



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:19 PM GMT

PDB ID : 4HW9
Title : Crystal Structure of Helicobacter pylori MscS (Closed State)
Authors : Lai, J.Y.; Poon, Y.S.; Kaiser, J.; Rees, D.C.
Deposited on : 2012-11-07
Resolution : 4.14 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

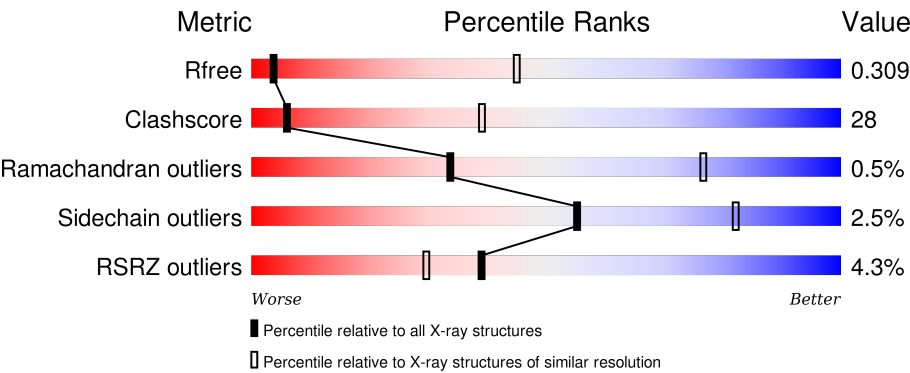
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.14 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}	91344	1023 (4.68-3.60)
Clashscore	102246	1122 (4.68-3.60)
Ramachandran outliers	100387	1068 (4.68-3.60)
Sidechain outliers	100360	1054 (4.68-3.60)
RSRZ outliers	91569	1027 (4.68-3.60)

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. 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	309	
1	B	309	
1	C	309	
1	D	309	
1	E	309	

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Mol	Chain	Length	Quality of chain
1	F	309	
1	G	309	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13797 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 Mechanosensitive channel MscS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	B	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	C	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	D	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	E	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	F	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0
1	G	253	Total 1971	C 1284	N 327	O 354	S 6	0	0	0

There are 266 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
A	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
A	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
A	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
A	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
A	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
A	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
A	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
A	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
A	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
A	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
A	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
A	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
A	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
A	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
A	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
A	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
A	200	THR	ALA	CONFLICT	UNP E8QGV2
A	202	GLU	ASP	CONFLICT	UNP E8QGV2
A	273	PRO	SER	CONFLICT	UNP E8QGV2
A	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
A	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
A	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
A	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
A	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
A	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
A	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
A	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
A	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
A	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
A	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
B	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
B	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
B	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
B	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
B	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
B	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
B	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
B	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
B	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
B	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
B	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
B	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
B	-5	SER	-	EXPRESSION TAG	UNP E8QGV2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
B	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
B	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
B	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
B	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
B	200	THR	ALA	CONFLICT	UNP E8QGV2
B	202	GLU	ASP	CONFLICT	UNP E8QGV2
B	273	PRO	SER	CONFLICT	UNP E8QGV2
B	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
B	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
B	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
B	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
B	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
B	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
B	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
B	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
B	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
B	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
B	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
C	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
C	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
C	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
C	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
C	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
C	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
C	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
C	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
C	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
C	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
C	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
C	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
C	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
C	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
C	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
C	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
C	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
C	200	THR	ALA	CONFLICT	UNP E8QGV2
C	202	GLU	ASP	CONFLICT	UNP E8QGV2
C	273	PRO	SER	CONFLICT	UNP E8QGV2
C	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
C	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
C	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
C	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
C	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
C	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
C	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
C	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
C	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
C	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
C	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
D	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
D	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
D	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
D	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
D	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
D	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
D	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
D	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
D	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
D	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
D	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
D	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
D	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
D	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
D	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
D	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
D	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
D	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
D	200	THR	ALA	CONFLICT	UNP E8QGV2
D	202	GLU	ASP	CONFLICT	UNP E8QGV2
D	273	PRO	SER	CONFLICT	UNP E8QGV2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
D	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
D	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
D	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
D	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
D	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
D	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
D	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
D	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
D	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
D	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
E	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
E	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
E	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
E	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
E	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
E	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
E	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
E	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
E	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
E	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
E	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
E	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
E	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
E	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
E	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
E	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
E	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
E	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
E	200	THR	ALA	CONFLICT	UNP E8QGV2
E	202	GLU	ASP	CONFLICT	UNP E8QGV2
E	273	PRO	SER	CONFLICT	UNP E8QGV2
E	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
E	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
E	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
E	278	ASP	-	EXPRESSION TAG	UNP E8QGV2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
E	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
E	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
E	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
E	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
E	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
E	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
F	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
F	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
F	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
F	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
F	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
F	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
F	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
F	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
F	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
F	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
F	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
F	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
F	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
F	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
F	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
F	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
F	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
F	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
F	200	THR	ALA	CONFLICT	UNP E8QGV2
F	202	GLU	ASP	CONFLICT	UNP E8QGV2
F	273	PRO	SER	CONFLICT	UNP E8QGV2
F	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
F	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
F	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
F	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
F	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
F	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
F	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
F	282	ASP	-	EXPRESSION TAG	UNP E8QGV2

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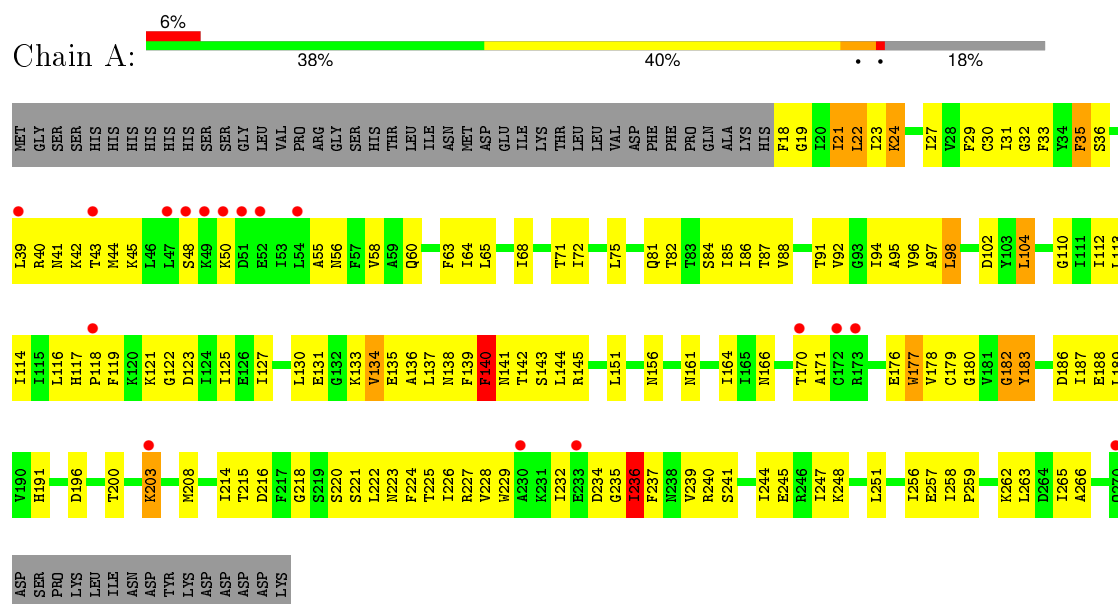
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Chain	Residue	Modelled	Actual	Comment	Reference
F	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
F	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
F	285	LYS	-	EXPRESSION TAG	UNP E8QGV2
G	-23	MET	-	EXPRESSION TAG	UNP E8QGV2
G	-22	GLY	-	EXPRESSION TAG	UNP E8QGV2
G	-21	SER	-	EXPRESSION TAG	UNP E8QGV2
G	-20	SER	-	EXPRESSION TAG	UNP E8QGV2
G	-19	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-18	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-17	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-16	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-15	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-14	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-13	SER	-	EXPRESSION TAG	UNP E8QGV2
G	-12	SER	-	EXPRESSION TAG	UNP E8QGV2
G	-11	GLY	-	EXPRESSION TAG	UNP E8QGV2
G	-10	LEU	-	EXPRESSION TAG	UNP E8QGV2
G	-9	VAL	-	EXPRESSION TAG	UNP E8QGV2
G	-8	PRO	-	EXPRESSION TAG	UNP E8QGV2
G	-7	ARG	-	EXPRESSION TAG	UNP E8QGV2
G	-6	GLY	-	EXPRESSION TAG	UNP E8QGV2
G	-5	SER	-	EXPRESSION TAG	UNP E8QGV2
G	-4	HIS	-	EXPRESSION TAG	UNP E8QGV2
G	-3	THR	-	EXPRESSION TAG	UNP E8QGV2
G	-2	LEU	-	EXPRESSION TAG	UNP E8QGV2
G	-1	ILE	-	EXPRESSION TAG	UNP E8QGV2
G	0	ASN	-	EXPRESSION TAG	UNP E8QGV2
G	200	THR	ALA	CONFLICT	UNP E8QGV2
G	202	GLU	ASP	CONFLICT	UNP E8QGV2
G	273	PRO	SER	CONFLICT	UNP E8QGV2
G	275	LEU	-	EXPRESSION TAG	UNP E8QGV2
G	276	ILE	-	EXPRESSION TAG	UNP E8QGV2
G	277	ASN	-	EXPRESSION TAG	UNP E8QGV2
G	278	ASP	-	EXPRESSION TAG	UNP E8QGV2
G	279	TYR	-	EXPRESSION TAG	UNP E8QGV2
G	280	LYS	-	EXPRESSION TAG	UNP E8QGV2
G	281	ASP	-	EXPRESSION TAG	UNP E8QGV2
G	282	ASP	-	EXPRESSION TAG	UNP E8QGV2
G	283	ASP	-	EXPRESSION TAG	UNP E8QGV2
G	284	ASP	-	EXPRESSION TAG	UNP E8QGV2
G	285	LYS	-	EXPRESSION TAG	UNP E8QGV2

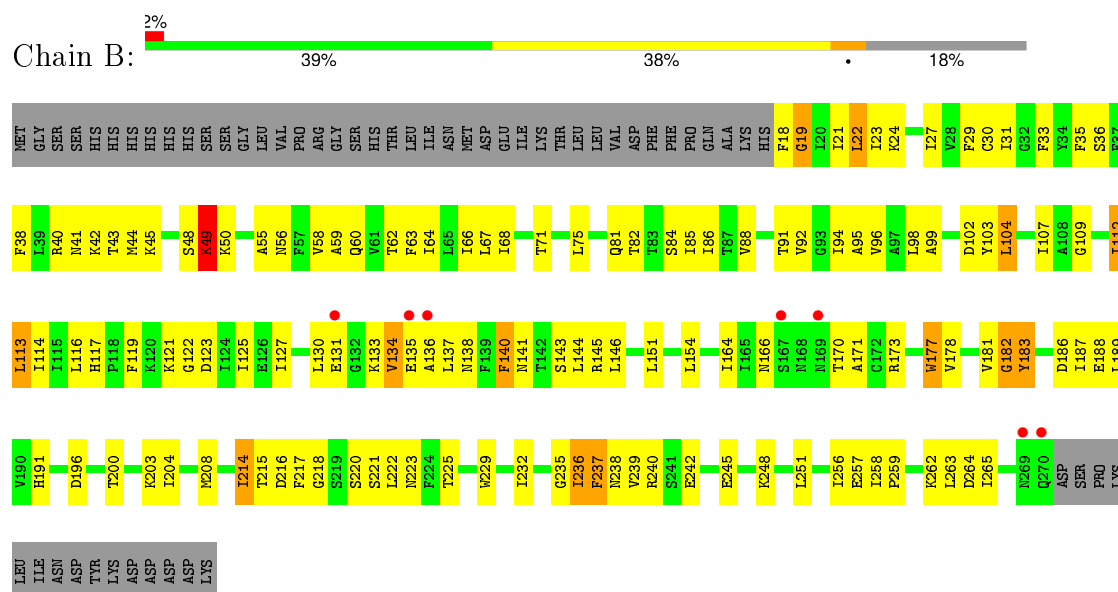
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

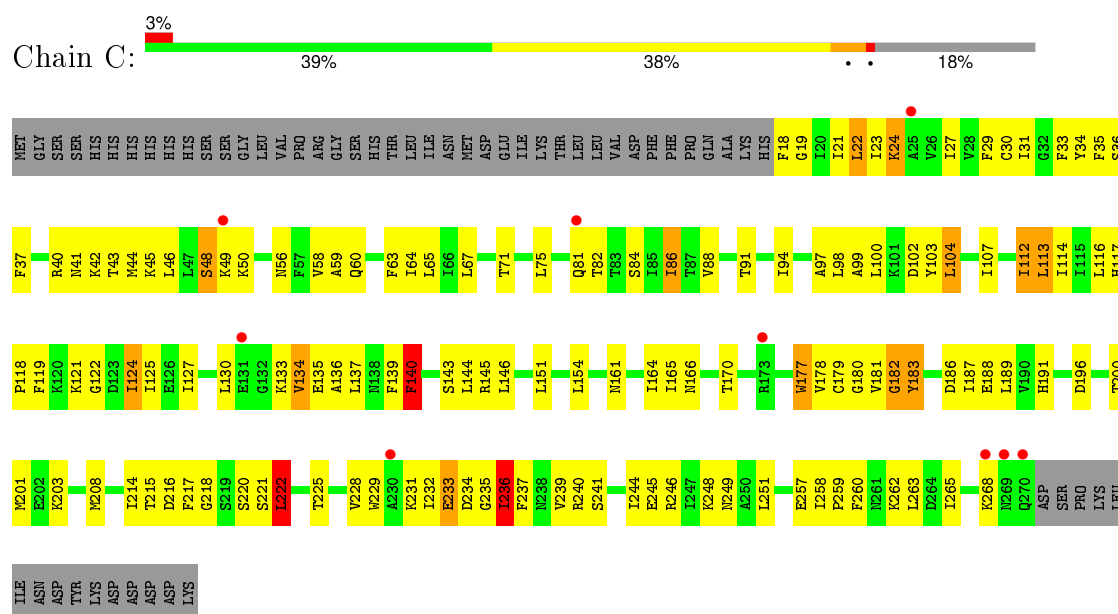
• Molecule 1: Mechanosensitive channel MscS



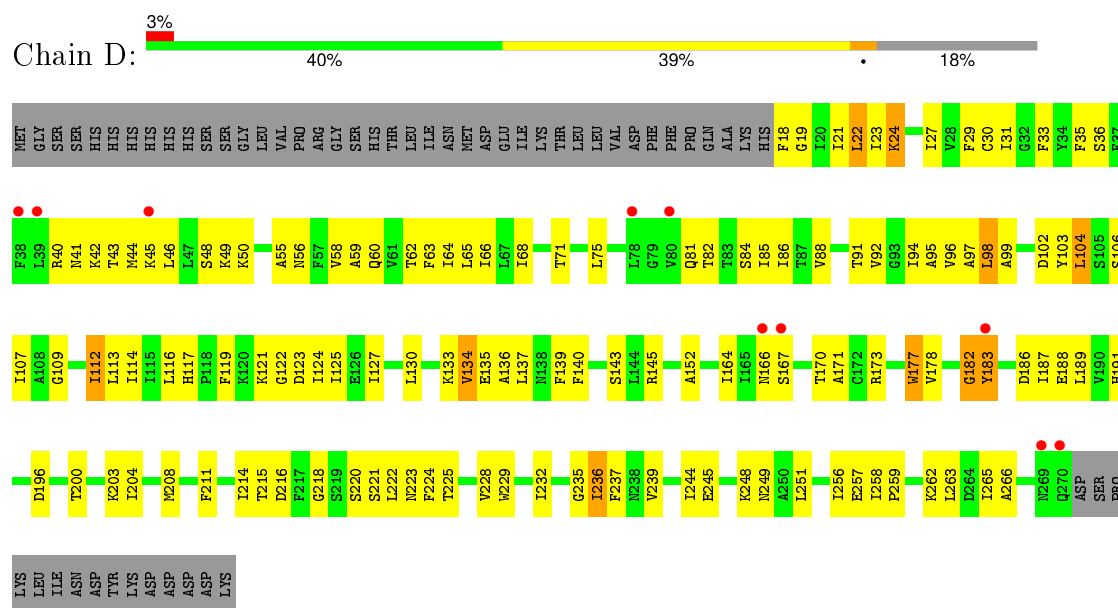
• Molecule 1: Mechanosensitive channel MscS



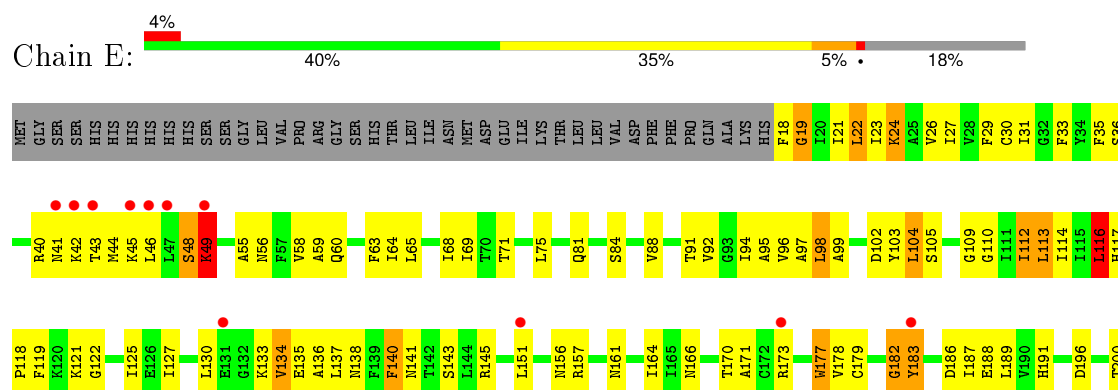
• Molecule 1: Mechanosensitive channel MscS

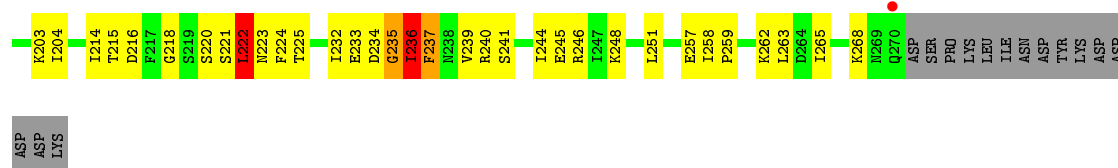


• Molecule 1: Mechanosensitive channel MscS

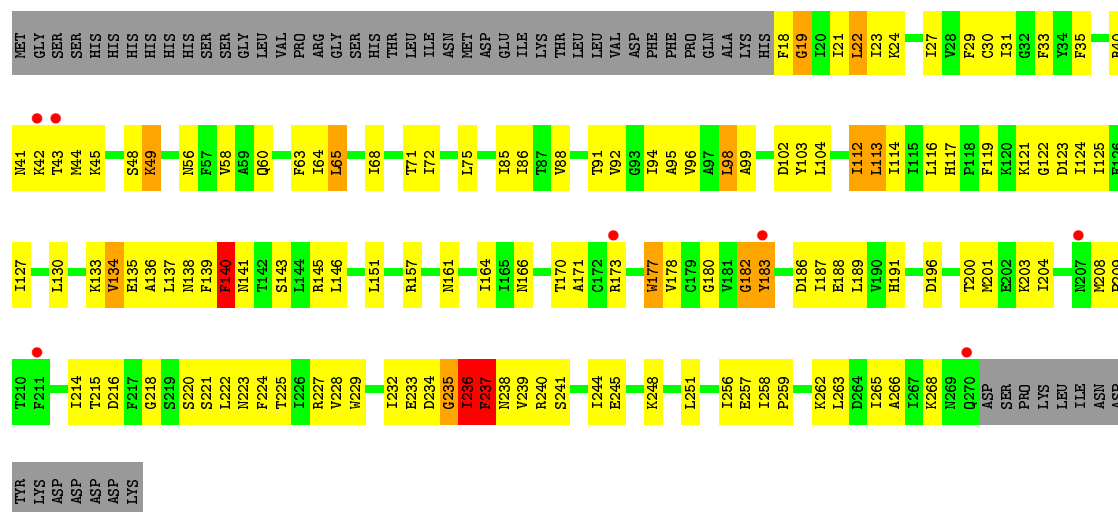


• Molecule 1: Mechanosensitive channel MscS

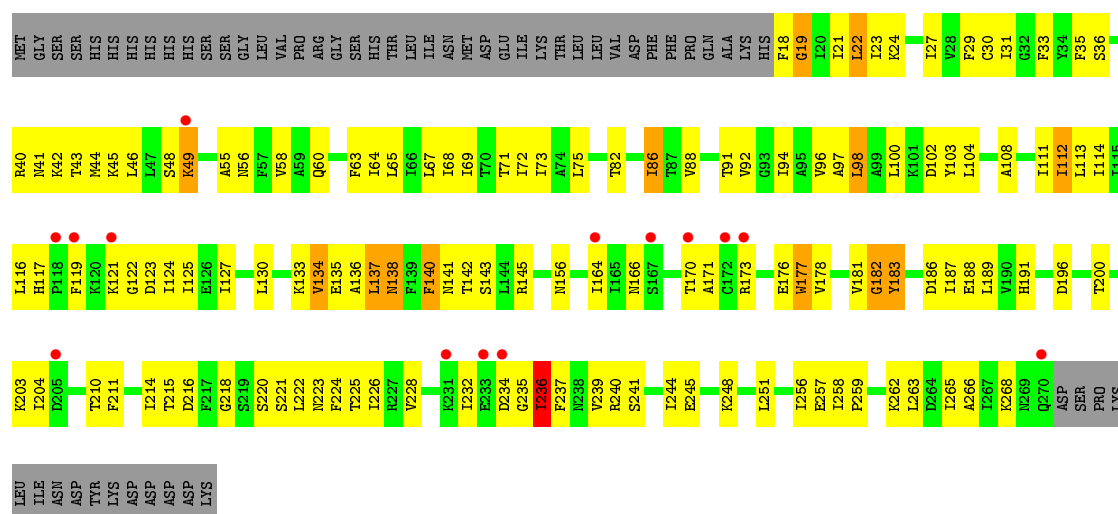




• Molecule 1: Mechanosensitive channel MscS



• Molecule 1: Mechanosensitive channel MscS



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.92Å 143.10Å 178.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.56 – 4.14 46.08 – 4.14	Depositor EDS
% Data completeness (in resolution range)	88.2 (44.56-4.14) 98.6 (46.08-4.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 4.14Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.244 , 0.304 0.250 , 0.309	Depositor DCC
R_{free} test set	1151 reflections (5.12%)	DCC
Wilson B-factor (Å ²)	183.3	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 134.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 22495 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	13797	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.97	3/2001 (0.1%)	1.35	20/2707 (0.7%)
1	B	0.97	1/2001 (0.0%)	1.30	18/2707 (0.7%)
1	C	1.05	6/2001 (0.3%)	1.38	34/2707 (1.3%)
1	D	0.99	1/2001 (0.0%)	1.32	16/2707 (0.6%)
1	E	0.98	3/2001 (0.1%)	1.40	29/2707 (1.1%)
1	F	0.94	2/2001 (0.1%)	1.37	26/2707 (1.0%)
1	G	0.97	2/2001 (0.1%)	1.39	21/2707 (0.8%)
All	All	0.98	18/14007 (0.1%)	1.36	164/18949 (0.9%)

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	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	2
1	G	0	1
All	All	0	7

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	179	CYS	CB-SG	9.23	1.98	1.82
1	C	48	SER	CB-OG	-8.33	1.31	1.42
1	C	177	TRP	CB-CG	-7.89	1.36	1.50
1	D	177	TRP	CB-CG	-7.83	1.36	1.50
1	G	177	TRP	CB-CG	-7.73	1.36	1.50
1	E	177	TRP	CB-CG	-7.33	1.37	1.50
1	C	236	ILE	CA-CB	6.40	1.69	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	236	ILE	CA-CB	6.30	1.69	1.54
1	B	177	TRP	CB-CG	-6.17	1.39	1.50
1	F	236	ILE	CA-CB	6.05	1.68	1.54
1	A	177	TRP	CB-CG	-5.89	1.39	1.50
1	E	236	ILE	C-O	5.86	1.34	1.23
1	C	233	GLU	CB-CG	-5.33	1.42	1.52
1	E	179	CYS	CB-SG	5.20	1.91	1.82
1	A	203	LYS	CG-CD	-5.08	1.35	1.52
1	F	177	TRP	CB-CG	-5.07	1.41	1.50
1	A	179	CYS	CB-SG	5.06	1.90	1.82
1	C	260	PHE	CB-CG	-5.03	1.42	1.51

All (164) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	236	ILE	CG1-CB-CG2	-15.14	78.09	111.40
1	A	21	ILE	CG1-CB-CG2	-15.02	78.36	111.40
1	G	86	ILE	CG1-CB-CG2	-12.79	83.25	111.40
1	G	104	LEU	CB-CG-CD2	-10.93	92.42	111.00
1	C	222	LEU	CA-CB-CG	10.36	139.13	115.30
1	E	222	LEU	CA-CB-CG	9.86	137.99	115.30
1	F	113	LEU	CB-CG-CD2	-9.76	94.42	111.00
1	C	104	LEU	CB-CG-CD2	-9.42	94.99	111.00
1	F	235	GLY	N-CA-C	9.15	135.97	113.10
1	G	49	LYS	CA-CB-CG	9.00	133.21	113.40
1	G	183	TYR	CB-CG-CD1	-9.00	115.60	121.00
1	A	183	TYR	CB-CG-CD1	-8.96	115.63	121.00
1	D	104	LEU	CB-CG-CD2	-8.94	95.81	111.00
1	C	183	TYR	CB-CG-CD1	-8.58	115.85	121.00
1	F	19	GLY	N-CA-C	8.40	134.11	113.10
1	F	183	TYR	CB-CG-CD1	-8.31	116.01	121.00
1	A	182	GLY	N-CA-C	-8.24	92.50	113.10
1	C	113	LEU	CB-CG-CD2	-8.23	97.01	111.00
1	D	183	TYR	CB-CG-CD1	-8.23	116.06	121.00
1	B	113	LEU	CB-CG-CD2	-8.18	97.09	111.00
1	G	19	GLY	N-CA-C	8.14	133.45	113.10
1	D	182	GLY	N-CA-C	-8.14	92.76	113.10
1	A	203	LYS	CD-CE-NZ	-8.10	93.06	111.70
1	E	104	LEU	CB-CG-CD2	-8.10	97.23	111.00
1	F	236	ILE	N-CA-C	-8.07	89.22	111.00
1	C	49	LYS	CA-CB-CG	8.05	131.11	113.40
1	E	183	TYR	CB-CG-CD1	-8.05	116.17	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	182	GLY	N-CA-C	-7.98	93.15	113.10
1	B	183	TYR	CB-CG-CD1	-7.96	116.23	121.00
1	B	19	GLY	N-CA-C	7.92	132.89	113.10
1	E	19	GLY	N-CA-C	7.82	132.65	113.10
1	E	49	LYS	CA-CB-CG	7.77	130.49	113.40
1	D	19	GLY	N-CA-C	7.75	132.47	113.10
1	E	182	GLY	N-CA-C	-7.68	93.89	113.10
1	C	50	LYS	N-CA-C	-7.50	90.74	111.00
1	A	19	GLY	N-CA-C	7.48	131.80	113.10
1	A	104	LEU	CB-CG-CD2	-7.48	98.29	111.00
1	F	130	LEU	CA-CB-CG	7.44	132.41	115.30
1	C	19	GLY	N-CA-C	7.41	131.62	113.10
1	F	104	LEU	CB-CG-CD2	-7.40	98.42	111.00
1	E	116	LEU	CB-CG-CD2	7.39	123.56	111.00
1	B	49	LYS	CA-CB-CG	7.38	129.63	113.40
1	E	177	TRP	CB-CG-CD2	-7.30	117.12	126.60
1	A	22	LEU	CA-CB-CG	7.27	132.01	115.30
1	C	183	TYR	CB-CG-CD2	7.26	125.36	121.00
1	D	130	LEU	CA-CB-CG	7.25	131.98	115.30
1	E	130	LEU	CA-CB-CG	7.24	131.95	115.30
1	G	177	TRP	N-CA-CB	7.24	123.64	110.60
1	B	182	GLY	N-CA-C	-7.24	95.00	113.10
1	B	104	LEU	CB-CG-CD2	-7.24	98.70	111.00
1	F	49	LYS	CA-CB-CG	7.17	129.18	113.40
1	F	183	TYR	CB-CG-CD2	7.16	125.29	121.00
1	G	130	LEU	CA-CB-CG	7.08	131.58	115.30
1	C	182	GLY	N-CA-C	-7.08	95.41	113.10
1	E	177	TRP	N-CA-CB	7.08	123.34	110.60
1	B	177	TRP	N-CA-CB	7.05	123.30	110.60
1	F	177	TRP	N-CA-CB	7.01	123.22	110.60
1	F	182	GLY	N-CA-C	-6.99	95.61	113.10
1	D	183	TYR	CB-CG-CD2	6.98	125.19	121.00
1	C	22	LEU	CA-CB-CG	6.97	131.34	115.30
1	C	86	ILE	CA-CB-CG1	-6.95	97.80	111.00
1	D	177	TRP	N-CA-CB	6.88	122.99	110.60
1	A	98	LEU	CA-CB-CG	-6.88	99.48	115.30
1	F	86	ILE	CA-CB-CG1	-6.88	97.93	111.00
1	F	98	LEU	CA-CB-CG	-6.88	99.47	115.30
1	E	183	TYR	CB-CG-CD2	6.86	125.12	121.00
1	C	177	TRP	N-CA-CB	6.84	122.91	110.60
1	C	222	LEU	CB-CG-CD2	6.83	122.62	111.00
1	E	246	ARG	NE-CZ-NH2	6.81	123.70	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	130	LEU	CA-CB-CG	6.79	130.92	115.30
1	C	177	TRP	CA-CB-CG	6.78	126.59	113.70
1	B	98	LEU	CA-CB-CG	-6.72	99.85	115.30
1	E	177	TRP	CA-CB-CG	6.69	126.41	113.70
1	A	183	TYR	CB-CG-CD2	6.68	125.00	121.00
1	E	233	GLU	CA-CB-CG	6.66	128.06	113.40
1	E	113	LEU	CB-CG-CD2	-6.54	99.89	111.00
1	G	183	TYR	CB-CG-CD2	6.51	124.90	121.00
1	A	130	LEU	CA-CB-CG	6.43	130.08	115.30
1	E	235	GLY	N-CA-C	6.40	129.10	113.10
1	E	22	LEU	CA-CB-CG	6.36	129.93	115.30
1	E	177	TRP	CB-CA-C	-6.30	97.79	110.40
1	C	139	PHE	CB-CG-CD1	6.30	125.21	120.80
1	D	22	LEU	CA-CB-CG	6.29	129.76	115.30
1	G	22	LEU	CA-CB-CG	6.28	129.74	115.30
1	A	112	ILE	CG1-CB-CG2	6.27	125.20	111.40
1	C	48	SER	CB-CA-C	-6.21	98.30	110.10
1	F	22	LEU	CA-CB-CG	6.21	129.59	115.30
1	B	146	LEU	CB-CG-CD2	-6.20	100.46	111.00
1	B	183	TYR	CB-CG-CD2	6.19	124.71	121.00
1	D	50	LYS	N-CA-C	-6.17	94.33	111.00
1	D	177	TRP	CB-CA-C	-6.16	98.08	110.40
1	E	177	TRP	CB-CG-CD1	6.16	135.01	127.00
1	B	22	LEU	CA-CB-CG	6.13	129.39	115.30
1	D	50	LYS	N-CA-CB	6.13	121.63	110.60
1	E	237	PHE	N-CA-CB	-6.12	99.58	110.60
1	E	98	LEU	CA-CB-CG	-6.08	101.31	115.30
1	F	102	ASP	N-CA-CB	-6.07	99.67	110.60
1	E	236	ILE	CA-C-N	-5.93	104.15	117.20
1	G	113	LEU	CB-CG-CD2	-5.91	100.96	111.00
1	F	65	LEU	CB-CG-CD1	-5.89	100.98	111.00
1	C	140	PHE	CB-CA-C	-5.87	98.66	110.40
1	E	236	ILE	C-N-CA	5.86	136.36	121.70
1	C	233	GLU	CG-CD-OE2	5.81	129.93	118.30
1	F	146	LEU	CB-CG-CD2	-5.81	101.12	111.00
1	A	177	TRP	CB-CA-C	-5.81	98.78	110.40
1	D	98	LEU	CA-CB-CG	-5.81	101.94	115.30
1	C	233	GLU	CA-CB-CG	5.80	126.17	113.40
1	G	236	ILE	N-CA-C	-5.80	95.34	111.00
1	F	237	PHE	N-CA-CB	-5.80	100.17	110.60
1	C	130	LEU	CA-CB-CG	5.77	128.56	115.30
1	C	48	SER	CA-CB-OG	5.76	126.75	111.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	236	ILE	C-N-CA	5.75	136.06	121.70
1	A	140	PHE	CB-CG-CD2	-5.74	116.78	120.80
1	E	102	ASP	N-CA-CB	-5.69	100.35	110.60
1	A	113	LEU	CB-CG-CD2	-5.67	101.36	111.00
1	B	177	TRP	CA-CB-CG	5.66	124.46	113.70
1	D	177	TRP	CA-CB-CG	5.65	124.44	113.70
1	B	102	ASP	N-CA-CB	-5.65	100.43	110.60
1	F	104	LEU	CA-CB-CG	5.65	128.29	115.30
1	C	102	ASP	N-CA-CB	-5.60	100.52	110.60
1	D	177	TRP	CB-CG-CD2	-5.59	119.34	126.60
1	F	177	TRP	CB-CA-C	-5.59	99.23	110.40
1	G	177	TRP	CB-CA-C	-5.54	99.31	110.40
1	C	177	TRP	CB-CA-C	-5.54	99.32	110.40
1	E	46	LEU	CB-CG-CD2	5.54	120.41	111.00
1	G	177	TRP	CB-CG-CD2	-5.53	119.41	126.60
1	F	236	ILE	C-N-CA	5.53	135.53	121.70
1	E	222	LEU	CB-CG-CD1	5.49	120.33	111.00
1	C	233	GLU	CG-CD-OE1	-5.44	107.42	118.30
1	C	67	LEU	CB-CG-CD1	-5.43	101.76	111.00
1	G	98	LEU	CA-CB-CG	-5.42	102.83	115.30
1	E	104	LEU	CA-CB-CG	5.41	127.73	115.30
1	F	177	TRP	CA-CB-CG	5.39	123.95	113.70
1	C	50	LYS	N-CA-CB	5.38	120.29	110.60
1	G	102	ASP	N-CA-CB	-5.34	100.98	110.60
1	C	177	TRP	CB-CG-CD2	-5.32	119.68	126.60
1	G	177	TRP	CA-CB-CG	5.32	123.80	113.70
1	D	24	LYS	CD-CE-NZ	5.30	123.89	111.70
1	A	203	LYS	CB-CG-CD	5.29	125.36	111.60
1	C	86	ILE	CG1-CB-CG2	-5.27	99.80	111.40
1	A	140	PHE	CB-CA-C	-5.27	99.86	110.40
1	E	237	PHE	CB-CG-CD2	-5.27	117.11	120.80
1	B	177	TRP	CB-CA-C	-5.25	99.89	110.40
1	G	100	LEU	CB-CG-CD1	-5.23	102.10	111.00
1	A	102	ASP	N-CA-CB	-5.23	101.19	110.60
1	C	24	LYS	CD-CE-NZ	5.20	123.66	111.70
1	B	67	LEU	CB-CG-CD1	-5.19	102.17	111.00
1	C	233	GLU	N-CA-CB	5.19	119.94	110.60
1	G	137	LEU	CB-CG-CD2	-5.17	102.22	111.00
1	A	50	LYS	N-CA-CB	5.16	119.89	110.60
1	C	233	GLU	CB-CA-C	-5.16	100.09	110.40
1	A	24	LYS	CD-CE-NZ	5.11	123.46	111.70
1	E	24	LYS	CD-CE-NZ	5.11	123.45	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	154	LEU	CB-CG-CD2	-5.08	102.36	111.00
1	B	177	TRP	CB-CG-CD2	-5.08	119.99	126.60
1	B	214	ILE	CB-CA-C	-5.08	101.44	111.60
1	F	236	ILE	N-CA-CB	5.08	122.48	110.80
1	F	177	TRP	CB-CG-CD2	-5.05	120.03	126.60
1	C	124	ILE	CG1-CB-CG2	5.05	122.51	111.40
1	F	140	PHE	CB-CA-C	-5.04	100.32	110.40
1	G	67	LEU	CB-CG-CD1	-5.04	102.44	111.00
1	C	146	LEU	CB-CG-CD2	-5.03	102.44	111.00
1	A	139	PHE	C-N-CA	5.01	134.22	121.70
1	D	139	PHE	CB-CG-CD1	5.00	124.30	120.80

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	49	LYS	Mainchain
1	C	236	ILE	Mainchain
1	D	102	ASP	Mainchain
1	E	237	PHE	Mainchain
1	F	234	ASP	Mainchain
1	F	236	ILE	Mainchain
1	G	234	ASP	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	1971	0	2079	135	0
1	B	1971	0	2079	135	0
1	C	1971	0	2079	134	0
1	D	1971	0	2079	142	0
1	E	1971	0	2079	133	0
1	F	1971	0	2079	135	0
1	G	1971	0	2079	134	0
All	All	13797	0	14553	805	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 28.

All (805) 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:C:236:ILE:HG23	1:C:237:PHE:H	1.30	0.95
1:D:236:ILE:HG23	1:D:237:PHE:H	1.33	0.91
1:F:220:SER:HB2	1:F:262:LYS:H	1.32	0.91
1:F:91:THR:HA	1:F:94:ILE:HD12	1.52	0.91
1:B:91:THR:HA	1:B:94:ILE:HD12	1.52	0.90
1:F:186:ASP:HB3	1:F:189:LEU:HG	1.54	0.89
1:G:186:ASP:HB3	1:G:189:LEU:HG	1.55	0.88
1:F:236:ILE:HG22	1:F:237:PHE:H	1.36	0.88
1:G:220:SER:HB2	1:G:262:LYS:H	1.38	0.87
1:E:186:ASP:HB3	1:E:189:LEU:HG	1.58	0.86
1:B:220:SER:HB2	1:B:262:LYS:H	1.41	0.86
1:D:220:SER:HB2	1:D:262:LYS:H	1.41	0.86
1:C:91:THR:HA	1:C:94:ILE:HD12	1.59	0.85
1:C:220:SER:HB2	1:C:262:LYS:H	1.39	0.85
1:G:91:THR:HA	1:G:94:ILE:HD12	1.59	0.85
1:E:220:SER:HB2	1:E:262:LYS:H	1.41	0.84
1:A:91:THR:HA	1:A:94:ILE:HD12	1.57	0.84
1:G:236:ILE:HG23	1:G:237:PHE:H	1.39	0.84
1:D:214:ILE:HG21	1:E:248:LYS:HE3	1.57	0.84
1:F:236:ILE:HG22	1:F:237:PHE:HB3	1.58	0.83
1:A:220:SER:HB2	1:A:262:LYS:H	1.44	0.82
1:A:186:ASP:HB3	1:A:189:LEU:HG	1.60	0.81
1:F:135:GLU:OE2	1:F:145:ARG:HB2	1.81	0.81
1:D:186:ASP:HB3	1:D:189:LEU:HG	1.61	0.81
1:A:237:PHE:CE2	1:G:211:PHE:HB3	2.18	0.79
1:E:44:MET:HA	1:E:48:SER:HB3	1.65	0.78
1:B:186:ASP:HB3	1:B:189:LEU:HG	1.65	0.78
1:A:215:THR:HG22	1:A:216:ASP:OD2	1.84	0.78
1:D:182:GLY:N	1:D:257:GLU:O	2.17	0.78
1:C:236:ILE:CG2	1:C:237:PHE:H	1.95	0.77
1:C:186:ASP:HB3	1:C:189:LEU:HG	1.66	0.77
1:D:30:CYS:HA	1:D:33:PHE:HB3	1.66	0.77
1:E:30:CYS:HA	1:E:33:PHE:HB3	1.65	0.77
1:B:214:ILE:HG21	1:C:248:LYS:HE3	1.66	0.77
1:A:248:LYS:HE3	1:G:214:ILE:HG21	1.66	0.77
1:C:214:ILE:HG21	1:D:248:LYS:HE3	1.67	0.77
1:B:18:PHE:HE2	1:B:22:LEU:HD13	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:GLY:HA2	1:A:133:LYS:HE3	1.67	0.76
1:E:117:HIS:HB2	1:E:119:PHE:O	1.86	0.76
1:G:214:ILE:HG23	1:G:222:LEU:HD21	1.68	0.76
1:C:122:GLY:HA2	1:C:133:LYS:HE3	1.68	0.76
1:F:44:MET:O	1:F:48:SER:OG	2.04	0.76
1:F:182:GLY:N	1:F:257:GLU:O	2.18	0.75
1:F:18:PHE:HE2	1:F:22:LEU:HD13	1.51	0.75
1:E:235:GLY:HA2	1:E:239:VAL:HG23	1.69	0.75
1:G:21:ILE:HG13	1:G:22:LEU:H	1.51	0.75
1:E:182:GLY:N	1:E:257:GLU:O	2.20	0.75
1:D:215:THR:HG22	1:D:216:ASP:OD2	1.87	0.75
1:A:237:PHE:CD2	1:G:211:PHE:HB3	2.22	0.75
1:G:30:CYS:HA	1:G:33:PHE:HB3	1.69	0.74
1:C:182:GLY:N	1:C:257:GLU:O	2.18	0.74
1:G:215:THR:HG22	1:G:216:ASP:OD2	1.87	0.74
1:A:82:THR:OG1	1:B:81:GLN:NE2	2.20	0.74
1:E:91:THR:HA	1:E:94:ILE:HD12	1.67	0.74
1:B:60:GLN:HG3	1:B:64:ILE:HD11	1.69	0.74
1:D:21:ILE:HG13	1:D:22:LEU:H	1.52	0.74
1:B:30:CYS:HA	1:B:33:PHE:HB3	1.70	0.74
1:A:30:CYS:HA	1:A:33:PHE:HB3	1.70	0.74
1:C:127:ILE:HD11	1:C:164:ILE:HG23	1.70	0.74
1:B:182:GLY:N	1:B:257:GLU:O	2.20	0.73
1:D:122:GLY:HA2	1:D:133:LYS:HE3	1.70	0.73
1:C:21:ILE:HG13	1:C:22:LEU:H	1.52	0.73
1:F:21:ILE:HG13	1:F:22:LEU:H	1.53	0.73
1:F:214:ILE:HG21	1:G:248:LYS:HE3	1.70	0.72
1:D:60:GLN:HG3	1:D:64:ILE:HD11	1.72	0.72
1:D:91:THR:HA	1:D:94:ILE:HD12	1.72	0.72
1:E:18:PHE:HE2	1:E:22:LEU:HD13	1.52	0.72
1:C:18:PHE:HE2	1:C:22:LEU:HD13	1.53	0.72
1:B:21:ILE:HG13	1:B:22:LEU:H	1.55	0.72
1:D:187:ILE:HG23	1:D:214:ILE:HD11	1.73	0.71
1:G:122:GLY:HA2	1:G:133:LYS:HE3	1.72	0.71
1:G:237:PHE:HE1	1:G:240:ARG:HH11	1.38	0.71
1:B:24:LYS:HA	1:B:27:ILE:HD12	1.72	0.71
1:A:135:GLU:OE2	1:A:145:ARG:HB2	1.90	0.71
1:A:60:GLN:HG3	1:A:64:ILE:HD11	1.72	0.70
1:C:30:CYS:HA	1:C:33:PHE:HB3	1.73	0.70
1:G:236:ILE:CG2	1:G:237:PHE:H	2.03	0.70
1:A:182:GLY:N	1:A:257:GLU:O	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:135:GLU:OE2	1:C:145:ARG:HB2	1.91	0.70
1:E:60:GLN:HG3	1:E:64:ILE:HD11	1.72	0.70
1:B:122:GLY:HA2	1:B:133:LYS:HE3	1.74	0.70
1:G:182:GLY:N	1:G:257:GLU:O	2.24	0.69
1:F:215:THR:HG22	1:F:216:ASP:OD2	1.92	0.69
1:F:30:CYS:HA	1:F:33:PHE:HB3	1.75	0.69
1:F:60:GLN:HG3	1:F:64:ILE:HD11	1.75	0.69
1:A:214:ILE:HG21	1:B:248:LYS:HE3	1.73	0.68
1:B:127:ILE:HD11	1:B:164:ILE:HG23	1.76	0.67
1:F:236:ILE:CG2	1:F:237:PHE:H	2.01	0.67
1:A:127:ILE:HD11	1:A:164:ILE:HG23	1.77	0.67
1:D:41:ASN:HA	1:D:44:MET:HB2	1.76	0.67
1:F:187:ILE:HG23	1:F:214:ILE:HD11	1.75	0.67
1:E:215:THR:HG22	1:E:216:ASP:OD2	1.95	0.67
1:G:44:MET:O	1:G:48:SER:OG	2.09	0.67
1:E:122:GLY:HA2	1:E:133:LYS:HE3	1.75	0.67
1:G:177:TRP:HE3	1:G:178:VAL:H	1.44	0.66
1:F:177:TRP:HE3	1:F:178:VAL:H	1.43	0.66
1:C:60:GLN:HG3	1:C:64:ILE:HD11	1.78	0.66
1:C:187:ILE:HG23	1:C:214:ILE:HD11	1.78	0.66
1:C:27:ILE:O	1:C:31:ILE:HG13	1.95	0.66
1:C:215:THR:HG22	1:C:216:ASP:OD2	1.94	0.66
1:D:116:LEU:HD13	1:E:140:PHE:CE2	2.31	0.65
1:G:92:VAL:O	1:G:96:VAL:HG23	1.96	0.65
1:A:187:ILE:HG23	1:A:214:ILE:HD11	1.78	0.65
1:A:24:LYS:HA	1:A:27:ILE:HD12	1.78	0.65
1:G:187:ILE:HG23	1:G:214:ILE:HD11	1.79	0.65
1:A:18:PHE:HE2	1:A:22:LEU:HD13	1.61	0.65
1:D:235:GLY:HA2	1:D:239:VAL:HG23	1.78	0.65
1:E:21:ILE:HG13	1:E:22:LEU:H	1.60	0.65
1:G:43:THR:CG2	1:G:58:VAL:HG12	2.27	0.65
1:D:177:TRP:HE3	1:D:178:VAL:H	1.42	0.65
1:G:237:PHE:CE1	1:G:240:ARG:NH1	2.65	0.65
1:G:125:ILE:HG22	1:G:166:ASN:HA	1.79	0.65
1:B:215:THR:HG22	1:B:216:ASP:OD2	1.96	0.64
1:F:122:GLY:HA2	1:F:133:LYS:HE3	1.78	0.64
1:F:116:LEU:HD13	1:G:140:PHE:CE2	2.32	0.64
1:B:221:SER:HB3	1:B:259:PRO:HG2	1.80	0.64
1:C:112:ILE:HG13	1:D:140:PHE:HE2	1.62	0.64
1:A:81:GLN:NE2	1:G:82:THR:OG1	2.26	0.64
1:G:18:PHE:HE2	1:G:22:LEU:HD13	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:218:GLY:HA3	1:G:221:SER:O	1.97	0.64
1:F:122:GLY:H	1:F:134:VAL:HG13	1.63	0.64
1:G:60:GLN:O	1:G:64:ILE:HG13	1.98	0.64
1:E:263:LEU:HD11	1:F:263:LEU:HD23	1.80	0.64
1:F:116:LEU:O	1:F:116:LEU:HD23	1.97	0.63
1:C:177:TRP:O	1:C:225:THR:HA	1.98	0.63
1:E:24:LYS:HA	1:E:27:ILE:HD12	1.81	0.63
1:B:235:GLY:HA2	1:B:239:VAL:HG23	1.81	0.63
1:D:18:PHE:HE2	1:D:22:LEU:HD13	1.63	0.63
1:B:263:LEU:HD11	1:C:263:LEU:HB3	1.81	0.63
1:C:114:ILE:HG13	1:C:137:LEU:HD21	1.80	0.63
1:B:177:TRP:O	1:B:225:THR:HA	1.99	0.62
1:G:60:GLN:HG3	1:G:64:ILE:HD11	1.81	0.62
1:E:214:ILE:HG21	1:F:248:LYS:HE3	1.81	0.62
1:F:263:LEU:HD11	1:G:263:LEU:HD23	1.80	0.62
1:E:48:SER:O	1:E:49:LYS:HG2	1.99	0.62
1:B:265:ILE:HD13	1:C:265:ILE:HD12	1.80	0.62
1:E:23:ILE:O	1:E:27:ILE:HG13	1.99	0.62
1:E:187:ILE:HG23	1:E:214:ILE:HD11	1.81	0.62
1:C:235:GLY:HA2	1:C:239:VAL:HG23	1.81	0.62
1:E:60:GLN:O	1:E:64:ILE:HG13	2.00	0.62
1:A:140:PHE:CD1	1:A:140:PHE:N	2.67	0.62
1:E:135:GLU:OE2	1:E:145:ARG:HB2	1.98	0.62
1:G:122:GLY:H	1:G:134:VAL:HG13	1.64	0.62
1:D:122:GLY:H	1:D:134:VAL:HG13	1.65	0.61
1:E:177:TRP:HE3	1:E:178:VAL:H	1.46	0.61
1:E:69:ILE:HD13	1:F:85:ILE:HG13	1.80	0.61
1:C:121:LYS:HG2	1:C:122:GLY:N	2.14	0.61
1:C:82:THR:OG1	1:D:81:GLN:NE2	2.30	0.61
1:D:218:GLY:HA3	1:D:221:SER:O	1.99	0.61
1:B:60:GLN:O	1:B:64:ILE:HG13	2.00	0.61
1:A:125:ILE:HG22	1:A:166:ASN:HA	1.81	0.61
1:D:82:THR:OG1	1:E:81:GLN:NE2	2.27	0.61
1:C:125:ILE:HG22	1:C:166:ASN:HA	1.81	0.61
1:A:140:PHE:HE2	1:G:112:ILE:HG13	1.64	0.61
1:C:117:HIS:HB2	1:C:119:PHE:O	2.00	0.61
1:C:24:LYS:HA	1:C:27:ILE:HD12	1.83	0.61
1:A:44:MET:O	1:A:48:SER:OG	2.16	0.61
1:F:71:THR:O	1:F:75:LEU:HG	2.00	0.61
1:A:84:SER:HA	1:G:86:ILE:HD11	1.82	0.61
1:D:221:SER:HB3	1:D:259:PRO:HG2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:MET:O	1:D:48:SER:OG	2.14	0.61
1:D:117:HIS:HB2	1:D:119:PHE:O	2.01	0.61
1:A:60:GLN:O	1:A:64:ILE:HG13	2.00	0.61
1:D:114:ILE:HG13	1:D:137:LEU:HD21	1.83	0.61
1:A:116:LEU:HD13	1:B:140:PHE:CE2	2.35	0.61
1:E:170:THR:OG1	1:F:151:LEU:HD21	2.01	0.61
1:G:21:ILE:HG13	1:G:22:LEU:N	2.16	0.60
1:A:263:LEU:HD23	1:G:263:LEU:HD11	1.83	0.60
1:B:218:GLY:HA3	1:B:221:SER:O	2.01	0.60
1:F:117:HIS:HB2	1:F:119:PHE:O	2.02	0.60
1:G:221:SER:HB3	1:G:259:PRO:HG2	1.83	0.60
1:G:196:ASP:O	1:G:200:THR:HG23	2.02	0.60
1:B:135:GLU:OE2	1:B:145:ARG:HB2	2.01	0.60
1:A:117:HIS:HB2	1:A:119:PHE:O	2.02	0.60
1:B:177:TRP:HE3	1:B:178:VAL:H	1.50	0.60
1:F:170:THR:O	1:F:232:ILE:HD11	2.01	0.60
1:G:24:LYS:HA	1:G:27:ILE:HD12	1.83	0.60
1:D:263:LEU:HD11	1:E:263:LEU:HB3	1.84	0.60
1:G:27:ILE:O	1:G:31:ILE:HG13	2.01	0.60
1:B:170:THR:O	1:B:232:ILE:HD11	2.02	0.60
1:A:114:ILE:HG13	1:A:137:LEU:HD21	1.82	0.60
1:F:235:GLY:HA2	1:F:239:VAL:HG23	1.83	0.59
1:F:218:GLY:HA3	1:F:221:SER:O	2.02	0.59
1:B:104:LEU:HG	1:C:99:ALA:HB2	1.82	0.59
1:D:211:PHE:CE1	1:E:236:ILE:HD12	2.37	0.59
1:E:27:ILE:O	1:E:31:ILE:HG13	2.02	0.59
1:C:177:TRP:HE3	1:C:178:VAL:H	1.50	0.59
1:C:97:ALA:HA	1:D:95:ALA:HB2	1.85	0.59
1:D:43:THR:CG2	1:D:58:VAL:HG12	2.33	0.59
1:G:181:VAL:HG23	1:G:182:GLY:O	2.02	0.59
1:E:170:THR:O	1:E:232:ILE:HD11	2.02	0.59
1:B:183:TYR:HH	1:B:217:PHE:HD2	1.50	0.59
1:A:41:ASN:HA	1:A:44:MET:HB2	1.83	0.59
1:B:187:ILE:HG23	1:B:214:ILE:HD11	1.85	0.58
1:F:44:MET:HA	1:F:48:SER:HB3	1.85	0.58
1:D:177:TRP:O	1:D:225:THR:HA	2.02	0.58
1:F:265:ILE:HD13	1:G:265:ILE:CD1	2.33	0.58
1:E:41:ASN:HA	1:E:44:MET:HB2	1.84	0.58
1:F:21:ILE:HG13	1:F:22:LEU:N	2.17	0.58
1:B:41:ASN:HA	1:B:44:MET:HB2	1.85	0.58
1:F:177:TRP:O	1:F:225:THR:HA	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ILE:HG23	1:B:222:LEU:HD21	1.86	0.58
1:F:161:ASN:HD21	1:G:103:TYR:HE2	1.51	0.58
1:A:218:GLY:HA3	1:A:221:SER:O	2.04	0.58
1:C:21:ILE:HG13	1:C:22:LEU:N	2.18	0.58
1:G:236:ILE:HG23	1:G:237:PHE:N	2.16	0.58
1:D:60:GLN:O	1:D:64:ILE:HG13	2.03	0.57
1:G:56:ASN:O	1:G:60:GLN:HB2	2.04	0.57
1:A:177:TRP:HE3	1:A:178:VAL:H	1.50	0.57
1:G:177:TRP:O	1:G:225:THR:HA	2.04	0.57
1:F:43:THR:CG2	1:F:58:VAL:HG12	2.35	0.57
1:A:86:ILE:HD12	1:B:84:SER:HA	1.87	0.57
1:C:56:ASN:O	1:C:60:GLN:HB2	2.04	0.57
1:C:116:LEU:HD13	1:D:140:PHE:CE2	2.39	0.57
1:D:170:THR:O	1:D:232:ILE:HD11	2.04	0.57
1:B:48:SER:HB2	1:B:55:ALA:HB1	1.87	0.57
1:A:227:ARG:HH22	1:B:236:ILE:CD1	2.18	0.57
1:D:36:SER:HB3	1:D:63:PHE:CE1	2.39	0.57
1:F:24:LYS:HA	1:F:27:ILE:HD12	1.86	0.57
1:G:127:ILE:HD11	1:G:164:ILE:HG23	1.87	0.57
1:F:183:TYR:OH	1:G:258:ILE:HG21	2.05	0.57
1:D:125:ILE:HG22	1:D:166:ASN:HA	1.87	0.57
1:D:21:ILE:HG13	1:D:22:LEU:N	2.19	0.57
1:B:236:ILE:O	1:B:238:ASN:N	2.31	0.57
1:A:136:ALA:HB3	1:A:143:SER:HB3	1.87	0.57
1:B:117:HIS:HB2	1:B:119:PHE:O	2.05	0.57
1:B:122:GLY:H	1:B:134:VAL:HG13	1.70	0.56
1:C:60:GLN:O	1:C:64:ILE:HG13	2.05	0.56
1:E:268:LYS:O	1:F:266:ALA:HA	2.05	0.56
1:A:121:LYS:HG2	1:A:122:GLY:N	2.20	0.56
1:G:121:LYS:HG2	1:G:122:GLY:N	2.20	0.56
1:E:56:ASN:O	1:E:60:GLN:HB2	2.05	0.56
1:E:114:ILE:HG13	1:E:137:LEU:HD21	1.87	0.56
1:D:125:ILE:HD12	1:D:127:ILE:HG12	1.88	0.56
1:F:220:SER:CB	1:F:262:LYS:H	2.14	0.56
1:C:127:ILE:CD1	1:C:164:ILE:HA	2.36	0.56
1:B:263:LEU:HD11	1:C:263:LEU:HD23	1.87	0.56
1:C:41:ASN:HA	1:C:44:MET:HB2	1.88	0.56
1:F:60:GLN:O	1:F:64:ILE:HG13	2.06	0.56
1:A:43:THR:CG2	1:A:58:VAL:HG12	2.36	0.56
1:E:183:TYR:OH	1:F:258:ILE:HG21	2.06	0.56
1:D:88:VAL:HA	1:D:91:THR:HG22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:ILE:HD13	1:C:265:ILE:CD1	2.36	0.55
1:B:41:ASN:O	1:B:45:LYS:HB2	2.06	0.55
1:G:43:THR:HG23	1:G:58:VAL:HG12	1.88	0.55
1:D:177:TRP:CZ2	1:D:244:ILE:HD12	2.41	0.55
1:F:136:ALA:HB3	1:F:143:SER:HB3	1.89	0.55
1:A:71:THR:O	1:A:75:LEU:HG	2.07	0.55
1:C:43:THR:CG2	1:C:58:VAL:HG12	2.37	0.55
1:C:88:VAL:HA	1:C:91:THR:HG22	1.87	0.55
1:C:29:PHE:HD2	1:C:30:CYS:HG	1.54	0.55
1:A:214:ILE:HG21	1:B:248:LYS:CE	2.36	0.55
1:G:117:HIS:HB2	1:G:119:PHE:O	2.07	0.55
1:G:72:ILE:HD13	1:G:86:ILE:HD12	1.89	0.55
1:A:88:VAL:HA	1:A:91:THR:HG22	1.88	0.55
1:A:258:ILE:HG21	1:G:183:TYR:OH	2.05	0.55
1:B:21:ILE:HG13	1:B:22:LEU:N	2.22	0.55
1:B:121:LYS:HG2	1:B:122:GLY:N	2.22	0.55
1:G:41:ASN:HA	1:G:44:MET:HB2	1.87	0.55
1:D:112:ILE:HG13	1:E:140:PHE:HE2	1.72	0.55
1:A:177:TRP:CZ2	1:A:244:ILE:HD12	2.40	0.55
1:B:116:LEU:HD13	1:C:140:PHE:CE2	2.41	0.55
1:E:221:SER:HB3	1:E:259:PRO:HG2	1.89	0.55
1:B:23:ILE:O	1:B:27:ILE:HG13	2.07	0.55
1:D:23:ILE:O	1:D:27:ILE:HG13	2.07	0.55
1:E:177:TRP:O	1:E:225:THR:HA	2.06	0.54
1:A:221:SER:HB3	1:A:259:PRO:HG2	1.88	0.54
1:A:245:GLU:HG2	1:G:214:ILE:HG13	1.89	0.54
1:D:263:LEU:HD11	1:E:263:LEU:HD23	1.88	0.54
1:E:218:GLY:HA3	1:E:221:SER:O	2.06	0.54
1:B:114:ILE:HG13	1:B:137:LEU:HD21	1.88	0.54
1:D:214:ILE:HG21	1:E:248:LYS:CE	2.34	0.54
1:G:117:HIS:O	1:G:117:HIS:ND1	2.40	0.54
1:B:44:MET:O	1:B:48:SER:OG	2.14	0.54
1:C:214:ILE:HG23	1:C:222:LEU:HD11	1.88	0.54
1:A:122:GLY:H	1:A:134:VAL:HG13	1.71	0.54
1:A:27:ILE:O	1:A:31:ILE:HG13	2.07	0.54
1:E:136:ALA:HB3	1:E:143:SER:HB3	1.89	0.54
1:F:41:ASN:HA	1:F:44:MET:HB2	1.90	0.54
1:D:116:LEU:O	1:D:116:LEU:HD23	2.07	0.54
1:D:117:HIS:O	1:D:117:HIS:ND1	2.41	0.54
1:D:27:ILE:O	1:D:31:ILE:HG13	2.07	0.54
1:C:268:LYS:O	1:D:266:ALA:HA	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:121:LYS:HG2	1:F:122:GLY:N	2.22	0.54
1:A:127:ILE:CD1	1:A:164:ILE:HA	2.38	0.54
1:A:263:LEU:HD11	1:B:263:LEU:HB3	1.90	0.54
1:F:18:PHE:CE2	1:F:22:LEU:HD13	2.39	0.54
1:B:56:ASN:O	1:B:60:GLN:HB2	2.08	0.54
1:D:42:LYS:HA	1:D:45:LYS:HB3	1.90	0.54
1:E:109:GLY:HA2	1:F:103:TYR:CE1	2.42	0.53
1:E:41:ASN:O	1:E:45:LYS:HB2	2.08	0.53
1:G:41:ASN:O	1:G:45:LYS:HB2	2.07	0.53
1:B:183:TYR:OH	1:C:258:ILE:HG21	2.07	0.53
1:D:135:GLU:OE2	1:D:145:ARG:HB2	2.09	0.53
1:C:218:GLY:HA3	1:C:221:SER:O	2.08	0.53
1:E:122:GLY:H	1:E:134:VAL:HG13	1.71	0.53
1:C:263:LEU:HD11	1:D:263:LEU:HD23	1.90	0.53
1:B:112:ILE:HG13	1:C:140:PHE:HE2	1.72	0.53
1:C:23:ILE:O	1:C:27:ILE:HG13	2.08	0.53
1:C:116:LEU:HD23	1:C:116:LEU:O	2.07	0.53
1:F:265:ILE:HD13	1:G:265:ILE:HD12	1.89	0.53
1:C:40:ARG:HB2	1:C:63:PHE:HD1	1.74	0.53
1:D:56:ASN:O	1:D:60:GLN:HB2	2.09	0.53
1:A:86:ILE:CD1	1:B:84:SER:HA	2.38	0.53
1:F:140:PHE:CD1	1:F:140:PHE:N	2.75	0.53
1:D:85:ILE:H	1:D:85:ILE:HD12	1.73	0.53
1:D:236:ILE:HG23	1:D:237:PHE:N	2.13	0.53
1:A:188:GLU:HA	1:A:191:HIS:CB	2.39	0.53
1:D:43:THR:HG23	1:D:58:VAL:HG12	1.91	0.53
1:E:138:ASN:HD22	1:E:141:ASN:HB2	1.74	0.53
1:A:196:ASP:O	1:A:200:THR:HG23	2.08	0.53
1:C:221:SER:HB3	1:C:259:PRO:HG2	1.91	0.53
1:E:88:VAL:HA	1:E:91:THR:HG22	1.90	0.53
1:G:170:THR:O	1:G:232:ILE:HD11	2.08	0.53
1:A:214:ILE:HG23	1:A:222:LEU:HD21	1.91	0.53
1:G:127:ILE:CD1	1:G:164:ILE:HA	2.39	0.53
1:C:112:ILE:HG13	1:D:140:PHE:CE2	2.44	0.52
1:F:196:ASP:O	1:F:200:THR:HG23	2.10	0.52
1:F:56:ASN:O	1:F:60:GLN:HB2	2.09	0.52
1:B:71:THR:O	1:B:75:LEU:HG	2.08	0.52
1:B:82:THR:OG1	1:C:81:GLN:NE2	2.32	0.52
1:A:140:PHE:CE2	1:G:116:LEU:HD13	2.44	0.52
1:B:140:PHE:N	1:B:140:PHE:CD1	2.76	0.52
1:A:36:SER:HB3	1:A:63:PHE:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:127:ILE:HD11	1:E:164:ILE:HG23	1.92	0.52
1:B:127:ILE:CD1	1:B:164:ILE:HA	2.39	0.52
1:C:122:GLY:H	1:C:134:VAL:HG13	1.74	0.52
1:F:214:ILE:HG12	1:F:224:PHE:CZ	2.45	0.52
1:F:23:ILE:O	1:F:27:ILE:HG13	2.09	0.52
1:B:264:ASP:HB2	1:C:262:LYS:HG3	1.92	0.52
1:G:178:VAL:HG12	1:G:223:ASN:HB3	1.92	0.52
1:D:123:ASP:O	1:D:134:VAL:HG12	2.10	0.52
1:E:109:GLY:HA2	1:F:103:TYR:CZ	2.45	0.52
1:D:86:ILE:CD1	1:E:84:SER:HA	2.40	0.52
1:G:135:GLU:OE2	1:G:145:ARG:HB2	2.09	0.52
1:C:183:TYR:OH	1:D:258:ILE:HG21	2.10	0.52
1:G:177:TRP:CZ2	1:G:244:ILE:HD12	2.44	0.52
1:B:181:VAL:HG23	1:B:222:LEU:HB3	1.92	0.52
1:D:24:LYS:HA	1:D:27:ILE:HD12	1.91	0.52
1:A:266:ALA:HA	1:G:268:LYS:O	2.09	0.52
1:E:71:THR:O	1:E:75:LEU:HG	2.10	0.52
1:D:41:ASN:O	1:D:45:LYS:HB2	2.09	0.52
1:C:265:ILE:HD13	1:D:265:ILE:CD1	2.40	0.52
1:D:203:LYS:O	1:D:204:ILE:HG13	2.10	0.52
1:D:136:ALA:HB3	1:D:143:SER:HB3	1.92	0.52
1:G:88:VAL:HA	1:G:91:THR:HG22	1.92	0.51
1:A:177:TRP:O	1:A:225:THR:HA	2.10	0.51
1:B:181:VAL:CG2	1:B:222:LEU:HB3	2.40	0.51
1:F:18:PHE:CD2	1:F:22:LEU:HD22	2.44	0.51
1:F:214:ILE:HG23	1:F:222:LEU:HD21	1.90	0.51
1:C:241:SER:O	1:C:244:ILE:HG22	2.10	0.51
1:E:121:LYS:HG2	1:E:122:GLY:N	2.24	0.51
1:E:43:THR:CG2	1:E:58:VAL:HG12	2.39	0.51
1:C:177:TRP:CZ2	1:C:244:ILE:HD12	2.45	0.51
1:C:144:LEU:O	1:C:151:LEU:HA	2.10	0.51
1:A:208:MET:HB2	1:A:229:TRP:HB2	1.92	0.51
1:C:18:PHE:CE2	1:C:22:LEU:HD13	2.41	0.51
1:A:187:ILE:O	1:A:191:HIS:HB2	2.11	0.51
1:D:188:GLU:HA	1:D:191:HIS:CB	2.40	0.51
1:A:42:LYS:HE2	1:A:45:LYS:NZ	2.26	0.51
1:B:119:PHE:CE1	1:B:125:ILE:HD13	2.45	0.51
1:G:119:PHE:CE1	1:G:125:ILE:HD13	2.46	0.51
1:F:123:ASP:O	1:F:134:VAL:HG12	2.11	0.51
1:E:104:LEU:HG	1:F:99:ALA:HB2	1.92	0.51
1:C:44:MET:HA	1:C:48:SER:OG	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:THR:HG23	1:C:58:VAL:HG12	1.93	0.51
1:F:125:ILE:HG22	1:F:166:ASN:HA	1.93	0.51
1:E:125:ILE:HG22	1:E:166:ASN:HA	1.93	0.50
1:A:18:PHE:CD2	1:A:22:LEU:HD22	2.46	0.50
1:B:125:ILE:HG22	1:B:166:ASN:HA	1.92	0.50
1:F:136:ALA:HB3	1:F:143:SER:CB	2.41	0.50
1:F:263:LEU:HD11	1:G:263:LEU:HB3	1.93	0.50
1:B:116:LEU:O	1:B:116:LEU:HD23	2.11	0.50
1:E:21:ILE:HG13	1:E:22:LEU:N	2.26	0.50
1:G:23:ILE:O	1:G:27:ILE:HG13	2.11	0.50
1:G:241:SER:O	1:G:244:ILE:HG22	2.12	0.50
1:B:251:LEU:HD22	1:B:256:ILE:HG21	1.93	0.50
1:F:43:THR:HG23	1:F:58:VAL:HG12	1.93	0.50
1:A:92:VAL:O	1:A:96:VAL:HG23	2.12	0.50
1:C:217:PHE:CE2	1:D:258:ILE:HG12	2.46	0.50
1:F:235:GLY:O	1:F:238:ASN:HB2	2.12	0.50
1:C:41:ASN:O	1:C:45:LYS:HB2	2.12	0.50
1:D:196:ASP:O	1:D:200:THR:HG23	2.12	0.50
1:C:196:ASP:O	1:C:200:THR:HG23	2.12	0.50
1:F:48:SER:O	1:F:49:LYS:HG2	2.12	0.50
1:E:177:TRP:CZ2	1:E:244:ILE:HD12	2.46	0.50
1:G:64:ILE:O	1:G:68:ILE:HG13	2.11	0.50
1:A:41:ASN:O	1:A:45:LYS:HB2	2.11	0.50
1:E:136:ALA:HB3	1:E:143:SER:CB	2.41	0.50
1:C:170:THR:O	1:C:232:ILE:HD11	2.11	0.50
1:C:236:ILE:CG2	1:C:237:PHE:N	2.71	0.50
1:F:187:ILE:O	1:F:191:HIS:HB2	2.12	0.50
1:C:263:LEU:HD11	1:D:263:LEU:HB3	1.93	0.50
1:G:71:THR:O	1:G:75:LEU:HG	2.12	0.50
1:F:251:LEU:HD22	1:F:256:ILE:HG21	1.94	0.50
1:A:56:ASN:O	1:A:60:GLN:HB2	2.11	0.49
1:F:27:ILE:O	1:F:31:ILE:HG13	2.12	0.49
1:B:18:PHE:CE2	1:B:22:LEU:HD13	2.39	0.49
1:D:121:LYS:HG2	1:D:122:GLY:N	2.27	0.49
1:E:18:PHE:CE2	1:E:22:LEU:HD13	2.40	0.49
1:E:118:PRO:HG2	1:F:141:ASN:ND2	2.26	0.49
1:G:36:SER:HB3	1:G:63:PHE:CE1	2.47	0.49
1:G:237:PHE:HE1	1:G:240:ARG:NH1	2.04	0.49
1:E:18:PHE:CD2	1:E:22:LEU:HD22	2.47	0.49
1:B:235:GLY:O	1:B:236:ILE:C	2.50	0.49
1:C:208:MET:HB2	1:C:229:TRP:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:183:TYR:OH	1:E:258:ILE:HG21	2.12	0.49
1:E:42:LYS:HG2	1:E:45:LYS:HE3	1.93	0.49
1:F:41:ASN:O	1:F:45:LYS:HB2	2.12	0.49
1:F:215:THR:CB	1:F:225:THR:HG1	2.22	0.49
1:A:42:LYS:HA	1:A:45:LYS:HB3	1.93	0.49
1:B:259:PRO:HB3	1:B:262:LYS:NZ	2.27	0.49
1:A:40:ARG:HB2	1:A:63:PHE:HD1	1.76	0.49
1:E:127:ILE:CD1	1:E:164:ILE:HA	2.43	0.49
1:F:178:VAL:HG12	1:F:223:ASN:HB3	1.94	0.49
1:A:183:TYR:OH	1:B:258:ILE:HG21	2.13	0.49
1:D:109:GLY:HA2	1:E:103:TYR:CZ	2.48	0.49
1:B:208:MET:HB2	1:B:229:TRP:HB2	1.94	0.49
1:C:18:PHE:CE1	1:C:21:ILE:HD11	2.48	0.49
1:B:36:SER:HB3	1:B:63:PHE:CE1	2.48	0.49
1:B:40:ARG:HB2	1:B:63:PHE:HD1	1.76	0.49
1:A:188:GLU:HA	1:A:191:HIS:HB2	1.95	0.49
1:F:127:ILE:HG23	1:F:127:ILE:HD12	1.56	0.49
1:B:44:MET:HA	1:B:48:SER:HB3	1.94	0.49
1:E:125:ILE:HD12	1:E:127:ILE:HG12	1.95	0.48
1:C:119:PHE:CE1	1:C:125:ILE:HD13	2.48	0.48
1:D:124:ILE:HG22	1:D:133:LYS:HB2	1.95	0.48
1:G:136:ALA:HB3	1:G:143:SER:HB3	1.94	0.48
1:F:18:PHE:CE2	1:F:22:LEU:HD22	2.47	0.48
1:F:268:LYS:O	1:G:266:ALA:HA	2.13	0.48
1:B:220:SER:CB	1:B:262:LYS:H	2.20	0.48
1:E:188:GLU:HA	1:E:191:HIS:CB	2.43	0.48
1:B:44:MET:HG2	1:B:59:ALA:HB2	1.95	0.48
1:B:48:SER:HB2	1:B:55:ALA:CB	2.44	0.48
1:E:178:VAL:HG12	1:E:223:ASN:HB3	1.94	0.48
1:F:235:GLY:C	1:F:236:ILE:O	2.45	0.48
1:D:214:ILE:HG23	1:D:222:LEU:HD21	1.94	0.48
1:A:180:GLY:HA2	1:A:222:LEU:O	2.12	0.48
1:B:85:ILE:HD12	1:B:85:ILE:H	1.79	0.48
1:D:98:LEU:HA	1:D:98:LEU:HD23	1.49	0.48
1:B:117:HIS:ND1	1:B:117:HIS:O	2.47	0.48
1:G:114:ILE:HG13	1:G:137:LEU:HD21	1.95	0.48
1:D:187:ILE:O	1:D:191:HIS:HB2	2.14	0.48
1:G:98:LEU:HA	1:G:98:LEU:HD23	1.54	0.48
1:G:235:GLY:HA2	1:G:239:VAL:HG23	1.95	0.48
1:B:42:LYS:HA	1:B:45:LYS:HB3	1.96	0.48
1:D:127:ILE:CD1	1:D:164:ILE:HA	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:LYS:HA	1:C:45:LYS:HB3	1.96	0.48
1:B:178:VAL:HG12	1:B:223:ASN:HB3	1.95	0.47
1:D:208:MET:HB2	1:D:229:TRP:HB2	1.96	0.47
1:G:215:THR:CB	1:G:225:THR:HG1	2.27	0.47
1:A:136:ALA:HB3	1:A:143:SER:CB	2.44	0.47
1:E:112:ILE:HG13	1:F:140:PHE:HE2	1.78	0.47
1:C:203:LYS:NZ	1:C:234:ASP:OD2	2.46	0.47
1:B:48:SER:O	1:B:49:LYS:HG2	2.13	0.47
1:E:42:LYS:HA	1:E:45:LYS:HB3	1.96	0.47
1:A:123:ASP:O	1:A:134:VAL:HG12	2.15	0.47
1:D:109:GLY:HA2	1:E:103:TYR:CE1	2.48	0.47
1:D:71:THR:O	1:D:75:LEU:HG	2.15	0.47
1:G:203:LYS:O	1:G:204:ILE:HG13	2.14	0.47
1:F:42:LYS:HG2	1:F:45:LYS:HE3	1.96	0.47
1:B:107:ILE:HG12	1:B:140:PHE:CD1	2.49	0.47
1:G:127:ILE:HD13	1:G:164:ILE:HA	1.95	0.47
1:F:221:SER:HB3	1:F:259:PRO:HG2	1.96	0.47
1:B:88:VAL:HA	1:B:91:THR:HG22	1.97	0.47
1:D:220:SER:CB	1:D:262:LYS:H	2.20	0.47
1:E:48:SER:HB2	1:E:55:ALA:HB1	1.96	0.47
1:E:18:PHE:CE1	1:E:21:ILE:HD11	2.50	0.47
1:A:140:PHE:CD2	1:G:116:LEU:HD13	2.50	0.47
1:E:171:ALA:HA	1:E:232:ILE:HD12	1.97	0.47
1:D:136:ALA:HB3	1:D:143:SER:CB	2.45	0.47
1:C:231:LYS:HE2	1:C:233:GLU:HG2	1.96	0.47
1:A:176:GLU:HA	1:A:226:ILE:O	2.15	0.47
1:G:186:ASP:HB3	1:G:189:LEU:CG	2.38	0.47
1:G:187:ILE:O	1:G:191:HIS:HB2	2.15	0.47
1:F:188:GLU:HA	1:F:191:HIS:CB	2.45	0.47
1:D:265:ILE:HD13	1:E:265:ILE:CD1	2.45	0.47
1:F:208:MET:HB2	1:F:229:TRP:HB2	1.96	0.47
1:E:220:SER:CB	1:E:262:LYS:H	2.20	0.47
1:F:214:ILE:HG13	1:G:245:GLU:HG2	1.97	0.47
1:B:235:GLY:O	1:B:237:PHE:N	2.48	0.47
1:C:36:SER:HB3	1:C:63:PHE:CE1	2.50	0.47
1:E:116:LEU:HD13	1:F:140:PHE:CE2	2.50	0.47
1:E:196:ASP:O	1:E:200:THR:HG23	2.14	0.47
1:E:161:ASN:OD1	1:F:157:ARG:HD3	2.15	0.47
1:E:42:LYS:HE2	1:E:45:LYS:NZ	2.30	0.47
1:D:112:ILE:HG13	1:E:140:PHE:CE2	2.50	0.47
1:B:215:THR:HG23	1:C:240:ARG:HH12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:42:LYS:HA	1:F:45:LYS:HB3	1.97	0.46
1:C:170:THR:HG21	1:D:145:ARG:CZ	2.45	0.46
1:B:203:LYS:O	1:B:204:ILE:HG13	2.15	0.46
1:A:241:SER:O	1:A:244:ILE:HG22	2.15	0.46
1:G:124:ILE:HG22	1:G:133:LYS:HB2	1.97	0.46
1:G:116:LEU:HD23	1:G:116:LEU:O	2.15	0.46
1:E:92:VAL:O	1:E:96:VAL:HG23	2.16	0.46
1:A:98:LEU:HA	1:A:98:LEU:HD23	1.46	0.46
1:B:19:GLY:O	1:B:22:LEU:HB3	2.15	0.46
1:G:42:LYS:NZ	1:G:46:LEU:HD11	2.30	0.46
1:F:116:LEU:HD13	1:G:140:PHE:CD2	2.51	0.46
1:E:187:ILE:O	1:E:191:HIS:HB2	2.16	0.46
1:D:127:ILE:HD11	1:D:164:ILE:HG23	1.98	0.46
1:A:170:THR:O	1:A:232:ILE:HD11	2.14	0.46
1:C:71:THR:O	1:C:75:LEU:HG	2.15	0.46
1:G:42:LYS:HA	1:G:45:LYS:HB3	1.97	0.46
1:B:136:ALA:HB3	1:B:143:SER:HB3	1.97	0.46
1:D:97:ALA:HA	1:E:95:ALA:HB2	1.97	0.46
1:F:98:LEU:HA	1:F:98:LEU:HD23	1.51	0.46
1:D:18:PHE:CE1	1:D:21:ILE:HD11	2.51	0.46
1:D:48:SER:HB2	1:D:55:ALA:HB1	1.97	0.46
1:A:23:ILE:O	1:A:27:ILE:HG13	2.16	0.46
1:A:263:LEU:HB3	1:G:263:LEU:HD11	1.96	0.46
1:A:251:LEU:HA	1:A:251:LEU:HD23	1.71	0.46
1:C:161:ASN:HD21	1:D:103:TYR:HE2	1.64	0.46
1:D:65:LEU:HA	1:D:65:LEU:HD12	1.70	0.46
1:E:65:LEU:HA	1:E:65:LEU:HD12	1.65	0.46
1:D:236:ILE:CG2	1:D:237:PHE:H	2.05	0.46
1:F:18:PHE:CE1	1:F:21:ILE:HD11	2.50	0.46
1:B:42:LYS:HE2	1:B:45:LYS:NZ	2.31	0.46
1:A:84:SER:CA	1:G:86:ILE:HD11	2.46	0.46
1:E:251:LEU:HD23	1:E:251:LEU:HA	1.60	0.46
1:E:44:MET:HG2	1:E:59:ALA:HB2	1.97	0.46
1:C:214:ILE:HG13	1:D:245:GLU:HG2	1.98	0.46
1:C:165:ILE:HA	1:D:152:ALA:HA	1.97	0.46
1:C:251:LEU:HA	1:C:251:LEU:HD23	1.75	0.46
1:B:86:ILE:CD1	1:C:84:SER:HA	2.46	0.46
1:B:18:PHE:CD2	1:B:22:LEU:HD22	2.51	0.46
1:A:265:ILE:CD1	1:G:265:ILE:HD13	2.46	0.46
1:A:235:GLY:O	1:A:236:ILE:C	2.55	0.46
1:D:40:ARG:HB2	1:D:63:PHE:HD1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:MET:O	1:C:48:SER:OG	2.29	0.45
1:F:88:VAL:HA	1:F:91:THR:HG22	1.98	0.45
1:C:117:HIS:ND1	1:C:117:HIS:O	2.48	0.45
1:A:18:PHE:CE2	1:A:22:LEU:HD22	2.50	0.45
1:D:265:ILE:HD13	1:E:265:ILE:HD12	1.98	0.45
1:G:251:LEU:HD22	1:G:256:ILE:HG21	1.99	0.45
1:F:259:PRO:HB3	1:F:262:LYS:NZ	2.31	0.45
1:C:18:PHE:CD2	1:C:22:LEU:HD22	2.51	0.45
1:F:177:TRP:HE1	1:F:244:ILE:HD12	1.81	0.45
1:B:215:THR:CB	1:B:225:THR:HG1	2.30	0.45
1:B:251:LEU:HA	1:B:251:LEU:HD23	1.75	0.45
1:D:214:ILE:HG12	1:D:224:PHE:CZ	2.52	0.45
1:D:29:PHE:O	1:D:33:PHE:HB2	2.17	0.45
1:B:123:ASP:O	1:B:134:VAL:HG12	2.17	0.45
1:D:42:LYS:HA	1:D:45:LYS:CB	2.46	0.45
1:E:127:ILE:HD13	1:E:164:ILE:HA	1.99	0.45
1:E:214:ILE:HG13	1:F:245:GLU:HG2	1.99	0.45
1:C:136:ALA:HB3	1:C:143:SER:HB3	1.99	0.45
1:D:92:VAL:O	1:D:96:VAL:HG23	2.16	0.45
1:G:108:ALA:HA	1:G:111:ILE:HB	1.98	0.45
1:G:236:ILE:CG2	1:G:237:PHE:N	2.77	0.45
1:D:177:TRP:HZ2	1:D:244:ILE:HD12	1.81	0.45
1:F:173:ARG:HE	1:F:173:ARG:HB3	1.57	0.45
1:D:188:GLU:HA	1:D:191:HIS:HB3	1.98	0.45
1:F:180:GLY:HA2	1:F:222:LEU:O	2.17	0.45
1:B:127:ILE:HD13	1:B:164:ILE:HA	1.97	0.45
1:E:29:PHE:O	1:E:33:PHE:HB2	2.17	0.45
1:G:48:SER:O	1:G:49:LYS:HG2	2.17	0.45
1:A:116:LEU:HD23	1:A:116:LEU:O	2.17	0.45
1:B:196:ASP:O	1:B:200:THR:HG23	2.16	0.45
1:A:95:ALA:HB2	1:G:97:ALA:HA	1.99	0.45
1:B:214:ILE:HG13	1:C:245:GLU:HG2	1.99	0.45
1:C:127:ILE:HD13	1:C:164:ILE:HA	1.97	0.44
1:F:29:PHE:O	1:F:33:PHE:CB	2.65	0.44
1:A:214:ILE:HG12	1:A:224:PHE:CZ	2.52	0.44
1:E:214:ILE:HG12	1:E:224:PHE:CZ	2.51	0.44
1:B:92:VAL:O	1:B:96:VAL:HG23	2.16	0.44
1:C:113:LEU:HD23	1:C:113:LEU:HA	1.52	0.44
1:A:21:ILE:H	1:A:21:ILE:HG13	1.65	0.44
1:C:42:LYS:NZ	1:C:46:LEU:HD11	2.32	0.44
1:A:87:THR:O	1:A:91:THR:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:GLU:HA	1:B:191:HIS:CB	2.47	0.44
1:A:64:ILE:O	1:A:68:ILE:HG13	2.18	0.44
1:A:127:ILE:HD13	1:A:164:ILE:HA	1.98	0.44
1:E:188:GLU:HA	1:E:191:HIS:HB2	1.98	0.44
1:A:140:PHE:HE2	1:G:112:ILE:CG1	2.30	0.44
1:E:43:THR:HG23	1:E:58:VAL:HG12	1.99	0.44
1:D:259:PRO:HB3	1:D:262:LYS:NZ	2.32	0.44
1:D:29:PHE:O	1:D:33:PHE:CB	2.65	0.44
1:F:265:ILE:HD13	1:G:265:ILE:HD11	1.99	0.44
1:F:117:HIS:ND1	1:F:117:HIS:O	2.51	0.44
1:E:40:ARG:HB2	1:E:63:PHE:HD1	1.82	0.44
1:B:217:PHE:CE2	1:C:258:ILE:HG12	2.53	0.44
1:A:65:LEU:HD12	1:A:65:LEU:HA	1.74	0.44
1:C:201:MET:HE3	1:C:246:ARG:HB2	1.97	0.44
1:E:235:GLY:HA2	1:E:239:VAL:CG2	2.45	0.44
1:G:123:ASP:O	1:G:134:VAL:HG12	2.17	0.44
1:C:42:LYS:HG2	1:C:45:LYS:HE3	1.98	0.44
1:A:251:LEU:HD22	1:A:256:ILE:HG21	1.99	0.44
1:D:107:ILE:HG12	1:D:140:PHE:CD1	2.53	0.44
1:C:116:LEU:HD13	1:D:140:PHE:CD2	2.52	0.44
1:A:48:SER:HB2	1:A:55:ALA:HB1	2.00	0.44
1:C:98:LEU:HD23	1:C:98:LEU:HA	1.55	0.44
1:A:39:LEU:O	1:A:43:THR:OG1	2.26	0.44
1:A:43:THR:HG23	1:A:58:VAL:HG12	2.00	0.44
1:E:112:ILE:HG13	1:F:140:PHE:CE2	2.52	0.44
1:F:138:ASN:HD22	1:F:141:ASN:HB2	1.82	0.44
1:D:62:THR:O	1:D:66:ILE:HG13	2.17	0.44
1:G:18:PHE:CE1	1:G:21:ILE:HD11	2.53	0.43
1:F:127:ILE:HA	1:F:127:ILE:HD13	1.70	0.43
1:E:116:LEU:HD11	1:F:139:PHE:HD2	1.83	0.43
1:A:171:ALA:O	1:A:232:ILE:HG13	2.17	0.43
1:E:36:SER:HB3	1:E:63:PHE:CE1	2.52	0.43
1:D:251:LEU:HD23	1:D:251:LEU:HA	1.73	0.43
1:G:210:THR:HG22	1:G:228:VAL:HG13	1.99	0.43
1:B:187:ILE:HG13	1:C:249:ASN:OD1	2.18	0.43
1:E:119:PHE:CE1	1:E:125:ILE:HD13	2.52	0.43
1:E:241:SER:O	1:E:244:ILE:HG22	2.18	0.43
1:C:114:ILE:CG1	1:C:137:LEU:HD21	2.48	0.43
1:C:265:ILE:HD13	1:D:265:ILE:HD12	2.00	0.43
1:A:114:ILE:CG1	1:A:137:LEU:HD21	2.46	0.43
1:E:173:ARG:HB3	1:E:173:ARG:HE	1.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:113:LEU:HA	1:F:113:LEU:HD23	1.48	0.43
1:G:188:GLU:HA	1:G:191:HIS:CB	2.48	0.43
1:A:248:LYS:CE	1:G:214:ILE:HG21	2.44	0.43
1:D:215:THR:HG23	1:E:240:ARG:HH12	1.83	0.43
1:C:125:ILE:HD12	1:C:127:ILE:HG12	2.00	0.43
1:E:19:GLY:O	1:E:22:LEU:HB3	2.17	0.43
1:F:40:ARG:HB2	1:F:63:PHE:HD1	1.84	0.43
1:C:104:LEU:HG	1:D:99:ALA:HB2	2.01	0.43
1:F:92:VAL:O	1:F:96:VAL:HG23	2.17	0.43
1:E:29:PHE:O	1:E:33:PHE:CB	2.66	0.43
1:G:19:GLY:O	1:G:22:LEU:HB3	2.17	0.43
1:F:177:TRP:CZ2	1:F:244:ILE:HD12	2.53	0.43
1:F:125:ILE:HD12	1:F:127:ILE:HG12	2.01	0.43
1:F:203:LYS:O	1:F:204:ILE:HG13	2.18	0.43
1:G:183:TYR:HD1	1:G:222:LEU:N	2.16	0.43
1:C:215:THR:CB	1:C:225:THR:HG1	2.29	0.43
1:A:116:LEU:O	1:A:118:PRO:HD3	2.18	0.43
1:G:40:ARG:HB2	1:G:63:PHE:HD1	1.82	0.43
1:A:247:ILE:O	1:A:251:LEU:HB2	2.18	0.43
1:D:103:TYR:O	1:D:106:SER:HB2	2.19	0.43
1:B:144:LEU:O	1:B:151:LEU:HA	2.19	0.43
1:D:188:GLU:HA	1:D:191:HIS:HB2	1.99	0.43
1:C:187:ILE:HG13	1:D:249:ASN:OD1	2.18	0.43
1:E:140:PHE:N	1:E:140:PHE:CD1	2.85	0.43
1:C:42:LYS:HE2	1:C:45:LYS:NZ	2.34	0.43
1:F:164:ILE:HD12	1:F:164:ILE:H	1.83	0.43
1:D:113:LEU:HA	1:D:113:LEU:HD23	1.66	0.43
1:A:97:ALA:HA	1:B:95:ALA:HB2	1.99	0.43
1:C:127:ILE:HD13	1:C:127:ILE:HA	1.74	0.43
1:A:145:ARG:CZ	1:G:170:THR:HG21	2.49	0.43
1:B:183:TYR:OH	1:B:217:PHE:HD2	2.01	0.43
1:B:112:ILE:CG1	1:C:140:PHE:CE2	3.02	0.43
1:D:86:ILE:HD12	1:E:84:SER:HA	2.00	0.43
1:A:226:ILE:HG22	1:A:228:VAL:HG23	2.00	0.43
1:B:154:LEU:HD12	1:B:154:LEU:N	2.34	0.43
1:B:109:GLY:O	1:B:113:LEU:HG	2.18	0.43
1:B:18:PHE:CE1	1:B:21:ILE:HD11	2.54	0.43
1:B:29:PHE:HD2	1:B:30:CYS:HG	1.67	0.43
1:B:27:ILE:O	1:B:31:ILE:HG13	2.18	0.43
1:G:42:LYS:HZ2	1:G:46:LEU:HD11	1.83	0.43
1:D:43:THR:HG21	1:D:58:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:PHE:CZ	1:B:125:ILE:HD13	2.54	0.43
1:C:86:ILE:HD11	1:D:84:SER:HA	2.01	0.43
1:E:235:GLY:O	1:E:236:ILE:C	2.56	0.43
1:F:214:ILE:HG21	1:G:248:LYS:CE	2.45	0.43
1:A:235:GLY:HA2	1:A:239:VAL:HG23	2.00	0.43
1:G:43:THR:HG21	1:G:58:VAL:O	2.19	0.42
1:F:112:ILE:HG13	1:G:140:PHE:HE2	1.84	0.42
1:C:265:ILE:HG21	1:D:265:ILE:HD12	2.01	0.42
1:F:42:LYS:HE2	1:F:45:LYS:NZ	2.34	0.42
1:E:18:PHE:CE2	1:E:22:LEU:HD22	2.54	0.42
1:A:42:LYS:HG2	1:A:45:LYS:HE3	2.00	0.42
1:A:44:MET:HA	1:A:48:SER:HB3	2.00	0.42
1:A:104:LEU:HG	1:B:99:ALA:HB2	2.00	0.42
1:E:64:ILE:O	1:E:68:ILE:HG13	2.19	0.42
1:B:86:ILE:HD12	1:C:84:SER:HA	2.01	0.42
1:A:138:ASN:HD22	1:A:141:ASN:HB2	1.85	0.42
1:A:203:LYS:NZ	1:A:234:ASP:OD2	2.31	0.42
1:B:127:ILE:HA	1:B:127:ILE:HD13	1.73	0.42
1:D:48:SER:O	1:D:49:LYS:HG2	2.18	0.42
1:E:214:ILE:HG23	1:E:222:LEU:HD11	2.00	0.42
1:C:265:ILE:HD13	1:D:265:ILE:HD11	2.01	0.42
1:A:140:PHE:CE2	1:G:112:ILE:HG13	2.51	0.42
1:B:112:ILE:CG1	1:C:140:PHE:HE2	2.32	0.42
1:D:85:ILE:O	1:D:86:ILE:C	2.56	0.42
1:G:136:ALA:HB3	1:G:143:SER:CB	2.49	0.42
1:E:97:ALA:HA	1:F:95:ALA:HB2	2.02	0.42
1:B:43:THR:HG23	1:B:58:VAL:HG12	2.01	0.42
1:E:186:ASP:HB3	1:E:189:LEU:CG	2.40	0.42
1:C:214:ILE:HG23	1:C:222:LEU:CD1	2.50	0.42
1:F:19:GLY:O	1:F:22:LEU:HB3	2.20	0.42
1:F:241:SER:O	1:F:244:ILE:HG22	2.20	0.42
1:A:188:GLU:HA	1:A:191:HIS:HB3	2.00	0.42
1:E:215:THR:OG1	1:E:225:THR:OG1	2.31	0.42
1:G:48:SER:HB2	1:G:55:ALA:HB1	2.01	0.42
1:A:265:ILE:HD13	1:B:265:ILE:CD1	2.50	0.42
1:D:228:VAL:HG12	1:D:229:TRP:N	2.35	0.42
1:C:188:GLU:HA	1:C:191:HIS:CB	2.49	0.42
1:E:203:LYS:O	1:E:204:ILE:HG13	2.19	0.42
1:E:113:LEU:HA	1:E:113:LEU:HD23	1.61	0.42
1:D:170:THR:OG1	1:E:151:LEU:HD21	2.18	0.42
1:D:104:LEU:HG	1:E:99:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:124:ILE:HG22	1:C:133:LYS:HB2	2.00	0.42
1:B:64:ILE:O	1:B:68:ILE:HG13	2.20	0.42
1:B:113:LEU:HA	1:B:113:LEU:HD23	1.42	0.42
1:E:110:GLY:HA3	1:E:156:ASN:HD22	1.84	0.42
1:E:98:LEU:HA	1:E:98:LEU:HD23	1.56	0.42
1:E:44:MET:CA	1:E:48:SER:HB3	2.44	0.42
1:A:215:THR:OG1	1:A:225:THR:OG1	2.23	0.42
1:F:64:ILE:HG13	1:F:64:ILE:H	1.68	0.42
1:A:265:ILE:HD13	1:B:265:ILE:HD12	2.01	0.42
1:F:119:PHE:CE1	1:F:125:ILE:HD13	2.55	0.42
1:E:105:SER:HB3	1:E:157:ARG:NH2	2.34	0.42
1:F:227:ARG:HH12	1:G:236:ILE:HD11	1.84	0.42
1:D:124:ILE:HG13	1:D:167:SER:HB2	2.00	0.42
1:G:171:ALA:O	1:G:232:ILE:HG13	2.20	0.42
1:C:177:TRP:CZ2	1:C:244:ILE:CD1	3.02	0.42
1:D:116:LEU:HD13	1:E:140:PHE:CD2	2.54	0.42
1:F:161:ASN:ND2	1:G:103:TYR:HE2	2.17	0.42
1:C:43:THR:HG21	1:C:58:VAL:O	2.20	0.42
1:A:161:ASN:HD21	1:B:103:TYR:HE2	1.68	0.42
1:C:34:TYR:O	1:C:37:PHE:N	2.51	0.42
1:F:29:PHE:O	1:F:33:PHE:HB2	2.20	0.41
1:F:64:ILE:O	1:F:68:ILE:HG13	2.20	0.41
1:A:125:ILE:HD12	1:A:127:ILE:HG12	2.02	0.41
1:E:215:THR:HG23	1:F:240:ARG:HH12	1.84	0.41
1:G:42:LYS:HG2	1:G:45:LYS:HE3	2.02	0.41
1:F:171:ALA:HA	1:F:232:ILE:HD12	2.01	0.41
1:B:173:ARG:HE	1:B:173:ARG:HB3	1.61	0.41
1:A:186:ASP:HB3	1:A:189:LEU:CG	2.43	0.41
1:C:177:TRP:HZ2	1:C:244:ILE:HD12	1.85	0.41
1:D:127:ILE:HD13	1:D:164:ILE:HA	2.03	0.41
1:C:228:VAL:HG12	1:C:229:TRP:N	2.35	0.41
1:D:251:LEU:HD22	1:D:256:ILE:HG21	2.02	0.41
1:A:142:THR:OG1	1:A:156:ASN:OD1	2.38	0.41
1:A:240:ARG:HH12	1:G:215:THR:HG23	1.85	0.41
1:A:29:PHE:O	1:A:33:PHE:CB	2.69	0.41
1:A:183:TYR:HD1	1:A:222:LEU:N	2.18	0.41
1:D:42:LYS:NZ	1:D:46:LEU:HD11	2.36	0.41
1:A:227:ARG:HH22	1:B:236:ILE:HD11	1.84	0.41
1:F:72:ILE:HD11	1:F:85:ILE:HG22	2.02	0.41
1:D:171:ALA:O	1:D:232:ILE:HG13	2.21	0.41
1:C:44:MET:HG2	1:C:59:ALA:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:228:VAL:HG12	1:F:229:TRP:N	2.36	0.41
1:B:43:THR:CG2	1:B:58:VAL:HG12	2.50	0.41
1:E:203:LYS:NZ	1:E:234:ASP:OD2	2.44	0.41
1:B:138:ASN:HD22	1:B:141:ASN:HB2	1.85	0.41
1:E:44:MET:HB3	1:E:44:MET:HE3	1.84	0.41
1:C:217:PHE:CD1	1:D:248:LYS:NZ	2.88	0.41
1:F:188:GLU:HA	1:F:191:HIS:HB3	2.01	0.41
1:E:214:ILE:HG21	1:E:214:ILE:HD13	1.88	0.41
1:E:116:LEU:HD13	1:F:140:PHE:CZ	2.56	0.41
1:F:65:LEU:HA	1:F:65:LEU:HD12	1.70	0.41
1:B:259:PRO:HB3	1:B:262:LYS:HZ2	1.83	0.41
1:D:214:ILE:HG13	1:E:245:GLU:HG2	2.01	0.41
1:D:127:ILE:HG23	1:D:127:ILE:HD12	1.77	0.41
1:A:72:ILE:HD11	1:A:85:ILE:HG22	2.02	0.41
1:B:62:THR:O	1:B:66:ILE:HG13	2.20	0.41
1:C:180:GLY:HA2	1:C:222:LEU:O	2.21	0.41
1:F:201:MET:HB3	1:F:204:ILE:HD12	2.03	0.41
1:B:242:GLU:O	1:B:245:GLU:N	2.53	0.41
1:D:64:ILE:HG13	1:D:64:ILE:H	1.71	0.41
1:A:140:PHE:CE2	1:G:112:ILE:CG1	3.04	0.41
1:A:220:SER:CB	1:A:262:LYS:H	2.23	0.41
1:B:187:ILE:O	1:B:191:HIS:HB2	2.21	0.41
1:A:263:LEU:HD11	1:B:263:LEU:HD23	2.03	0.41
1:A:117:HIS:O	1:A:117:HIS:ND1	2.54	0.41
1:G:127:ILE:HA	1:G:127:ILE:HD13	1.77	0.41
1:F:208:MET:HA	1:F:209:PRO:HD3	1.96	0.41
1:G:65:LEU:O	1:G:69:ILE:HG13	2.20	0.41
1:C:220:SER:CB	1:C:262:LYS:H	2.21	0.41
1:A:178:VAL:HG12	1:A:223:ASN:HB3	2.02	0.41
1:A:215:THR:CB	1:A:225:THR:HG1	2.28	0.41
1:G:29:PHE:O	1:G:33:PHE:CB	2.69	0.41
1:A:125:ILE:O	1:A:131:GLU:HG3	2.21	0.41
1:F:124:ILE:HG22	1:F:133:LYS:HB2	2.01	0.41
1:B:38:PHE:O	1:B:42:LYS:HB2	2.21	0.41
1:G:127:ILE:HG23	1:G:127:ILE:HD12	1.85	0.41
1:B:109:GLY:HA2	1:C:103:TYR:CZ	2.56	0.41
1:F:114:ILE:HG13	1:F:137:LEU:HD21	2.02	0.41
1:A:32:GLY:O	1:A:35:PHE:N	2.54	0.41
1:E:26:VAL:HG23	1:E:26:VAL:H	1.60	0.41
1:A:144:LEU:O	1:A:151:LEU:HA	2.19	0.41
1:D:64:ILE:O	1:D:68:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:ILE:HG12	1:B:140:PHE:CE1	2.55	0.41
1:C:107:ILE:HG12	1:C:140:PHE:CD1	2.55	0.41
1:C:100:LEU:O	1:C:104:LEU:HB3	2.20	0.41
1:A:110:GLY:HA3	1:A:156:ASN:HD22	1.86	0.41
1:A:85:ILE:HD11	1:G:73:ILE:HD11	2.02	0.41
1:E:117:HIS:O	1:E:117:HIS:ND1	2.54	0.40
1:C:181:VAL:O	1:C:259:PRO:HD3	2.21	0.40
1:D:18:PHE:CD2	1:D:22:LEU:HD22	2.56	0.40
1:F:177:TRP:NE1	1:F:244:ILE:HD12	2.37	0.40
1:C:112:ILE:CG1	1:D:140:PHE:CE2	3.04	0.40
1:E:263:LEU:HD11	1:F:263:LEU:HB3	2.02	0.40
1:B:125:ILE:O	1:B:131:GLU:HG3	2.21	0.40
1:G:138:ASN:HD22	1:G:141:ASN:HB2	1.86	0.40
1:G:214:ILE:HG12	1:G:224:PHE:CZ	2.56	0.40
1:D:44:MET:HG2	1:D:59:ALA:HB2	2.03	0.40
1:G:42:LYS:HE2	1:G:45:LYS:NZ	2.35	0.40
1:F:251:LEU:HD23	1:F:251:LEU:HA	1.68	0.40
1:G:173:ARG:HE	1:G:173:ARG:HB3	1.53	0.40
1:A:215:THR:HG23	1:B:240:ARG:HH12	1.86	0.40
1:G:178:VAL:CG1	1:G:223:ASN:HB3	2.52	0.40
1:B:171:ALA:HA	1:B:232:ILE:HD12	2.02	0.40
1:G:176:GLU:HA	1:G:226:ILE:O	2.22	0.40
1:G:142:THR:OG1	1:G:156:ASN:OD1	2.38	0.40
1:F:220:SER:HB2	1:F:262:LYS:N	2.16	0.40
1:C:259:PRO:HB3	1:C:262:LYS:NZ	2.35	0.40
1:B:188:GLU:HA	1:B:191:HIS:HB2	2.02	0.40
1:D:44:MET:HA	1:D:48:SER:HB3	2.04	0.40
1:D:178:VAL:HG12	1:D:223:ASN:HB3	2.02	0.40
1:D:173:ARG:HB3	1:D:173:ARG:HE	1.59	0.40
1:C:65:LEU:HD12	1:C:65:LEU:HA	1.78	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	251/309 (81%)	235 (94%)	15 (6%)	1 (0%)	39	79
1	B	251/309 (81%)	236 (94%)	14 (6%)	1 (0%)	39	79
1	C	251/309 (81%)	232 (92%)	17 (7%)	2 (1%)	24	69
1	D	251/309 (81%)	234 (93%)	16 (6%)	1 (0%)	39	79
1	E	251/309 (81%)	234 (93%)	16 (6%)	1 (0%)	39	79
1	F	251/309 (81%)	232 (92%)	18 (7%)	1 (0%)	39	79
1	G	251/309 (81%)	232 (92%)	17 (7%)	2 (1%)	24	69
All	All	1757/2163 (81%)	1635 (93%)	113 (6%)	9 (0%)	34	76

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	ILE
1	D	236	ILE
1	E	236	ILE
1	F	236	ILE
1	G	236	ILE
1	C	236	ILE
1	G	138	ASN
1	B	237	PHE
1	C	118	PRO

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	220/272 (81%)	216 (98%)	4 (2%)	66	87
1	B	220/272 (81%)	214 (97%)	6 (3%)	52	80
1	C	220/272 (81%)	214 (97%)	6 (3%)	52	80
1	D	220/272 (81%)	217 (99%)	3 (1%)	74	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	220/272 (81%)	211 (96%)	9 (4%)	37	73
1	F	220/272 (81%)	213 (97%)	7 (3%)	46	78
1	G	220/272 (81%)	216 (98%)	4 (2%)	66	87
All	All	1540/1904 (81%)	1501 (98%)	39 (2%)	55	82

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	PHE
1	A	134	VAL
1	A	140	PHE
1	A	236	ILE
1	B	35	PHE
1	B	50	LYS
1	B	112	ILE
1	B	134	VAL
1	B	140	PHE
1	B	236	ILE
1	C	35	PHE
1	C	112	ILE
1	C	134	VAL
1	C	140	PHE
1	C	222	LEU
1	C	236	ILE
1	D	35	PHE
1	D	112	ILE
1	D	134	VAL
1	E	35	PHE
1	E	48	SER
1	E	49	LYS
1	E	112	ILE
1	E	116	LEU
1	E	134	VAL
1	E	140	PHE
1	E	222	LEU
1	E	236	ILE
1	F	35	PHE
1	F	112	ILE
1	F	134	VAL
1	F	140	PHE
1	F	233	GLU

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Mol	Chain	Res	Type
1	F	236	ILE
1	F	237	PHE
1	G	35	PHE
1	G	112	ILE
1	G	134	VAL
1	G	140	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	A	169	ASN
1	A	270	GLN
1	B	138	ASN
1	B	169	ASN
1	B	207	ASN
1	B	270	GLN
1	C	138	ASN
1	C	169	ASN
1	C	270	GLN
1	D	138	ASN
1	D	169	ASN
1	D	270	GLN
1	E	138	ASN
1	E	168	ASN
1	E	207	ASN
1	E	238	ASN
1	E	270	GLN
1	F	138	ASN
1	F	141	ASN
1	F	169	ASN
1	F	238	ASN
1	F	270	GLN
1	G	138	ASN
1	G	169	ASN
1	G	270	GLN

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	253/309 (81%)	0.37	17 (6%) 21 14	46, 121, 198, 228	0
1	B	253/309 (81%)	0.09	7 (2%) 56 45	52, 120, 196, 222	0
1	C	253/309 (81%)	0.06	9 (3%) 46 36	52, 119, 191, 234	0
1	D	253/309 (81%)	0.00	10 (3%) 42 32	55, 117, 190, 216	0
1	E	253/309 (81%)	0.09	12 (4%) 35 27	55, 117, 191, 221	0
1	F	253/309 (81%)	-0.01	7 (2%) 56 45	54, 117, 189, 235	0
1	G	253/309 (81%)	0.12	14 (5%) 29 21	53, 120, 188, 221	0
All	All	1771/2163 (81%)	0.10	76 (4%) 39 30	46, 119, 194, 235	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	49	LYS	9.5
1	D	270	GLN	5.0
1	A	270	GLN	5.0
1	C	270	GLN	4.8
1	B	136	ALA	4.4
1	D	167	SER	4.2
1	G	205	ASP	4.1
1	A	47	LEU	4.1
1	D	269	ASN	4.1
1	F	270	GLN	4.0
1	B	131	GLU	4.0
1	E	49	LYS	3.9
1	E	42	LYS	3.8
1	E	43	THR	3.7
1	A	48	SER	3.6
1	D	38	PHE	3.4
1	A	51	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	G	49	LYS	3.4
1	G	270	GLN	3.4
1	B	135	GLU	3.3
1	E	45	LYS	3.3
1	A	172	CYS	3.0
1	A	43	THR	3.0
1	E	41	ASN	3.0
1	A	50	LYS	3.0
1	F	207	ASN	3.0
1	E	46	LEU	2.9
1	A	173	ARG	2.9
1	B	270	GLN	2.9
1	E	47	LEU	2.8
1	C	81	GLN	2.8
1	C	268	LYS	2.8
1	E	270	GLN	2.7
1	G	170	THR	2.7
1	D	166	ASN	2.7
1	E	173	ARG	2.6
1	A	118	PRO	2.6
1	G	118	PRO	2.6
1	C	49	LYS	2.6
1	D	45	LYS	2.6
1	G	234	ASP	2.6
1	B	269	ASN	2.6
1	G	231	LYS	2.5
1	B	169	ASN	2.5
1	G	119	PHE	2.5
1	A	170	THR	2.5
1	F	42	LYS	2.5
1	F	173	ARG	2.5
1	A	39	LEU	2.5
1	C	131	GLU	2.5
1	A	52	GLU	2.5
1	G	173	ARG	2.5
1	D	183	TYR	2.4
1	A	54	LEU	2.4
1	E	131	GLU	2.4
1	D	80	VAL	2.4
1	G	121	LYS	2.3
1	B	167	SER	2.3
1	F	183	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	211	PHE	2.2
1	E	151	LEU	2.2
1	G	172	CYS	2.2
1	A	233	GLU	2.2
1	C	173	ARG	2.2
1	G	233	GLU	2.2
1	C	25	ALA	2.1
1	E	183	TYR	2.1
1	A	230	ALA	2.1
1	C	230	ALA	2.1
1	F	43	THR	2.0
1	G	164	ILE	2.0
1	A	203	LYS	2.0
1	C	269	ASN	2.0
1	G	167	SER	2.0
1	D	78	LEU	2.0
1	D	39	LEU	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 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.