



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:52 AM UTC

PDB ID : 3IA0 / pdb_00003ia0
Title : Ethanolamine Utilization Microcompartment Shell Subunit, EutS-G39V mutant
Authors : Tanaka, S.; Sawaya, M.R.; Yeates, T.O.
Deposited on : 2009-07-13
Resolution : 2.50 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:

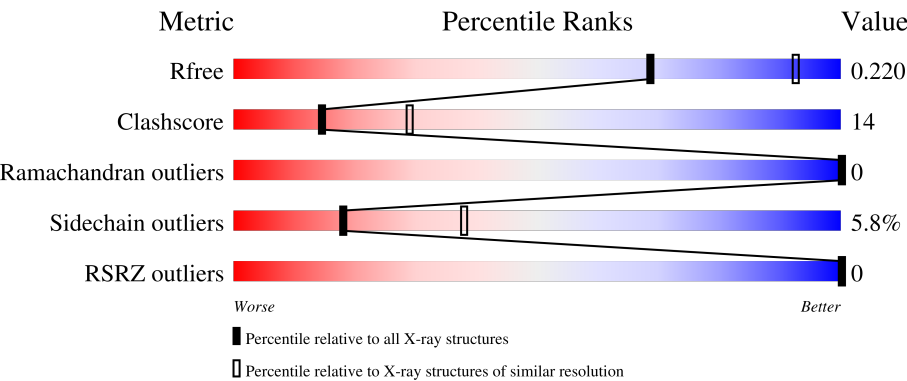
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	119	71%21%• 7%
1	B	119	71%21%• 7%
1	C	119	71%21%• 7%
1	D	119	71%21%• 7%
1	E	119	70%22%• 7%

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Mol	Chain	Length	Quality of chain
1	F	119	
1	G	119	
1	H	119	
1	I	119	
1	J	119	
1	K	119	
1	L	119	
1	M	119	
1	N	119	
1	O	119	
1	P	119	
1	Q	119	
1	R	119	
1	S	119	
1	T	119	
1	U	119	
1	V	119	
1	W	119	
1	X	119	
1	Y	119	
1	Z	119	
1	a	119	
1	b	119	
1	c	119	
1	d	119	

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Mol	Chain	Length	Quality of chain
1	e	119	 71%19%7%
1	f	119	 71%20%7%
1	g	119	 71%20%7%
1	h	119	 72%19%7%
1	i	119	 74%18%7%
1	j	119	 70%21%7%
1	k	119	 69%23%7%
1	l	119	 68%24%7%
1	m	119	 65%27%7%
1	n	119	 71%19%7%
1	o	119	 72%19%7%
1	p	119	 71%20%7%
1	q	119	 69%23%7%
1	r	119	 71%21%7%
1	s	119	 71%21%7%
1	t	119	 71%20%7%
1	u	119	 72%19%7%
1	v	119	 71%21%7%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 39312 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 Ethanolamine utilization protein eutS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	B	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	C	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	D	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	E	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	F	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	G	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	H	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	I	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	J	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	K	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	L	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	M	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	N	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	O	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	P	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	R	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	S	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	T	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	U	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	V	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	W	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	X	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	Y	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	Z	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	a	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	b	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	c	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	d	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	e	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	f	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	g	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	h	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	i	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	j	111	Total 819	C 524	N 136	O 155	S 4	0	0	0
1	k	111	Total 819	C 524	N 136	O 155	S 4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	l	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	m	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	n	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	o	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	p	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	q	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	r	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	s	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	t	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	u	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			
1	v	111	Total	C	N	O	S	0	0	0
			819	524	136	155	4			

There are 432 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	VAL	GLY	engineered mutation	UNP P63746
A	112	LEU	-	expression tag	UNP P63746
A	113	GLU	-	expression tag	UNP P63746
A	114	HIS	-	expression tag	UNP P63746
A	115	HIS	-	expression tag	UNP P63746
A	116	HIS	-	expression tag	UNP P63746
A	117	HIS	-	expression tag	UNP P63746
A	118	HIS	-	expression tag	UNP P63746
A	119	HIS	-	expression tag	UNP P63746
B	39	VAL	GLY	engineered mutation	UNP P63746
B	112	LEU	-	expression tag	UNP P63746
B	113	GLU	-	expression tag	UNP P63746
B	114	HIS	-	expression tag	UNP P63746
B	115	HIS	-	expression tag	UNP P63746
B	116	HIS	-	expression tag	UNP P63746
B	117	HIS	-	expression tag	UNP P63746
B	118	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
B	119	HIS	-	expression tag	UNP P63746
C	39	VAL	GLY	engineered mutation	UNP P63746
C	112	LEU	-	expression tag	UNP P63746
C	113	GLU	-	expression tag	UNP P63746
C	114	HIS	-	expression tag	UNP P63746
C	115	HIS	-	expression tag	UNP P63746
C	116	HIS	-	expression tag	UNP P63746
C	117	HIS	-	expression tag	UNP P63746
C	118	HIS	-	expression tag	UNP P63746
C	119	HIS	-	expression tag	UNP P63746
D	39	VAL	GLY	engineered mutation	UNP P63746
D	112	LEU	-	expression tag	UNP P63746
D	113	GLU	-	expression tag	UNP P63746
D	114	HIS	-	expression tag	UNP P63746
D	115	HIS	-	expression tag	UNP P63746
D	116	HIS	-	expression tag	UNP P63746
D	117	HIS	-	expression tag	UNP P63746
D	118	HIS	-	expression tag	UNP P63746
D	119	HIS	-	expression tag	UNP P63746
E	39	VAL	GLY	engineered mutation	UNP P63746
E	112	LEU	-	expression tag	UNP P63746
E	113	GLU	-	expression tag	UNP P63746
E	114	HIS	-	expression tag	UNP P63746
E	115	HIS	-	expression tag	UNP P63746
E	116	HIS	-	expression tag	UNP P63746
E	117	HIS	-	expression tag	UNP P63746
E	118	HIS	-	expression tag	UNP P63746
E	119	HIS	-	expression tag	UNP P63746
F	39	VAL	GLY	engineered mutation	UNP P63746
F	112	LEU	-	expression tag	UNP P63746
F	113	GLU	-	expression tag	UNP P63746
F	114	HIS	-	expression tag	UNP P63746
F	115	HIS	-	expression tag	UNP P63746
F	116	HIS	-	expression tag	UNP P63746
F	117	HIS	-	expression tag	UNP P63746
F	118	HIS	-	expression tag	UNP P63746
F	119	HIS	-	expression tag	UNP P63746
G	39	VAL	GLY	engineered mutation	UNP P63746
G	112	LEU	-	expression tag	UNP P63746
G	113	GLU	-	expression tag	UNP P63746
G	114	HIS	-	expression tag	UNP P63746
G	115	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
G	116	HIS	-	expression tag	UNP P63746
G	117	HIS	-	expression tag	UNP P63746
G	118	HIS	-	expression tag	UNP P63746
G	119	HIS	-	expression tag	UNP P63746
H	39	VAL	GLY	engineered mutation	UNP P63746
H	112	LEU	-	expression tag	UNP P63746
H	113	GLU	-	expression tag	UNP P63746
H	114	HIS	-	expression tag	UNP P63746
H	115	HIS	-	expression tag	UNP P63746
H	116	HIS	-	expression tag	UNP P63746
H	117	HIS	-	expression tag	UNP P63746
H	118	HIS	-	expression tag	UNP P63746
H	119	HIS	-	expression tag	UNP P63746
I	39	VAL	GLY	engineered mutation	UNP P63746
I	112	LEU	-	expression tag	UNP P63746
I	113	GLU	-	expression tag	UNP P63746
I	114	HIS	-	expression tag	UNP P63746
I	115	HIS	-	expression tag	UNP P63746
I	116	HIS	-	expression tag	UNP P63746
I	117	HIS	-	expression tag	UNP P63746
I	118	HIS	-	expression tag	UNP P63746
I	119	HIS	-	expression tag	UNP P63746
J	39	VAL	GLY	engineered mutation	UNP P63746
J	112	LEU	-	expression tag	UNP P63746
J	113	GLU	-	expression tag	UNP P63746
J	114	HIS	-	expression tag	UNP P63746
J	115	HIS	-	expression tag	UNP P63746
J	116	HIS	-	expression tag	UNP P63746
J	117	HIS	-	expression tag	UNP P63746
J	118	HIS	-	expression tag	UNP P63746
J	119	HIS	-	expression tag	UNP P63746
K	39	VAL	GLY	engineered mutation	UNP P63746
K	112	LEU	-	expression tag	UNP P63746
K	113	GLU	-	expression tag	UNP P63746
K	114	HIS	-	expression tag	UNP P63746
K	115	HIS	-	expression tag	UNP P63746
K	116	HIS	-	expression tag	UNP P63746
K	117	HIS	-	expression tag	UNP P63746
K	118	HIS	-	expression tag	UNP P63746
K	119	HIS	-	expression tag	UNP P63746
L	39	VAL	GLY	engineered mutation	UNP P63746
L	112	LEU	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
L	113	GLU	-	expression tag	UNP P63746
L	114	HIS	-	expression tag	UNP P63746
L	115	HIS	-	expression tag	UNP P63746
L	116	HIS	-	expression tag	UNP P63746
L	117	HIS	-	expression tag	UNP P63746
L	118	HIS	-	expression tag	UNP P63746
L	119	HIS	-	expression tag	UNP P63746
M	39	VAL	GLY	engineered mutation	UNP P63746
M	112	LEU	-	expression tag	UNP P63746
M	113	GLU	-	expression tag	UNP P63746
M	114	HIS	-	expression tag	UNP P63746
M	115	HIS	-	expression tag	UNP P63746
M	116	HIS	-	expression tag	UNP P63746
M	117	HIS	-	expression tag	UNP P63746
M	118	HIS	-	expression tag	UNP P63746
M	119	HIS	-	expression tag	UNP P63746
N	39	VAL	GLY	engineered mutation	UNP P63746
N	112	LEU	-	expression tag	UNP P63746
N	113	GLU	-	expression tag	UNP P63746
N	114	HIS	-	expression tag	UNP P63746
N	115	HIS	-	expression tag	UNP P63746
N	116	HIS	-	expression tag	UNP P63746
N	117	HIS	-	expression tag	UNP P63746
N	118	HIS	-	expression tag	UNP P63746
N	119	HIS	-	expression tag	UNP P63746
O	39	VAL	GLY	engineered mutation	UNP P63746
O	112	LEU	-	expression tag	UNP P63746
O	113	GLU	-	expression tag	UNP P63746
O	114	HIS	-	expression tag	UNP P63746
O	115	HIS	-	expression tag	UNP P63746
O	116	HIS	-	expression tag	UNP P63746
O	117	HIS	-	expression tag	UNP P63746
O	118	HIS	-	expression tag	UNP P63746
O	119	HIS	-	expression tag	UNP P63746
P	39	VAL	GLY	engineered mutation	UNP P63746
P	112	LEU	-	expression tag	UNP P63746
P	113	GLU	-	expression tag	UNP P63746
P	114	HIS	-	expression tag	UNP P63746
P	115	HIS	-	expression tag	UNP P63746
P	116	HIS	-	expression tag	UNP P63746
P	117	HIS	-	expression tag	UNP P63746
P	118	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
P	119	HIS	-	expression tag	UNP P63746
Q	39	VAL	GLY	engineered mutation	UNP P63746
Q	112	LEU	-	expression tag	UNP P63746
Q	113	GLU	-	expression tag	UNP P63746
Q	114	HIS	-	expression tag	UNP P63746
Q	115	HIS	-	expression tag	UNP P63746
Q	116	HIS	-	expression tag	UNP P63746
Q	117	HIS	-	expression tag	UNP P63746
Q	118	HIS	-	expression tag	UNP P63746
Q	119	HIS	-	expression tag	UNP P63746
R	39	VAL	GLY	engineered mutation	UNP P63746
R	112	LEU	-	expression tag	UNP P63746
R	113	GLU	-	expression tag	UNP P63746
R	114	HIS	-	expression tag	UNP P63746
R	115	HIS	-	expression tag	UNP P63746
R	116	HIS	-	expression tag	UNP P63746
R	117	HIS	-	expression tag	UNP P63746
R	118	HIS	-	expression tag	UNP P63746
R	119	HIS	-	expression tag	UNP P63746
S	39	VAL	GLY	engineered mutation	UNP P63746
S	112	LEU	-	expression tag	UNP P63746
S	113	GLU	-	expression tag	UNP P63746
S	114	HIS	-	expression tag	UNP P63746
S	115	HIS	-	expression tag	UNP P63746
S	116	HIS	-	expression tag	UNP P63746
S	117	HIS	-	expression tag	UNP P63746
S	118	HIS	-	expression tag	UNP P63746
S	119	HIS	-	expression tag	UNP P63746
T	39	VAL	GLY	engineered mutation	UNP P63746
T	112	LEU	-	expression tag	UNP P63746
T	113	GLU	-	expression tag	UNP P63746
T	114	HIS	-	expression tag	UNP P63746
T	115	HIS	-	expression tag	UNP P63746
T	116	HIS	-	expression tag	UNP P63746
T	117	HIS	-	expression tag	UNP P63746
T	118	HIS	-	expression tag	UNP P63746
T	119	HIS	-	expression tag	UNP P63746
U	39	VAL	GLY	engineered mutation	UNP P63746
U	112	LEU	-	expression tag	UNP P63746
U	113	GLU	-	expression tag	UNP P63746
U	114	HIS	-	expression tag	UNP P63746
U	115	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
U	116	HIS	-	expression tag	UNP P63746
U	117	HIS	-	expression tag	UNP P63746
U	118	HIS	-	expression tag	UNP P63746
U	119	HIS	-	expression tag	UNP P63746
V	39	VAL	GLY	engineered mutation	UNP P63746
V	112	LEU	-	expression tag	UNP P63746
V	113	GLU	-	expression tag	UNP P63746
V	114	HIS	-	expression tag	UNP P63746
V	115	HIS	-	expression tag	UNP P63746
V	116	HIS	-	expression tag	UNP P63746
V	117	HIS	-	expression tag	UNP P63746
V	118	HIS	-	expression tag	UNP P63746
V	119	HIS	-	expression tag	UNP P63746
W	39	VAL	GLY	engineered mutation	UNP P63746
W	112	LEU	-	expression tag	UNP P63746
W	113	GLU	-	expression tag	UNP P63746
W	114	HIS	-	expression tag	UNP P63746
W	115	HIS	-	expression tag	UNP P63746
W	116	HIS	-	expression tag	UNP P63746
W	117	HIS	-	expression tag	UNP P63746
W	118	HIS	-	expression tag	UNP P63746
W	119	HIS	-	expression tag	UNP P63746
X	39	VAL	GLY	engineered mutation	UNP P63746
X	112	LEU	-	expression tag	UNP P63746
X	113	GLU	-	expression tag	UNP P63746
X	114	HIS	-	expression tag	UNP P63746
X	115	HIS	-	expression tag	UNP P63746
X	116	HIS	-	expression tag	UNP P63746
X	117	HIS	-	expression tag	UNP P63746
X	118	HIS	-	expression tag	UNP P63746
X	119	HIS	-	expression tag	UNP P63746
Y	39	VAL	GLY	engineered mutation	UNP P63746
Y	112	LEU	-	expression tag	UNP P63746
Y	113	GLU	-	expression tag	UNP P63746
Y	114	HIS	-	expression tag	UNP P63746
Y	115	HIS	-	expression tag	UNP P63746
Y	116	HIS	-	expression tag	UNP P63746
Y	117	HIS	-	expression tag	UNP P63746
Y	118	HIS	-	expression tag	UNP P63746
Y	119	HIS	-	expression tag	UNP P63746
Z	39	VAL	GLY	engineered mutation	UNP P63746
Z	112	LEU	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	113	GLU	-	expression tag	UNP P63746
Z	114	HIS	-	expression tag	UNP P63746
Z	115	HIS	-	expression tag	UNP P63746
Z	116	HIS	-	expression tag	UNP P63746
Z	117	HIS	-	expression tag	UNP P63746
Z	118	HIS	-	expression tag	UNP P63746
Z	119	HIS	-	expression tag	UNP P63746
a	39	VAL	GLY	engineered mutation	UNP P63746
a	112	LEU	-	expression tag	UNP P63746
a	113	GLU	-	expression tag	UNP P63746
a	114	HIS	-	expression tag	UNP P63746
a	115	HIS	-	expression tag	UNP P63746
a	116	HIS	-	expression tag	UNP P63746
a	117	HIS	-	expression tag	UNP P63746
a	118	HIS	-	expression tag	UNP P63746
a	119	HIS	-	expression tag	UNP P63746
b	39	VAL	GLY	engineered mutation	UNP P63746
b	112	LEU	-	expression tag	UNP P63746
b	113	GLU	-	expression tag	UNP P63746
b	114	HIS	-	expression tag	UNP P63746
b	115	HIS	-	expression tag	UNP P63746
b	116	HIS	-	expression tag	UNP P63746
b	117	HIS	-	expression tag	UNP P63746
b	118	HIS	-	expression tag	UNP P63746
b	119	HIS	-	expression tag	UNP P63746
c	39	VAL	GLY	engineered mutation	UNP P63746
c	112	LEU	-	expression tag	UNP P63746
c	113	GLU	-	expression tag	UNP P63746
c	114	HIS	-	expression tag	UNP P63746
c	115	HIS	-	expression tag	UNP P63746
c	116	HIS	-	expression tag	UNP P63746
c	117	HIS	-	expression tag	UNP P63746
c	118	HIS	-	expression tag	UNP P63746
c	119	HIS	-	expression tag	UNP P63746
d	39	VAL	GLY	engineered mutation	UNP P63746
d	112	LEU	-	expression tag	UNP P63746
d	113	GLU	-	expression tag	UNP P63746
d	114	HIS	-	expression tag	UNP P63746
d	115	HIS	-	expression tag	UNP P63746
d	116	HIS	-	expression tag	UNP P63746
d	117	HIS	-	expression tag	UNP P63746
d	118	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
d	119	HIS	-	expression tag	UNP P63746
e	39	VAL	GLY	engineered mutation	UNP P63746
e	112	LEU	-	expression tag	UNP P63746
e	113	GLU	-	expression tag	UNP P63746
e	114	HIS	-	expression tag	UNP P63746
e	115	HIS	-	expression tag	UNP P63746
e	116	HIS	-	expression tag	UNP P63746
e	117	HIS	-	expression tag	UNP P63746
e	118	HIS	-	expression tag	UNP P63746
e	119	HIS	-	expression tag	UNP P63746
f	39	VAL	GLY	engineered mutation	UNP P63746
f	112	LEU	-	expression tag	UNP P63746
f	113	GLU	-	expression tag	UNP P63746
f	114	HIS	-	expression tag	UNP P63746
f	115	HIS	-	expression tag	UNP P63746
f	116	HIS	-	expression tag	UNP P63746
f	117	HIS	-	expression tag	UNP P63746
f	118	HIS	-	expression tag	UNP P63746
f	119	HIS	-	expression tag	UNP P63746
g	39	VAL	GLY	engineered mutation	UNP P63746
g	112	LEU	-	expression tag	UNP P63746
g	113	GLU	-	expression tag	UNP P63746
g	114	HIS	-	expression tag	UNP P63746
g	115	HIS	-	expression tag	UNP P63746
g	116	HIS	-	expression tag	UNP P63746
g	117	HIS	-	expression tag	UNP P63746
g	118	HIS	-	expression tag	UNP P63746
g	119	HIS	-	expression tag	UNP P63746
h	39	VAL	GLY	engineered mutation	UNP P63746
h	112	LEU	-	expression tag	UNP P63746
h	113	GLU	-	expression tag	UNP P63746
h	114	HIS	-	expression tag	UNP P63746
h	115	HIS	-	expression tag	UNP P63746
h	116	HIS	-	expression tag	UNP P63746
h	117	HIS	-	expression tag	UNP P63746
h	118	HIS	-	expression tag	UNP P63746
h	119	HIS	-	expression tag	UNP P63746
i	39	VAL	GLY	engineered mutation	UNP P63746
i	112	LEU	-	expression tag	UNP P63746
i	113	GLU	-	expression tag	UNP P63746
i	114	HIS	-	expression tag	UNP P63746
i	115	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
i	116	HIS	-	expression tag	UNP P63746
i	117	HIS	-	expression tag	UNP P63746
i	118	HIS	-	expression tag	UNP P63746
i	119	HIS	-	expression tag	UNP P63746
j	39	VAL	GLY	engineered mutation	UNP P63746
j	112	LEU	-	expression tag	UNP P63746
j	113	GLU	-	expression tag	UNP P63746
j	114	HIS	-	expression tag	UNP P63746
j	115	HIS	-	expression tag	UNP P63746
j	116	HIS	-	expression tag	UNP P63746
j	117	HIS	-	expression tag	UNP P63746
j	118	HIS	-	expression tag	UNP P63746
j	119	HIS	-	expression tag	UNP P63746
k	39	VAL	GLY	engineered mutation	UNP P63746
k	112	LEU	-	expression tag	UNP P63746
k	113	GLU	-	expression tag	UNP P63746
k	114	HIS	-	expression tag	UNP P63746
k	115	HIS	-	expression tag	UNP P63746
k	116	HIS	-	expression tag	UNP P63746
k	117	HIS	-	expression tag	UNP P63746
k	118	HIS	-	expression tag	UNP P63746
k	119	HIS	-	expression tag	UNP P63746
l	39	VAL	GLY	engineered mutation	UNP P63746
l	112	LEU	-	expression tag	UNP P63746
l	113	GLU	-	expression tag	UNP P63746
l	114	HIS	-	expression tag	UNP P63746
l	115	HIS	-	expression tag	UNP P63746
l	116	HIS	-	expression tag	UNP P63746
l	117	HIS	-	expression tag	UNP P63746
l	118	HIS	-	expression tag	UNP P63746
l	119	HIS	-	expression tag	UNP P63746
m	39	VAL	GLY	engineered mutation	UNP P63746
m	112	LEU	-	expression tag	UNP P63746
m	113	GLU	-	expression tag	UNP P63746
m	114	HIS	-	expression tag	UNP P63746
m	115	HIS	-	expression tag	UNP P63746
m	116	HIS	-	expression tag	UNP P63746
m	117	HIS	-	expression tag	UNP P63746
m	118	HIS	-	expression tag	UNP P63746
m	119	HIS	-	expression tag	UNP P63746
n	39	VAL	GLY	engineered mutation	UNP P63746
n	112	LEU	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
n	113	GLU	-	expression tag	UNP P63746
n	114	HIS	-	expression tag	UNP P63746
n	115	HIS	-	expression tag	UNP P63746
n	116	HIS	-	expression tag	UNP P63746
n	117	HIS	-	expression tag	UNP P63746
n	118	HIS	-	expression tag	UNP P63746
n	119	HIS	-	expression tag	UNP P63746
o	39	VAL	GLY	engineered mutation	UNP P63746
o	112	LEU	-	expression tag	UNP P63746
o	113	GLU	-	expression tag	UNP P63746
o	114	HIS	-	expression tag	UNP P63746
o	115	HIS	-	expression tag	UNP P63746
o	116	HIS	-	expression tag	UNP P63746
o	117	HIS	-	expression tag	UNP P63746
o	118	HIS	-	expression tag	UNP P63746
o	119	HIS	-	expression tag	UNP P63746
p	39	VAL	GLY	engineered mutation	UNP P63746
p	112	LEU	-	expression tag	UNP P63746
p	113	GLU	-	expression tag	UNP P63746
p	114	HIS	-	expression tag	UNP P63746
p	115	HIS	-	expression tag	UNP P63746
p	116	HIS	-	expression tag	UNP P63746
p	117	HIS	-	expression tag	UNP P63746
p	118	HIS	-	expression tag	UNP P63746
p	119	HIS	-	expression tag	UNP P63746
q	39	VAL	GLY	engineered mutation	UNP P63746
q	112	LEU	-	expression tag	UNP P63746
q	113	GLU	-	expression tag	UNP P63746
q	114	HIS	-	expression tag	UNP P63746
q	115	HIS	-	expression tag	UNP P63746
q	116	HIS	-	expression tag	UNP P63746
q	117	HIS	-	expression tag	UNP P63746
q	118	HIS	-	expression tag	UNP P63746
q	119	HIS	-	expression tag	UNP P63746
r	39	VAL	GLY	engineered mutation	UNP P63746
r	112	LEU	-	expression tag	UNP P63746
r	113	GLU	-	expression tag	UNP P63746
r	114	HIS	-	expression tag	UNP P63746
r	115	HIS	-	expression tag	UNP P63746
r	116	HIS	-	expression tag	UNP P63746
r	117	HIS	-	expression tag	UNP P63746
r	118	HIS	-	expression tag	UNP P63746

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Chain	Residue	Modelled	Actual	Comment	Reference
r	119	HIS	-	expression tag	UNP P63746
s	39	VAL	GLY	engineered mutation	UNP P63746
s	112	LEU	-	expression tag	UNP P63746
s	113	GLU	-	expression tag	UNP P63746
s	114	HIS	-	expression tag	UNP P63746
s	115	HIS	-	expression tag	UNP P63746
s	116	HIS	-	expression tag	UNP P63746
s	117	HIS	-	expression tag	UNP P63746
s	118	HIS	-	expression tag	UNP P63746
s	119	HIS	-	expression tag	UNP P63746
t	39	VAL	GLY	engineered mutation	UNP P63746
t	112	LEU	-	expression tag	UNP P63746
t	113	GLU	-	expression tag	UNP P63746
t	114	HIS	-	expression tag	UNP P63746
t	115	HIS	-	expression tag	UNP P63746
t	116	HIS	-	expression tag	UNP P63746
t	117	HIS	-	expression tag	UNP P63746
t	118	HIS	-	expression tag	UNP P63746
t	119	HIS	-	expression tag	UNP P63746
u	39	VAL	GLY	engineered mutation	UNP P63746
u	112	LEU	-	expression tag	UNP P63746
u	113	GLU	-	expression tag	UNP P63746
u	114	HIS	-	expression tag	UNP P63746
u	115	HIS	-	expression tag	UNP P63746
u	116	HIS	-	expression tag	UNP P63746
u	117	HIS	-	expression tag	UNP P63746
u	118	HIS	-	expression tag	UNP P63746
u	119	HIS	-	expression tag	UNP P63746
v	39	VAL	GLY	engineered mutation	UNP P63746
v	112	LEU	-	expression tag	UNP P63746
v	113	GLU	-	expression tag	UNP P63746
v	114	HIS	-	expression tag	UNP P63746
v	115	HIS	-	expression tag	UNP P63746
v	116	HIS	-	expression tag	UNP P63746
v	117	HIS	-	expression tag	UNP P63746
v	118	HIS	-	expression tag	UNP P63746
v	119	HIS	-	expression tag	UNP P63746

3 Residue-property plots [i](#)

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

- Molecule 1: Ethanolamine utilization protein eutS

Chain A: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain B: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain C: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain D: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain E: 



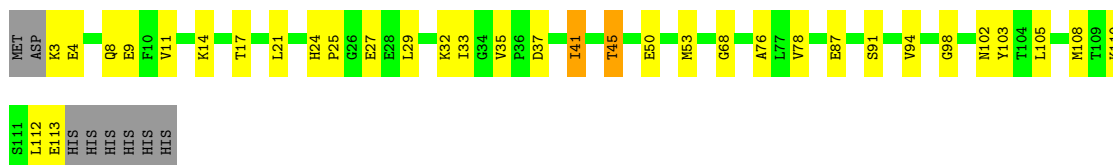
- Molecule 1: Ethanolamine utilization protein eutS

Chain F: 



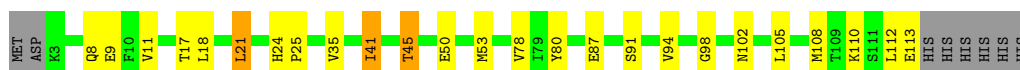
- Molecule 1: Ethanolamine utilization protein eutS

Chain G: 65% 27% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain H: 72% 18% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain I: 73% 18% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain J: 72% 19% 7%



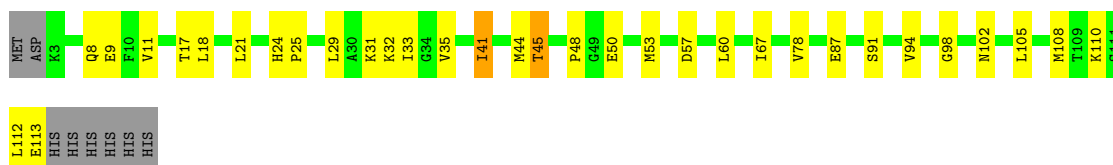
- Molecule 1: Ethanolamine utilization protein eutS

Chain K: 71% 21% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain L: 66% 26% 7%



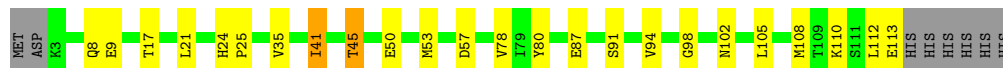
- Molecule 1: Ethanolamine utilization protein eutS

Chain M: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain N: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain O: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain P: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain Q: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain R: 



- Molecule 1: Ethanolamine utilization protein eutS

Chain S: 



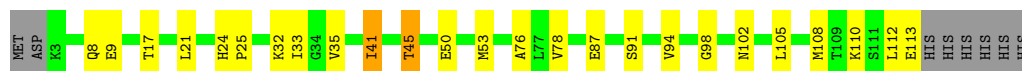
- Molecule 1: Ethanolamine utilization protein eutS

Chain T:  74% 17% 7%



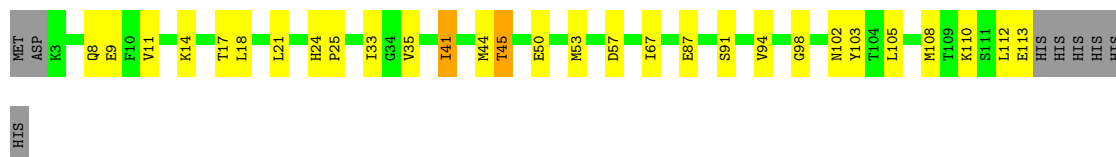
- Molecule 1: Ethanolamine utilization protein eutS

Chain U:  72% 19% 7%



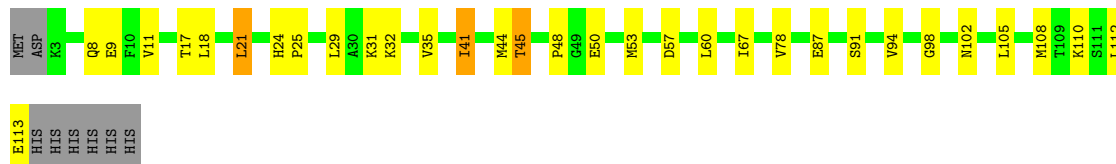
- Molecule 1: Ethanolamine utilization protein eutS

Chain V:  69% 23% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain W:  66% 24% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain X:  71% 21% 7%



- Molecule 1: Ethanolamine utilization protein eutS

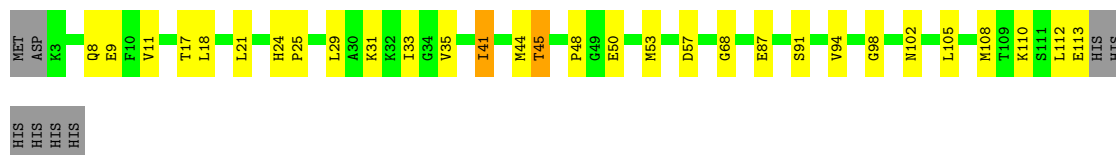
Chain Y:  70% 22% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain Z:  69% 23% 7%

- Molecule 1: Ethanolamine utilization protein eutS



- Molecule 1: Ethanolamine utilization protein eutS



- Molecule 1: Ethanolamine utilization protein eutS



- Molecule 1: Ethanolamine utilization protein eutS



- Molecule 1: Ethanolamine utilization protein eutS



- Molecule 1: Ethanolamine utilization protein eutS



• Molecule 1: Ethanolamine utilization protein eutS

Chain g:  71% 20% 7%

• Molecule 1: Ethanolamine utilization protein eutS

Chain h:  72% 19% 7%

• Molecule 1: Ethanolamine utilization protein eutS

Chain i:  74% 18% 7%

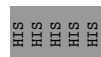
• Molecule 1: Ethanolamine utilization protein eutS

Chain j:  70% 21% 7%

• Molecule 1: Ethanolamine utilization protein eutS

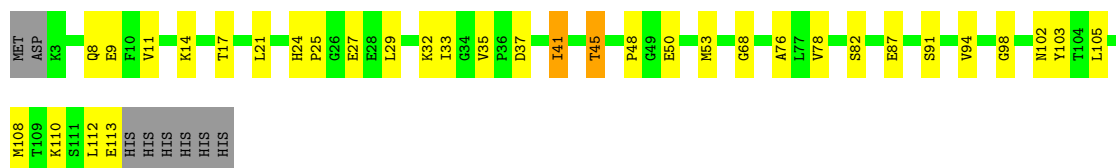
Chain k:  69% 23% 7%

• Molecule 1: Ethanolamine utilization protein eutS

Chain l:  68% 24% 7%

• Molecule 1: Ethanolamine utilization protein eutS

Chain m:  65% 27% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain n: 71% 19% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain o: 72% 19% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain p: 71% 20% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain q: 69% 23% 7%



- Molecule 1: Ethanolamine utilization protein eutS

Chain r: 71% 21% 7%

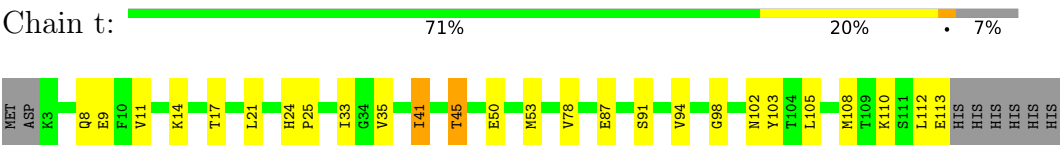


- Molecule 1: Ethanolamine utilization protein eutS

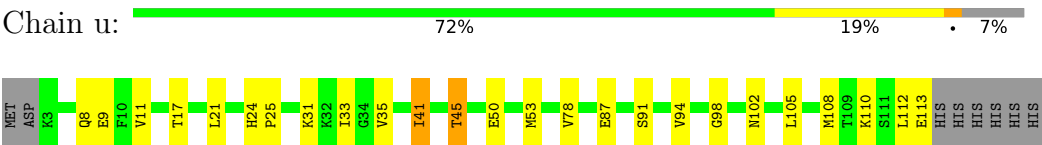
Chain s: 71% 21% 7%



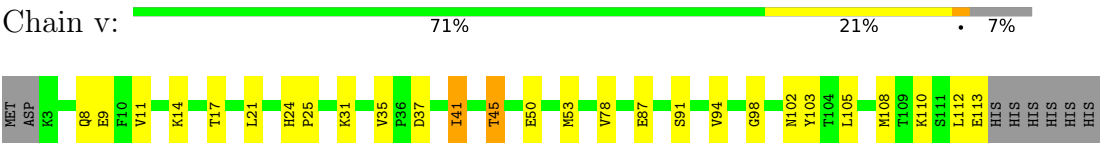
• Molecule 1: Ethanolamine utilization protein eutS



• Molecule 1: Ethanolamine utilization protein eutS



• Molecule 1: Ethanolamine utilization protein eutS



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.58Å 151.39Å 127.46Å 90.00° 90.39° 90.00°	Depositor
Resolution (Å)	58.88 – 2.50 58.88 – 2.50	Depositor EDS
% Data completeness (in resolution range)	80.2 (58.88-2.50) 88.9 (58.88-2.50)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.4_4	Depositor
R, R_{free}	0.217 , 0.239 0.220 , 0.220	Depositor DCC
R_{free} test set	8725 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.760	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.408 for h,-k,-l 0.408 for -h,-k,l 0.388 for -h,k,-l	Xtriage
Reported twinning fraction	0.463 for -h,-k,l	Depositor
Outliers	0 of 173036 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	39312	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.88% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.39	0/830	0.80	1/1123 (0.1%)
1	B	0.37	0/830	0.78	0/1123
1	C	0.38	0/830	0.78	0/1123
1	D	0.39	0/830	0.78	0/1123
1	E	0.38	0/830	0.78	0/1123
1	F	0.38	0/830	0.78	0/1123
1	G	0.38	0/830	0.80	1/1123 (0.1%)
1	H	0.39	0/830	0.77	0/1123
1	I	0.40	0/830	0.80	0/1123
1	J	0.38	0/830	0.78	0/1123
1	K	0.38	0/830	0.80	0/1123
1	L	0.40	0/830	0.79	0/1123
1	M	0.40	0/830	0.77	0/1123
1	N	0.38	0/830	0.79	0/1123
1	O	0.35	0/830	0.78	0/1123
1	P	0.37	0/830	0.77	0/1123
1	Q	0.39	0/830	0.78	0/1123
1	R	0.38	0/830	0.78	0/1123
1	S	0.37	0/830	0.80	1/1123 (0.1%)
1	T	0.38	0/830	0.76	0/1123
1	U	0.38	0/830	0.78	0/1123
1	V	0.38	0/830	0.79	0/1123
1	W	0.40	0/830	0.78	0/1123
1	X	0.38	0/830	0.79	0/1123
1	Y	0.39	0/830	0.78	0/1123
1	Z	0.39	0/830	0.79	0/1123
1	a	0.37	0/830	0.79	1/1123 (0.1%)
1	b	0.39	0/830	0.77	0/1123
1	c	0.39	0/830	0.78	0/1123
1	d	0.38	0/830	0.78	0/1123
1	e	0.39	0/830	0.79	0/1123
1	f	0.37	0/830	0.79	0/1123
1	g	0.37	0/830	0.78	1/1123 (0.1%)
1	h	0.38	0/830	0.79	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	i	0.38	0/830	0.78	0/1123
1	j	0.40	0/830	0.78	0/1123
1	k	0.39	0/830	0.80	0/1123
1	l	0.39	0/830	0.80	0/1123
1	m	0.37	0/830	0.80	1/1123 (0.1%)
1	n	0.39	0/830	0.77	0/1123
1	o	0.41	0/830	0.79	0/1123
1	p	0.39	0/830	0.80	1/1123 (0.1%)
1	q	0.38	0/830	0.76	0/1123
1	r	0.37	0/830	0.80	0/1123
1	s	0.37	0/830	0.78	0/1123
1	t	0.38	0/830	0.79	0/1123
1	u	0.39	0/830	0.78	0/1123
1	v	0.36	0/830	0.78	0/1123
All	All	0.38	0/39840	0.78	7/53904 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	68	GLY	N-CA-C	-5.34	106.31	112.50
1	g	68	GLY	N-CA-C	-5.31	106.07	112.49
1	p	68	GLY	N-CA-C	-5.22	106.44	112.50
1	S	68	GLY	N-CA-C	-5.12	106.30	112.49
1	m	68	GLY	N-CA-C	-5.06	106.36	112.49
1	A	68	GLY	N-CA-C	-5.04	106.39	112.49
1	a	68	GLY	N-CA-C	-5.03	106.67	112.50

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	819	0	851	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	819	0	851	31	0
1	C	819	0	851	38	0
1	D	819	0	851	43	0
1	E	819	0	851	33	0
1	F	819	0	851	32	0
1	G	819	0	851	52	0
1	H	819	0	851	29	0
1	I	819	0	851	26	0
1	J	819	0	851	29	0
1	K	819	0	851	33	0
1	L	819	0	851	52	0
1	M	819	0	851	31	0
1	N	819	0	851	27	0
1	O	819	0	851	31	0
1	P	819	0	851	33	0
1	Q	819	0	851	43	0
1	R	819	0	851	38	0
1	S	819	0	851	39	0
1	T	819	0	851	27	0
1	U	819	0	851	30	0
1	V	819	0	851	35	0
1	W	819	0	851	39	0
1	X	819	0	851	42	0
1	Y	819	0	851	37	0
1	Z	819	0	851	38	0
1	a	819	0	851	35	0
1	b	819	0	851	34	0
1	c	819	0	851	38	0
1	d	819	0	851	39	0
1	e	819	0	851	45	0
1	f	819	0	851	40	0
1	g	819	0	851	28	0
1	h	819	0	851	29	0
1	i	819	0	851	30	0
1	j	819	0	851	31	0
1	k	819	0	851	32	0
1	l	819	0	851	47	0
1	m	819	0	851	47	0
1	n	819	0	851	33	0
1	o	819	0	851	32	0
1	p	819	0	851	33	0
1	q	819	0	851	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	r	819	0	851	30	0
1	s	819	0	851	35	0
1	t	819	0	851	33	0
1	u	819	0	851	40	0
1	v	819	0	851	42	0
All	All	39312	0	40848	1119	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 14.

All (1119) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:35:VAL:HG21	1:e:41:ILE:HD11	1.27	1.17
1:p:35:VAL:HG21	1:p:41:ILE:HD11	1.26	1.15
1:Q:35:VAL:HG21	1:Q:41:ILE:HD11	1.28	1.14
1:T:35:VAL:HG21	1:T:41:ILE:HD11	1.29	1.14
1:N:35:VAL:HG21	1:N:41:ILE:HD11	1.29	1.13
1:c:35:VAL:HG21	1:c:41:ILE:HD11	1.25	1.13
1:D:35:VAL:HG21	1:D:41:ILE:HD11	1.31	1.13
1:M:35:VAL:HG21	1:M:41:ILE:HD11	1.28	1.13
1:U:35:VAL:HG21	1:U:41:ILE:HD11	1.29	1.13
1:l:35:VAL:HG21	1:l:41:ILE:HD11	1.30	1.13
1:H:35:VAL:HG21	1:H:41:ILE:HD11	1.30	1.12
1:I:35:VAL:HG21	1:I:41:ILE:HD11	1.28	1.12
1:i:35:VAL:HG21	1:i:41:ILE:HD11	1.30	1.12
1:L:35:VAL:HG21	1:L:41:ILE:HD11	1.29	1.12
1:o:35:VAL:HG21	1:o:41:ILE:HD11	1.30	1.12
1:a:35:VAL:HG21	1:a:41:ILE:HD11	1.32	1.11
1:d:37:ASP:HB2	1:l:31:LYS:HZ1	1.12	1.11
1:h:35:VAL:HG21	1:h:41:ILE:HD11	1.30	1.11
1:s:35:VAL:HG21	1:s:41:ILE:HD11	1.32	1.11
1:A:35:VAL:HG21	1:A:41:ILE:HD11	1.32	1.11
1:O:35:VAL:HG21	1:O:41:ILE:HD11	1.30	1.11
1:g:35:VAL:HG21	1:g:41:ILE:HD11	1.27	1.11
1:Y:35:VAL:HG21	1:Y:41:ILE:HD11	1.29	1.11
1:v:35:VAL:HG21	1:v:41:ILE:HD11	1.30	1.10
1:F:35:VAL:HG21	1:F:41:ILE:HD11	1.31	1.10
1:r:35:VAL:HG21	1:r:41:ILE:HD11	1.29	1.10
1:P:35:VAL:HG21	1:P:41:ILE:HD11	1.28	1.10
1:u:35:VAL:HG21	1:u:41:ILE:HD11	1.30	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:35:VAL:HG21	1:V:41:ILE:HD11	1.29	1.09
1:k:35:VAL:HG21	1:k:41:ILE:HD11	1.30	1.09
1:X:35:VAL:HG21	1:X:41:ILE:HD11	1.28	1.09
1:J:35:VAL:HG21	1:J:41:ILE:HD11	1.29	1.09
1:j:35:VAL:HG21	1:j:41:ILE:HD11	1.30	1.09
1:E:35:VAL:HG21	1:E:41:ILE:HD11	1.31	1.09
1:q:35:VAL:HG21	1:q:41:ILE:HD11	1.31	1.09
1:W:35:VAL:HG21	1:W:41:ILE:HD11	1.30	1.09
1:C:35:VAL:HG21	1:C:41:ILE:HD11	1.27	1.08
1:R:35:VAL:HG21	1:R:41:ILE:HD11	1.32	1.08
1:t:35:VAL:HG21	1:t:41:ILE:HD11	1.29	1.08
1:K:31:LYS:HE2	1:M:27:GLU:OE1	1.51	1.08
1:G:35:VAL:HG21	1:G:41:ILE:HD11	1.31	1.08
1:S:35:VAL:HG21	1:S:41:ILE:HD11	1.29	1.08
1:Z:35:VAL:HG21	1:Z:41:ILE:HD11	1.31	1.08
1:n:35:VAL:HG21	1:n:41:ILE:HD11	1.30	1.08
1:f:35:VAL:HG21	1:f:41:ILE:HD11	1.29	1.07
1:K:35:VAL:HG21	1:K:41:ILE:HD11	1.31	1.07
1:d:35:VAL:HG21	1:d:41:ILE:HD11	1.31	1.07
1:B:35:VAL:HG21	1:B:41:ILE:HD11	1.30	1.07
1:m:35:VAL:HG21	1:m:41:ILE:HD11	1.30	1.06
1:b:35:VAL:HG21	1:b:41:ILE:HD11	1.30	1.06
1:d:37:ASP:CB	1:l:31:LYS:HZ1	1.71	1.03
1:d:37:ASP:HB2	1:l:31:LYS:NZ	1.73	1.02
1:Y:27:GLU:OE1	1:k:31:LYS:HE2	1.58	1.01
1:j:31:LYS:HE2	1:q:27:GLU:OE1	1.62	1.00
1:F:27:GLU:OE1	1:W:31:LYS:HE2	1.61	0.98
1:G:27:GLU:OE1	1:Q:31:LYS:HE3	1.65	0.95
1:d:37:ASP:CB	1:l:31:LYS:NZ	2.28	0.95
1:D:31:LYS:HE3	1:S:27:GLU:OE1	1.68	0.94
1:L:31:LYS:HZ1	1:R:37:ASP:HB2	1.33	0.94
1:d:37:ASP:H	1:l:31:LYS:HZ3	1.19	0.91
1:d:37:ASP:H	1:l:31:LYS:NZ	1.67	0.90
1:E:37:ASP:H	1:X:31:LYS:HZ1	1.21	0.89
1:b:87:GLU:OE1	1:g:82:SER:HB2	1.74	0.87
1:A:8:GLN:NE2	1:F:8:GLN:HE22	1.74	0.85
1:c:31:LYS:HE3	1:m:27:GLU:OE1	1.76	0.85
1:f:27:GLU:OE1	1:u:31:LYS:HG3	1.76	0.85
1:Y:8:GLN:HE22	1:Z:8:GLN:NE2	1.74	0.85
1:L:31:LYS:HZ1	1:R:37:ASP:CB	1.89	0.85
1:M:8:GLN:HE22	1:N:8:GLN:NE2	1.75	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:8:GLN:HE22	1:u:8:GLN:NE2	1.75	0.83
1:G:27:GLU:CD	1:Q:31:LYS:HG3	2.03	0.83
1:Y:8:GLN:NE2	1:d:8:GLN:HE22	1.76	0.82
1:e:31:LYS:NZ	1:v:37:ASP:H	1.77	0.82
1:a:87:GLU:HG3	1:a:108:MET:HE1	1.62	0.82
1:B:87:GLU:HG3	1:B:108:MET:HE1	1.62	0.82
1:n:8:GLN:HE22	1:o:8:GLN:NE2	1.78	0.82
1:b:8:GLN:HE22	1:c:8:GLN:NE2	1.78	0.81
1:e:8:GLN:HE22	1:f:8:GLN:NE2	1.78	0.81
1:q:8:GLN:NE2	1:v:8:GLN:HE22	1.78	0.81
1:D:8:GLN:HE22	1:E:8:GLN:NE2	1.79	0.81
1:e:31:LYS:HZ1	1:v:37:ASP:CB	1.93	0.80
1:L:31:LYS:NZ	1:R:37:ASP:HB2	1.95	0.80
1:u:8:GLN:HE22	1:v:8:GLN:NE2	1.80	0.80
1:M:8:GLN:NE2	1:R:8:GLN:HE22	1.77	0.80
1:Q:87:GLU:HG3	1:Q:108:MET:HE1	1.64	0.80
1:c:31:LYS:HG3	1:m:27:GLU:CD	2.06	0.80
1:S:8:GLN:NE2	1:X:8:GLN:HE22	1.80	0.79
1:U:87:GLU:HG3	1:U:108:MET:HE1	1.63	0.79
1:D:87:GLU:HG3	1:D:108:MET:HE1	1.64	0.79
1:E:8:GLN:HE22	1:F:8:GLN:NE2	1.80	0.79
1:S:87:GLU:HG3	1:S:108:MET:HE1	1.64	0.79
1:h:87:GLU:HG3	1:h:108:MET:HE1	1.63	0.79
1:E:87:GLU:HG3	1:E:108:MET:HE1	1.64	0.79
1:c:87:GLU:HG3	1:c:108:MET:HE1	1.65	0.79
1:q:8:GLN:HE22	1:r:8:GLN:NE2	1.81	0.79
1:L:87:GLU:HG3	1:L:108:MET:HE1	1.65	0.78
1:A:8:GLN:HE22	1:B:8:GLN:NE2	1.81	0.78
1:Z:87:GLU:HG3	1:Z:108:MET:HE1	1.65	0.78
1:s:87:GLU:HG3	1:s:108:MET:HE1	1.66	0.78
1:o:87:GLU:HG3	1:o:108:MET:HE1	1.65	0.78
1:v:87:GLU:HG3	1:v:108:MET:HE1	1.66	0.78
1:p:87:GLU:HG3	1:p:108:MET:HE1	1.66	0.78
1:C:8:GLN:HE22	1:D:8:GLN:NE2	1.82	0.78
1:A:87:GLU:HG3	1:A:108:MET:HE1	1.65	0.78
1:f:27:GLU:OE1	1:u:31:LYS:HE3	1.84	0.78
1:r:87:GLU:HG3	1:r:108:MET:HE1	1.66	0.78
1:d:37:ASP:N	1:l:31:LYS:NZ	2.31	0.77
1:J:8:GLN:HE22	1:K:8:GLN:NE2	1.82	0.77
1:J:87:GLU:HG3	1:J:108:MET:HE1	1.66	0.77
1:N:87:GLU:HG3	1:N:108:MET:HE1	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:87:GLU:HG3	1:P:108:MET:HE1	1.65	0.77
1:P:8:GLN:HE22	1:Q:8:GLN:NE2	1.83	0.77
1:F:87:GLU:HG3	1:F:108:MET:HE1	1.65	0.77
1:r:8:GLN:HE22	1:s:8:GLN:NE2	1.82	0.77
1:u:87:GLU:HG3	1:u:108:MET:HE1	1.67	0.77
1:H:8:GLN:HE22	1:I:8:GLN:NE2	1.83	0.77
1:W:8:GLN:HE22	1:X:8:GLN:NE2	1.83	0.77
1:c:31:LYS:NZ	1:m:37:ASP:OD2	2.17	0.77
1:G:8:GLN:HE22	1:H:8:GLN:NE2	1.82	0.77
1:V:87:GLU:HG3	1:V:108:MET:HE1	1.67	0.76
1:t:8:GLN:HE22	1:u:8:GLN:CD	1.92	0.76
1:i:87:GLU:HG3	1:i:108:MET:HE1	1.67	0.76
1:O:87:GLU:HG3	1:O:108:MET:HE1	1.66	0.76
1:b:87:GLU:HG3	1:b:108:MET:HE1	1.65	0.76
1:e:8:GLN:NE2	1:j:8:GLN:HE22	1.83	0.76
1:f:27:GLU:CD	1:u:31:LYS:HG3	2.10	0.76
1:C:87:GLU:HG3	1:C:108:MET:HE1	1.67	0.76
1:e:31:LYS:HZ1	1:v:37:ASP:HB2	1.50	0.76
1:X:87:GLU:HG3	1:X:108:MET:HE1	1.67	0.76
1:f:87:GLU:HG3	1:f:108:MET:HE1	1.67	0.76
1:d:87:GLU:HG3	1:d:108:MET:HE1	1.68	0.76
1:L:31:LYS:NZ	1:R:37:ASP:CB	2.47	0.76
1:G:87:GLU:HG3	1:G:108:MET:HE1	1.68	0.75
1:I:87:GLU:HG3	1:I:108:MET:HE1	1.68	0.75
1:m:87:GLU:HG3	1:m:108:MET:HE1	1.68	0.75
1:o:8:GLN:HE22	1:p:8:GLN:NE2	1.84	0.75
1:G:37:ASP:OD2	1:Q:31:LYS:NZ	2.19	0.75
1:t:87:GLU:HG3	1:t:108:MET:HE1	1.65	0.75
1:R:87:GLU:HG3	1:R:108:MET:HE1	1.68	0.75
1:q:87:GLU:HG3	1:q:108:MET:HE1	1.65	0.75
1:l:8:GLN:HE22	1:m:8:GLN:NE2	1.84	0.75
1:M:87:GLU:HG3	1:M:108:MET:HE1	1.67	0.75
1:k:8:GLN:HE22	1:l:8:GLN:NE2	1.85	0.75
1:Y:87:GLU:HG3	1:Y:108:MET:HE1	1.67	0.74
1:e:87:GLU:HG3	1:e:108:MET:HE1	1.68	0.74
1:s:9:GLU:HA	1:t:11:VAL:O	1.86	0.74
1:Y:8:GLN:HE22	1:Z:8:GLN:CD	1.94	0.74
1:n:87:GLU:HG3	1:n:108:MET:HE1	1.67	0.74
1:K:8:GLN:HE22	1:L:8:GLN:NE2	1.86	0.74
1:l:87:GLU:HG3	1:l:108:MET:HE1	1.68	0.74
1:g:87:GLU:HG3	1:g:108:MET:HE1	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:8:GLN:HE22	1:b:8:GLN:NE2	1.86	0.73
1:I:8:GLN:HE22	1:J:8:GLN:NE2	1.85	0.73
1:Q:9:GLU:HA	1:R:11:VAL:O	1.89	0.73
1:g:112:LEU:O	1:g:113:GLU:HB2	1.88	0.73
1:f:53:MET:HE1	1:g:78:VAL:HG21	1.71	0.73
1:H:87:GLU:HG3	1:H:108:MET:HE1	1.67	0.73
1:K:112:LEU:O	1:K:113:GLU:HB2	1.89	0.73
1:r:112:LEU:O	1:r:113:GLU:HB2	1.88	0.73
1:m:82:SER:HB2	1:s:87:GLU:OE1	1.89	0.73
1:T:87:GLU:HG3	1:T:108:MET:HE1	1.67	0.73
1:M:53:MET:HE1	1:N:78:VAL:HG21	1.71	0.73
1:f:8:GLN:HE22	1:g:8:GLN:NE2	1.87	0.73
1:A:8:GLN:CD	1:F:8:GLN:HE22	1.95	0.73
1:V:8:GLN:HE22	1:W:8:GLN:NE2	1.86	0.73
1:Y:112:LEU:O	1:Y:113:GLU:HB2	1.89	0.72
1:W:87:GLU:HG3	1:W:108:MET:HE1	1.69	0.72
1:n:112:LEU:O	1:n:113:GLU:HB2	1.89	0.72
1:D:112:LEU:O	1:D:113:GLU:HB2	1.89	0.72
1:j:87:GLU:HG3	1:j:108:MET:HE1	1.70	0.72
1:O:8:GLN:HE22	1:P:8:GLN:NE2	1.88	0.72
1:d:37:ASP:N	1:l:31:LYS:HZ1	1.87	0.72
1:P:112:LEU:O	1:P:113:GLU:HB2	1.89	0.72
1:V:94:VAL:HG12	1:V:105:LEU:HD23	1.72	0.72
1:Y:53:MET:HE1	1:Z:78:VAL:HG21	1.71	0.72
1:Z:112:LEU:O	1:Z:113:GLU:HB2	1.90	0.72
1:i:94:VAL:HG12	1:i:105:LEU:HD23	1.72	0.72
1:m:8:GLN:HE22	1:n:8:GLN:CD	1.98	0.72
1:l:112:LEU:O	1:l:113:GLU:HB2	1.90	0.72
1:p:112:LEU:O	1:p:113:GLU:HB2	1.90	0.72
1:Q:112:LEU:O	1:Q:113:GLU:HB2	1.89	0.71
1:k:87:GLU:HG3	1:k:108:MET:HE1	1.70	0.71
1:q:112:LEU:O	1:q:113:GLU:HB2	1.90	0.71
1:H:112:LEU:O	1:H:113:GLU:HB2	1.88	0.71
1:L:31:LYS:NZ	1:R:37:ASP:H	1.88	0.71
1:S:8:GLN:HE22	1:T:8:GLN:NE2	1.88	0.71
1:c:94:VAL:HG12	1:c:105:LEU:HD23	1.72	0.71
1:e:31:LYS:HZ1	1:v:37:ASP:H	1.35	0.71
1:e:112:LEU:O	1:e:113:GLU:HB2	1.90	0.71
1:W:112:LEU:O	1:W:113:GLU:HB2	1.90	0.71
1:U:8:GLN:HE22	1:V:8:GLN:NE2	1.89	0.71
1:k:112:LEU:O	1:k:113:GLU:HB2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:112:LEU:O	1:N:113:GLU:HB2	1.90	0.71
1:T:112:LEU:O	1:T:113:GLU:HB2	1.89	0.71
1:f:50:GLU:HB2	1:g:45:THR:HG22	1.71	0.71
1:K:87:GLU:HG3	1:K:108:MET:HE1	1.70	0.71
1:h:9:GLU:HA	1:i:11:VAL:O	1.90	0.71
1:d:112:LEU:O	1:d:113:GLU:HB2	1.89	0.71
1:A:112:LEU:O	1:A:113:GLU:HB2	1.90	0.70
1:C:112:LEU:O	1:C:113:GLU:HB2	1.91	0.70
1:l:53:MET:HE1	1:m:78:VAL:HG21	1.73	0.70
1:F:112:LEU:O	1:F:113:GLU:HB2	1.89	0.70
1:I:112:LEU:O	1:I:113:GLU:HB2	1.91	0.70
1:L:112:LEU:O	1:L:113:GLU:HB2	1.89	0.70
1:M:112:LEU:O	1:M:113:GLU:HB2	1.90	0.70
1:X:112:LEU:O	1:X:113:GLU:HB2	1.88	0.70
1:c:112:LEU:O	1:c:113:GLU:HB2	1.90	0.70
1:u:112:LEU:O	1:u:113:GLU:HB2	1.91	0.70
1:a:112:LEU:O	1:a:113:GLU:HB2	1.92	0.70
1:i:112:LEU:O	1:i:113:GLU:HB2	1.92	0.70
1:j:112:LEU:O	1:j:113:GLU:HB2	1.91	0.70
1:k:8:GLN:NE2	1:p:8:GLN:HE22	1.88	0.70
1:R:112:LEU:O	1:R:113:GLU:HB2	1.91	0.70
1:U:112:LEU:O	1:U:113:GLU:HB2	1.91	0.70
1:b:112:LEU:O	1:b:113:GLU:HB2	1.89	0.70
1:q:8:GLN:HE22	1:r:8:GLN:CD	1.99	0.70
1:J:112:LEU:O	1:J:113:GLU:HB2	1.90	0.69
1:X:94:VAL:HG12	1:X:105:LEU:HD23	1.73	0.69
1:E:112:LEU:O	1:E:113:GLU:HB2	1.91	0.69
1:f:112:LEU:O	1:f:113:GLU:HB2	1.91	0.69
1:m:8:GLN:HE22	1:n:8:GLN:NE2	1.91	0.69
1:s:8:GLN:HE22	1:t:8:GLN:NE2	1.90	0.69
1:D:31:LYS:HG3	1:S:27:GLU:CD	2.17	0.69
1:Q:8:GLN:HE22	1:R:8:GLN:NE2	1.90	0.69
1:v:112:LEU:O	1:v:113:GLU:HB2	1.91	0.69
1:B:112:LEU:O	1:B:113:GLU:HB2	1.91	0.69
1:Q:94:VAL:HG12	1:Q:105:LEU:HD23	1.73	0.69
1:s:112:LEU:O	1:s:113:GLU:HB2	1.93	0.69
1:F:94:VAL:HG12	1:F:105:LEU:HD23	1.75	0.69
1:O:50:GLU:HB2	1:P:45:THR:HG22	1.74	0.68
1:Z:9:GLU:HA	1:a:11:VAL:O	1.94	0.68
1:o:112:LEU:O	1:o:113:GLU:HB2	1.90	0.68
1:G:8:GLN:NE2	1:L:8:GLN:HE22	1.90	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:112:LEU:O	1:t:113:GLU:HB2	1.92	0.68
1:C:8:GLN:HE22	1:D:8:GLN:CD	2.02	0.68
1:V:112:LEU:O	1:V:113:GLU:HB2	1.92	0.68
1:a:94:VAL:HG12	1:a:105:LEU:HD23	1.75	0.68
1:D:31:LYS:HG3	1:S:27:GLU:OE1	1.94	0.68
1:H:94:VAL:HG12	1:H:105:LEU:HD23	1.76	0.68
1:O:94:VAL:HG12	1:O:105:LEU:HD23	1.76	0.68
1:T:94:VAL:HG12	1:T:105:LEU:HD23	1.76	0.68
1:s:94:VAL:HG12	1:s:105:LEU:HD23	1.74	0.68
1:R:94:VAL:HG12	1:R:105:LEU:HD23	1.75	0.68
1:e:94:VAL:HG12	1:e:105:LEU:HD23	1.76	0.67
1:e:31:LYS:HZ1	1:v:37:ASP:N	1.92	0.67
1:c:9:GLU:HA	1:d:11:VAL:O	1.92	0.67
1:k:94:VAL:HG12	1:k:105:LEU:HD23	1.76	0.67
1:m:112:LEU:O	1:m:113:GLU:HB2	1.93	0.67
1:M:50:GLU:HB2	1:N:45:THR:HG22	1.76	0.67
1:O:53:MET:HE1	1:P:78:VAL:HG21	1.76	0.67
1:S:112:LEU:O	1:S:113:GLU:HB2	1.93	0.67
1:O:112:LEU:O	1:O:113:GLU:HB2	1.93	0.67
1:c:8:GLN:HE22	1:d:8:GLN:NE2	1.91	0.67
1:u:94:VAL:HG12	1:u:105:LEU:HD23	1.77	0.67
1:B:94:VAL:HG12	1:B:105:LEU:HD23	1.77	0.67
1:L:94:VAL:HG12	1:L:105:LEU:HD23	1.76	0.67
1:p:94:VAL:HG12	1:p:105:LEU:HD23	1.77	0.67
1:G:112:LEU:O	1:G:113:GLU:HB2	1.93	0.67
1:I:94:VAL:HG12	1:I:105:LEU:HD23	1.77	0.67
1:b:53:MET:HE1	1:c:78:VAL:HG21	1.77	0.67
1:h:112:LEU:O	1:h:113:GLU:HB2	1.92	0.67
1:q:78:VAL:HG21	1:v:53:MET:HE1	1.77	0.67
1:t:94:VAL:HG12	1:t:105:LEU:HD23	1.76	0.67
1:M:94:VAL:HG12	1:M:105:LEU:HD23	1.77	0.67
1:U:94:VAL:HG12	1:U:105:LEU:HD23	1.77	0.67
1:b:8:GLN:HE22	1:c:8:GLN:CD	2.03	0.67
1:l:94:VAL:HG12	1:l:105:LEU:HD23	1.77	0.66
1:v:94:VAL:HG12	1:v:105:LEU:HD23	1.77	0.66
1:l:50:GLU:HB2	1:m:45:THR:HG22	1.77	0.66
1:m:9:GLU:HA	1:n:11:VAL:O	1.94	0.66
1:B:8:GLN:HE22	1:C:8:GLN:NE2	1.94	0.66
1:G:50:GLU:HB2	1:H:45:THR:HG22	1.77	0.66
1:i:8:GLN:HE22	1:j:8:GLN:NE2	1.94	0.66
1:k:8:GLN:HE22	1:l:8:GLN:CD	2.04	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:9:GLU:HA	1:b:11:VAL:O	1.95	0.65
1:d:94:VAL:HG12	1:d:105:LEU:HD23	1.78	0.65
1:e:45:THR:HG22	1:j:50:GLU:HB2	1.78	0.65
1:j:94:VAL:HG12	1:j:105:LEU:HD23	1.78	0.65
1:J:94:VAL:HG12	1:J:105:LEU:HD23	1.78	0.65
1:h:94:VAL:HG12	1:h:105:LEU:HD23	1.78	0.65
1:M:8:GLN:HE22	1:N:8:GLN:CD	2.03	0.65
1:U:9:GLU:HA	1:V:11:VAL:O	1.97	0.65
1:T:53:MET:HE1	1:U:78:VAL:HG21	1.78	0.65
1:M:8:GLN:CD	1:R:8:GLN:HE22	2.04	0.65
1:S:50:GLU:HB2	1:T:45:THR:HG22	1.78	0.65
1:e:8:GLN:CD	1:j:8:GLN:HE22	2.05	0.65
1:N:94:VAL:HG12	1:N:105:LEU:HD23	1.79	0.65
1:b:94:VAL:HG12	1:b:105:LEU:HD23	1.78	0.65
1:s:8:GLN:HE22	1:t:8:GLN:CD	2.04	0.65
1:G:94:VAL:HG12	1:G:105:LEU:HD23	1.78	0.65
1:c:8:GLN:HE22	1:d:8:GLN:CD	2.05	0.65
1:n:94:VAL:HG12	1:n:105:LEU:HD23	1.78	0.65
1:B:9:GLU:HA	1:C:11:VAL:O	1.97	0.64
1:C:94:VAL:HG12	1:C:105:LEU:HD23	1.77	0.64
1:O:8:GLN:HE22	1:P:8:GLN:CD	2.05	0.64
1:G:8:GLN:HE22	1:H:8:GLN:CD	2.06	0.64
1:K:94:VAL:HG12	1:K:105:LEU:HD23	1.78	0.64
1:E:53:MET:HE1	1:F:78:VAL:HG21	1.80	0.64
1:E:94:VAL:HG12	1:E:105:LEU:HD23	1.78	0.64
1:Q:8:GLN:HE22	1:R:8:GLN:CD	2.05	0.64
1:q:94:VAL:HG12	1:q:105:LEU:HD23	1.77	0.64
1:m:94:VAL:HG12	1:m:105:LEU:HD23	1.79	0.64
1:Y:8:GLN:NE2	1:Z:8:GLN:CD	2.56	0.64
1:c:31:LYS:HG3	1:m:27:GLU:OE1	1.98	0.64
1:a:8:GLN:HE22	1:b:8:GLN:CD	2.06	0.64
1:g:94:VAL:HG12	1:g:105:LEU:HD23	1.79	0.64
1:D:94:VAL:HG12	1:D:105:LEU:HD23	1.79	0.63
1:c:8:GLN:CD	1:d:8:GLN:HB3	2.23	0.63
1:S:8:GLN:CD	1:X:8:GLN:HE22	2.07	0.63
1:d:37:ASP:CA	1:l:31:LYS:HZ1	2.10	0.63
1:q:8:GLN:CD	1:v:8:GLN:HE22	2.07	0.63
1:A:94:VAL:HG12	1:A:105:LEU:HD23	1.81	0.63
1:J:8:GLN:HE22	1:K:8:GLN:CD	2.07	0.63
1:T:8:GLN:HE22	1:U:8:GLN:NE2	1.97	0.63
1:e:31:LYS:NZ	1:v:37:ASP:CB	2.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:8:GLN:HE22	1:J:8:GLN:CD	2.06	0.62
1:A:8:GLN:CD	1:F:8:GLN:NE2	2.57	0.62
1:Y:50:GLU:HB2	1:Z:45:THR:HG22	1.80	0.62
1:b:50:GLU:HB2	1:c:45:THR:HG22	1.81	0.62
1:k:9:GLU:HA	1:l:11:VAL:O	1.99	0.62
1:E:8:GLN:HE22	1:F:8:GLN:CD	2.07	0.62
1:P:94:VAL:HG12	1:P:105:LEU:HD23	1.79	0.62
1:a:50:GLU:HB2	1:b:45:THR:HG22	1.81	0.62
1:t:53:MET:HE1	1:u:78:VAL:HG21	1.80	0.62
1:W:8:GLN:HE22	1:X:8:GLN:CD	2.08	0.62
1:r:50:GLU:HB2	1:s:45:THR:HG22	1.80	0.62
1:W:94:VAL:HG12	1:W:105:LEU:HD23	1.80	0.62
1:Z:94:VAL:HG12	1:Z:105:LEU:HD23	1.79	0.62
1:b:87:GLU:OE1	1:g:82:SER:CB	2.47	0.62
1:u:8:GLN:HE22	1:v:8:GLN:CD	2.07	0.62
1:E:37:ASP:N	1:X:31:LYS:HZ1	1.95	0.62
1:G:27:GLU:OE1	1:Q:31:LYS:HG3	1.98	0.62
1:B:8:GLN:HE22	1:C:8:GLN:CD	2.06	0.62
1:L:31:LYS:HZ1	1:R:37:ASP:N	1.96	0.62
1:t:8:GLN:NE2	1:u:8:GLN:CD	2.58	0.62
1:e:8:GLN:HE22	1:f:8:GLN:CD	2.08	0.61
1:e:78:VAL:HG21	1:j:53:MET:HE1	1.82	0.61
1:o:94:VAL:HG12	1:o:105:LEU:HD23	1.82	0.61
1:r:94:VAL:HG12	1:r:105:LEU:HD23	1.80	0.61
1:G:45:THR:HG22	1:L:50:GLU:HB2	1.81	0.61
1:W:67:ILE:HB	1:X:32:LYS:HE3	1.82	0.61
1:D:8:GLN:HE22	1:E:8:GLN:CD	2.09	0.61
1:V:8:GLN:HE22	1:W:8:GLN:CD	2.08	0.61
1:U:8:GLN:HE22	1:V:8:GLN:CD	2.09	0.61
1:Q:9:GLU:HG2	1:R:11:VAL:HG23	1.83	0.61
1:h:8:GLN:HE22	1:i:8:GLN:NE2	1.98	0.61
1:S:94:VAL:HG12	1:S:105:LEU:HD23	1.81	0.61
1:Y:94:VAL:HG12	1:Y:105:LEU:HD23	1.81	0.61
1:q:45:THR:HG22	1:v:50:GLU:HB2	1.82	0.61
1:G:78:VAL:HG21	1:L:53:MET:HE1	1.82	0.61
1:c:9:GLU:HG2	1:d:11:VAL:HG23	1.82	0.61
1:o:50:GLU:HB2	1:p:45:THR:HG22	1.82	0.61
1:G:8:GLN:CD	1:L:8:GLN:HE22	2.09	0.60
1:S:53:MET:HE1	1:T:78:VAL:HG21	1.83	0.60
1:f:94:VAL:HG12	1:f:105:LEU:HD23	1.83	0.60
1:Y:45:THR:HG22	1:d:50:GLU:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:THR:HG22	1:F:50:GLU:HB2	1.82	0.60
1:a:53:MET:HE1	1:b:78:VAL:HG21	1.83	0.60
1:A:11:VAL:O	1:F:9:GLU:HA	2.00	0.60
1:C:9:GLU:HA	1:D:11:VAL:O	2.02	0.60
1:A:8:GLN:HB3	1:F:8:GLN:CD	2.26	0.60
1:V:50:GLU:HB2	1:W:45:THR:HG22	1.82	0.60
1:E:50:GLU:HB2	1:F:45:THR:HG22	1.83	0.60
1:G:27:GLU:OE2	1:Q:31:LYS:HG3	2.00	0.60
1:q:9:GLU:HA	1:r:11:VAL:O	2.02	0.60
1:m:53:MET:HE1	1:n:78:VAL:HG21	1.84	0.60
1:G:53:MET:HE1	1:H:78:VAL:HG21	1.84	0.59
1:T:50:GLU:HB2	1:U:45:THR:HG22	1.84	0.59
1:Z:53:MET:CE	1:a:33:ILE:HG23	2.32	0.59
1:K:8:GLN:HE22	1:L:8:GLN:CD	2.11	0.59
1:V:53:MET:HE1	1:W:78:VAL:HG21	1.84	0.59
1:g:53:MET:HE1	1:h:78:VAL:HG21	1.85	0.59
1:s:9:GLU:HG2	1:t:11:VAL:HG23	1.84	0.59
1:I:50:GLU:HB2	1:J:45:THR:HG22	1.84	0.59
1:i:50:GLU:HB2	1:j:45:THR:HG22	1.83	0.59
1:o:8:GLN:HE22	1:p:8:GLN:CD	2.10	0.59
1:K:9:GLU:HA	1:L:11:VAL:O	2.02	0.59
1:t:50:GLU:HB2	1:u:45:THR:HG22	1.85	0.59
1:Y:78:VAL:HG21	1:d:53:MET:HE1	1.84	0.59
1:g:8:GLN:HE22	1:h:8:GLN:NE2	2.01	0.59
1:n:8:GLN:HE22	1:o:8:GLN:CD	2.11	0.59
1:u:50:GLU:HB2	1:v:45:THR:HG22	1.84	0.59
1:X:112:LEU:O	1:X:113:GLU:CB	2.52	0.58
1:l:8:GLN:HE22	1:m:8:GLN:CD	2.11	0.58
1:C:67:ILE:HB	1:D:32:LYS:HE3	1.85	0.58
1:g:112:LEU:O	1:g:113:GLU:CB	2.52	0.58
1:q:50:GLU:HB2	1:r:45:THR:HG22	1.84	0.58
1:t:8:GLN:CD	1:u:8:GLN:HB3	2.27	0.58
1:A:11:VAL:HG23	1:F:9:GLU:HG2	1.84	0.58
1:C:53:MET:HE1	1:D:78:VAL:HG21	1.86	0.58
1:a:9:GLU:HG2	1:b:11:VAL:HG23	1.86	0.58
1:D:50:GLU:HB2	1:E:45:THR:HG22	1.86	0.57
1:L:112:LEU:O	1:L:113:GLU:CB	2.52	0.57
1:Q:8:GLN:CD	1:R:8:GLN:HB3	2.29	0.57
1:W:53:MET:HE1	1:X:78:VAL:HG21	1.86	0.57
1:D:31:LYS:CE	1:S:27:GLU:OE1	2.49	0.57
1:f:8:GLN:HE22	1:g:8:GLN:CD	2.11	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:50:GLU:HB2	1:n:45:THR:HG22	1.85	0.57
1:K:112:LEU:O	1:K:113:GLU:CB	2.52	0.57
1:P:53:MET:HE1	1:Q:78:VAL:HG21	1.85	0.57
1:n:112:LEU:O	1:n:113:GLU:CB	2.53	0.57
1:u:9:GLU:HA	1:v:11:VAL:O	2.03	0.57
1:f:50:GLU:HB2	1:g:45:THR:CG2	2.34	0.57
1:D:112:LEU:O	1:D:113:GLU:CB	2.52	0.57
1:Q:112:LEU:O	1:Q:113:GLU:CB	2.52	0.57
1:e:11:VAL:O	1:j:9:GLU:HA	2.05	0.57
1:m:8:GLN:CD	1:n:8:GLN:HB3	2.28	0.57
1:r:112:LEU:O	1:r:113:GLU:CB	2.53	0.57
1:c:31:LYS:CE	1:m:37:ASP:OD2	2.53	0.57
1:i:8:GLN:HE22	1:j:8:GLN:CD	2.11	0.57
1:d:112:LEU:O	1:d:113:GLU:CB	2.53	0.56
1:T:112:LEU:O	1:T:113:GLU:CB	2.52	0.56
1:h:8:GLN:HE22	1:i:8:GLN:CD	2.12	0.56
1:A:50:GLU:HB2	1:B:45:THR:HG22	1.87	0.56
1:H:112:LEU:O	1:H:113:GLU:CB	2.52	0.56
1:K:31:LYS:CE	1:M:27:GLU:OE1	2.42	0.56
1:P:112:LEU:O	1:P:113:GLU:CB	2.53	0.56
1:Z:112:LEU:O	1:Z:113:GLU:CB	2.53	0.56
1:q:112:LEU:O	1:q:113:GLU:CB	2.53	0.56
1:M:8:GLN:NE2	1:N:8:GLN:CD	2.63	0.56
1:o:112:LEU:O	1:o:113:GLU:CB	2.54	0.56
1:A:78:VAL:HG21	1:F:53:MET:HE1	1.88	0.56
1:J:53:MET:HE1	1:K:78:VAL:HG21	1.87	0.56
1:O:8:GLN:CD	1:P:8:GLN:HB3	2.31	0.56
1:O:9:GLU:HA	1:P:11:VAL:O	2.05	0.56
1:P:8:GLN:HE22	1:Q:8:GLN:CD	2.14	0.56
1:q:8:GLN:NE2	1:r:8:GLN:CD	2.63	0.56
1:q:8:GLN:CD	1:r:8:GLN:HB3	2.31	0.56
1:F:112:LEU:O	1:F:113:GLU:CB	2.53	0.56
1:W:57:ASP:HA	1:X:29:LEU:HD22	1.87	0.56
1:W:112:LEU:O	1:W:113:GLU:CB	2.54	0.56
1:S:11:VAL:O	1:X:9:GLU:HA	2.06	0.56
1:u:9:GLU:HG2	1:v:11:VAL:HG23	1.88	0.56
1:c:31:LYS:HE2	1:m:37:ASP:OD2	2.06	0.56
1:f:112:LEU:O	1:f:113:GLU:CB	2.54	0.56
1:c:112:LEU:O	1:c:113:GLU:CB	2.53	0.55
1:k:50:GLU:HB2	1:l:45:THR:HG22	1.89	0.55
1:q:53:MET:HE1	1:r:78:VAL:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:MET:HE1	1:B:78:VAL:HG21	1.87	0.55
1:W:9:GLU:HA	1:X:11:VAL:O	2.06	0.55
1:l:24:HIS:N	1:l:25:PRO:HD3	2.21	0.55
1:C:112:LEU:O	1:C:113:GLU:CB	2.54	0.55
1:i:53:MET:HE1	1:j:78:VAL:HG21	1.88	0.55
1:p:112:LEU:O	1:p:113:GLU:CB	2.54	0.55
1:M:78:VAL:HG21	1:R:53:MET:HE1	1.89	0.55
1:h:112:LEU:O	1:h:113:GLU:CB	2.55	0.55
1:u:112:LEU:O	1:u:113:GLU:CB	2.54	0.55
1:M:8:GLN:CD	1:R:8:GLN:NE2	2.64	0.55
1:M:112:LEU:O	1:M:113:GLU:CB	2.54	0.55
1:e:112:LEU:O	1:e:113:GLU:CB	2.52	0.55
1:U:24:HIS:N	1:U:25:PRO:HD3	2.20	0.55
1:J:112:LEU:O	1:J:113:GLU:CB	2.55	0.55
1:b:112:LEU:O	1:b:113:GLU:CB	2.53	0.55
1:k:8:GLN:CD	1:l:8:GLN:HB3	2.32	0.55
1:s:24:HIS:N	1:s:25:PRO:HD3	2.22	0.55
1:G:29:LEU:HD22	1:L:57:ASP:HA	1.88	0.55
1:N:8:GLN:HE22	1:O:8:GLN:NE2	2.04	0.55
1:e:8:GLN:NE2	1:f:8:GLN:CD	2.65	0.55
1:G:24:HIS:N	1:G:25:PRO:HD3	2.21	0.55
1:k:112:LEU:O	1:k:113:GLU:CB	2.54	0.55
1:d:24:HIS:N	1:d:25:PRO:HD3	2.22	0.55
1:E:24:HIS:N	1:E:25:PRO:HD3	2.22	0.54
1:e:24:HIS:N	1:e:25:PRO:HD3	2.22	0.54
1:h:9:GLU:HG2	1:i:11:VAL:HG23	1.89	0.54
1:M:50:GLU:HB2	1:N:45:THR:CG2	2.37	0.54
1:Q:24:HIS:N	1:Q:25:PRO:HD3	2.22	0.54
1:C:8:GLN:NE2	1:D:8:GLN:CD	2.64	0.54
1:N:24:HIS:N	1:N:25:PRO:HD3	2.22	0.54
1:g:24:HIS:N	1:g:25:PRO:HD3	2.23	0.54
1:l:112:LEU:O	1:l:113:GLU:CB	2.53	0.54
1:v:112:LEU:O	1:v:113:GLU:CB	2.55	0.54
1:B:112:LEU:O	1:B:113:GLU:CB	2.55	0.54
1:G:32:LYS:HE3	1:L:67:ILE:HB	1.88	0.54
1:b:24:HIS:N	1:b:25:PRO:HD3	2.21	0.54
1:i:112:LEU:O	1:i:113:GLU:CB	2.55	0.54
1:V:112:LEU:O	1:V:113:GLU:CB	2.56	0.54
1:U:112:LEU:O	1:U:113:GLU:CB	2.54	0.54
1:Z:24:HIS:N	1:Z:25:PRO:HD3	2.22	0.54
1:g:50:GLU:HB2	1:h:45:THR:HG22	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:24:HIS:N	1:h:25:PRO:HD3	2.22	0.54
1:r:53:MET:HE1	1:s:78:VAL:HG21	1.89	0.54
1:C:24:HIS:N	1:C:25:PRO:HD3	2.23	0.54
1:G:11:VAL:O	1:L:9:GLU:HA	2.07	0.54
1:L:24:HIS:N	1:L:25:PRO:HD3	2.22	0.54
1:N:112:LEU:O	1:N:113:GLU:CB	2.54	0.54
1:P:24:HIS:N	1:P:25:PRO:HD3	2.23	0.54
1:f:24:HIS:N	1:f:25:PRO:HD3	2.23	0.54
1:j:112:LEU:O	1:j:113:GLU:CB	2.55	0.54
1:v:24:HIS:N	1:v:25:PRO:HD3	2.22	0.54
1:V:24:HIS:N	1:V:25:PRO:HD3	2.23	0.54
1:h:53:MET:CE	1:i:33:ILE:HG23	2.38	0.54
1:k:45:THR:HG22	1:p:50:GLU:HB2	1.90	0.54
1:m:8:GLN:NE2	1:n:8:GLN:CD	2.66	0.54
1:C:53:MET:CE	1:D:33:ILE:HG23	2.38	0.54
1:D:31:LYS:NZ	1:S:37:ASP:OD2	2.39	0.54
1:I:53:MET:HE1	1:J:78:VAL:HG21	1.89	0.54
1:I:112:LEU:O	1:I:113:GLU:CB	2.54	0.54
1:O:24:HIS:N	1:O:25:PRO:HD3	2.23	0.54
1:b:8:GLN:NE2	1:c:8:GLN:CD	2.66	0.54
1:c:31:LYS:HG3	1:m:27:GLU:OE2	2.08	0.54
1:m:24:HIS:N	1:m:25:PRO:HD3	2.23	0.54
1:u:8:GLN:CD	1:v:8:GLN:HB3	2.33	0.54
1:B:24:HIS:N	1:B:25:PRO:HD3	2.23	0.54
1:c:24:HIS:N	1:c:25:PRO:HD3	2.23	0.54
1:m:112:LEU:O	1:m:113:GLU:CB	2.56	0.54
1:A:24:HIS:N	1:A:25:PRO:HD3	2.23	0.53
1:W:50:GLU:HB2	1:X:45:THR:HG22	1.91	0.53
1:i:35:VAL:HG21	1:i:41:ILE:CD1	2.22	0.53
1:k:78:VAL:HG21	1:p:53:MET:HE1	1.91	0.53
1:R:24:HIS:N	1:R:25:PRO:HD3	2.23	0.53
1:a:112:LEU:O	1:a:113:GLU:CB	2.56	0.53
1:X:24:HIS:N	1:X:25:PRO:HD3	2.22	0.53
1:L:31:LYS:HZ1	1:R:37:ASP:H	1.49	0.53
1:f:37:ASP:OD2	1:u:31:LYS:HE2	2.08	0.53
1:p:24:HIS:N	1:p:25:PRO:HD3	2.23	0.53
1:A:112:LEU:O	1:A:113:GLU:CB	2.54	0.53
1:D:9:GLU:HA	1:E:11:VAL:O	2.08	0.53
1:Y:24:HIS:N	1:Y:25:PRO:HD3	2.24	0.53
1:a:8:GLN:CD	1:b:8:GLN:HB3	2.34	0.53
1:c:50:GLU:HB2	1:d:45:THR:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:9:GLU:HA	1:j:11:VAL:O	2.09	0.53
1:R:112:LEU:O	1:R:113:GLU:CB	2.54	0.53
1:S:8:GLN:CD	1:X:8:GLN:NE2	2.67	0.53
1:T:24:HIS:N	1:T:25:PRO:HD3	2.22	0.53
1:k:9:GLU:HG2	1:l:11:VAL:HG23	1.91	0.53
1:n:24:HIS:N	1:n:25:PRO:HD3	2.24	0.53
1:D:24:HIS:N	1:D:25:PRO:HD3	2.24	0.53
1:J:24:HIS:N	1:J:25:PRO:HD3	2.24	0.53
1:S:24:HIS:N	1:S:25:PRO:HD3	2.23	0.53
1:U:9:GLU:HG2	1:V:11:VAL:HG23	1.90	0.53
1:Y:27:GLU:OE1	1:k:31:LYS:CE	2.45	0.53
1:u:8:GLN:NE2	1:v:8:GLN:CD	2.67	0.53
1:J:50:GLU:HB2	1:K:45:THR:HG22	1.90	0.53
1:e:9:GLU:HA	1:f:11:VAL:O	2.08	0.53
1:M:11:VAL:O	1:R:9:GLU:HA	2.09	0.53
1:r:24:HIS:N	1:r:25:PRO:HD3	2.23	0.53
1:s:8:GLN:CD	1:t:8:GLN:HB3	2.34	0.53
1:M:45:THR:HG22	1:R:50:GLU:HB2	1.91	0.53
1:m:9:GLU:HG2	1:n:11:VAL:HG23	1.91	0.53
1:I:9:GLU:HA	1:J:11:VAL:O	2.09	0.52
1:O:112:LEU:O	1:O:113:GLU:CB	2.57	0.52
1:Y:112:LEU:O	1:Y:113:GLU:CB	2.53	0.52
1:f:37:ASP:OD2	1:u:31:LYS:NZ	2.39	0.52
1:E:112:LEU:O	1:E:113:GLU:CB	2.55	0.52
1:P:50:GLU:HB2	1:Q:45:THR:HG22	1.91	0.52
1:S:8:GLN:HE22	1:T:8:GLN:CD	2.18	0.52
1:q:24:HIS:N	1:q:25:PRO:HD3	2.24	0.52
1:P:35:VAL:HG21	1:P:41:ILE:CD1	2.19	0.52
1:V:8:GLN:CD	1:W:8:GLN:HB3	2.34	0.52
1:W:24:HIS:N	1:W:25:PRO:HD3	2.23	0.52
1:a:24:HIS:N	1:a:25:PRO:HD3	2.24	0.52
1:q:8:GLN:CD	1:v:8:GLN:NE2	2.68	0.52
1:s:112:LEU:O	1:s:113:GLU:CB	2.56	0.52
1:H:8:GLN:HE22	1:I:8:GLN:CD	2.17	0.52
1:N:9:GLU:HA	1:O:11:VAL:O	2.10	0.52
1:u:24:HIS:N	1:u:25:PRO:HD3	2.24	0.52
1:G:112:LEU:O	1:G:113:GLU:CB	2.56	0.52
1:K:24:HIS:N	1:K:25:PRO:HD3	2.23	0.52
1:G:50:GLU:HB2	1:H:45:THR:CG2	2.40	0.52
1:k:24:HIS:N	1:k:25:PRO:HD3	2.24	0.52
1:t:24:HIS:N	1:t:25:PRO:HD3	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:9:GLU:HA	1:H:11:VAL:O	2.10	0.52
1:I:24:HIS:N	1:I:25:PRO:HD3	2.24	0.52
1:S:112:LEU:O	1:S:113:GLU:CB	2.56	0.52
1:Y:8:GLN:CD	1:Z:8:GLN:HB3	2.35	0.52
1:o:24:HIS:N	1:o:25:PRO:HD3	2.23	0.52
1:S:50:GLU:HB2	1:T:45:THR:CG2	2.40	0.52
1:i:24:HIS:N	1:i:25:PRO:HD3	2.24	0.52
1:j:24:HIS:N	1:j:25:PRO:HD3	2.24	0.52
1:s:50:GLU:HB2	1:t:45:THR:HG22	1.92	0.52
1:J:8:GLN:NE2	1:K:8:GLN:CD	2.68	0.51
1:M:24:HIS:N	1:M:25:PRO:HD3	2.23	0.51
1:i:8:GLN:CD	1:j:8:GLN:HB3	2.35	0.51
1:F:24:HIS:N	1:F:25:PRO:HD3	2.24	0.51
1:q:9:GLU:HG2	1:r:11:VAL:HG23	1.92	0.51
1:r:8:GLN:HE22	1:s:8:GLN:CD	2.18	0.51
1:t:112:LEU:O	1:t:113:GLU:CB	2.55	0.51
1:f:50:GLU:CB	1:g:45:THR:HG22	2.40	0.51
1:I:8:GLN:CD	1:J:8:GLN:HB3	2.36	0.51
1:G:37:ASP:OD2	1:Q:31:LYS:CE	2.59	0.51
1:e:50:GLU:HB2	1:f:45:THR:HG22	1.93	0.51
1:C:35:VAL:HG21	1:C:41:ILE:CD1	2.19	0.51
1:f:27:GLU:OE1	1:u:31:LYS:CE	2.58	0.51
1:D:8:GLN:NE2	1:E:8:GLN:CD	2.69	0.51
1:G:8:GLN:NE2	1:H:8:GLN:CD	2.68	0.51
1:G:27:GLU:CD	1:Q:31:LYS:HE3	2.34	0.51
1:K:53:MET:CE	1:L:33:ILE:HG23	2.40	0.51
1:W:8:GLN:NE2	1:X:8:GLN:CD	2.68	0.51
1:f:27:GLU:HB2	1:u:31:LYS:HE2	1.91	0.51
1:n:8:GLN:NE2	1:o:8:GLN:CD	2.69	0.51
1:W:35:VAL:HG21	1:W:41:ILE:CD1	2.21	0.50
1:k:8:GLN:CD	1:p:8:GLN:HE22	2.19	0.50
1:O:35:VAL:HG21	1:O:41:ILE:CD1	2.22	0.50
1:O:50:GLU:HB2	1:P:45:THR:CG2	2.40	0.50
1:a:35:VAL:HG21	1:a:41:ILE:CD1	2.23	0.50
1:e:8:GLN:HB3	1:j:8:GLN:CD	2.37	0.50
1:e:31:LYS:HZ3	1:v:37:ASP:H	1.55	0.50
1:B:53:MET:HE1	1:C:78:VAL:HG21	1.93	0.50
1:E:8:GLN:NE2	1:F:8:GLN:CD	2.69	0.50
1:U:35:VAL:HG21	1:U:41:ILE:CD1	2.21	0.50
1:Z:53:MET:HB3	1:a:33:ILE:HD11	1.91	0.50
1:a:8:GLN:NE2	1:b:8:GLN:CD	2.70	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:27:GLU:CD	1:u:31:LYS:CG	2.82	0.50
1:r:50:GLU:HB2	1:s:45:THR:CG2	2.40	0.50
1:N:53:MET:CE	1:O:33:ILE:HG23	2.42	0.50
1:d:37:ASP:HB3	1:l:31:LYS:NZ	2.23	0.50
1:o:8:GLN:CD	1:p:8:GLN:HB3	2.37	0.50
1:D:9:GLU:HG2	1:E:11:VAL:HG23	1.94	0.50
1:d:37:ASP:CB	1:l:31:LYS:HZ2	2.17	0.50
1:C:57:ASP:HA	1:D:29:LEU:HD22	1.92	0.50
1:b:50:GLU:HB2	1:c:45:THR:CG2	2.40	0.50
1:e:45:THR:CG2	1:j:50:GLU:HB2	2.41	0.50
1:B:8:GLN:CD	1:C:8:GLN:HB3	2.37	0.50
1:P:67:ILE:HB	1:Q:32:LYS:HE3	1.94	0.49
1:n:67:ILE:HB	1:o:32:LYS:HE3	1.93	0.49
1:J:35:VAL:HG21	1:J:41:ILE:CD1	2.21	0.49
1:K:53:MET:HB3	1:L:33:ILE:HD11	1.94	0.49
1:D:8:GLN:CD	1:E:8:GLN:HB3	2.37	0.49
1:H:80:TYR:OH	1:O:31:LYS:HE2	2.12	0.49
1:Y:45:THR:CG2	1:d:50:GLU:HB2	2.43	0.49
1:U:8:GLN:CD	1:V:8:GLN:HB3	2.37	0.49
1:B:50:GLU:HB2	1:C:45:THR:HG22	1.93	0.49
1:O:8:GLN:NE2	1:P:8:GLN:CD	2.70	0.49
1:t:9:GLU:HA	1:u:11:VAL:O	2.13	0.49
1:U:53:MET:CE	1:V:33:ILE:HG23	2.43	0.49
1:V:9:GLU:HA	1:W:11:VAL:O	2.12	0.49
1:V:35:VAL:HG21	1:V:41:ILE:CD1	2.21	0.49
1:Z:48:PRO:HG2	1:a:45:THR:HG21	1.95	0.49
1:H:24:HIS:N	1:H:25:PRO:HD3	2.26	0.49
1:e:8:GLN:CD	1:j:8:GLN:NE2	2.69	0.49
1:b:8:GLN:CD	1:c:8:GLN:HB3	2.37	0.49
1:g:67:ILE:HB	1:h:32:LYS:HE3	1.95	0.49
1:k:8:GLN:NE2	1:l:8:GLN:CD	2.69	0.49
1:l:50:GLU:HB2	1:m:45:THR:CG2	2.43	0.49
1:u:53:MET:HE1	1:v:78:VAL:HG21	1.95	0.49
1:C:50:GLU:HB2	1:D:45:THR:HG22	1.95	0.49
1:Q:8:GLN:NE2	1:R:8:GLN:CD	2.71	0.49
1:Z:48:PRO:CG	1:a:45:THR:HG21	2.42	0.49
1:Z:57:ASP:HB2	1:a:29:LEU:CD2	2.43	0.49
1:o:9:GLU:HA	1:p:11:VAL:O	2.13	0.49
1:K:8:GLN:NE2	1:L:8:GLN:CD	2.71	0.48
1:l:8:GLN:NE2	1:m:8:GLN:CD	2.71	0.48
1:E:50:GLU:HB2	1:F:45:THR:CG2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:37:ASP:OD2	1:Q:31:LYS:HE2	2.13	0.48
1:J:9:GLU:HA	1:K:11:VAL:O	2.14	0.48
1:K:35:VAL:HG21	1:K:41:ILE:CD1	2.22	0.48
1:N:53:MET:CE	1:O:33:ILE:HG12	2.43	0.48
1:C:53:MET:HB3	1:D:33:ILE:HD11	1.95	0.48
1:k:35:VAL:HG21	1:k:41:ILE:CD1	2.22	0.48
1:I:8:GLN:NE2	1:J:8:GLN:CD	2.71	0.48
1:A:67:ILE:HB	1:B:32:LYS:HE3	1.96	0.48
1:C:8:GLN:CD	1:D:8:GLN:HB3	2.38	0.48
1:U:8:GLN:NE2	1:V:8:GLN:CD	2.72	0.48
1:W:57:ASP:CA	1:X:29:LEU:HD22	2.44	0.48
1:Y:9:GLU:HA	1:Z:11:VAL:O	2.12	0.48
1:h:50:GLU:HB2	1:i:45:THR:HG22	1.95	0.48
1:s:8:GLN:NE2	1:t:8:GLN:CD	2.69	0.48
1:X:35:VAL:HG21	1:X:41:ILE:CD1	2.21	0.48
1:a:17:THR:HB	1:a:45:THR:OG1	2.14	0.48
1:c:35:VAL:CG2	1:c:41:ILE:HD11	2.19	0.48
1:o:53:MET:HE1	1:p:78:VAL:HG21	1.96	0.48
1:E:37:ASP:H	1:X:31:LYS:NZ	2.01	0.48
1:S:9:GLU:HA	1:T:11:VAL:O	2.14	0.48
1:V:98:GLY:O	1:V:102:ASN:HA	2.14	0.48
1:o:50:GLU:HB2	1:p:45:THR:CG2	2.43	0.48
1:Y:8:GLN:CD	1:d:8:GLN:HE22	2.20	0.48
1:h:35:VAL:HG21	1:h:41:ILE:CD1	2.22	0.48
1:T:17:THR:HB	1:T:45:THR:OG1	2.15	0.47
1:V:8:GLN:NE2	1:W:8:GLN:CD	2.72	0.47
1:Y:17:THR:HB	1:Y:45:THR:OG1	2.14	0.47
1:Z:53:MET:CE	1:a:33:ILE:HG12	2.43	0.47
1:b:39:VAL:HG12	1:s:38:ALA:HB1	1.96	0.47
1:d:17:THR:HB	1:d:45:THR:OG1	2.14	0.47
1:j:17:THR:HB	1:j:45:THR:OG1	2.14	0.47
1:q:45:THR:CG2	1:v:50:GLU:HB2	2.44	0.47
1:H:17:THR:HB	1:H:45:THR:OG1	2.14	0.47
1:U:53:MET:CE	1:V:33:ILE:HG12	2.45	0.47
1:c:8:GLN:NE2	1:d:8:GLN:CD	2.71	0.47
1:t:35:VAL:HG21	1:t:41:ILE:CD1	2.21	0.47
1:M:8:GLN:NE2	1:N:8:GLN:NE2	2.55	0.47
1:Q:98:GLY:O	1:Q:102:ASN:HA	2.15	0.47
1:Y:8:GLN:NE2	1:Z:8:GLN:NE2	2.54	0.47
1:c:17:THR:HB	1:c:45:THR:OG1	2.14	0.47
1:r:35:VAL:HG21	1:r:41:ILE:CD1	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:35:VAL:HG21	1:u:41:ILE:CD1	2.22	0.47
1:M:35:VAL:HG21	1:M:41:ILE:CD1	2.21	0.47
1:j:35:VAL:HG21	1:j:41:ILE:CD1	2.22	0.47
1:r:17:THR:HB	1:r:45:THR:OG1	2.14	0.47
1:u:50:GLU:HB2	1:v:45:THR:CG2	2.44	0.47
1:G:8:GLN:CD	1:H:8:GLN:HB3	2.40	0.47
1:Y:67:ILE:HB	1:Z:32:LYS:HE3	1.95	0.47
1:p:98:GLY:O	1:p:102:ASN:HA	2.15	0.47
1:r:98:GLY:O	1:r:102:ASN:HA	2.14	0.47
1:A:8:GLN:HE22	1:B:8:GLN:CD	2.22	0.47
1:W:53:MET:CE	1:X:33:ILE:HG23	2.44	0.47
1:Y:5:ARG:NH2	1:b:15:GLN:OE1	2.37	0.47
1:G:8:GLN:HB3	1:L:8:GLN:CD	2.40	0.47
1:G:29:LEU:HB2	1:L:60:LEU:HD12	1.97	0.47
1:W:53:MET:HB3	1:X:33:ILE:HD11	1.97	0.47
1:b:35:VAL:HG21	1:b:41:ILE:CD1	2.22	0.47
1:f:17:THR:HB	1:f:45:THR:OG1	2.15	0.47
1:f:37:ASP:OD2	1:u:31:LYS:CE	2.63	0.47
1:g:17:THR:HB	1:g:45:THR:OG1	2.14	0.47
1:m:17:THR:HB	1:m:45:THR:OG1	2.15	0.47
1:v:35:VAL:HG21	1:v:41:ILE:CD1	2.22	0.47
1:G:8:GLN:CD	1:L:8:GLN:NE2	2.73	0.47
1:G:17:THR:HB	1:G:45:THR:OG1	2.13	0.47
1:L:17:THR:HB	1:L:45:THR:OG1	2.14	0.47
1:P:8:GLN:NE2	1:Q:8:GLN:CD	2.73	0.47
1:P:35:VAL:CG2	1:P:41:ILE:HD11	2.21	0.47
1:Q:35:VAL:HG21	1:Q:41:ILE:CD1	2.20	0.47
1:X:98:GLY:O	1:X:102:ASN:HA	2.15	0.47
1:e:31:LYS:NZ	1:v:37:ASP:HB2	2.22	0.47
1:h:53:MET:HB3	1:i:33:ILE:HD11	1.96	0.47
1:L:35:VAL:HG21	1:L:41:ILE:CD1	2.22	0.47
1:V:17:THR:HB	1:V:45:THR:OG1	2.15	0.47
1:W:17:THR:HB	1:W:45:THR:OG1	2.14	0.47
1:c:35:VAL:HG21	1:c:41:ILE:CD1	2.18	0.47
1:s:53:MET:HE1	1:t:78:VAL:HG21	1.96	0.47
1:v:17:THR:HB	1:v:45:THR:OG1	2.15	0.47
1:l:57:ASP:HA	1:m:29:LEU:HD22	1.96	0.47
1:m:53:MET:HE2	1:n:33:ILE:HD13	1.97	0.47
1:G:27:GLU:CD	1:Q:31:LYS:CG	2.82	0.46
1:S:33:ILE:HG23	1:X:53:MET:CE	2.45	0.46
1:Z:8:GLN:HE22	1:a:8:GLN:NE2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:98:GLY:O	1:u:102:ASN:HA	2.15	0.46
1:A:45:THR:CG2	1:F:50:GLU:HB2	2.44	0.46
1:B:87:GLU:HG3	1:B:108:MET:CE	2.40	0.46
1:E:17:THR:HB	1:E:45:THR:OG1	2.14	0.46
1:G:45:THR:HG21	1:L:48:PRO:HG2	1.97	0.46
1:e:9:GLU:HG2	1:f:11:VAL:HG23	1.98	0.46
1:h:87:GLU:HG3	1:h:108:MET:CE	2.41	0.46
1:o:8:GLN:NE2	1:p:8:GLN:CD	2.74	0.46
1:A:17:THR:HB	1:A:45:THR:OG1	2.15	0.46
1:f:35:VAL:HG21	1:f:41:ILE:CD1	2.21	0.46
1:g:98:GLY:O	1:g:102:ASN:HA	2.15	0.46
1:k:98:GLY:O	1:k:102:ASN:HA	2.15	0.46
1:B:17:THR:HB	1:B:45:THR:OG1	2.15	0.46
1:C:17:THR:HB	1:C:45:THR:OG1	2.15	0.46
1:M:17:THR:HB	1:M:45:THR:OG1	2.16	0.46
1:h:48:PRO:HG2	1:i:45:THR:HG21	1.97	0.46
1:i:17:THR:HB	1:i:45:THR:OG1	2.16	0.46
1:m:35:VAL:HG21	1:m:41:ILE:CD1	2.22	0.46
1:H:98:GLY:O	1:H:102:ASN:HA	2.15	0.46
1:h:8:GLN:CD	1:i:8:GLN:HB3	2.41	0.46
1:J:17:THR:HB	1:J:45:THR:OG1	2.16	0.46
1:N:17:THR:HB	1:N:45:THR:OG1	2.15	0.46
1:Y:98:GLY:O	1:Y:102:ASN:HA	2.16	0.46
1:p:87:GLU:HG3	1:p:108:MET:CE	2.43	0.46
1:E:35:VAL:HG21	1:E:41:ILE:CD1	2.22	0.46
1:H:9:GLU:HA	1:I:11:VAL:O	2.16	0.46
1:P:17:THR:HB	1:P:45:THR:OG1	2.16	0.46
1:e:11:VAL:HG23	1:j:9:GLU:HG2	1.98	0.46
1:f:8:GLN:NE2	1:g:8:GLN:CD	2.74	0.46
1:i:98:GLY:O	1:i:102:ASN:HA	2.16	0.46
1:M:98:GLY:O	1:M:102:ASN:HA	2.16	0.46
1:N:53:MET:HB3	1:O:33:ILE:HD11	1.97	0.46
1:e:17:THR:HB	1:e:45:THR:OG1	2.15	0.46
1:e:53:MET:HE2	1:f:33:ILE:HD13	1.98	0.46
1:h:53:MET:CE	1:i:33:ILE:HG12	2.46	0.46
1:F:17:THR:HB	1:F:45:THR:OG1	2.16	0.46
1:F:98:GLY:O	1:F:102:ASN:HA	2.16	0.46
1:I:98:GLY:O	1:I:102:ASN:HA	2.16	0.46
1:N:53:MET:HE2	1:O:33:ILE:HG12	1.97	0.46
1:S:33:ILE:HD11	1:X:53:MET:HB3	1.98	0.46
1:V:67:ILE:HB	1:W:32:LYS:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:17:THR:HB	1:l:45:THR:OG1	2.15	0.46
1:q:17:THR:HB	1:q:45:THR:OG1	2.15	0.46
1:E:9:GLU:HA	1:F:11:VAL:O	2.16	0.46
1:U:50:GLU:HB2	1:V:45:THR:HG22	1.98	0.46
1:Z:50:GLU:HB2	1:a:45:THR:HG22	1.97	0.46
1:g:35:VAL:HG21	1:g:41:ILE:CD1	2.20	0.46
1:n:98:GLY:O	1:n:102:ASN:HA	2.16	0.46
1:o:17:THR:HB	1:o:45:THR:OG1	2.16	0.46
1:o:87:GLU:HG3	1:o:108:MET:CE	2.42	0.46
1:u:17:THR:HB	1:u:45:THR:OG1	2.16	0.46
1:M:33:ILE:HG23	1:R:53:MET:CE	2.46	0.45
1:Q:87:GLU:HG3	1:Q:108:MET:CE	2.41	0.45
1:X:17:THR:HB	1:X:45:THR:OG1	2.16	0.45
1:Z:53:MET:HE2	1:a:33:ILE:HG12	1.97	0.45
1:a:31:LYS:HE2	1:n:80:TYR:OH	2.16	0.45
1:I:17:THR:HB	1:I:45:THR:OG1	2.15	0.45
1:L:31:LYS:HZ3	1:R:37:ASP:H	1.60	0.45
1:K:98:GLY:O	1:K:102:ASN:HA	2.17	0.45
1:O:17:THR:HB	1:O:45:THR:OG1	2.16	0.45
1:S:11:VAL:HG23	1:X:9:GLU:HG2	1.97	0.45
1:o:98:GLY:O	1:o:102:ASN:HA	2.16	0.45
1:t:50:GLU:HB2	1:u:45:THR:CG2	2.46	0.45
1:U:87:GLU:HG3	1:U:108:MET:CE	2.42	0.45
1:a:87:GLU:HG3	1:a:108:MET:CE	2.41	0.45
1:h:17:THR:HB	1:h:45:THR:OG1	2.16	0.45
1:i:87:GLU:HG3	1:i:108:MET:CE	2.44	0.45
1:k:17:THR:HB	1:k:45:THR:OG1	2.16	0.45
1:o:9:GLU:HG2	1:p:11:VAL:HG23	1.96	0.45
1:o:35:VAL:HG21	1:o:41:ILE:CD1	2.22	0.45
1:B:8:GLN:NE2	1:C:8:GLN:CD	2.73	0.45
1:J:53:MET:HE2	1:K:33:ILE:HD13	1.98	0.45
1:T:35:VAL:HG21	1:T:41:ILE:CD1	2.21	0.45
1:t:17:THR:HB	1:t:45:THR:OG1	2.16	0.45
1:D:50:GLU:HB2	1:E:45:THR:CG2	2.47	0.45
1:D:87:GLU:HG3	1:D:108:MET:CE	2.42	0.45
1:K:53:MET:HE1	1:L:78:VAL:HG21	1.99	0.45
1:T:8:GLN:HE22	1:U:8:GLN:CD	2.23	0.45
1:C:57:ASP:CA	1:D:29:LEU:HD22	2.47	0.45
1:F:82:SER:HB2	1:K:87:GLU:OE1	2.16	0.45
1:G:29:LEU:HD22	1:L:57:ASP:CA	2.47	0.45
1:G:33:ILE:HG23	1:L:53:MET:CE	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:98:GLY:O	1:L:102:ASN:HA	2.17	0.45
1:C:67:ILE:HD12	1:D:32:LYS:HG3	1.99	0.45
1:O:35:VAL:CG2	1:O:41:ILE:HD11	2.23	0.45
1:P:53:MET:CE	1:Q:33:ILE:HG23	2.46	0.45
1:S:17:THR:HB	1:S:45:THR:OG1	2.16	0.45
1:a:48:PRO:HG2	1:b:45:THR:HG21	1.99	0.45
1:i:50:GLU:HB2	1:j:45:THR:CG2	2.47	0.45
1:C:57:ASP:HB2	1:D:29:LEU:CD2	2.47	0.45
1:Y:50:GLU:HB2	1:Z:45:THR:CG2	2.45	0.45
1:c:87:GLU:HG3	1:c:108:MET:CE	2.43	0.45
1:e:35:VAL:HG21	1:e:41:ILE:CD1	2.20	0.45
1:n:8:GLN:NE2	1:o:8:GLN:NE2	2.58	0.45
1:n:17:THR:HB	1:n:45:THR:OG1	2.16	0.45
1:q:53:MET:CE	1:r:33:ILE:HG23	2.46	0.45
1:T:98:GLY:O	1:T:102:ASN:HA	2.16	0.45
1:W:98:GLY:O	1:W:102:ASN:HA	2.17	0.45
1:Z:35:VAL:HG21	1:Z:41:ILE:CD1	2.23	0.45
1:D:98:GLY:O	1:D:102:ASN:HA	2.18	0.44
1:O:98:GLY:O	1:O:102:ASN:HA	2.18	0.44
1:P:87:GLU:HG3	1:P:108:MET:CE	2.43	0.44
1:Q:17:THR:HB	1:Q:45:THR:OG1	2.16	0.44
1:Q:53:MET:CE	1:R:33:ILE:HG12	2.47	0.44
1:R:98:GLY:O	1:R:102:ASN:HA	2.17	0.44
1:U:17:THR:HB	1:U:45:THR:OG1	2.16	0.44
1:b:50:GLU:CB	1:c:45:THR:HG22	2.46	0.44
1:p:17:THR:HB	1:p:45:THR:OG1	2.17	0.44
1:s:17:THR:HB	1:s:45:THR:OG1	2.17	0.44
1:G:33:ILE:HD11	1:L:53:MET:HB3	1.99	0.44
1:C:87:GLU:HG3	1:C:108:MET:CE	2.44	0.44
1:G:27:GLU:HB2	1:Q:31:LYS:CE	2.47	0.44
1:H:87:GLU:HG3	1:H:108:MET:CE	2.44	0.44
1:R:17:THR:HB	1:R:45:THR:OG1	2.17	0.44
1:S:35:VAL:HG21	1:S:41:ILE:CD1	2.21	0.44
1:S:87:GLU:HG3	1:S:108:MET:CE	2.42	0.44
1:q:57:ASP:HA	1:r:29:LEU:HD22	1.98	0.44
1:q:87:GLU:HG3	1:q:108:MET:CE	2.42	0.44
1:J:98:GLY:O	1:J:102:ASN:HA	2.17	0.44
1:W:57:ASP:HB2	1:X:29:LEU:CD2	2.47	0.44
1:Z:87:GLU:HG3	1:Z:108:MET:CE	2.43	0.44
1:b:17:THR:HB	1:b:45:THR:OG1	2.16	0.44
1:m:98:GLY:O	1:m:102:ASN:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:9:GLU:HA	1:o:11:VAL:O	2.18	0.44
1:n:53:MET:CE	1:o:33:ILE:HG23	2.47	0.44
1:p:35:VAL:HG21	1:p:41:ILE:CD1	2.19	0.44
1:D:31:LYS:CG	1:S:27:GLU:CD	2.88	0.44
1:E:98:GLY:O	1:E:102:ASN:HA	2.17	0.44
1:K:17:THR:HB	1:K:45:THR:OG1	2.17	0.44
1:Q:50:GLU:HB2	1:R:45:THR:HG22	1.98	0.44
1:T:87:GLU:HG3	1:T:108:MET:CE	2.44	0.44
1:e:53:MET:HE1	1:f:78:VAL:HG21	1.99	0.44
1:P:57:ASP:HA	1:Q:29:LEU:HD22	1.99	0.44
1:T:53:MET:HE2	1:U:33:ILE:HD13	1.99	0.44
1:d:35:VAL:HG21	1:d:41:ILE:CD1	2.23	0.44
1:t:98:GLY:O	1:t:102:ASN:HA	2.17	0.44
1:V:50:GLU:HB2	1:W:45:THR:CG2	2.46	0.44
1:W:67:ILE:HD12	1:X:32:LYS:HG3	1.99	0.44
1:Y:45:THR:HG22	1:d:50:GLU:CB	2.48	0.44
1:f:9:GLU:HA	1:g:11:VAL:O	2.17	0.44
1:q:98:GLY:O	1:q:102:ASN:HA	2.18	0.44
1:r:50:GLU:CB	1:s:45:THR:HG22	2.45	0.44
1:r:87:GLU:HG3	1:r:108:MET:CE	2.43	0.44
1:s:53:MET:HB3	1:t:33:ILE:HD11	2.00	0.44
1:B:9:GLU:HG2	1:C:11:VAL:HG23	2.00	0.44
1:I:9:GLU:HG2	1:J:11:VAL:HG23	2.00	0.44
1:L:87:GLU:HG3	1:L:108:MET:CE	2.43	0.44
1:M:50:GLU:CB	1:N:45:THR:HG22	2.44	0.44
1:Y:57:ASP:HA	1:Z:29:LEU:HD22	1.99	0.44
1:Z:17:THR:HB	1:Z:45:THR:OG1	2.18	0.44
1:a:98:GLY:O	1:a:102:ASN:HA	2.18	0.44
1:k:53:MET:HE1	1:l:78:VAL:HG21	1.99	0.44
1:s:98:GLY:O	1:s:102:ASN:HA	2.18	0.44
1:u:87:GLU:HG3	1:u:108:MET:CE	2.43	0.44
1:D:53:MET:HE1	1:E:78:VAL:HG21	2.00	0.44
1:Q:35:VAL:CG2	1:Q:41:ILE:HD11	2.21	0.44
1:c:98:GLY:O	1:c:102:ASN:HA	2.18	0.44
1:n:53:MET:CE	1:o:33:ILE:HG12	2.48	0.44
1:A:8:GLN:NE2	1:B:8:GLN:NE2	2.59	0.43
1:A:98:GLY:O	1:A:102:ASN:HA	2.16	0.43
1:G:9:GLU:HG2	1:H:11:VAL:HG23	2.00	0.43
1:S:33:ILE:HG12	1:X:53:MET:CE	2.47	0.43
1:l:50:GLU:OE2	1:m:76:ALA:HB2	2.18	0.43
1:m:48:PRO:HG2	1:n:45:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:8:GLN:NE2	1:I:8:GLN:CD	2.75	0.43
1:K:9:GLU:HG2	1:L:11:VAL:HG23	2.00	0.43
1:K:53:MET:CE	1:L:33:ILE:HG12	2.48	0.43
1:M:8:GLN:CD	1:N:8:GLN:HB3	2.43	0.43
1:S:98:GLY:O	1:S:102:ASN:HA	2.18	0.43
1:X:105:LEU:HD12	1:X:105:LEU:N	2.33	0.43
1:Y:53:MET:HB3	1:Z:33:ILE:HD11	1.99	0.43
1:l:98:GLY:O	1:l:102:ASN:HA	2.18	0.43
1:B:98:GLY:O	1:B:102:ASN:HA	2.19	0.43
1:G:98:GLY:O	1:G:102:ASN:HA	2.18	0.43
1:c:8:GLN:OE1	1:d:8:GLN:HB3	2.17	0.43
1:H:53:MET:CE	1:I:33:ILE:HG12	2.48	0.43
1:K:50:GLU:HB2	1:L:45:THR:HG22	2.01	0.43
1:h:87:GLU:CG	1:h:108:MET:HE1	2.43	0.43
1:m:82:SER:HB2	1:s:87:GLU:CD	2.43	0.43
1:E:8:GLN:CD	1:F:8:GLN:HB3	2.43	0.43
1:N:98:GLY:O	1:N:102:ASN:HA	2.17	0.43
1:O:9:GLU:HG2	1:P:11:VAL:HG23	1.99	0.43
1:W:60:LEU:HD12	1:X:29:LEU:HB2	2.00	0.43
1:e:8:GLN:NE2	1:f:8:GLN:NE2	2.57	0.43
1:e:45:THR:HG22	1:j:50:GLU:CB	2.47	0.43
1:W:21:LEU:C	1:W:21:LEU:HD13	2.44	0.43
1:Y:8:GLN:NE2	1:d:8:GLN:NE2	2.55	0.43
1:a:50:GLU:HB2	1:b:45:THR:CG2	2.48	0.43
1:l:9:GLU:HA	1:m:11:VAL:O	2.18	0.43
1:O:87:GLU:HG3	1:O:108:MET:CE	2.44	0.43
1:V:87:GLU:HG3	1:V:108:MET:CE	2.44	0.43
1:f:27:GLU:HB2	1:u:31:LYS:CE	2.48	0.43
1:v:87:GLU:HG3	1:v:108:MET:CE	2.44	0.43
1:B:53:MET:HE2	1:C:33:ILE:HD13	2.01	0.43
1:I:50:GLU:HB2	1:J:45:THR:CG2	2.47	0.43
1:n:57:ASP:HB2	1:o:29:LEU:CD2	2.48	0.43
1:q:8:GLN:HB3	1:v:8:GLN:CD	2.44	0.43
1:v:98:GLY:O	1:v:102:ASN:HA	2.18	0.43
1:I:35:VAL:CG2	1:I:41:ILE:HD11	2.21	0.43
1:Y:8:GLN:CD	1:d:8:GLN:NE2	2.76	0.43
1:f:98:GLY:O	1:f:102:ASN:HA	2.19	0.43
1:l:53:MET:CE	1:m:33:ILE:HG23	2.49	0.43
1:E:53:MET:HE2	1:F:33:ILE:HD13	2.00	0.43
1:I:31:LYS:NZ	1:N:80:TYR:OH	2.46	0.43
1:L:31:LYS:NZ	1:R:37:ASP:HB3	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:87:GLU:HG3	1:N:108:MET:CE	2.43	0.43
1:b:105:LEU:HD12	1:b:105:LEU:N	2.34	0.43
1:c:31:LYS:CG	1:m:27:GLU:CD	2.86	0.43
1:j:18:LEU:O	1:j:44:MET:HA	2.19	0.43
1:l:48:PRO:HG2	1:m:45:THR:HG21	2.00	0.43
1:D:17:THR:HB	1:D:45:THR:OG1	2.18	0.42
1:D:35:VAL:HG21	1:D:41:ILE:CD1	2.23	0.42
1:P:98:GLY:O	1:P:102:ASN:HA	2.18	0.42
1:S:45:THR:HG22	1:X:50:GLU:HB2	2.00	0.42
1:T:50:GLU:HB2	1:U:45:THR:CG2	2.47	0.42
1:U:53:MET:HB3	1:V:33:ILE:HD11	2.01	0.42
1:W:8:GLN:CD	1:X:8:GLN:HB3	2.44	0.42
1:d:98:GLY:O	1:d:102:ASN:HA	2.18	0.42
1:k:8:GLN:CD	1:p:8:GLN:NE2	2.77	0.42
1:l:53:MET:HB3	1:m:33:ILE:HD11	2.00	0.42
1:s:87:GLU:HG3	1:s:108:MET:CE	2.43	0.42
1:D:31:LYS:HG3	1:S:27:GLU:OE2	2.20	0.42
1:E:50:GLU:CB	1:F:45:THR:HG22	2.49	0.42
1:T:50:GLU:OE2	1:U:76:ALA:HB2	2.18	0.42
1:l:60:LEU:HD12	1:m:29:LEU:HB2	2.01	0.42
1:A:87:GLU:HG3	1:A:108:MET:CE	2.43	0.42
1:F:87:GLU:HG3	1:F:108:MET:CE	2.42	0.42
1:M:35:VAL:CG2	1:M:41:ILE:HD11	2.21	0.42
1:X:87:GLU:HG3	1:X:108:MET:CE	2.45	0.42
1:b:98:GLY:O	1:b:102:ASN:HA	2.19	0.42
1:e:36:PRO:HA	1:v:31:LYS:NZ	2.34	0.42
1:e:87:GLU:HG3	1:e:108:MET:CE	2.45	0.42
1:j:21:LEU:C	1:j:21:LEU:HD13	2.44	0.42
1:k:33:ILE:HD11	1:p:53:MET:HB3	2.02	0.42
1:l:67:ILE:HB	1:m:32:LYS:HE3	2.00	0.42
1:A:8:GLN:NE2	1:B:8:GLN:CD	2.77	0.42
1:I:87:GLU:HG3	1:I:108:MET:CE	2.44	0.42
1:P:9:GLU:HA	1:Q:11:VAL:O	2.20	0.42
1:a:57:ASP:HA	1:b:29:LEU:HD22	2.01	0.42
1:l:35:VAL:HG21	1:l:41:ILE:CD1	2.23	0.42
1:o:105:LEU:N	1:o:105:LEU:HD12	2.35	0.42
1:r:8:GLN:NE2	1:s:8:GLN:CD	2.77	0.42
1:s:53:MET:HE2	1:t:33:ILE:HD13	2.01	0.42
1:C:98:GLY:O	1:C:102:ASN:HA	2.19	0.42
1:K:67:ILE:HB	1:L:32:LYS:HE3	2.02	0.42
1:U:53:MET:HE2	1:V:33:ILE:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:31:LYS:NZ	1:v:37:ASP:HB3	2.35	0.42
1:s:3:LYS:HB3	1:s:4:GLU:H	1.75	0.42
1:E:3:LYS:HB3	1:E:4:GLU:H	1.74	0.42
1:Z:98:GLY:O	1:Z:102:ASN:HA	2.19	0.42
1:h:98:GLY:O	1:h:102:ASN:HA	2.19	0.42
1:q:45:THR:HG22	1:v:50:GLU:CB	2.49	0.42
1:S:87:GLU:CG	1:S:108:MET:HE1	2.44	0.42
1:T:67:ILE:HB	1:U:32:LYS:HE3	2.02	0.42
1:g:105:LEU:HD12	1:g:105:LEU:N	2.35	0.42
1:G:35:VAL:HG21	1:G:41:ILE:CD1	2.23	0.42
1:J:87:GLU:HG3	1:J:108:MET:CE	2.44	0.42
1:M:8:GLN:NE2	1:R:8:GLN:NE2	2.57	0.42
1:N:57:ASP:HB2	1:O:29:LEU:CD2	2.49	0.42
1:S:8:GLN:NE2	1:T:8:GLN:CD	2.78	0.42
1:Y:87:GLU:HG3	1:Y:108:MET:CE	2.45	0.42
1:d:37:ASP:CA	1:l:31:LYS:NZ	2.78	0.42
1:j:3:LYS:HB3	1:j:4:GLU:H	1.74	0.42
1:p:18:LEU:O	1:p:44:MET:HA	2.20	0.42
1:q:105:LEU:HD12	1:q:105:LEU:N	2.35	0.42
1:H:21:LEU:C	1:H:21:LEU:HD13	2.45	0.42
1:P:18:LEU:HG	1:P:45:THR:HG23	2.02	0.42
1:R:105:LEU:N	1:R:105:LEU:HD12	2.34	0.42
1:U:35:VAL:CG2	1:U:41:ILE:HD11	2.22	0.42
1:V:14:LYS:HD2	1:V:103:TYR:CE2	2.55	0.42
1:e:36:PRO:HA	1:v:31:LYS:HZ3	1.85	0.42
1:k:33:ILE:HG23	1:p:53:MET:CE	2.50	0.42
1:G:32:LYS:HG3	1:L:67:ILE:HD12	2.02	0.42
1:J:8:GLN:CD	1:K:8:GLN:HB3	2.45	0.42
1:Y:50:GLU:OE2	1:Z:76:ALA:HB2	2.20	0.42
1:s:18:LEU:O	1:s:44:MET:HA	2.20	0.42
1:C:48:PRO:HG2	1:D:45:THR:HG21	2.01	0.41
1:G:27:GLU:CD	1:Q:31:LYS:CE	2.92	0.41
1:O:18:LEU:O	1:O:44:MET:HA	2.20	0.41
1:W:48:PRO:HG2	1:X:45:THR:HG21	2.01	0.41
1:e:8:GLN:CD	1:f:8:GLN:HB3	2.45	0.41
1:h:8:GLN:NE2	1:i:8:GLN:CD	2.76	0.41
1:p:105:LEU:N	1:p:105:LEU:HD12	2.34	0.41
1:q:8:GLN:NE2	1:v:8:GLN:NE2	2.58	0.41
1:q:48:PRO:HG2	1:r:45:THR:HG21	2.02	0.41
1:D:31:LYS:HE2	1:S:37:ASP:OD2	2.20	0.41
1:M:8:GLN:HB3	1:R:8:GLN:CD	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:18:LEU:O	1:a:44:MET:HA	2.20	0.41
1:g:53:MET:HB3	1:h:33:ILE:HD11	2.02	0.41
1:k:50:GLU:HB2	1:l:45:THR:CG2	2.49	0.41
1:n:87:GLU:HG3	1:n:108:MET:CE	2.44	0.41
1:A:14:LYS:HD2	1:A:103:TYR:CE2	2.55	0.41
1:A:57:ASP:HA	1:B:29:LEU:HD22	2.00	0.41
1:F:21:LEU:C	1:F:21:LEU:HD13	2.46	0.41
1:G:76:ALA:HB2	1:L:50:GLU:OE2	2.20	0.41
1:L:18:LEU:O	1:L:44:MET:HA	2.20	0.41
1:f:21:LEU:HD13	1:f:21:LEU:C	2.46	0.41
1:h:48:PRO:CG	1:i:45:THR:HG21	2.49	0.41
1:i:8:GLN:NE2	1:j:8:GLN:CD	2.77	0.41
1:v:14:LYS:HD2	1:v:103:TYR:CE2	2.55	0.41
1:k:11:VAL:O	1:p:9:GLU:HA	2.20	0.41
1:l:14:LYS:HD2	1:l:103:TYR:CE2	2.55	0.41
1:n:53:MET:HB3	1:o:33:ILE:HD11	2.01	0.41
1:q:11:VAL:O	1:v:9:GLU:HA	2.20	0.41
1:C:105:LEU:HD12	1:C:105:LEU:N	2.35	0.41
1:G:14:LYS:HD2	1:G:103:TYR:CE2	2.56	0.41
1:L:31:LYS:HZ1	1:R:37:ASP:CA	2.32	0.41
1:U:98:GLY:O	1:U:102:ASN:HA	2.20	0.41
1:Y:105:LEU:HD12	1:Y:105:LEU:N	2.36	0.41
1:o:50:GLU:CB	1:p:45:THR:HG22	2.49	0.41
1:s:53:MET:CE	1:t:33:ILE:HG23	2.50	0.41
1:s:105:LEU:N	1:s:105:LEU:HD12	2.36	0.41
1:t:53:MET:HE2	1:u:33:ILE:HD13	2.03	0.41
1:C:35:VAL:CG2	1:C:41:ILE:HD11	2.20	0.41
1:G:45:THR:CG2	1:L:50:GLU:HB2	2.49	0.41
1:W:18:LEU:O	1:W:44:MET:HA	2.20	0.41
1:Z:57:ASP:HA	1:a:29:LEU:HD22	2.01	0.41
1:e:98:GLY:O	1:e:102:ASN:HA	2.20	0.41
1:n:21:LEU:HD13	1:n:21:LEU:C	2.46	0.41
1:A:50:GLU:HB2	1:B:45:THR:CG2	2.51	0.41
1:F:105:LEU:N	1:F:105:LEU:HD12	2.35	0.41
1:N:50:GLU:HB2	1:O:45:THR:HG22	2.02	0.41
1:S:21:LEU:HD13	1:S:21:LEU:C	2.46	0.41
1:Z:105:LEU:N	1:Z:105:LEU:HD12	2.36	0.41
1:c:18:LEU:HG	1:c:45:THR:HG23	2.02	0.41
1:k:3:LYS:HB3	1:k:4:GLU:H	1.75	0.41
1:m:53:MET:CE	1:n:33:ILE:HG23	2.51	0.41
1:C:9:GLU:HG2	1:D:11:VAL:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:35:VAL:HG21	1:R:41:ILE:CD1	2.24	0.41
1:Y:53:MET:CE	1:Z:33:ILE:HG23	2.50	0.41
1:g:18:LEU:HG	1:g:45:THR:HG23	2.03	0.41
1:m:14:LYS:HD2	1:m:103:TYR:CE2	2.55	0.41
1:G:11:VAL:HG23	1:L:9:GLU:HG2	2.02	0.41
1:G:87:GLU:HG3	1:G:108:MET:CE	2.46	0.41
1:S:8:GLN:HB3	1:X:8:GLN:CD	2.45	0.41
1:T:21:LEU:HD13	1:T:21:LEU:C	2.46	0.41
1:V:18:LEU:O	1:V:44:MET:HA	2.21	0.41
1:Z:57:ASP:CA	1:a:29:LEU:HD22	2.51	0.41
1:e:21:LEU:HD13	1:e:21:LEU:C	2.46	0.41
1:j:98:GLY:O	1:j:102:ASN:HA	2.21	0.41
1:k:45:THR:CG2	1:p:50:GLU:HB2	2.51	0.41
1:s:18:LEU:HG	1:s:45:THR:HG23	2.02	0.41
1:E:14:LYS:HD2	1:E:103:TYR:CE2	2.56	0.41
1:G:27:GLU:OE1	1:Q:31:LYS:CE	2.52	0.41
1:G:50:GLU:CB	1:H:45:THR:HG22	2.45	0.41
1:H:35:VAL:HG21	1:H:41:ILE:CD1	2.23	0.41
1:V:105:LEU:HD12	1:V:105:LEU:N	2.35	0.41
1:e:105:LEU:HD12	1:e:105:LEU:N	2.36	0.41
1:f:48:PRO:HG2	1:g:45:THR:HG21	2.03	0.41
1:q:67:ILE:HB	1:r:32:LYS:HE3	2.03	0.41
1:B:18:LEU:O	1:B:44:MET:HA	2.21	0.40
1:Q:87:GLU:CG	1:Q:108:MET:HE1	2.44	0.40
1:S:33:ILE:HG12	1:X:53:MET:HE2	2.03	0.40
1:V:94:VAL:CG1	1:V:105:LEU:HD23	2.48	0.40
1:t:50:GLU:CB	1:u:45:THR:HG22	2.51	0.40
1:A:53:MET:CE	1:B:33:ILE:HG23	2.52	0.40
1:B:105:LEU:N	1:B:105:LEU:HD12	2.36	0.40
1:H:18:LEU:HG	1:H:45:THR:HG23	2.03	0.40
1:O:48:PRO:HG2	1:P:45:THR:HG21	2.04	0.40
1:P:53:MET:HB3	1:Q:33:ILE:HD11	2.04	0.40
1:W:9:GLU:HG2	1:X:11:VAL:HG23	2.04	0.40
1:Z:87:GLU:CG	1:Z:108:MET:HE1	2.45	0.40
1:g:87:GLU:HG3	1:g:108:MET:CE	2.45	0.40
1:m:53:MET:HB3	1:n:33:ILE:HD11	2.02	0.40
1:o:8:GLN:OE1	1:p:8:GLN:HB3	2.22	0.40
1:u:50:GLU:CB	1:v:45:THR:HG22	2.51	0.40
1:H:50:GLU:HB2	1:I:45:THR:HG22	2.03	0.40
1:L:105:LEU:HD12	1:L:105:LEU:N	2.37	0.40
1:c:31:LYS:CE	1:m:27:GLU:HB2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:14:LYS:HD2	1:t:103:TYR:CE2	2.56	0.40
1:B:53:MET:CE	1:C:33:ILE:HG12	2.51	0.40
1:J:14:LYS:HD2	1:J:103:TYR:CE2	2.56	0.40
1:K:57:ASP:HA	1:L:29:LEU:HD22	2.02	0.40
1:S:9:GLU:HG2	1:T:11:VAL:HG23	2.03	0.40
1:V:57:ASP:HA	1:W:29:LEU:HD22	2.03	0.40
1:Y:18:LEU:O	1:Y:44:MET:HA	2.22	0.40
1:d:37:ASP:HB2	1:l:31:LYS:HZ2	1.72	0.40
1:e:53:MET:CE	1:f:33:ILE:HG12	2.51	0.40
1:h:105:LEU:N	1:h:105:LEU:HD12	2.37	0.40
1:k:33:ILE:HD13	1:p:53:MET:HE2	2.02	0.40
1:l:87:GLU:HG3	1:l:108:MET:CE	2.47	0.40
1:q:18:LEU:O	1:q:44:MET:HA	2.22	0.40
1:r:18:LEU:O	1:r:44:MET:HA	2.21	0.40
1:s:53:MET:CE	1:t:33:ILE:HG12	2.51	0.40
1:G:3:LYS:HB3	1:G:4:GLU:H	1.73	0.40
1:J:53:MET:CE	1:K:33:ILE:HG23	2.52	0.40
1:M:32:LYS:HE3	1:R:67:ILE:HB	2.02	0.40
1:P:105:LEU:N	1:P:105:LEU:HD12	2.36	0.40
1:Q:18:LEU:HG	1:Q:45:THR:HG23	2.04	0.40
1:Y:5:ARG:HH22	1:b:15:GLN:CD	2.27	0.40
1:c:50:GLU:HB2	1:d:45:THR:CG2	2.51	0.40
1:e:18:LEU:HG	1:e:45:THR:HG23	2.03	0.40
1:k:18:LEU:O	1:k:44:MET:HA	2.22	0.40
1:t:105:LEU:N	1:t:105:LEU:HD12	2.36	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	109/119 (92%)	109 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	109/119 (92%)	107 (98%)	2 (2%)	0	100	100
1	C	109/119 (92%)	109 (100%)	0	0	100	100
1	D	109/119 (92%)	109 (100%)	0	0	100	100
1	E	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	F	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	G	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	H	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	I	109/119 (92%)	109 (100%)	0	0	100	100
1	J	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	K	109/119 (92%)	109 (100%)	0	0	100	100
1	L	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	M	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	N	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	O	109/119 (92%)	107 (98%)	2 (2%)	0	100	100
1	P	109/119 (92%)	109 (100%)	0	0	100	100
1	Q	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	R	109/119 (92%)	109 (100%)	0	0	100	100
1	S	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	T	109/119 (92%)	109 (100%)	0	0	100	100
1	U	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	V	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	W	109/119 (92%)	107 (98%)	2 (2%)	0	100	100
1	X	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	Y	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	Z	109/119 (92%)	109 (100%)	0	0	100	100
1	a	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	b	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	c	109/119 (92%)	109 (100%)	0	0	100	100
1	d	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	e	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	f	109/119 (92%)	108 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	g	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	h	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	i	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	j	109/119 (92%)	109 (100%)	0	0	100	100
1	k	109/119 (92%)	109 (100%)	0	0	100	100
1	l	109/119 (92%)	109 (100%)	0	0	100	100
1	m	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	n	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	o	109/119 (92%)	109 (100%)	0	0	100	100
1	p	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	q	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	r	109/119 (92%)	109 (100%)	0	0	100	100
1	s	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	t	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	u	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
1	v	109/119 (92%)	108 (99%)	1 (1%)	0	100	100
All	All	5232/5712 (92%)	5196 (99%)	36 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	B	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	C	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	D	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	E	86/94 (92%)	81 (94%)	5 (6%)	18	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	G	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	H	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	I	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	J	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	K	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	L	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	M	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	N	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	O	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	P	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	Q	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	R	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	S	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	T	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	U	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	V	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	W	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	X	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	Y	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	Z	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	a	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	b	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	c	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	d	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	e	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	f	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	g	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	h	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	i	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	j	86/94 (92%)	81 (94%)	5 (6%)	18	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	k	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	l	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	m	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	n	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	o	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	p	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	q	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	r	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	s	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	t	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	u	86/94 (92%)	81 (94%)	5 (6%)	18	38
1	v	86/94 (92%)	81 (94%)	5 (6%)	18	38
All	All	4128/4512 (92%)	3888 (94%)	240 (6%)	18	38

All (240) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	41	ILE
1	A	45	THR
1	A	91	SER
1	A	110	LYS
1	B	21	LEU
1	B	41	ILE
1	B	45	THR
1	B	91	SER
1	B	110	LYS
1	C	21	LEU
1	C	41	ILE
1	C	45	THR
1	C	91	SER
1	C	110	LYS
1	D	21	LEU
1	D	41	ILE
1	D	45	THR
1	D	91	SER
1	D	110	LYS
1	E	21	LEU

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Mol	Chain	Res	Type
1	E	41	ILE
1	E	45	THR
1	E	91	SER
1	E	110	LYS
1	F	21	LEU
1	F	41	ILE
1	F	45	THR
1	F	91	SER
1	F	110	LYS
1	G	21	LEU
1	G	41	ILE
1	G	45	THR
1	G	91	SER
1	G	110	LYS
1	H	21	LEU
1	H	41	ILE
1	H	45	THR
1	H	91	SER
1	H	110	LYS
1	I	21	LEU
1	I	41	ILE
1	I	45	THR
1	I	91	SER
1	I	110	LYS
1	J	21	LEU
1	J	41	ILE
1	J	45	THR
1	J	91	SER
1	J	110	LYS
1	K	21	LEU
1	K	41	ILE
1	K	45	THR
1	K	91	SER
1	K	110	LYS
1	L	21	LEU
1	L	41	ILE
1	L	45	THR
1	L	91	SER
1	L	110	LYS
1	M	21	LEU
1	M	41	ILE
1	M	45	THR

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Mol	Chain	Res	Type
1	M	91	SER
1	M	110	LYS
1	N	21	LEU
1	N	41	ILE
1	N	45	THR
1	N	91	SER
1	N	110	LYS
1	O	21	LEU
1	O	41	ILE
1	O	45	THR
1	O	91	SER
1	O	110	LYS
1	P	21	LEU
1	P	41	ILE
1	P	45	THR
1	P	91	SER
1	P	110	LYS
1	Q	21	LEU
1	Q	41	ILE
1	Q	45	THR
1	Q	91	SER
1	Q	110	LYS
1	R	21	LEU
1	R	41	ILE
1	R	45	THR
1	R	91	SER
1	R	110	LYS
1	S	21	LEU
1	S	41	ILE
1	S	45	THR
1	S	91	SER
1	S	110	LYS
1	T	21	LEU
1	T	41	ILE
1	T	45	THR
1	T	91	SER
1	T	110	LYS
1	U	21	LEU
1	U	41	ILE
1	U	45	THR
1	U	91	SER
1	U	110	LYS

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Mol	Chain	Res	Type
1	V	21	LEU
1	V	41	ILE
1	V	45	THR
1	V	91	SER
1	V	110	LYS
1	W	21	LEU
1	W	41	ILE
1	W	45	THR
1	W	91	SER
1	W	110	LYS
1	X	21	LEU
1	X	41	ILE
1	X	45	THR
1	X	91	SER
1	X	110	LYS
1	Y	21	LEU
1	Y	41	ILE
1	Y	45	THR
1	Y	91	SER
1	Y	110	LYS
1	Z	21	LEU
1	Z	41	ILE
1	Z	45	THR
1	Z	91	SER
1	Z	110	LYS
1	a	21	LEU
1	a	41	ILE
1	a	45	THR
1	a	91	SER
1	a	110	LYS
1	b	21	LEU
1	b	41	ILE
1	b	45	THR
1	b	91	SER
1	b	110	LYS
1	c	21	LEU
1	c	41	ILE
1	c	45	THR
1	c	91	SER
1	c	110	LYS
1	d	21	LEU
1	d	41	ILE

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Mol	Chain	Res	Type
1	d	45	THR
1	d	91	SER
1	d	110	LYS
1	e	21	LEU
1	e	41	ILE
1	e	45	THR
1	e	91	SER
1	e	110	LYS
1	f	21	LEU
1	f	41	ILE
1	f	45	THR
1	f	91	SER
1	f	110	LYS
1	g	21	LEU
1	g	41	ILE
1	g	45	THR
1	g	91	SER
1	g	110	LYS
1	h	21	LEU
1	h	41	ILE
1	h	45	THR
1	h	91	SER
1	h	110	LYS
1	i	21	LEU
1	i	41	ILE
1	i	45	THR
1	i	91	SER
1	i	110	LYS
1	j	21	LEU
1	j	41	ILE
1	j	45	THR
1	j	91	SER
1	j	110	LYS
1	k	21	LEU
1	k	41	ILE
1	k	45	THR
1	k	91	SER
1	k	110	LYS
1	l	21	LEU
1	l	41	ILE
1	l	45	THR
1	l	91	SER

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Mol	Chain	Res	Type
1	l	110	LYS
1	m	21	LEU
1	m	41	ILE
1	m	45	THR
1	m	91	SER
1	m	110	LYS
1	n	21	LEU
1	n	41	ILE
1	n	45	THR
1	n	91	SER
1	n	110	LYS
1	o	21	LEU
1	o	41	ILE
1	o	45	THR
1	o	91	SER
1	o	110	LYS
1	p	21	LEU
1	p	41	ILE
1	p	45	THR
1	p	91	SER
1	p	110	LYS
1	q	21	LEU
1	q	41	ILE
1	q	45	THR
1	q	91	SER
1	q	110	LYS
1	r	21	LEU
1	r	41	ILE
1	r	45	THR
1	r	91	SER
1	r	110	LYS
1	s	21	LEU
1	s	41	ILE
1	s	45	THR
1	s	91	SER
1	s	110	LYS
1	t	21	LEU
1	t	41	ILE
1	t	45	THR
1	t	91	SER
1	t	110	LYS
1	u	21	LEU

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Mol	Chain	Res	Type
1	u	41	ILE
1	u	45	THR
1	u	91	SER
1	u	110	LYS
1	v	21	LEU
1	v	41	ILE
1	v	45	THR
1	v	91	SER
1	v	110	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	8	GLN
1	D	8	GLN
1	D	66	HIS
1	F	8	GLN
1	F	24	HIS
1	G	8	GLN
1	H	66	HIS
1	I	8	GLN
1	J	66	HIS
1	K	8	GLN
1	L	66	HIS
1	M	8	GLN
1	O	8	GLN
1	O	66	HIS
1	Q	8	GLN
1	Q	66	HIS
1	R	66	HIS
1	T	8	GLN
1	U	66	HIS
1	V	8	GLN
1	V	66	HIS
1	X	8	GLN
1	X	66	HIS
1	Y	8	GLN
1	Z	66	HIS
1	a	8	GLN
1	a	66	HIS
1	b	24	HIS
1	b	66	HIS

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Mol	Chain	Res	Type
1	c	8	GLN
1	d	66	HIS
1	e	66	HIS
1	f	8	GLN
1	f	66	HIS
1	g	66	HIS
1	h	8	GLN
1	h	66	HIS
1	j	8	GLN
1	j	66	HIS
1	k	8	GLN
1	l	66	HIS
1	m	8	GLN
1	m	24	HIS
1	n	66	HIS
1	o	8	GLN
1	o	66	HIS
1	p	66	HIS
1	q	8	GLN
1	r	66	HIS
1	s	8	GLN
1	t	66	HIS
1	u	8	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	111/119 (93%)	-1.12	0 100 100	53, 64, 90, 105	0
1	B	111/119 (93%)	-1.17	0 100 100	53, 63, 90, 107	0
1	C	111/119 (93%)	-1.22	0 100 100	54, 64, 90, 109	0
1	D	111/119 (93%)	-1.14	0 100 100	54, 64, 91, 106	0
1	E	111/119 (93%)	-1.13	0 100 100	50, 64, 89, 107	0
1	F	111/119 (93%)	-1.16	0 100 100	52, 62, 89, 107	0
1	G	111/119 (93%)	-1.12	0 100 100	52, 64, 89, 108	0
1	H	111/119 (93%)	-1.20	0 100 100	52, 63, 90, 104	0
1	I	111/119 (93%)	-1.19	0 100 100	52, 63, 89, 106	0
1	J	111/119 (93%)	-1.14	0 100 100	54, 63, 90, 106	0
1	K	111/119 (93%)	-1.12	0 100 100	51, 62, 91, 104	0
1	L	111/119 (93%)	-1.22	0 100 100	54, 62, 88, 106	0
1	M	111/119 (93%)	-1.11	0 100 100	51, 63, 89, 108	0
1	N	111/119 (93%)	-1.07	0 100 100	53, 64, 90, 105	0
1	O	111/119 (93%)	-1.18	0 100 100	53, 64, 88, 106	0
1	P	111/119 (93%)	-1.13	0 100 100	53, 63, 90, 107	0
1	Q	111/119 (93%)	-1.19	0 100 100	53, 64, 90, 106	0
1	R	111/119 (93%)	-1.20	0 100 100	52, 63, 89, 104	0
1	S	111/119 (93%)	-1.14	0 100 100	53, 65, 91, 108	0
1	T	111/119 (93%)	-1.14	0 100 100	51, 63, 90, 107	0
1	U	111/119 (93%)	-1.13	0 100 100	51, 63, 90, 105	0
1	V	111/119 (93%)	-1.19	0 100 100	53, 63, 90, 105	0
1	W	111/119 (93%)	-1.20	0 100 100	49, 63, 91, 105	0
1	X	111/119 (93%)	-1.17	0 100 100	54, 64, 91, 106	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å²)	Q<0.9		
1	Y	111/119 (93%)	-1.17	0	100	100	51, 63, 89, 106	0
1	Z	111/119 (93%)	-1.18	0	100	100	53, 63, 90, 106	0
1	a	111/119 (93%)	-1.15	0	100	100	52, 63, 89, 107	0
1	b	111/119 (93%)	-1.22	0	100	100	54, 64, 91, 107	0
1	c	111/119 (93%)	-1.18	0	100	100	52, 64, 89, 103	0
1	d	111/119 (93%)	-1.17	0	100	100	53, 63, 90, 104	0
1	e	111/119 (93%)	-1.14	0	100	100	54, 63, 90, 106	0
1	f	111/119 (93%)	-1.19	0	100	100	54, 64, 90, 106	0
1	g	111/119 (93%)	-1.12	0	100	100	50, 64, 90, 107	0
1	h	111/119 (93%)	-1.23	0	100	100	50, 63, 90, 106	0
1	i	111/119 (93%)	-1.15	0	100	100	53, 64, 91, 105	0
1	j	111/119 (93%)	-1.10	0	100	100	50, 63, 90, 107	0
1	k	111/119 (93%)	-1.17	0	100	100	53, 63, 90, 103	0
1	l	111/119 (93%)	-1.20	0	100	100	53, 63, 88, 106	0
1	m	111/119 (93%)	-1.11	0	100	100	51, 64, 90, 108	0
1	n	111/119 (93%)	-1.17	0	100	100	53, 63, 89, 106	0
1	o	111/119 (93%)	-1.19	0	100	100	54, 63, 90, 106	0
1	p	111/119 (93%)	-1.13	0	100	100	53, 63, 91, 107	0
1	q	111/119 (93%)	-1.09	0	100	100	52, 63, 89, 107	0
1	r	111/119 (93%)	-1.14	0	100	100	53, 64, 90, 104	0
1	s	111/119 (93%)	-1.16	0	100	100	51, 64, 90, 106	0
1	t	111/119 (93%)	-1.16	0	100	100	54, 63, 89, 108	0
1	u	111/119 (93%)	-1.19	0	100	100	54, 64, 90, 108	0
1	v	111/119 (93%)	-1.14	0	100	100	52, 64, 90, 105	0
All	All	5328/5712 (93%)	-1.16	0	100	100	49, 64, 91, 109	0

There are no RSRZ outliers to report.

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.