91%)	97 (96%)	4 (4%)	0	100	100
2	U	101/111 (91%)	99 (98%)	2 (2%)	0	100	100
2	V	101/111 (91%)	96 (95%)	5 (5%)	0	100	100
2	W	101/111 (91%)	99 (98%)	2 (2%)	0	100	100
2	X	101/111 (91%)	100 (99%)	1 (1%)	0	100	100
All	All	2646/2892 (92%)	2551 (96%)	92 (4%)	3 (0%)	48	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	37	GLN
2	S	26	ARG
2	S	25	GLU

5.3.2 Protein sidechains [i](#)

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	98/109 (90%)	96 (98%)	2 (2%)	48	65
1	B	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	C	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	D	98/109 (90%)	96 (98%)	2 (2%)	48	65
1	E	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	F	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	G	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	H	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	I	97/109 (89%)	94 (97%)	3 (3%)	35	59
1	J	98/109 (90%)	94 (96%)	4 (4%)	27	52
1	K	98/109 (90%)	95 (97%)	3 (3%)	35	59
1	L	98/109 (90%)	94 (96%)	4 (4%)	27	52
2	M	90/98 (92%)	86 (96%)	4 (4%)	25	51
2	N	90/98 (92%)	85 (94%)	5 (6%)	19	46
2	O	90/98 (92%)	85 (94%)	5 (6%)	19	46
2	P	90/98 (92%)	86 (96%)	4 (4%)	25	51
2	Q	95/98 (97%)	84 (88%)	11 (12%)	5	20
2	R	90/98 (92%)	86 (96%)	4 (4%)	25	51
2	S	90/98 (92%)	84 (93%)	6 (7%)	15	41
2	T	90/98 (92%)	86 (96%)	4 (4%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	90/98 (92%)	86 (96%)	4 (4%)	25	51
2	V	90/98 (92%)	86 (96%)	4 (4%)	25	51
2	W	90/98 (92%)	87 (97%)	3 (3%)	33	57
2	X	90/98 (92%)	84 (93%)	6 (7%)	15	41
All	All	2260/2484 (91%)	2164 (96%)	96 (4%)	26	52

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	THR
1	A	37	GLN
1	B	23	THR
1	B	37	GLN
1	B	101	ASP
1	C	23	THR
1	C	37	GLN
1	C	101	ASP
1	D	23	THR
1	D	101	ASP
1	E	23	THR
1	E	37	GLN
1	E	101	ASP
1	F	23	THR
1	F	37	GLN
1	F	101	ASP
1	G	23	THR
1	G	37	GLN
1	G	101	ASP
1	H	23	THR
1	H	37	GLN
1	H	101	ASP
1	I	23	THR
1	I	70	VAL
1	I	101	ASP
1	J	23	THR
1	J	37	GLN
1	J	101	ASP
1	J	102	ARG
1	K	23	THR
1	K	37	GLN
1	K	101	ASP

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Mol	Chain	Res	Type
1	L	23	THR
1	L	37	GLN
1	L	69	ARG
1	L	101	ASP
2	M	13	LEU
2	M	50	ASP
2	M	68	LYS
2	M	70	ARG
2	N	13	LEU
2	N	68	LYS
2	N	70	ARG
2	N	93	GLU
2	N	98	LEU
2	O	13	LEU
2	O	61	THR
2	O	68	LYS
2	O	70	ARG
2	O	102	THR
2	P	13	LEU
2	P	61	THR
2	P	68	LYS
2	P	70	ARG
2	Q	3	GLU
2	Q	13	LEU
2	Q	25	GLU
2	Q	57	VAL
2	Q	61	THR
2	Q	62	ASP
2	Q	68	LYS
2	Q	70	ARG
2	Q	92	ARG
2	Q	93	GLU
2	Q	99	ARG
2	R	13	LEU
2	R	39	SER
2	R	68	LYS
2	R	70	ARG
2	S	13	LEU
2	S	17	LYS
2	S	25	GLU
2	S	68	LYS
2	S	70	ARG

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Mol	Chain	Res	Type
2	S	93	GLU
2	T	13	LEU
2	T	68	LYS
2	T	70	ARG
2	T	102	THR
2	U	13	LEU
2	U	52	GLU
2	U	68	LYS
2	U	70	ARG
2	V	43	GLU
2	V	46	SER
2	V	68	LYS
2	V	70	ARG
2	W	13	LEU
2	W	68	LYS
2	W	70	ARG
2	X	13	LEU
2	X	37	LEU
2	X	66	LYS
2	X	68	LYS
2	X	70	ARG
2	X	93	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	E	37	GLN
1	F	37	GLN
1	F	100	GLN
1	G	37	GLN
1	H	37	GLN
1	I	100	GLN
1	J	100	GLN
1	K	37	GLN
1	L	37	GLN
2	M	91	ASN
2	N	91	ASN
2	O	20	HIS
2	O	51	HIS
2	O	91	ASN
2	P	51	HIS

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Mol	Chain	Res	Type
2	P	91	ASN
2	Q	20	HIS
2	Q	51	HIS
2	Q	91	ASN
2	Q	107	HIS
2	R	20	HIS
2	R	51	HIS
2	R	91	ASN
2	S	51	HIS
2	S	91	ASN
2	T	51	HIS
2	U	91	ASN
2	V	20	HIS
2	V	51	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	117/130 (90%)	-0.12	1 (0%) 81 68	40, 62, 85, 126	12 (10%)
1	B	117/130 (90%)	-0.02	4 (3%) 48 35	39, 62, 80, 147	12 (10%)
1	C	117/130 (90%)	0.01	2 (1%) 69 54	45, 71, 100, 139	12 (10%)
1	D	117/130 (90%)	-0.10	3 (2%) 57 42	39, 60, 86, 125	12 (10%)
1	E	117/130 (90%)	-0.10	4 (3%) 48 35	37, 66, 90, 142	12 (10%)
1	F	117/130 (90%)	-0.01	1 (0%) 81 68	37, 67, 91, 119	12 (10%)
1	G	117/130 (90%)	-0.23	2 (1%) 69 54	34, 65, 87, 124	12 (10%)
1	H	117/130 (90%)	-0.10	2 (1%) 69 54	35, 62, 89, 124	12 (10%)
1	I	117/130 (90%)	-0.09	3 (2%) 57 42	35, 64, 86, 113	12 (10%)
1	J	117/130 (90%)	-0.09	1 (0%) 81 68	39, 64, 87, 141	12 (10%)
1	K	117/130 (90%)	-0.21	0 100 100	37, 63, 88, 111	12 (10%)
1	L	117/130 (90%)	-0.03	3 (2%) 57 42	37, 67, 91, 137	12 (10%)
2	M	103/111 (92%)	-0.20	1 (0%) 79 66	56, 80, 108, 120	0
2	N	103/111 (92%)	-0.15	1 (0%) 79 66	57, 82, 110, 135	0
2	O	103/111 (92%)	-0.23	0 100 100	58, 77, 109, 138	0
2	P	103/111 (92%)	-0.28	1 (0%) 79 66	48, 67, 96, 122	0
2	Q	109/111 (98%)	-0.20	0 100 100	51, 71, 98, 114	0
2	R	103/111 (92%)	-0.27	0 100 100	51, 67, 91, 114	0
2	S	103/111 (92%)	-0.33	2 (1%) 66 51	45, 67, 100, 119	0
2	T	103/111 (92%)	-0.18	1 (0%) 79 66	54, 70, 103, 124	0
2	U	103/111 (92%)	-0.29	0 100 100	52, 72, 98, 115	0
2	V	103/111 (92%)	-0.25	1 (0%) 79 66	48, 70, 105, 117	0
2	W	103/111 (92%)	-0.22	1 (0%) 79 66	52, 71, 99, 117	0
2	X	103/111 (92%)	-0.22	1 (0%) 79 66	43, 70, 100, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	2646/2892 (91%)	-0.16	35 (1%) 75 61	34, 68, 102, 147	144 (5%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	T	103	GLY	4.3
2	S	103	GLY	3.7
2	P	103	GLY	3.5
2	X	103	GLY	3.4
1	H	76	ARG	3.2
1	E	76	ARG	2.7
1	C	97	ASP	2.7
2	M	103	GLY	2.7
2	N	103	GLY	2.5
1	C	76	ARG	2.5
1	A	1	MET	2.5
1	B	117	ASP	2.5
2	V	103	GLY	2.4
1	E	51	GLU	2.4
1	G	1	MET	2.4
1	F	76	ARG	2.3
1	G	12	GLU	2.3
1	L	93	LEU	2.3
1	L	12	GLU	2.2
1	D	43	ALA	2.2
1	J	73	LEU	2.2
1	L	76	ARG	2.2
2	S	88	ALA	2.2
1	I	51	GLU	2.1
1	B	12	GLU	2.1
1	E	12	GLU	2.1
1	I	47	PHE	2.1
1	I	76	ARG	2.1
2	W	103	GLY	2.1
1	B	97	ASP	2.1
1	D	117	ASP	2.1
1	H	12	GLU	2.1
1	B	93	LEU	2.0
1	E	1	MET	2.0
1	D	51	GLU	2.0

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.