



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 02:07 pm BST

PDB ID : 4EMH  
Title : Crystal structure of SpLsm4  
Authors : Jiang, S.M.; Wu, D.H.; Song, H.W.  
Deposited on : 2012-04-12  
Resolution : 2.20 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

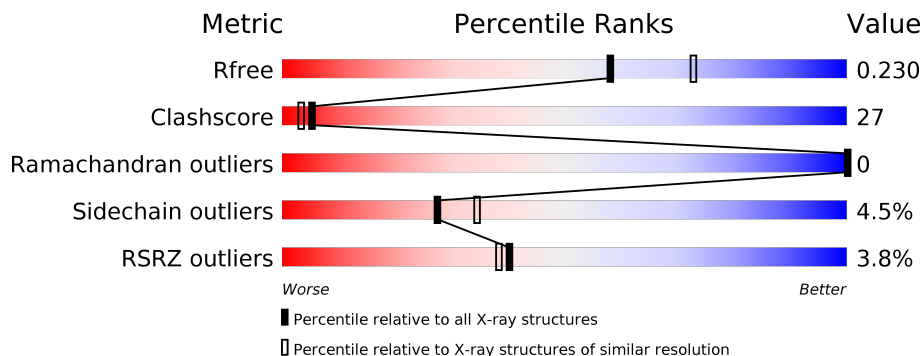
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	105	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 39%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 17%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">2%    39%    17%    •    43%</p>
1	B	105	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 36%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 20%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">2%    36%    20%    •    43%</p>
1	C	105	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 39%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 17%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">%    39%    17%    •    43%</p>
1	D	105	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 13%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">3%    43%    13%    •    43%</p>
1	E	105	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 38%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 18%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">2%    38%    18%    •    43%</p>
1	F	105	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 38%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 18%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">38%    18%    •    43%</p>

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Mol	Chain	Length	Quality of chain
1	G	105	<p>2% 38% 18% 43%</p>
1	H	105	<p>1% 40% 16% 43%</p>
1	I	105	<p>2% 41% 15% 43%</p>
1	J	105	<p>2% 40% 15% 43%</p>
1	K	105	<p>4% 39% 18% 43%</p>
1	L	105	<p>3% 39% 17% 43%</p>
1	M	105	<p>3% 40% 16% 43%</p>
1	N	105	<p>2% 36% 19% 43%</p>
1	O	105	<p>1% 40% 16% 43%</p>
1	P	105	<p>2% 42% 13% 43%</p>
1	Q	105	<p>2% 40% 15% 43%</p>
1	R	105	<p>6% 42% 15% 43%</p>
1	T	105	<p>4% 38% 19% 43%</p>
1	U	105	<p>1% 36% 20% 43%</p>
1	V	105	<p>1% 37% 20% 43%</p>
1	W	105	<p>4% 37% 19% 43%</p>
1	X	105	<p>2% 36% 19% 43%</p>
1	Y	105	<p>1% 41% 14% 43%</p>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 12991 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 Probable U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	60	497	314	90	89	2	2	0	0	0
1	B	60	497	314	90	89	2	2	0	0	0
1	C	60	497	314	90	89	2	2	0	0	0
1	D	60	497	314	90	89	2	2	0	0	0
1	E	60	497	314	90	89	2	2	0	0	0
1	F	60	497	314	90	89	2	2	0	0	0
1	G	60	497	314	90	89	2	2	0	0	0
1	H	60	497	314	90	89	2	2	0	0	0
1	I	60	497	314	90	89	2	2	0	0	0
1	J	60	497	314	90	89	2	2	0	0	0
1	K	60	497	314	90	89	2	2	0	0	0
1	L	60	497	314	90	89	2	2	0	0	0
1	M	60	497	314	90	89	2	2	0	0	0
1	N	60	497	314	90	89	2	2	0	0	0
1	O	60	497	314	90	89	2	2	0	0	0
1	P	60	497	314	90	89	2	2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S	Se			
1	Q	60	497	314	90	89	2	2	0	0	0
1	R	60	497	314	90	89	2	2	0	0	0
1	T	60	497	314	90	89	2	2	0	0	0
1	U	60	497	314	90	89	2	2	0	0	0
1	V	60	497	314	90	89	2	2	0	0	0
1	W	60	497	314	90	89	2	2	0	0	0
1	X	60	497	314	90	89	2	2	0	0	0
1	Y	60	497	314	90	89	2	2	0	0	0

There are 336 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MSE	-	EXPRESSION TAG	UNP O14352
A	-12	GLY	-	EXPRESSION TAG	UNP O14352
A	-11	SER	-	EXPRESSION TAG	UNP O14352
A	-10	SER	-	EXPRESSION TAG	UNP O14352
A	-9	HIS	-	EXPRESSION TAG	UNP O14352
A	-8	HIS	-	EXPRESSION TAG	UNP O14352
A	-7	HIS	-	EXPRESSION TAG	UNP O14352
A	-6	HIS	-	EXPRESSION TAG	UNP O14352
A	-5	HIS	-	EXPRESSION TAG	UNP O14352
A	-4	HIS	-	EXPRESSION TAG	UNP O14352
A	-3	SER	-	EXPRESSION TAG	UNP O14352
A	-2	GLN	-	EXPRESSION TAG	UNP O14352
A	-1	ASP	-	EXPRESSION TAG	UNP O14352
A	0	PRO	-	EXPRESSION TAG	UNP O14352
B	-13	MSE	-	EXPRESSION TAG	UNP O14352
B	-12	GLY	-	EXPRESSION TAG	UNP O14352
B	-11	SER	-	EXPRESSION TAG	UNP O14352
B	-10	SER	-	EXPRESSION TAG	UNP O14352
B	-9	HIS	-	EXPRESSION TAG	UNP O14352
B	-8	HIS	-	EXPRESSION TAG	UNP O14352
B	-7	HIS	-	EXPRESSION TAG	UNP O14352
B	-6	HIS	-	EXPRESSION TAG	UNP O14352
B	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	EXPRESSION TAG	UNP O14352
B	-3	SER	-	EXPRESSION TAG	UNP O14352
B	-2	GLN	-	EXPRESSION TAG	UNP O14352
B	-1	ASP	-	EXPRESSION TAG	UNP O14352
B	0	PRO	-	EXPRESSION TAG	UNP O14352
C	-13	MSE	-	EXPRESSION TAG	UNP O14352
C	-12	GLY	-	EXPRESSION TAG	UNP O14352
C	-11	SER	-	EXPRESSION TAG	UNP O14352
C	-10	SER	-	EXPRESSION TAG	UNP O14352
C	-9	HIS	-	EXPRESSION TAG	UNP O14352
C	-8	HIS	-	EXPRESSION TAG	UNP O14352
C	-7	HIS	-	EXPRESSION TAG	UNP O14352
C	-6	HIS	-	EXPRESSION TAG	UNP O14352
C	-5	HIS	-	EXPRESSION TAG	UNP O14352
C	-4	HIS	-	EXPRESSION TAG	UNP O14352
C	-3	SER	-	EXPRESSION TAG	UNP O14352
C	-2	GLN	-	EXPRESSION TAG	UNP O14352
C	-1	ASP	-	EXPRESSION TAG	UNP O14352
C	0	PRO	-	EXPRESSION TAG	UNP O14352
D	-13	MSE	-	EXPRESSION TAG	UNP O14352
D	-12	GLY	-	EXPRESSION TAG	UNP O14352
D	-11	SER	-	EXPRESSION TAG	UNP O14352
D	-10	SER	-	EXPRESSION TAG	UNP O14352
D	-9	HIS	-	EXPRESSION TAG	UNP O14352
D	-8	HIS	-	EXPRESSION TAG	UNP O14352
D	-7	HIS	-	EXPRESSION TAG	UNP O14352
D	-6	HIS	-	EXPRESSION TAG	UNP O14352
D	-5	HIS	-	EXPRESSION TAG	UNP O14352
D	-4	HIS	-	EXPRESSION TAG	UNP O14352
D	-3	SER	-	EXPRESSION TAG	UNP O14352
D	-2	GLN	-	EXPRESSION TAG	UNP O14352
D	-1	ASP	-	EXPRESSION TAG	UNP O14352
D	0	PRO	-	EXPRESSION TAG	UNP O14352
E	-13	MSE	-	EXPRESSION TAG	UNP O14352
E	-12	GLY	-	EXPRESSION TAG	UNP O14352
E	-11	SER	-	EXPRESSION TAG	UNP O14352
E	-10	SER	-	EXPRESSION TAG	UNP O14352
E	-9	HIS	-	EXPRESSION TAG	UNP O14352
E	-8	HIS	-	EXPRESSION TAG	UNP O14352
E	-7	HIS	-	EXPRESSION TAG	UNP O14352
E	-6	HIS	-	EXPRESSION TAG	UNP O14352
E	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	EXPRESSION TAG	UNP O14352
E	-3	SER	-	EXPRESSION TAG	UNP O14352
E	-2	GLN	-	EXPRESSION TAG	UNP O14352
E	-1	ASP	-	EXPRESSION TAG	UNP O14352
E	0	PRO	-	EXPRESSION TAG	UNP O14352
F	-13	MSE	-	EXPRESSION TAG	UNP O14352
F	-12	GLY	-	EXPRESSION TAG	UNP O14352
F	-11	SER	-	EXPRESSION TAG	UNP O14352
F	-10	SER	-	EXPRESSION TAG	UNP O14352
F	-9	HIS	-	EXPRESSION TAG	UNP O14352
F	-8	HIS	-	EXPRESSION TAG	UNP O14352
F	-7	HIS	-	EXPRESSION TAG	UNP O14352
F	-6	HIS	-	EXPRESSION TAG	UNP O14352
F	-5	HIS	-	EXPRESSION TAG	UNP O14352
F	-4	HIS	-	EXPRESSION TAG	UNP O14352
F	-3	SER	-	EXPRESSION TAG	UNP O14352
F	-2	GLN	-	EXPRESSION TAG	UNP O14352
F	-1	ASP	-	EXPRESSION TAG	UNP O14352
F	0	PRO	-	EXPRESSION TAG	UNP O14352
G	-13	MSE	-	EXPRESSION TAG	UNP O14352
G	-12	GLY	-	EXPRESSION TAG	UNP O14352
G	-11	SER	-	EXPRESSION TAG	UNP O14352
G	-10	SER	-	EXPRESSION TAG	UNP O14352
G	-9	HIS	-	EXPRESSION TAG	UNP O14352
G	-8	HIS	-	EXPRESSION TAG	UNP O14352
G	-7	HIS	-	EXPRESSION TAG	UNP O14352
G	-6	HIS	-	EXPRESSION TAG	UNP O14352
G	-5	HIS	-	EXPRESSION TAG	UNP O14352
G	-4	HIS	-	EXPRESSION TAG	UNP O14352
G	-3	SER	-	EXPRESSION TAG	UNP O14352
G	-2	GLN	-	EXPRESSION TAG	UNP O14352
G	-1	ASP	-	EXPRESSION TAG	UNP O14352
G	0	PRO	-	EXPRESSION TAG	UNP O14352
H	-13	MSE	-	EXPRESSION TAG	UNP O14352
H	-12	GLY	-	EXPRESSION TAG	UNP O14352
H	-11	SER	-	EXPRESSION TAG	UNP O14352
H	-10	SER	-	EXPRESSION TAG	UNP O14352
H	-9	HIS	-	EXPRESSION TAG	UNP O14352
H	-8	HIS	-	EXPRESSION TAG	UNP O14352
H	-7	HIS	-	EXPRESSION TAG	UNP O14352
H	-6	HIS	-	EXPRESSION TAG	UNP O14352
H	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-4	HIS	-	EXPRESSION TAG	UNP O14352
H	-3	SER	-	EXPRESSION TAG	UNP O14352
H	-2	GLN	-	EXPRESSION TAG	UNP O14352
H	-1	ASP	-	EXPRESSION TAG	UNP O14352
H	0	PRO	-	EXPRESSION TAG	UNP O14352
I	-13	MSE	-	EXPRESSION TAG	UNP O14352
I	-12	GLY	-	EXPRESSION TAG	UNP O14352
I	-11	SER	-	EXPRESSION TAG	UNP O14352
I	-10	SER	-	EXPRESSION TAG	UNP O14352
I	-9	HIS	-	EXPRESSION TAG	UNP O14352
I	-8	HIS	-	EXPRESSION TAG	UNP O14352
I	-7	HIS	-	EXPRESSION TAG	UNP O14352
I	-6	HIS	-	EXPRESSION TAG	UNP O14352
I	-5	HIS	-	EXPRESSION TAG	UNP O14352
I	-4	HIS	-	EXPRESSION TAG	UNP O14352
I	-3	SER	-	EXPRESSION TAG	UNP O14352
I	-2	GLN	-	EXPRESSION TAG	UNP O14352
I	-1	ASP	-	EXPRESSION TAG	UNP O14352
I	0	PRO	-	EXPRESSION TAG	UNP O14352
J	-13	MSE	-	EXPRESSION TAG	UNP O14352
J	-12	GLY	-	EXPRESSION TAG	UNP O14352
J	-11	SER	-	EXPRESSION TAG	UNP O14352
J	-10	SER	-	EXPRESSION TAG	UNP O14352
J	-9	HIS	-	EXPRESSION TAG	UNP O14352
J	-8	HIS	-	EXPRESSION TAG	UNP O14352
J	-7	HIS	-	EXPRESSION TAG	UNP O14352
J	-6	HIS	-	EXPRESSION TAG	UNP O14352
J	-5	HIS	-	EXPRESSION TAG	UNP O14352
J	-4	HIS	-	EXPRESSION TAG	UNP O14352
J	-3	SER	-	EXPRESSION TAG	UNP O14352
J	-2	GLN	-	EXPRESSION TAG	UNP O14352
J	-1	ASP	-	EXPRESSION TAG	UNP O14352
J	0	PRO	-	EXPRESSION TAG	UNP O14352
K	-13	MSE	-	EXPRESSION TAG	UNP O14352
K	-12	GLY	-	EXPRESSION TAG	UNP O14352
K	-11	SER	-	EXPRESSION TAG	UNP O14352
K	-10	SER	-	EXPRESSION TAG	UNP O14352
K	-9	HIS	-	EXPRESSION TAG	UNP O14352
K	-8	HIS	-	EXPRESSION TAG	UNP O14352
K	-7	HIS	-	EXPRESSION TAG	UNP O14352
K	-6	HIS	-	EXPRESSION TAG	UNP O14352
K	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-4	HIS	-	EXPRESSION TAG	UNP O14352
K	-3	SER	-	EXPRESSION TAG	UNP O14352
K	-2	GLN	-	EXPRESSION TAG	UNP O14352
K	-1	ASP	-	EXPRESSION TAG	UNP O14352
K	0	PRO	-	EXPRESSION TAG	UNP O14352
L	-13	MSE	-	EXPRESSION TAG	UNP O14352
L	-12	GLY	-	EXPRESSION TAG	UNP O14352
L	-11	SER	-	EXPRESSION TAG	UNP O14352
L	-10	SER	-	EXPRESSION TAG	UNP O14352
L	-9	HIS	-	EXPRESSION TAG	UNP O14352
L	-8	HIS	-	EXPRESSION TAG	UNP O14352
L	-7	HIS	-	EXPRESSION TAG	UNP O14352
L	-6	HIS	-	EXPRESSION TAG	UNP O14352
L	-5	HIS	-	EXPRESSION TAG	UNP O14352
L	-4	HIS	-	EXPRESSION TAG	UNP O14352
L	-3	SER	-	EXPRESSION TAG	UNP O14352
L	-2	GLN	-	EXPRESSION TAG	UNP O14352
L	-1	ASP	-	EXPRESSION TAG	UNP O14352
L	0	PRO	-	EXPRESSION TAG	UNP O14352
M	-13	MSE	-	EXPRESSION TAG	UNP O14352
M	-12	GLY	-	EXPRESSION TAG	UNP O14352
M	-11	SER	-	EXPRESSION TAG	UNP O14352
M	-10	SER	-	EXPRESSION TAG	UNP O14352
M	-9	HIS	-	EXPRESSION TAG	UNP O14352
M	-8	HIS	-	EXPRESSION TAG	UNP O14352
M	-7	HIS	-	EXPRESSION TAG	UNP O14352
M	-6	HIS	-	EXPRESSION TAG	UNP O14352
M	-5	HIS	-	EXPRESSION TAG	UNP O14352
M	-4	HIS	-	EXPRESSION TAG	UNP O14352
M	-3	SER	-	EXPRESSION TAG	UNP O14352
M	-2	GLN	-	EXPRESSION TAG	UNP O14352
M	-1	ASP	-	EXPRESSION TAG	UNP O14352
M	0	PRO	-	EXPRESSION TAG	UNP O14352
N	-13	MSE	-	EXPRESSION TAG	UNP O14352
N	-12	GLY	-	EXPRESSION TAG	UNP O14352
N	-11	SER	-	EXPRESSION TAG	UNP O14352
N	-10	SER	-	EXPRESSION TAG	UNP O14352
N	-9	HIS	-	EXPRESSION TAG	UNP O14352
N	-8	HIS	-	EXPRESSION TAG	UNP O14352
N	-7	HIS	-	EXPRESSION TAG	UNP O14352
N	-6	HIS	-	EXPRESSION TAG	UNP O14352
N	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
N	-4	HIS	-	EXPRESSION TAG	UNP O14352
N	-3	SER	-	EXPRESSION TAG	UNP O14352
N	-2	GLN	-	EXPRESSION TAG	UNP O14352
N	-1	ASP	-	EXPRESSION TAG	UNP O14352
N	0	PRO	-	EXPRESSION TAG	UNP O14352
O	-13	MSE	-	EXPRESSION TAG	UNP O14352
O	-12	GLY	-	EXPRESSION TAG	UNP O14352
O	-11	SER	-	EXPRESSION TAG	UNP O14352
O	-10	SER	-	EXPRESSION TAG	UNP O14352
O	-9	HIS	-	EXPRESSION TAG	UNP O14352
O	-8	HIS	-	EXPRESSION TAG	UNP O14352
O	-7	HIS	-	EXPRESSION TAG	UNP O14352
O	-6	HIS	-	EXPRESSION TAG	UNP O14352
O	-5	HIS	-	EXPRESSION TAG	UNP O14352
O	-4	HIS	-	EXPRESSION TAG	UNP O14352
O	-3	SER	-	EXPRESSION TAG	UNP O14352
O	-2	GLN	-	EXPRESSION TAG	UNP O14352
O	-1	ASP	-	EXPRESSION TAG	UNP O14352
O	0	PRO	-	EXPRESSION TAG	UNP O14352
P	-13	MSE	-	EXPRESSION TAG	UNP O14352
P	-12	GLY	-	EXPRESSION TAG	UNP O14352
P	-11	SER	-	EXPRESSION TAG	UNP O14352
P	-10	SER	-	EXPRESSION TAG	UNP O14352
P	-9	HIS	-	EXPRESSION TAG	UNP O14352
P	-8	HIS	-	EXPRESSION TAG	UNP O14352
P	-7	HIS	-	EXPRESSION TAG	UNP O14352
P	-6	HIS	-	EXPRESSION TAG	UNP O14352
P	-5	HIS	-	EXPRESSION TAG	UNP O14352
P	-4	HIS	-	EXPRESSION TAG	UNP O14352
P	-3	SER	-	EXPRESSION TAG	UNP O14352
P	-2	GLN	-	EXPRESSION TAG	UNP O14352
P	-1	ASP	-	EXPRESSION TAG	UNP O14352
P	0	PRO	-	EXPRESSION TAG	UNP O14352
Q	-13	MSE	-	EXPRESSION TAG	UNP O14352
Q	-12	GLY	-	EXPRESSION TAG	UNP O14352
Q	-11	SER	-	EXPRESSION TAG	UNP O14352
Q	-10	SER	-	EXPRESSION TAG	UNP O14352
Q	-9	HIS	-	EXPRESSION TAG	UNP O14352
Q	-8	HIS	-	EXPRESSION TAG	UNP O14352
Q	-7	HIS	-	EXPRESSION TAG	UNP O14352
Q	-6	HIS	-	EXPRESSION TAG	UNP O14352
Q	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-4	HIS	-	EXPRESSION TAG	UNP O14352
Q	-3	SER	-	EXPRESSION TAG	UNP O14352
Q	-2	GLN	-	EXPRESSION TAG	UNP O14352
Q	-1	ASP	-	EXPRESSION TAG	UNP O14352
Q	0	PRO	-	EXPRESSION TAG	UNP O14352
R	-13	MSE	-	EXPRESSION TAG	UNP O14352
R	-12	GLY	-	EXPRESSION TAG	UNP O14352
R	-11	SER	-	EXPRESSION TAG	UNP O14352
R	-10	SER	-	EXPRESSION TAG	UNP O14352
R	-9	HIS	-	EXPRESSION TAG	UNP O14352
R	-8	HIS	-	EXPRESSION TAG	UNP O14352
R	-7	HIS	-	EXPRESSION TAG	UNP O14352
R	-6	HIS	-	EXPRESSION TAG	UNP O14352
R	-5	HIS	-	EXPRESSION TAG	UNP O14352
R	-4	HIS	-	EXPRESSION TAG	UNP O14352
R	-3	SER	-	EXPRESSION TAG	UNP O14352
R	-2	GLN	-	EXPRESSION TAG	UNP O14352
R	-1	ASP	-	EXPRESSION TAG	UNP O14352
R	0	PRO	-	EXPRESSION TAG	UNP O14352
T	-13	MSE	-	EXPRESSION TAG	UNP O14352
T	-12	GLY	-	EXPRESSION TAG	UNP O14352
T	-11	SER	-	EXPRESSION TAG	UNP O14352
T	-10	SER	-	EXPRESSION TAG	UNP O14352
T	-9	HIS	-	EXPRESSION TAG	UNP O14352
T	-8	HIS	-	EXPRESSION TAG	UNP O14352
T	-7	HIS	-	EXPRESSION TAG	UNP O14352
T	-6	HIS	-	EXPRESSION TAG	UNP O14352
T	-5	HIS	-	EXPRESSION TAG	UNP O14352
T	-4	HIS	-	EXPRESSION TAG	UNP O14352
T	-3	SER	-	EXPRESSION TAG	UNP O14352
T	-2	GLN	-	EXPRESSION TAG	UNP O14352
T	-1	ASP	-	EXPRESSION TAG	UNP O14352
T	0	PRO	-	EXPRESSION TAG	UNP O14352
U	-13	MSE	-	EXPRESSION TAG	UNP O14352
U	-12	GLY	-	EXPRESSION TAG	UNP O14352
U	-11	SER	-	EXPRESSION TAG	UNP O14352
U	-10	SER	-	EXPRESSION TAG	UNP O14352
U	-9	HIS	-	EXPRESSION TAG	UNP O14352
U	-8	HIS	-	EXPRESSION TAG	UNP O14352
U	-7	HIS	-	EXPRESSION TAG	UNP O14352
U	-6	HIS	-	EXPRESSION TAG	UNP O14352
U	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
U	-4	HIS	-	EXPRESSION TAG	UNP O14352
U	-3	SER	-	EXPRESSION TAG	UNP O14352
U	-2	GLN	-	EXPRESSION TAG	UNP O14352
U	-1	ASP	-	EXPRESSION TAG	UNP O14352
U	0	PRO	-	EXPRESSION TAG	UNP O14352
V	-13	MSE	-	EXPRESSION TAG	UNP O14352
V	-12	GLY	-	EXPRESSION TAG	UNP O14352
V	-11	SER	-	EXPRESSION TAG	UNP O14352
V	-10	SER	-	EXPRESSION TAG	UNP O14352
V	-9	HIS	-	EXPRESSION TAG	UNP O14352
V	-8	HIS	-	EXPRESSION TAG	UNP O14352
V	-7	HIS	-	EXPRESSION TAG	UNP O14352
V	-6	HIS	-	EXPRESSION TAG	UNP O14352
V	-5	HIS	-	EXPRESSION TAG	UNP O14352
V	-4	HIS	-	EXPRESSION TAG	UNP O14352
V	-3	SER	-	EXPRESSION TAG	UNP O14352
V	-2	GLN	-	EXPRESSION TAG	UNP O14352
V	-1	ASP	-	EXPRESSION TAG	UNP O14352
V	0	PRO	-	EXPRESSION TAG	UNP O14352
W	-13	MSE	-	EXPRESSION TAG	UNP O14352
W	-12	GLY	-	EXPRESSION TAG	UNP O14352
W	-11	SER	-	EXPRESSION TAG	UNP O14352
W	-10	SER	-	EXPRESSION TAG	UNP O14352
W	-9	HIS	-	EXPRESSION TAG	UNP O14352
W	-8	HIS	-	EXPRESSION TAG	UNP O14352
W	-7	HIS	-	EXPRESSION TAG	UNP O14352
W	-6	HIS	-	EXPRESSION TAG	UNP O14352
W	-5	HIS	-	EXPRESSION TAG	UNP O14352
W	-4	HIS	-	EXPRESSION TAG	UNP O14352
W	-3	SER	-	EXPRESSION TAG	UNP O14352
W	-2	GLN	-	EXPRESSION TAG	UNP O14352
W	-1	ASP	-	EXPRESSION TAG	UNP O14352
W	0	PRO	-	EXPRESSION TAG	UNP O14352
X	-13	MSE	-	EXPRESSION TAG	UNP O14352
X	-12	GLY	-	EXPRESSION TAG	UNP O14352
X	-11	SER	-	EXPRESSION TAG	UNP O14352
X	-10	SER	-	EXPRESSION TAG	UNP O14352
X	-9	HIS	-	EXPRESSION TAG	UNP O14352
X	-8	HIS	-	EXPRESSION TAG	UNP O14352
X	-7	HIS	-	EXPRESSION TAG	UNP O14352
X	-6	HIS	-	EXPRESSION TAG	UNP O14352
X	-5	HIS	-	EXPRESSION TAG	UNP O14352

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Chain	Residue	Modelled	Actual	Comment	Reference
X	-4	HIS	-	EXPRESSION TAG	UNP O14352
X	-3	SER	-	EXPRESSION TAG	UNP O14352
X	-2	GLN	-	EXPRESSION TAG	UNP O14352
X	-1	ASP	-	EXPRESSION TAG	UNP O14352
X	0	PRO	-	EXPRESSION TAG	UNP O14352
Y	-13	MSE	-	EXPRESSION TAG	UNP O14352
Y	-12	GLY	-	EXPRESSION TAG	UNP O14352
Y	-11	SER	-	EXPRESSION TAG	UNP O14352
Y	-10	SER	-	EXPRESSION TAG	UNP O14352
Y	-9	HIS	-	EXPRESSION TAG	UNP O14352
Y	-8	HIS	-	EXPRESSION TAG	UNP O14352
Y	-7	HIS	-	EXPRESSION TAG	UNP O14352
Y	-6	HIS	-	EXPRESSION TAG	UNP O14352
Y	-5	HIS	-	EXPRESSION TAG	UNP O14352
Y	-4	HIS	-	EXPRESSION TAG	UNP O14352
Y	-3	SER	-	EXPRESSION TAG	UNP O14352
Y	-2	GLN	-	EXPRESSION TAG	UNP O14352
Y	-1	ASP	-	EXPRESSION TAG	UNP O14352
Y	0	PRO	-	EXPRESSION TAG	UNP O14352

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	50	Total O 50 50	0	0
2	B	48	Total O 48 48	0	0
2	C	49	Total O 49 49	0	0
2	D	42	Total O 42 42	0	0
2	E	45	Total O 45 45	0	0
2	F	33	Total O 33 33	0	0
2	G	65	Total O 65 65	0	0
2	H	49	Total O 49 49	0	0
2	I	59	Total O 59 59	0	0
2	J	53	Total O 53 53	0	0

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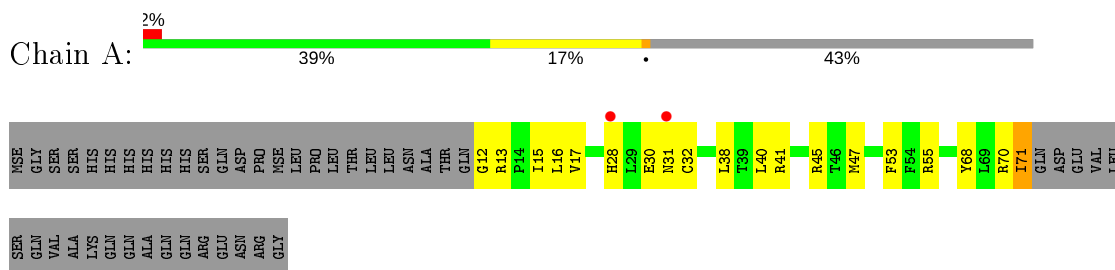
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	K	31	Total 31	O 31	0	0
2	L	43	Total 43	O 43	0	0
2	M	42	Total 42	O 42	0	0
2	N	37	Total 37	O 37	0	0
2	O	27	Total 27	O 27	0	0
2	P	49	Total 49	O 49	0	0
2	Q	54	Total 54	O 54	0	0
2	R	48	Total 48	O 48	0	0
2	T	36	Total 36	O 36	0	0
2	U	24	Total 24	O 24	0	0
2	V	28	Total 28	O 28	0	0
2	W	56	Total 56	O 56	0	0
2	X	39	Total 39	O 39	0	0
2	Y	56	Total 56	O 56	0	0

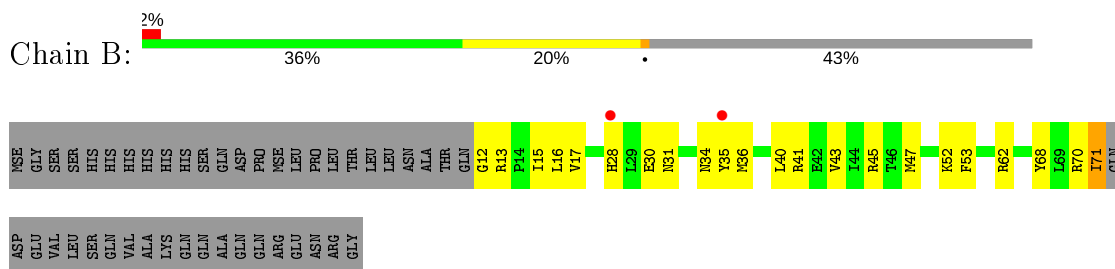
### 3 Residue-property plots [i](#)

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

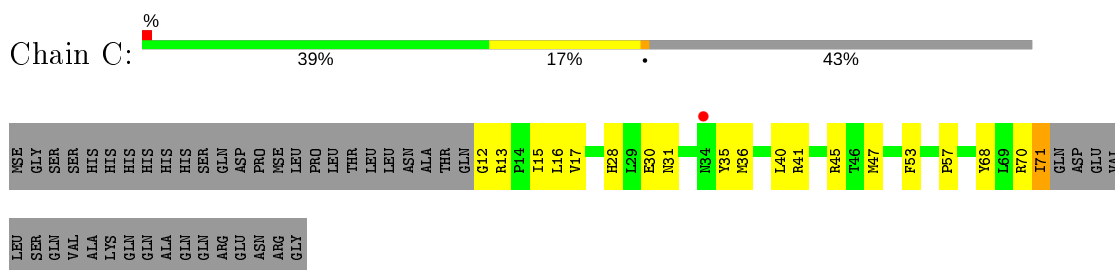
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



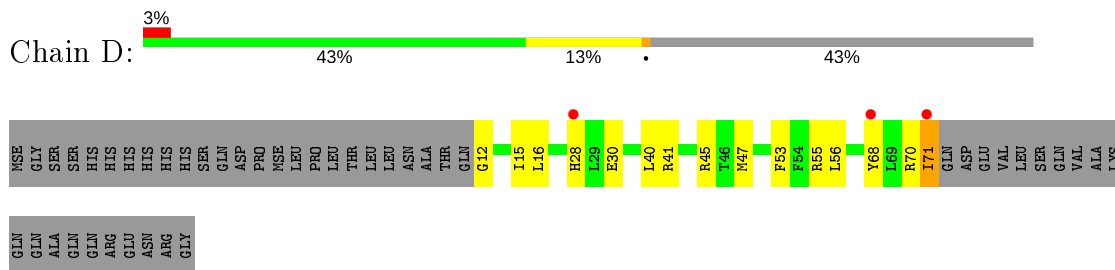
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4

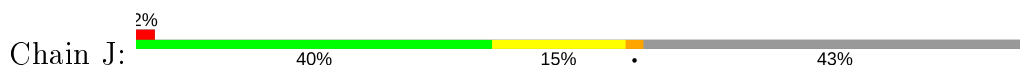


- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4

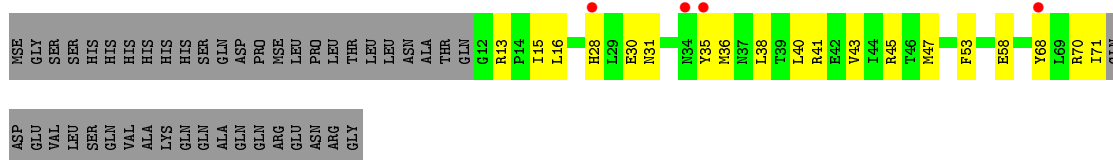




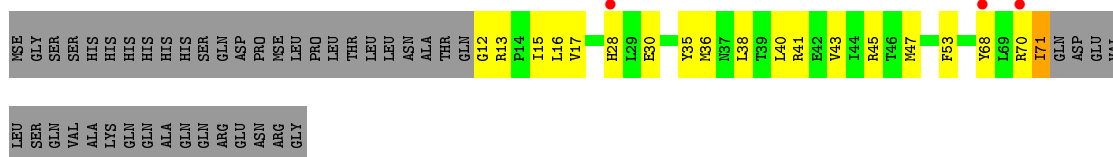




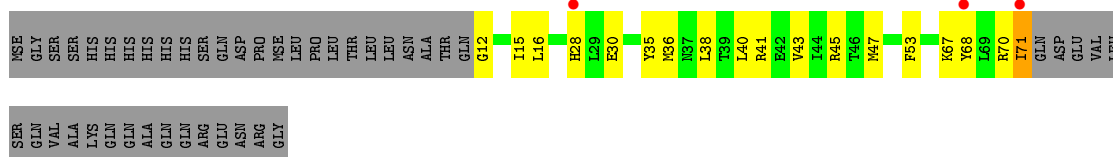
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



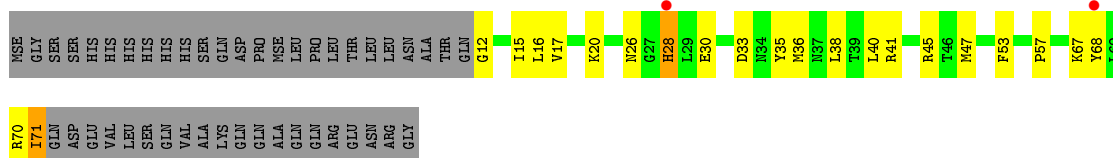
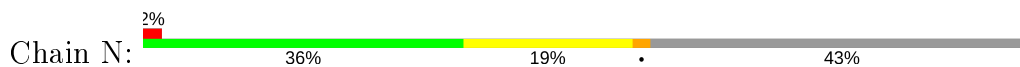
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



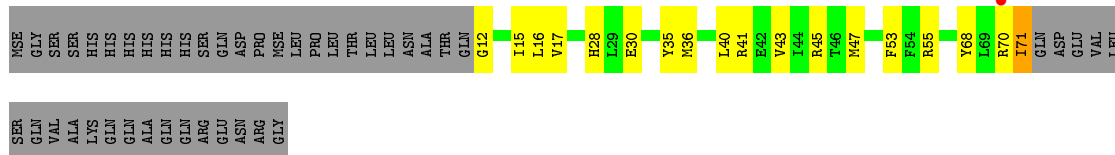
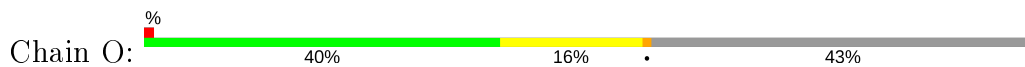
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



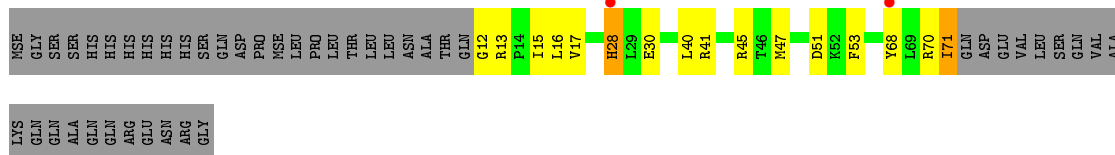
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



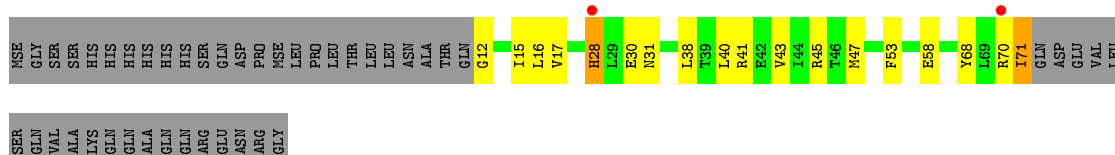
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



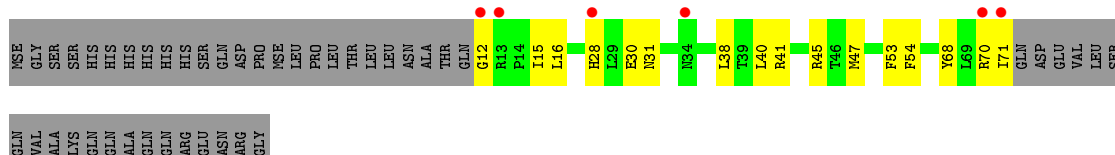
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



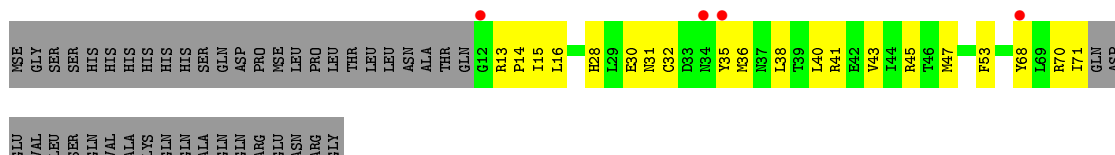
- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



- Molecule 1: Probable U6 snRNA-associated Sm-like protein LSm4



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	185.12Å 124.47Å 131.57Å 90.00° 135.07° 90.00°	Depositor
Resolution (Å)	92.56 – 2.20 92.92 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (92.56-2.20) 92.6 (92.92-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, $R_{free}$	0.237 , 0.253 0.234 , 0.230	Depositor DCC
$R_{free}$ test set	6586 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.8	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.045 for -h-2*1,k,h+1 0.024 for h,-k,-h-l 0.026 for h+2*1,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12991	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.82 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3200e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.61	1/504 (0.2%)	0.68	0/674
1	B	0.47	0/504	0.65	0/674
1	C	0.47	0/504	0.64	0/674
1	D	0.45	0/504	0.61	0/674
1	E	0.51	0/504	0.63	0/674
1	F	0.43	0/504	0.62	0/674
1	G	0.52	0/504	0.65	0/674
1	H	0.50	0/504	0.64	0/674
1	I	0.48	0/504	0.68	0/674
1	J	0.45	0/504	0.66	0/674
1	K	0.45	0/504	0.63	0/674
1	L	0.48	0/504	0.65	0/674
1	M	0.47	0/504	0.64	0/674
1	N	0.47	0/504	0.63	0/674
1	O	0.46	0/504	0.63	0/674
1	P	0.48	0/504	0.63	0/674
1	Q	0.50	0/504	0.68	0/674
1	R	0.47	0/504	0.66	0/674
1	T	0.51	0/504	0.65	0/674
1	U	0.42	0/504	0.61	0/674
1	V	0.50	0/504	0.63	0/674
1	W	0.50	0/504	0.69	0/674
1	X	0.47	0/504	0.60	0/674
1	Y	0.51	0/504	0.65	0/674
All	All	0.48	1/12096 (0.0%)	0.64	0/16176

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	32	CYS	CB-SG	-8.34	1.68	1.82

There are no bond angle outliers.

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	497	0	496	27	0
1	B	497	0	496	27	2
1	C	497	0	496	27	0
1	D	497	0	496	28	0
1	E	497	0	496	26	2
1	F	497	0	496	23	0
1	G	497	0	496	36	0
1	H	497	0	496	20	1
1	I	497	0	496	25	0
1	J	497	0	496	25	0
1	K	497	0	496	24	1
1	L	497	0	496	22	0
1	M	497	0	496	24	1
1	N	497	0	496	30	2
1	O	497	0	496	20	0
1	P	497	0	496	24	0
1	Q	497	0	496	27	0
1	R	497	0	496	27	0
1	T	497	0	496	24	1
1	U	497	0	496	27	0
1	V	497	0	496	28	0
1	W	497	0	496	33	0
1	X	497	0	496	35	0
1	Y	497	0	496	31	1
2	A	50	0	0	4	0
2	B	48	0	0	4	0
2	C	49	0	0	10	0
2	D	42	0	0	10	0
2	E	45	0	0	6	0
2	F	33	0	0	4	0
2	G	65	0	0	17	0
2	H	49	0	0	6	1
2	I	59	0	0	5	0
2	J	53	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	31	0	0	7	0
2	L	43	0	0	4	0
2	M	42	0	0	6	0
2	N	37	0	0	9	0
2	O	27	0	0	0	0
2	P	49	0	0	9	0
2	Q	54	0	0	10	0
2	R	48	0	0	8	0
2	T	36	0	0	7	0
2	U	24	0	0	4	0
2	V	28	0	0	7	0
2	W	56	0	0	10	0
2	X	39	0	0	13	0
2	Y	56	0	0	15	0
All	All	12991	0	11904	632	6

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 27.

All (632) 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:I:12:GLY:N	2:I:134:HOH:O	1.93	1.00
1:B:13:ARG:HG3	2:E:118:HOH:O	1.62	0.98
1:J:47:MSE:SE	2:J:139:HOH:O	2.32	0.97
1:B:47:MSE:SE	2:B:121:HOH:O	2.31	0.96
1:M:47:MSE:SE	2:M:117:HOH:O	2.34	0.95
1:D:12:GLY:N	1:D:71:ILE:HD13	1.82	0.94
1:U:47:MSE:HE3	1:U:53:PHE:CE2	2.02	0.94
1:W:35:TYR:O	2:W:130:HOH:O	1.87	0.93
1:C:71:ILE:O	2:C:119:HOH:O	1.86	0.93
1:N:28:HIS:HB3	2:N:120:HOH:O	1.67	0.93
1:V:13:ARG:NH2	2:V:128:HOH:O	1.99	0.93
1:I:12:GLY:CA	2:I:134:HOH:O	2.17	0.93
1:H:47:MSE:HE3	1:H:53:PHE:CE2	2.03	0.93
1:T:36:MSE:SE	2:T:119:HOH:O	2.35	0.92
1:K:47:MSE:HE3	1:K:53:PHE:CE2	2.05	0.92
1:A:12:GLY:HA3	1:A:71:ILE:HD13	1.51	0.92
1:M:47:MSE:HE3	1:M:53:PHE:CE2	2.05	0.92
1:R:31:ASN:HB2	2:R:138:HOH:O	1.67	0.92
1:X:47:MSE:HE3	1:X:53:PHE:CE2	2.05	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:41:ARG:HG2	2:K:129:HOH:O	1.71	0.91
1:R:47:MSE:HE3	1:R:53:PHE:CE2	2.05	0.91
1:N:47:MSE:HE3	1:N:53:PHE:CE2	2.06	0.91
1:G:47:MSE:HE3	1:G:53:PHE:CE2	2.05	0.90
1:B:47:MSE:HE3	1:B:53:PHE:CE2	2.07	0.90
1:E:47:MSE:HE3	1:E:53:PHE:CE2	2.07	0.90
1:A:47:MSE:HE3	1:A:53:PHE:CE2	2.08	0.89
1:I:47:MSE:SE	2:I:140:HOH:O	2.39	0.89
1:M:70:ARG:NH1	2:M:115:HOH:O	2.04	0.89
1:I:12:GLY:HA3	1:I:71:ILE:HD13	1.53	0.88
1:C:47:MSE:HE3	1:C:53:PHE:CE2	2.08	0.88
1:A:47:MSE:SE	2:A:132:HOH:O	2.40	0.88
1:C:12:GLY:HA3	1:C:71:ILE:HD13	1.56	0.88
1:W:47:MSE:HE3	1:W:53:PHE:CE2	2.09	0.88
1:E:36:MSE:SE	2:E:124:HOH:O	2.40	0.88
1:G:70:ARG:NH1	2:G:148:HOH:O	2.07	0.87
1:D:47:MSE:HE3	1:D:53:PHE:CE2	2.10	0.87
1:J:47:MSE:HE3	1:J:53:PHE:CE2	2.10	0.87
1:D:12:GLY:HA2	2:D:115:HOH:O	1.72	0.87
1:F:47:MSE:HE3	1:F:53:PHE:CE2	2.08	0.87
1:I:47:MSE:HE3	1:I:53:PHE:CE2	2.11	0.86
1:Y:28:HIS:NE2	2:Y:110:HOH:O	2.03	0.86
1:F:47:MSE:SE	2:F:116:HOH:O	2.44	0.86
1:Q:47:MSE:HE3	1:Q:53:PHE:CE2	2.11	0.86
1:O:47:MSE:HE3	1:O:53:PHE:CE2	2.10	0.85
1:Y:41:ARG:NE	2:Y:151:HOH:O	2.08	0.85
1:U:33:ASP:OD2	2:U:120:HOH:O	1.94	0.85
1:D:68:TYR:CE1	2:D:116:HOH:O	2.29	0.84
1:D:12:GLY:CA	2:D:115:HOH:O	2.24	0.84
1:C:47:MSE:SE	2:C:136:HOH:O	2.46	0.84
1:T:47:MSE:HE3	1:T:53:PHE:CE2	2.12	0.84
1:J:28:HIS:HB3	2:J:124:HOH:O	1.77	0.84
1:L:47:MSE:HE3	1:L:53:PHE:CE2	2.13	0.83
1:K:58:GLU:HB2	2:K:129:HOH:O	1.77	0.83
1:G:12:GLY:N	2:G:127:HOH:O	2.12	0.83
1:Q:12:GLY:CA	2:Q:144:HOH:O	2.27	0.82
1:W:35:TYR:HE1	2:W:153:HOH:O	1.63	0.81
1:D:12:GLY:N	2:D:115:HOH:O	2.13	0.81
1:T:13:ARG:NH2	2:T:134:HOH:O	2.12	0.81
1:P:47:MSE:HE3	1:P:53:PHE:CE2	2.15	0.81
1:W:41:ARG:CZ	2:W:150:HOH:O	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:41:ARG:NH1	2:W:150:HOH:O	2.14	0.80
1:D:70:ARG:NH1	2:D:116:HOH:O	2.13	0.79
1:B:31:ASN:HA	1:E:34:ASN:ND2	1.98	0.79
1:V:47:MSE:HE3	1:V:53:PHE:CE2	2.17	0.79
1:C:12:GLY:N	2:C:146:HOH:O	2.14	0.79
1:G:12:GLY:CA	2:G:127:HOH:O	2.30	0.78
1:Y:47:MSE:HE3	1:Y:53:PHE:CE2	2.17	0.78
1:P:71:ILE:O	2:P:145:HOH:O	2.01	0.78
1:X:35:TYR:O	2:X:127:HOH:O	2.02	0.78
1:W:35:TYR:CE1	2:W:153:HOH:O	2.35	0.77
1:V:15:ILE:HG22	1:V:71:ILE:HG12	1.66	0.77
1:F:31:ASN:ND2	2:F:115:HOH:O	2.18	0.76
1:G:12:GLY:HA2	2:G:127:HOH:O	1.86	0.76
1:V:42:GLU:OE2	2:V:106:HOH:O	2.03	0.76
1:V:12:GLY:N	1:V:71:ILE:HG21	2.01	0.76
1:A:55:ARG:HD2	2:C:143:HOH:O	1.86	0.75
1:P:28:HIS:NE2	2:P:126:HOH:O	2.16	0.75
1:X:30:GLU:OE2	2:X:137:HOH:O	2.03	0.75
1:L:12:GLY:N	2:L:122:HOH:O	2.18	0.75
1:X:13:ARG:HD3	2:X:109:HOH:O	1.87	0.75
1:N:47:MSE:SE	2:N:128:HOH:O	2.53	0.75
1:D:68:TYR:CZ	2:D:116:HOH:O	2.39	0.75
1:Q:12:GLY:N	2:Q:144:HOH:O	2.20	0.74
1:B:34:ASN:ND2	1:E:31:ASN:HA	2.03	0.74
1:M:45:ARG:NH2	2:M:138:HOH:O	2.21	0.73
1:N:26:ASN:ND2	2:N:133:HOH:O	2.19	0.73
1:G:37:ASN:O	2:G:153:HOH:O	2.07	0.73
1:R:31:ASN:ND2	2:R:112:HOH:O	2.20	0.73
1:Y:45:ARG:NE	1:Y:47:MSE:HE1	2.04	0.73
1:P:12:GLY:N	1:P:71:ILE:HD13	2.04	0.73
1:M:68:TYR:CE1	2:M:115:HOH:O	2.41	0.73
1:H:47:MSE:HE3	1:H:53:PHE:HE2	1.52	0.73
1:U:47:MSE:HE3	1:U:53:PHE:HE2	1.52	0.73
1:X:37:ASN:OD1	2:X:118:HOH:O	2.07	0.73
1:G:45:ARG:CZ	1:G:47:MSE:HE1	2.18	0.73
1:G:47:MSE:SE	2:G:137:HOH:O	2.57	0.72
1:K:47:MSE:SE	2:K:110:HOH:O	2.56	0.72
1:Q:45:ARG:NE	1:Q:47:MSE:HE1	2.04	0.72
2:Q:143:HOH:O	1:R:47:MSE:SE	2.57	0.72
1:D:45:ARG:NE	1:D:47:MSE:HE1	2.05	0.72
1:Y:12:GLY:N	2:Y:101:HOH:O	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:28:HIS:HB2	2:N:114:HOH:O	1.88	0.72
1:E:45:ARG:NE	1:E:47:MSE:HE1	2.05	0.72
1:M:45:ARG:NE	1:M:47:MSE:HE1	2.04	0.72
1:M:45:ARG:CZ	1:M:47:MSE:HE1	2.20	0.72
1:T:45:ARG:NE	1:T:47:MSE:HE1	2.03	0.72
1:B:45:ARG:CZ	1:B:47:MSE:HE1	2.20	0.72
1:N:45:ARG:CZ	1:N:47:MSE:HE1	2.19	0.72
1:I:45:ARG:NE	1:I:47:MSE:HE1	2.04	0.71
1:N:45:ARG:NE	1:N:47:MSE:HE1	2.05	0.71
1:A:31:ASN:OD1	2:A:136:HOH:O	2.08	0.71
1:R:47:MSE:HE3	1:R:53:PHE:HE2	1.55	0.71
1:L:45:ARG:CZ	1:L:47:MSE:HE1	2.20	0.71
1:N:47:MSE:HE3	1:N:53:PHE:HE2	1.55	0.71
1:F:45:ARG:CZ	1:F:47:MSE:HE1	2.20	0.71
1:F:55:ARG:O	2:F:130:HOH:O	2.07	0.71
1:K:41:ARG:NE	2:K:129:HOH:O	2.17	0.71
1:V:45:ARG:CZ	1:V:47:MSE:HE1	2.20	0.71
1:E:47:MSE:HE3	1:E:53:PHE:HE2	1.54	0.71
1:C:45:ARG:NE	1:C:47:MSE:HE1	2.06	0.71
1:R:12:GLY:N	2:R:113:HOH:O	2.23	0.71
1:D:45:ARG:CZ	1:D:47:MSE:HE1	2.21	0.70
1:C:30:GLU:HG3	1:C:41:ARG:HG3	1.72	0.70
1:I:45:ARG:CZ	1:I:47:MSE:HE1	2.21	0.70
1:G:45:ARG:NE	1:G:47:MSE:HE1	2.05	0.70
1:X:45:ARG:CZ	1:X:47:MSE:HE1	2.21	0.70
1:C:45:ARG:CZ	1:C:47:MSE:HE1	2.22	0.70
1:A:30:GLU:HG3	1:A:41:ARG:HG3	1.74	0.70
1:V:30:GLU:HG3	1:V:41:ARG:HG3	1.74	0.70
1:L:45:ARG:NE	1:L:47:MSE:HE1	2.07	0.70
1:Y:47:MSE:SE	2:Y:142:HOH:O	2.60	0.70
1:W:45:ARG:CZ	1:W:47:MSE:HE1	2.22	0.70
1:E:45:ARG:CZ	1:E:47:MSE:HE1	2.21	0.70
1:K:45:ARG:CZ	1:K:47:MSE:HE1	2.22	0.69
1:K:47:MSE:HE3	1:K:53:PHE:HE2	1.53	0.69
1:N:30:GLU:HG3	1:N:41:ARG:HG3	1.74	0.69
1:T:45:ARG:CZ	1:T:47:MSE:HE1	2.21	0.69
1:J:30:GLU:HG3	1:J:41:ARG:HG3	1.74	0.69
1:V:45:ARG:NE	1:V:47:MSE:HE1	2.07	0.69
1:Q:45:ARG:CZ	1:Q:47:MSE:HE1	2.21	0.69
1:G:37:ASN:OD1	2:G:112:HOH:O	2.10	0.69
1:O:45:ARG:CZ	1:O:47:MSE:HE1	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:ARG:HD2	2:D:116:HOH:O	1.92	0.69
1:G:47:MSE:HE3	1:G:53:PHE:HE2	1.55	0.69
1:J:28:HIS:HB2	2:J:128:HOH:O	1.93	0.69
1:J:45:ARG:NE	1:J:47:MSE:HE1	2.08	0.69
1:F:45:ARG:NE	1:F:47:MSE:HE1	2.08	0.69
1:W:45:ARG:NE	1:W:47:MSE:HE1	2.07	0.69
1:Y:45:ARG:CZ	1:Y:47:MSE:HE1	2.23	0.69
1:D:30:GLU:HG3	1:D:41:ARG:HG3	1.75	0.68
1:G:70:ARG:NE	2:G:106:HOH:O	2.25	0.68
1:P:45:ARG:CZ	1:P:47:MSE:HE1	2.22	0.68
1:Q:47:MSE:HE3	1:Q:53:PHE:HE2	1.59	0.68
1:F:47:MSE:HE3	1:F:53:PHE:HE2	1.58	0.68
1:Y:30:GLU:HG3	1:Y:41:ARG:HG3	1.74	0.68
1:B:45:ARG:NE	1:B:47:MSE:HE1	2.08	0.68
1:P:13:ARG:NH1	2:P:136:HOH:O	2.20	0.68
1:J:45:ARG:CZ	1:J:47:MSE:HE1	2.24	0.68
1:X:47:MSE:HE3	1:X:53:PHE:HE2	1.58	0.68
1:E:30:GLU:HG3	1:E:41:ARG:HG3	1.76	0.68
1:O:45:ARG:NE	1:O:47:MSE:HE1	2.09	0.68
1:Q:30:GLU:HG3	1:Q:41:ARG:HG3	1.76	0.68
1:R:45:ARG:CZ	1:R:47:MSE:HE1	2.24	0.68
1:A:45:ARG:CZ	1:A:47:MSE:HE1	2.24	0.67
1:H:45:ARG:CZ	1:H:47:MSE:HE1	2.24	0.67
1:P:45:ARG:NE	1:P:47:MSE:HE1	2.09	0.67
1:I:30:GLU:HG3	1:I:41:ARG:HG3	1.76	0.67
1:L:12:GLY:CA	2:L:122:HOH:O	2.43	0.67
1:O:47:MSE:HE3	1:O:53:PHE:HE2	1.59	0.67
1:T:36:MSE:CE	2:T:119:HOH:O	2.43	0.67
1:H:45:ARG:NE	1:H:47:MSE:HE1	2.10	0.67
1:B:52:LYS:NZ	2:B:114:HOH:O	2.18	0.67
1:G:70:ARG:CZ	2:G:106:HOH:O	2.43	0.67
1:G:30:GLU:HG3	1:G:41:ARG:HG3	1.75	0.67
1:X:45:ARG:NE	1:X:47:MSE:HE1	2.10	0.67
1:Y:41:ARG:CZ	2:Y:151:HOH:O	2.41	0.67
1:V:12:GLY:N	1:V:71:ILE:CG2	2.58	0.67
1:F:30:GLU:HG3	1:F:41:ARG:HG3	1.77	0.67
1:O:30:GLU:HG3	1:O:41:ARG:HG3	1.77	0.67
1:M:68:TYR:CZ	2:M:115:HOH:O	2.48	0.66
1:X:28:HIS:HE1	2:X:137:HOH:O	1.79	0.66
1:M:30:GLU:HG3	1:M:41:ARG:HG3	1.76	0.66
1:M:47:MSE:HE3	1:M:53:PHE:HE2	1.56	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:47:MSE:SE	2:Q:152:HOH:O	2.63	0.66
1:A:45:ARG:NE	1:A:47:MSE:HE1	2.10	0.66
1:C:47:MSE:HE3	1:C:53:PHE:HE2	1.55	0.66
1:K:45:ARG:NE	1:K:47:MSE:HE1	2.10	0.66
1:K:30:GLU:HG3	1:K:41:ARG:HG3	1.76	0.66
1:V:71:ILE:O	2:V:101:HOH:O	2.12	0.66
1:X:30:GLU:HG3	1:X:41:ARG:HG3	1.77	0.66
1:B:47:MSE:HE3	1:B:53:PHE:HE2	1.54	0.66
1:R:41:ARG:NH2	2:R:120:HOH:O	2.28	0.66
1:J:12:GLY:HA3	1:J:71:ILE:HD13	1.77	0.66
1:W:47:MSE:HE3	1:W:53:PHE:HE2	1.55	0.66
1:P:13:ARG:NH2	2:P:136:HOH:O	2.28	0.65
1:H:57:PRO:HG2	1:I:55:ARG:HB2	1.78	0.65
1:L:47:MSE:HE3	1:L:53:PHE:HE2	1.61	0.65
1:P:30:GLU:HG3	1:P:41:ARG:HG3	1.79	0.65
1:T:30:GLU:HG3	1:T:41:ARG:HG3	1.78	0.65
1:U:30:GLU:HG3	1:U:41:ARG:HG3	1.76	0.65
1:H:30:GLU:HG3	1:H:41:ARG:HG3	1.78	0.65
1:G:70:ARG:NH2	2:G:106:HOH:O	2.29	0.65
1:R:45:ARG:NE	1:R:47:MSE:HE1	2.11	0.65
1:W:30:GLU:HG3	1:W:41:ARG:HG3	1.77	0.65
1:W:30:GLU:HG3	1:W:41:ARG:HD2	1.79	0.65
1:L:30:GLU:HG3	1:L:41:ARG:HG3	1.77	0.65
1:U:55:ARG:NH1	2:U:121:HOH:O	2.29	0.65
1:D:47:MSE:HE3	1:D:53:PHE:HE2	1.60	0.64
1:I:47:MSE:HE3	1:I:53:PHE:HE2	1.60	0.64
1:N:70:ARG:NH1	2:N:119:HOH:O	2.28	0.64
1:A:55:ARG:CD	2:C:143:HOH:O	2.44	0.64
1:U:45:ARG:CZ	1:U:47:MSE:HE1	2.28	0.64
1:V:32:CYS:N	2:V:116:HOH:O	2.30	0.64
1:L:13:ARG:NE	2:L:124:HOH:O	2.30	0.64
1:Q:12:GLY:HA3	1:Q:71:ILE:HD13	1.78	0.64
1:U:45:ARG:NE	1:U:47:MSE:HE1	2.12	0.64
1:R:30:GLU:HG3	1:R:41:ARG:HD2	1.80	0.64
1:A:47:MSE:HE3	1:A:53:PHE:HE2	1.56	0.64
1:P:47:MSE:HE3	1:P:53:PHE:HE2	1.63	0.64
1:W:13:ARG:NH2	2:W:141:HOH:O	2.13	0.63
1:K:47:MSE:CE	1:K:53:PHE:CE2	2.82	0.63
1:X:13:ARG:NH1	2:X:109:HOH:O	2.11	0.63
1:V:30:GLU:HG3	1:V:41:ARG:HD2	1.80	0.63
1:X:28:HIS:HB3	2:X:131:HOH:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:GLU:HG3	1:B:41:ARG:HG3	1.78	0.63
1:B:30:GLU:HG3	1:B:41:ARG:HD2	1.81	0.63
1:X:30:GLU:HG3	1:X:41:ARG:HD2	1.81	0.63
1:H:13:ARG:NH1	2:H:145:HOH:O	2.31	0.63
1:M:12:GLY:HA3	1:M:71:ILE:HD13	1.78	0.63
1:A:47:MSE:CE	1:A:53:PHE:CE2	2.82	0.62
1:J:47:MSE:HE3	1:J:53:PHE:HE2	1.60	0.62
1:A:30:GLU:HG3	1:A:41:ARG:HD2	1.80	0.62
1:R:30:GLU:HG3	1:R:41:ARG:HG3	1.80	0.62
1:J:30:GLU:HG3	1:J:41:ARG:HD2	1.82	0.62
1:G:30:GLU:HG3	1:G:41:ARG:HD2	1.80	0.62
1:V:34:ASN:CG	2:V:115:HOH:O	2.38	0.62
1:D:71:ILE:O	2:D:121:HOH:O	2.16	0.61
1:C:13:ARG:NH2	2:C:121:HOH:O	2.31	0.61
1:D:30:GLU:HG3	1:D:41:ARG:HD2	1.82	0.61
1:U:12:GLY:HA3	1:U:71:ILE:HD13	1.83	0.61
1:M:30:GLU:HG3	1:M:41:ARG:HD2	1.82	0.61
1:R:47:MSE:CE	1:R:53:PHE:CE2	2.83	0.61
1:C:31:ASN:ND2	2:C:145:HOH:O	2.32	0.60
1:M:45:ARG:CZ	2:M:138:HOH:O	2.48	0.60
1:N:15:ILE:HD11	1:N:40:LEU:HD21	1.84	0.60
1:O:30:GLU:HG3	1:O:41:ARG:HD2	1.83	0.60
1:Y:30:GLU:HG3	1:Y:41:ARG:HD2	1.83	0.60
1:C:30:GLU:HG3	1:C:41:ARG:HD2	1.83	0.60
1:K:30:GLU:HG3	1:K:41:ARG:HD2	1.83	0.60
1:O:12:GLY:HA3	1:O:71:ILE:HD13	1.83	0.60
1:H:30:GLU:OE2	2:H:120:HOH:O	2.17	0.60
1:R:41:ARG:CZ	2:R:121:HOH:O	2.50	0.60
1:D:12:GLY:N	1:D:71:ILE:CD1	2.62	0.60
1:Q:28:HIS:HB3	2:Q:147:HOH:O	2.01	0.60
1:F:30:GLU:HG3	1:F:41:ARG:HD2	1.84	0.60
1:K:15:ILE:HD11	1:K:40:LEU:HD21	1.84	0.60
1:U:30:GLU:HG3	1:U:41:ARG:HD2	1.83	0.60
1:Y:15:ILE:HD11	1:Y:40:LEU:HD21	1.84	0.60
1:I:30:GLU:HG3	1:I:41:ARG:HD2	1.84	0.59
1:L:16:LEU:HD23	1:L:16:LEU:C	2.23	0.59
1:E:30:GLU:HG3	1:E:41:ARG:HD2	1.84	0.59
1:E:36:MSE:CE	2:E:124:HOH:O	2.51	0.59
1:P:51:ASP:OD2	2:P:133:HOH:O	2.17	0.59
1:K:58:GLU:CB	2:K:129:HOH:O	2.44	0.59
1:X:15:ILE:HD11	1:X:40:LEU:HD21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:16:LEU:C	1:F:16:LEU:HD23	2.22	0.59
1:T:30:GLU:HG3	1:T:41:ARG:HD2	1.85	0.58
1:N:30:GLU:HG3	1:N:41:ARG:HD2	1.84	0.58
1:Y:13:ARG:NH2	2:Y:129:HOH:O	2.33	0.58
1:B:12:GLY:HA3	1:B:71:ILE:HD13	1.85	0.58
1:G:12:GLY:HA3	1:G:71:ILE:HD13	1.85	0.58
1:V:15:ILE:HD11	1:V:40:LEU:HD21	1.84	0.58
1:V:34:ASN:HB2	2:V:115:HOH:O	2.02	0.58
1:Q:30:GLU:HG3	1:Q:41:ARG:HD2	1.84	0.58
1:W:16:LEU:HD23	1:W:16:LEU:C	2.23	0.58
1:Y:12:GLY:CA	2:Y:127:HOH:O	2.50	0.58
1:M:16:LEU:HD23	1:M:16:LEU:C	2.24	0.58
1:Q:47:MSE:CE	1:Q:53:PHE:CE2	2.85	0.58
1:U:15:ILE:HD11	1:U:40:LEU:HD21	1.85	0.58
1:T:47:MSE:HE3	1:T:53:PHE:HE2	1.62	0.58
1:X:12:GLY:HA3	1:X:71:ILE:HD13	1.85	0.58
1:E:15:ILE:HD11	1:E:40:LEU:HD21	1.86	0.58
2:H:139:HOH:O	1:I:55:ARG:CD	2.52	0.57
1:Y:47:MSE:HE3	1:Y:53:PHE:HE2	1.67	0.57
1:P:16:LEU:C	1:P:16:LEU:HD23	2.24	0.57
1:R:16:LEU:HD23	1:R:16:LEU:C	2.24	0.57
1:F:15:ILE:HD11	1:F:40:LEU:HD21	1.85	0.57
1:Q:15:ILE:HD11	1:Q:40:LEU:HD21	1.86	0.57
1:C:12:GLY:CA	2:C:146:HOH:O	2.51	0.57
1:I:12:GLY:HA2	2:I:134:HOH:O	1.93	0.57
1:W:15:ILE:HD11	1:W:40:LEU:HD21	1.85	0.57
1:I:47:MSE:CE	1:I:53:PHE:CE2	2.87	0.57
1:Q:16:LEU:C	1:Q:16:LEU:HD23	2.25	0.57
1:G:47:MSE:CE	1:G:53:PHE:CE2	2.83	0.57
1:R:15:ILE:HD11	1:R:40:LEU:HD21	1.87	0.57
1:V:34:ASN:CB	2:V:115:HOH:O	2.51	0.57
1:W:13:ARG:NE	2:W:141:HOH:O	2.36	0.57
1:E:16:LEU:HD23	1:E:16:LEU:C	2.25	0.56
1:T:16:LEU:HD23	1:T:16:LEU:C	2.25	0.56
1:X:16:LEU:C	1:X:16:LEU:HD23	2.25	0.56
1:A:13:ARG:NH1	2:A:141:HOH:O	2.38	0.56
1:H:30:GLU:HG3	1:H:41:ARG:HD2	1.88	0.56
1:D:16:LEU:HD23	1:D:16:LEU:C	2.26	0.56
1:W:12:GLY:HA3	1:W:71:ILE:HD13	1.88	0.56
1:I:15:ILE:HD11	1:I:40:LEU:HD21	1.87	0.56
1:T:47:MSE:CE	1:T:53:PHE:CE2	2.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:15:ILE:HD11	1:H:40:LEU:HD21	1.87	0.55
1:D:47:MSE:CE	1:D:53:PHE:CE2	2.88	0.55
1:E:47:MSE:CE	1:E:53:PHE:CE2	2.85	0.55
1:O:16:LEU:HD23	1:O:16:LEU:C	2.26	0.55
1:G:16:LEU:C	1:G:16:LEU:HD23	2.27	0.55
1:K:58:GLU:CG	2:K:129:HOH:O	2.53	0.55
1:Q:28:HIS:HB2	2:Q:151:HOH:O	2.05	0.55
1:Y:12:GLY:N	2:Y:127:HOH:O	2.38	0.55
1:P:30:GLU:HG3	1:P:41:ARG:HD2	1.87	0.55
1:Q:31:ASN:CB	2:Q:130:HOH:O	2.55	0.55
1:C:15:ILE:HD11	1:C:40:LEU:HD21	1.88	0.55
1:B:16:LEU:C	1:B:16:LEU:HD23	2.27	0.55
1:L:15:ILE:HD11	1:L:40:LEU:HD21	1.89	0.55
1:M:15:ILE:HD11	1:M:40:LEU:HD21	1.87	0.55
1:R:41:ARG:NH1	2:R:121:HOH:O	2.39	0.55
1:A:15:ILE:HD11	1:A:40:LEU:HD21	1.87	0.55
1:A:16:LEU:HD23	1:A:16:LEU:C	2.27	0.55
1:L:30:GLU:HG3	1:L:41:ARG:HD2	1.88	0.55
1:N:16:LEU:HD23	1:N:16:LEU:C	2.28	0.55
1:Y:16:LEU:HD23	1:Y:16:LEU:C	2.28	0.54
1:N:47:MSE:CE	1:N:53:PHE:CE2	2.85	0.54
1:V:47:MSE:HE3	1:V:53:PHE:HE2	1.66	0.54
1:H:16:LEU:C	1:H:16:LEU:HD23	2.27	0.54
1:O:15:ILE:HD11	1:O:40:LEU:HD21	1.89	0.54
1:W:47:MSE:CE	1:W:53:PHE:CE2	2.89	0.54
1:J:70:ARG:NE	2:J:135:HOH:O	2.02	0.54
1:T:32:CYS:SG	2:T:119:HOH:O	2.44	0.54
1:U:16:LEU:C	1:U:16:LEU:HD23	2.26	0.54
1:W:31:ASN:HB2	2:W:129:HOH:O	2.07	0.54
1:W:35:TYR:CE2	2:W:144:HOH:O	2.53	0.54
1:Y:30:GLU:CG	1:Y:41:ARG:HG3	2.37	0.54
1:V:16:LEU:C	1:V:16:LEU:HD23	2.28	0.54
1:C:16:LEU:C	1:C:16:LEU:HD23	2.28	0.54
1:G:15:ILE:HD11	1:G:40:LEU:HD21	1.90	0.54
1:T:36:MSE:HE1	2:T:119:HOH:O	2.06	0.54
1:C:41:ARG:HD2	2:C:147:HOH:O	2.08	0.54
1:D:15:ILE:HD11	1:D:40:LEU:HD21	1.89	0.53
1:P:15:ILE:HD11	1:P:40:LEU:HD21	1.89	0.53
1:B:15:ILE:HD11	1:B:40:LEU:HD21	1.89	0.53
1:J:47:MSE:CE	1:J:53:PHE:CE2	2.89	0.53
1:G:55:ARG:CZ	2:G:144:HOH:O	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:58:GLU:HB3	1:R:54:PHE:HB2	1.90	0.53
1:K:16:LEU:C	1:K:16:LEU:HD23	2.29	0.53
1:P:12:GLY:N	1:P:71:ILE:CD1	2.72	0.53
1:E:13:ARG:NH1	2:E:139:HOH:O	1.96	0.53
1:T:15:ILE:HD11	1:T:40:LEU:HD21	1.89	0.53
1:J:16:LEU:HD23	1:J:16:LEU:C	2.29	0.52
1:Y:41:ARG:NH2	2:Y:151:HOH:O	2.40	0.52
1:C:47:MSE:CE	1:C:53:PHE:CE2	2.88	0.52
1:P:41:ARG:NH2	2:P:129:HOH:O	2.35	0.52
1:Q:31:ASN:HB3	2:Q:130:HOH:O	2.10	0.52
1:Y:13:ARG:NH1	2:Y:152:HOH:O	2.27	0.52
1:Y:30:GLU:HG3	1:Y:41:ARG:CG	2.40	0.52
1:V:47:MSE:CE	1:V:53:PHE:CE2	2.90	0.52
1:G:30:GLU:HG3	1:G:41:ARG:CG	2.40	0.52
1:J:30:GLU:CG	1:J:41:ARG:HG3	2.40	0.52
1:G:55:ARG:NH2	2:G:144:HOH:O	2.42	0.51
1:B:47:MSE:CE	1:B:53:PHE:CE2	2.87	0.51
1:V:30:GLU:HG3	1:V:41:ARG:CG	2.39	0.51
1:Y:12:GLY:N	1:Y:71:ILE:HD13	2.24	0.51
1:Y:28:HIS:CD2	2:Y:110:HOH:O	2.56	0.51
1:H:47:MSE:CE	1:H:53:PHE:CE2	2.87	0.51
1:C:30:GLU:HG3	1:C:41:ARG:CG	2.40	0.51
2:H:139:HOH:O	1:I:55:ARG:HD2	2.09	0.51
1:E:12:GLY:HA3	1:E:71:ILE:HD13	1.93	0.51
1:E:36:MSE:HE1	2:E:124:HOH:O	2.10	0.50
1:Q:45:ARG:CD	1:Q:47:MSE:HE1	2.41	0.50
1:I:16:LEU:HD23	1:I:16:LEU:C	2.32	0.50
1:R:31:ASN:ND2	2:R:138:HOH:O	2.32	0.50
1:J:30:GLU:HG3	1:J:41:ARG:CG	2.40	0.50
1:D:30:GLU:CG	1:D:41:ARG:HG3	2.41	0.50
2:D:132:HOH:O	1:E:55:ARG:HD3	2.11	0.50
1:G:34:ASN:CB	2:G:159:HOH:O	2.58	0.50
1:V:30:GLU:CG	1:V:41:ARG:HG3	2.41	0.50
1:A:30:GLU:HG3	1:A:41:ARG:CG	2.41	0.50
1:X:30:GLU:HG3	1:X:41:ARG:CG	2.42	0.50
1:G:70:ARG:HD2	2:G:148:HOH:O	2.11	0.50
1:W:30:GLU:HG3	1:W:41:ARG:CG	2.42	0.50
1:U:47:MSE:CE	1:U:53:PHE:CE2	2.86	0.49
1:F:12:GLY:HA3	1:F:71:ILE:HD13	1.93	0.49
1:G:30:GLU:CG	1:G:41:ARG:HG3	2.41	0.49
1:I:45:ARG:CD	1:I:47:MSE:HE1	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:30:GLU:CG	1:I:41:ARG:HG3	2.41	0.49
1:U:45:ARG:CD	1:U:47:MSE:HE1	2.43	0.49
1:W:16:LEU:HD23	1:W:17:VAL:N	2.27	0.49
1:W:30:GLU:CG	1:W:41:ARG:HG3	2.42	0.49
1:Y:55:ARG:NH1	2:Y:143:HOH:O	2.45	0.49
1:B:35:TYR:O	1:B:36:MSE:HB2	2.12	0.49
1:F:35:TYR:O	1:F:36:MSE:HB2	2.13	0.49
1:N:30:GLU:HG3	1:N:41:ARG:CG	2.41	0.49
1:V:30:GLU:HG3	1:V:41:ARG:CD	2.43	0.49
1:W:55:ARG:CD	2:Y:147:HOH:O	2.61	0.49
1:D:30:GLU:HG3	1:D:41:ARG:CG	2.41	0.49
1:K:30:GLU:HG3	1:K:41:ARG:CG	2.41	0.48
1:K:30:GLU:CG	1:K:41:ARG:HG3	2.42	0.48
1:O:30:GLU:HG3	1:O:41:ARG:CG	2.43	0.48
1:H:13:ARG:NH2	2:H:140:HOH:O	2.46	0.48
1:J:15:ILE:HD11	1:J:40:LEU:HD21	1.94	0.48
1:L:16:LEU:HD23	1:L:17:VAL:N	2.28	0.48
1:F:30:GLU:HG3	1:F:41:ARG:CG	2.43	0.48
1:P:30:GLU:CG	1:P:41:ARG:HG3	2.43	0.48
1:P:47:MSE:CE	1:P:53:PHE:CE2	2.91	0.48
1:N:30:GLU:CG	1:N:41:ARG:HG3	2.41	0.48
1:X:31:ASN:ND2	2:X:126:HOH:O	2.31	0.48
1:E:45:ARG:CD	1:E:47:MSE:HE1	2.43	0.48
1:M:30:GLU:CG	1:M:41:ARG:HG3	2.42	0.48
1:U:57:PRO:HG2	1:V:55:ARG:HB2	1.94	0.48
1:G:34:ASN:HB3	2:G:159:HOH:O	2.13	0.48
1:H:30:GLU:CG	1:H:41:ARG:HG3	2.42	0.48
1:C:41:ARG:NH2	2:C:129:HOH:O	2.29	0.47
1:G:30:GLU:HG3	1:G:41:ARG:CD	2.44	0.47
1:P:13:ARG:CZ	2:P:136:HOH:O	2.54	0.47
1:Q:38:LEU:HD12	1:Q:38:LEU:C	2.35	0.47
1:R:30:GLU:CG	1:R:41:ARG:HG3	2.44	0.47
1:U:30:GLU:HG3	1:U:41:ARG:CG	2.42	0.47
1:I:30:GLU:HG3	1:I:41:ARG:CG	2.42	0.47
1:I:31:ASN:HB3	2:I:157:HOH:O	2.14	0.47
1:O:35:TYR:O	1:O:36:MSE:HB2	2.14	0.47
1:Y:47:MSE:CE	1:Y:53:PHE:CE2	2.93	0.47
1:B:68:TYR:CE1	1:B:70:ARG:HD2	2.50	0.47
1:M:30:GLU:HG3	1:M:41:ARG:CG	2.42	0.47
1:A:30:GLU:CG	1:A:41:ARG:HG3	2.44	0.47
1:A:30:GLU:HG3	1:A:41:ARG:CD	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:30:GLU:CG	1:Q:41:ARG:HG3	2.43	0.47
1:K:45:ARG:CD	1:K:47:MSE:HE1	2.45	0.47
1:O:30:GLU:CG	1:O:41:ARG:HG3	2.43	0.47
1:Q:30:GLU:HG3	1:Q:41:ARG:CG	2.42	0.47
1:H:30:GLU:HG3	1:H:41:ARG:CG	2.44	0.47
1:W:30:GLU:HG3	1:W:41:ARG:CD	2.44	0.46
1:X:35:TYR:O	1:X:36:MSE:HB2	2.14	0.46
1:G:45:ARG:CD	1:G:47:MSE:HE1	2.44	0.46
1:W:35:TYR:HE2	2:W:144:HOH:O	1.94	0.46
1:H:12:GLY:HA3	1:H:71:ILE:HD13	1.96	0.46
1:J:30:GLU:HG3	1:J:41:ARG:CD	2.45	0.46
1:J:45:ARG:CD	1:J:47:MSE:HE1	2.45	0.46
1:L:47:MSE:CE	1:L:53:PHE:CE2	2.94	0.46
1:Y:12:GLY:HA2	2:Y:127:HOH:O	2.11	0.46
1:D:45:ARG:CD	1:D:47:MSE:HE1	2.45	0.46
1:E:30:GLU:HG3	1:E:41:ARG:CG	2.43	0.46
1:F:30:GLU:CG	1:F:41:ARG:HG3	2.44	0.46
1:W:55:ARG:HD2	2:Y:147:HOH:O	2.15	0.46
1:X:47:MSE:CE	1:X:53:PHE:CE2	2.89	0.46
1:B:30:GLU:HG3	1:B:41:ARG:CG	2.44	0.46
1:D:55:ARG:HD3	2:F:125:HOH:O	2.14	0.46
1:K:35:TYR:O	1:K:36:MSE:HB2	2.15	0.46
1:T:45:ARG:CD	1:T:47:MSE:HE1	2.45	0.46
1:C:30:GLU:HG3	1:C:41:ARG:CD	2.46	0.46
1:E:30:GLU:CG	1:E:41:ARG:HG3	2.45	0.46
1:R:30:GLU:HG3	1:R:41:ARG:CG	2.45	0.46
1:G:35:TYR:O	1:G:36:MSE:HB2	2.16	0.46
1:U:30:GLU:CG	1:U:41:ARG:HG3	2.43	0.46
1:F:47:MSE:CE	1:F:53:PHE:CE2	2.91	0.46
1:M:30:GLU:HG3	1:M:41:ARG:CD	2.46	0.46
1:T:30:GLU:HG3	1:T:41:ARG:CG	2.44	0.45
1:W:68:TYR:HE1	1:W:70:ARG:HD2	1.81	0.45
1:Q:12:GLY:HA2	2:Q:144:HOH:O	2.02	0.45
1:N:35:TYR:O	1:N:36:MSE:HB2	2.17	0.45
1:Q:16:LEU:HD23	1:Q:17:VAL:N	2.30	0.45
1:W:68:TYR:CE1	1:W:70:ARG:HD2	2.52	0.45
1:X:45:ARG:CD	1:X:47:MSE:HE1	2.45	0.45
1:X:68:TYR:CE1	1:X:70:ARG:HD2	2.52	0.45
1:R:30:GLU:HG3	1:R:41:ARG:CD	2.46	0.45
1:D:30:GLU:HG3	1:D:41:ARG:CD	2.46	0.45
1:E:35:TYR:O	1:E:36:MSE:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:30:GLU:HG3	1:L:41:ARG:CG	2.45	0.45
1:M:47:MSE:CE	1:M:53:PHE:CE2	2.90	0.45
1:P:30:GLU:HG3	1:P:41:ARG:CG	2.45	0.45
1:K:47:MSE:CE	1:K:53:PHE:CD2	3.00	0.45
1:M:35:TYR:O	1:M:36:MSE:HB2	2.17	0.45
1:N:57:PRO:HG2	1:O:55:ARG:HB2	1.98	0.45
1:Y:30:GLU:HG3	1:Y:41:ARG:CD	2.46	0.45
1:B:45:ARG:CD	1:B:47:MSE:HE1	2.47	0.45
1:C:30:GLU:CG	1:C:41:ARG:HG3	2.44	0.45
1:E:68:TYR:OH	2:E:135:HOH:O	2.20	0.45
1:G:12:GLY:CA	1:G:71:ILE:HD13	2.47	0.45
1:M:45:ARG:CD	1:M:47:MSE:HE1	2.47	0.45
1:V:30:GLU:CG	1:V:41:ARG:HD2	2.47	0.45
1:B:30:GLU:HG3	1:B:41:ARG:CD	2.46	0.44
1:D:68:TYR:CE1	1:D:70:ARG:HD2	2.52	0.44
1:N:12:GLY:N	1:N:71:ILE:HD13	2.31	0.44
1:G:68:TYR:CE1	1:G:70:ARG:HD2	2.52	0.44
1:U:68:TYR:CE1	1:U:70:ARG:HD2	2.51	0.44
1:X:34:ASN:CG	2:X:138:HOH:O	2.55	0.44
1:K:13:ARG:NH2	2:K:119:HOH:O	2.49	0.44
1:O:68:TYR:CE1	1:O:70:ARG:HD2	2.52	0.44
1:Q:31:ASN:HB2	2:Q:130:HOH:O	2.15	0.44
1:T:13:ARG:NE	2:T:114:HOH:O	2.33	0.44
1:T:30:GLU:CG	1:T:41:ARG:HG3	2.44	0.44
1:U:30:GLU:HG3	1:U:41:ARG:CD	2.47	0.44
1:K:30:GLU:HG3	1:K:41:ARG:CD	2.47	0.44
1:O:47:MSE:CE	1:O:53:PHE:CE2	2.93	0.44
1:C:12:GLY:CA	1:C:71:ILE:HD13	2.38	0.44
1:L:12:GLY:HA3	1:L:71:ILE:HD13	1.99	0.44
1:X:30:GLU:HG3	1:X:41:ARG:CD	2.45	0.44
1:T:38:LEU:HD12	1:T:38:LEU:C	2.39	0.44
1:U:35:TYR:O	1:U:36:MSE:HB2	2.18	0.44
1:U:47:MSE:HE3	1:U:53:PHE:CD2	2.52	0.44
1:C:45:ARG:CD	1:C:47:MSE:HE1	2.48	0.44
1:M:68:TYR:CE1	1:M:70:ARG:HD2	2.52	0.44
1:N:30:GLU:HG3	1:N:41:ARG:CD	2.48	0.44
1:T:31:ASN:HB2	2:T:112:HOH:O	2.18	0.44
1:T:35:TYR:O	1:T:36:MSE:HB2	2.18	0.44
1:G:16:LEU:HD23	1:G:17:VAL:N	2.34	0.43
1:H:16:LEU:HD23	1:H:17:VAL:N	2.33	0.43
1:P:41:ARG:HD3	2:P:126:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:30:GLU:CG	1:R:41:ARG:HD2	2.47	0.43
1:A:16:LEU:HD23	1:A:17:VAL:N	2.33	0.43
1:E:68:TYR:CE1	1:E:70:ARG:HD2	2.53	0.43
1:I:30:GLU:HG3	1:I:41:ARG:CD	2.48	0.43
1:J:13:ARG:N	1:J:14:PRO:HD2	2.33	0.43
1:N:38:LEU:HD12	1:N:38:LEU:C	2.38	0.43
1:N:45:ARG:CD	1:N:47:MSE:HE1	2.47	0.43
1:R:47:MSE:CE	1:R:53:PHE:CD2	3.02	0.43
1:U:33:ASP:HB3	2:U:120:HOH:O	2.17	0.43
1:W:30:GLU:CG	1:W:41:ARG:HD2	2.47	0.43
1:X:30:GLU:CG	1:X:41:ARG:HG3	2.45	0.43
1:F:16:LEU:HD23	1:F:17:VAL:N	2.33	0.43
1:F:68:TYR:CE1	1:F:70:ARG:HD2	2.53	0.43
1:Y:68:TYR:CE1	1:Y:70:ARG:HD2	2.54	0.43
1:E:30:GLU:HG3	1:E:41:ARG:CD	2.48	0.43
1:T:13:ARG:H	1:T:14:PRO:HD2	1.84	0.43
1:X:19:LEU:HB3	2:X:105:HOH:O	2.18	0.43
1:Y:16:LEU:HD23	1:Y:17:VAL:N	2.33	0.43
1:L:35:TYR:O	1:L:36:MSE:HB2	2.19	0.43
1:N:68:TYR:CE1	1:N:70:ARG:HD2	2.53	0.43
1:W:38:LEU:C	1:W:38:LEU:HD12	2.39	0.43
1:X:16:LEU:HD23	1:X:17:VAL:N	2.33	0.43
1:A:30:GLU:CG	1:A:41:ARG:HD2	2.48	0.43
1:L:71:ILE:HD12	2:L:117:HOH:O	2.19	0.43
1:N:12:GLY:HA3	1:N:71:ILE:HD13	2.01	0.43
1:Y:30:GLU:CG	1:Y:41:ARG:HD2	2.47	0.43
1:A:47:MSE:CE	1:A:53:PHE:CD2	3.02	0.43
1:B:30:GLU:CG	1:B:41:ARG:HG3	2.47	0.43
1:B:68:TYR:HE1	1:B:70:ARG:HD2	1.83	0.43
1:M:38:LEU:C	1:M:38:LEU:HD12	2.40	0.43
1:T:68:TYR:CE1	1:T:70:ARG:HD2	2.54	0.43
1:U:16:LEU:HD23	1:U:17:VAL:N	2.33	0.43
1:A:55:ARG:HB2	1:C:57:PRO:HG2	2.01	0.42
1:O:30:GLU:HG3	1:O:41:ARG:CD	2.47	0.42
1:W:45:ARG:CD	1:W:47:MSE:HE1	2.49	0.42
2:H:139:HOH:O	1:I:55:ARG:HD3	2.14	0.42
1:O:45:ARG:CD	1:O:47:MSE:HE1	2.50	0.42
1:R:31:ASN:CB	2:R:138:HOH:O	2.46	0.42
1:W:16:LEU:CD2	1:W:16:LEU:C	2.87	0.42
1:X:13:ARG:CD	2:X:109:HOH:O	2.56	0.42
1:B:16:LEU:HD23	1:B:17:VAL:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:ARG:NE	2:B:140:HOH:O	1.85	0.42
1:D:56:LEU:HD12	1:D:56:LEU:N	2.34	0.42
1:G:47:MSE:CE	1:G:53:PHE:CD2	3.02	0.42
1:I:38:LEU:HD12	1:I:38:LEU:C	2.40	0.42
1:B:30:GLU:CG	1:B:41:ARG:HD2	2.49	0.42
1:C:16:LEU:HD23	1:C:17:VAL:N	2.35	0.42
1:K:68:TYR:CE1	1:K:70:ARG:HD2	2.54	0.42
1:N:68:TYR:CE1	2:N:119:HOH:O	2.71	0.42
1:F:30:GLU:HG3	1:F:41:ARG:CD	2.48	0.42
1:O:30:GLU:CG	1:O:41:ARG:HD2	2.49	0.42
1:P:12:GLY:N	2:P:122:HOH:O	2.52	0.42
1:P:16:LEU:HD23	1:P:17:VAL:N	2.35	0.42
1:Q:68:TYR:CE1	1:Q:70:ARG:HD2	2.55	0.42
1:H:68:TYR:CE1	1:H:70:ARG:HD2	2.54	0.42
1:L:30:GLU:CG	1:L:41:ARG:HG3	2.44	0.42
1:L:68:TYR:CE1	1:L:70:ARG:HD2	2.54	0.42
1:A:68:TYR:CE1	1:A:70:ARG:HD2	2.53	0.42
1:H:45:ARG:CD	1:H:47:MSE:HE1	2.50	0.42
1:J:16:LEU:HD23	1:J:17:VAL:N	2.35	0.42
1:G:71:ILE:HD12	2:G:142:HOH:O	2.18	0.42
1:R:45:ARG:CD	1:R:47:MSE:HE1	2.50	0.42
1:X:28:HIS:CB	2:X:130:HOH:O	2.68	0.42
1:U:47:MSE:CE	1:U:53:PHE:CD2	3.03	0.42
1:V:35:TYR:O	1:V:36:MSE:HB2	2.20	0.42
1:X:47:MSE:HE3	1:X:53:PHE:CD2	2.54	0.42
1:X:68:TYR:HE1	1:X:70:ARG:HD2	1.85	0.42
1:H:35:TYR:O	1:H:36:MSE:HB2	2.20	0.41
1:L:16:LEU:CD2	1:L:16:LEU:C	2.88	0.41
1:Y:45:ARG:CD	1:Y:47:MSE:HE1	2.50	0.41
1:A:38:LEU:HD12	1:A:38:LEU:C	2.40	0.41
1:F:16:LEU:C	1:F:16:LEU:CD2	2.88	0.41
1:A:13:ARG:NH1	2:A:113:HOH:O	2.52	0.41
1:X:30:GLU:CG	1:X:41:ARG:HD2	2.49	0.41
1:C:68:TYR:CE1	1:C:70:ARG:HD2	2.55	0.41
1:D:30:GLU:CG	1:D:41:ARG:HD2	2.49	0.41
1:J:12:GLY:CA	1:J:71:ILE:HD13	2.47	0.41
1:U:31:ASN:ND2	2:U:118:HOH:O	2.52	0.41
1:V:68:TYR:CE1	1:V:70:ARG:HD2	2.55	0.41
1:R:68:TYR:CE1	1:R:70:ARG:HD2	2.55	0.41
1:X:47:MSE:CE	1:X:53:PHE:CD2	3.04	0.41
1:A:45:ARG:CD	1:A:47:MSE:HE1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:16:LEU:HD23	1:E:17:VAL:N	2.36	0.41
1:I:68:TYR:CE1	1:I:70:ARG:HD2	2.56	0.41
1:O:16:LEU:HD23	1:O:17:VAL:N	2.36	0.41
1:Q:30:GLU:HG3	1:Q:41:ARG:CD	2.48	0.41
1:U:38:LEU:C	1:U:38:LEU:HD12	2.41	0.41
1:W:35:TYR:O	1:W:36:MSE:HB2	2.20	0.41
1:G:71:ILE:CD1	2:G:142:HOH:O	2.69	0.41
1:K:38:LEU:C	1:K:38:LEU:HD12	2.41	0.41
1:N:68:TYR:CZ	2:N:119:HOH:O	2.56	0.41
1:R:38:LEU:C	1:R:38:LEU:HD12	2.41	0.41
1:A:47:MSE:HE2	1:A:53:PHE:CD2	2.56	0.41
2:D:132:HOH:O	1:E:55:ARG:CD	2.67	0.41
1:L:38:LEU:C	1:L:38:LEU:HD12	2.41	0.41
1:B:12:GLY:CA	2:B:144:HOH:O	2.69	0.41
1:F:38:LEU:C	1:F:38:LEU:HD12	2.42	0.41
1:J:71:ILE:HD12	1:J:71:ILE:C	2.41	0.41
1:U:30:GLU:CG	1:U:41:ARG:HD2	2.50	0.41
1:V:45:ARG:CD	1:V:47:MSE:HE1	2.51	0.41
1:D:68:TYR:HE1	1:D:70:ARG:HD2	1.87	0.40
1:J:30:GLU:CG	1:J:41:ARG:HD2	2.49	0.40
1:L:30:GLU:HG3	1:L:41:ARG:CD	2.52	0.40
1:P:68:TYR:CE1	1:P:70:ARG:HD2	2.56	0.40
1:T:30:GLU:HG3	1:T:41:ARG:CD	2.49	0.40
1:J:68:TYR:CE1	1:J:70:ARG:HD2	2.56	0.40
1:N:16:LEU:HD23	1:N:17:VAL:N	2.36	0.40
1:U:58:GLU:HB3	1:V:54:PHE:HB2	2.04	0.40
1:X:38:LEU:C	1:X:38:LEU:HD12	2.41	0.40
1:Y:68:TYR:HE1	1:Y:70:ARG:HD2	1.86	0.40
1:M:30:GLU:CG	1:M:41:ARG:HD2	2.49	0.40
1:X:28:HIS:HB3	2:X:130:HOH:O	2.20	0.40
1:J:38:LEU:C	1:J:38:LEU:HD12	2.42	0.40
1:N:33:ASP:C	1:N:33:ASP:OD1	2.60	0.40
1:O:68:TYR:HE1	1:O:70:ARG:HD2	1.85	0.40
1:B:71:ILE:HD12	1:B:71:ILE:C	2.41	0.40
1:C:35:TYR:O	1:C:36:MSE:HB2	2.21	0.40
1:F:68:TYR:HE1	1:F:70:ARG:HD2	1.86	0.40
1:F:71:ILE:C	1:F:71:ILE:HD12	2.42	0.40
1:N:20:LYS:CE	2:N:121:HOH:O	2.70	0.40
1:N:28:HIS:CB	2:N:120:HOH:O	2.46	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:ASN:OD1	1:E:30:GLU:OE1[2_657]	1.95	0.25
1:M:67:LYS:NZ	1:Y:30:GLU:OE2[4_556]	2.11	0.09
1:N:67:LYS:NZ	2:H:120:HOH:O[4_556]	2.12	0.08
1:H:41:ARG:NH1	1:N:67:LYS:NZ[4_546]	2.16	0.04
1:K:31:ASN:OD1	1:T:30:GLU:OE1[3_454]	2.16	0.04
1:B:31:ASN:OD1	1:E:30:GLU:CD[2_657]	2.19	0.01

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	B	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	C	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	D	58/105 (55%)	58 (100%)	0	0	100	100
1	E	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	F	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	G	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	H	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	I	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	J	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	K	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	L	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	M	58/105 (55%)	58 (100%)	0	0	100	100
1	N	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	O	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	P	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	Q	58/105 (55%)	56 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	T	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	U	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	V	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	W	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
1	X	58/105 (55%)	56 (97%)	2 (3%)	0	100	100
1	Y	58/105 (55%)	57 (98%)	1 (2%)	0	100	100
All	All	1392/2520 (55%)	1357 (98%)	35 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	B	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	C	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	D	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	E	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	F	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	G	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	H	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	I	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	J	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	K	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	L	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	M	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	N	55/91 (60%)	53 (96%)	2 (4%)	35	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	P	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	Q	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	R	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	T	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	U	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	V	55/91 (60%)	54 (98%)	1 (2%)	59	72
1	W	55/91 (60%)	52 (94%)	3 (6%)	21	26
1	X	55/91 (60%)	53 (96%)	2 (4%)	35	45
1	Y	55/91 (60%)	52 (94%)	3 (6%)	21	26
All	All	1320/2184 (60%)	1260 (96%)	60 (4%)	27	34

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	HIS
1	A	71	ILE
1	B	28	HIS
1	B	43	VAL
1	B	71	ILE
1	C	28	HIS
1	C	71	ILE
1	D	28	HIS
1	D	71	ILE
1	E	28	HIS
1	E	71	ILE
1	F	28	HIS
1	F	43	VAL
1	F	71	ILE
1	G	28	HIS
1	G	43	VAL
1	G	71	ILE
1	H	28	HIS
1	H	71	ILE
1	I	28	HIS
1	I	43	VAL
1	I	71	ILE
1	J	28	HIS

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Mol	Chain	Res	Type
1	J	43	VAL
1	J	71	ILE
1	K	28	HIS
1	K	43	VAL
1	K	71	ILE
1	L	28	HIS
1	L	43	VAL
1	L	71	ILE
1	M	28	HIS
1	M	43	VAL
1	M	71	ILE
1	N	28	HIS
1	N	71	ILE
1	O	28	HIS
1	O	43	VAL
1	O	71	ILE
1	P	28	HIS
1	P	71	ILE
1	Q	28	HIS
1	Q	43	VAL
1	Q	71	ILE
1	R	28	HIS
1	R	71	ILE
1	T	28	HIS
1	T	43	VAL
1	T	71	ILE
1	U	28	HIS
1	U	71	ILE
1	V	28	HIS
1	W	28	HIS
1	W	43	VAL
1	W	71	ILE
1	X	28	HIS
1	X	71	ILE
1	Y	28	HIS
1	Y	43	VAL
1	Y	71	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	64	ASN
1	B	31	ASN
1	B	34	ASN
1	B	64	ASN
1	C	34	ASN
1	C	64	ASN
1	D	34	ASN
1	D	64	ASN
1	E	34	ASN
1	E	64	ASN
1	F	34	ASN
1	F	64	ASN
1	G	34	ASN
1	G	64	ASN
1	H	64	ASN
1	I	34	ASN
1	I	64	ASN
1	J	34	ASN
1	K	34	ASN
1	K	64	ASN
1	L	34	ASN
1	L	64	ASN
1	M	64	ASN
1	N	34	ASN
1	N	64	ASN
1	O	34	ASN
1	O	64	ASN
1	Q	64	ASN
1	R	34	ASN
1	R	64	ASN
1	T	34	ASN
1	T	64	ASN
1	U	34	ASN
1	U	64	ASN
1	V	34	ASN
1	V	64	ASN
1	W	34	ASN
1	W	64	ASN
1	X	34	ASN
1	X	64	ASN
1	Y	34	ASN
1	Y	64	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data i

### 6.1 Protein, DNA and RNA chains i

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	58/105 (55%)	-0.00	2 (3%) 45 43	19, 26, 43, 49	0
1	B	58/105 (55%)	-0.10	2 (3%) 45 43	19, 26, 44, 50	0
1	C	58/105 (55%)	-0.18	1 (1%) 70 68	19, 26, 43, 49	0
1	D	58/105 (55%)	0.05	3 (5%) 27 26	19, 26, 43, 49	0
1	E	58/105 (55%)	-0.14	2 (3%) 45 43	20, 26, 43, 51	0
1	F	58/105 (55%)	-0.16	0 100 100	20, 27, 44, 50	0
1	G	58/105 (55%)	0.00	2 (3%) 45 43	18, 25, 43, 49	0
1	H	58/105 (55%)	0.07	1 (1%) 70 68	18, 24, 42, 48	0
1	I	58/105 (55%)	0.10	2 (3%) 45 43	17, 24, 42, 48	0
1	J	58/105 (55%)	-0.09	2 (3%) 45 43	18, 25, 43, 49	0
1	K	58/105 (55%)	0.07	4 (6%) 16 15	21, 26, 46, 51	0
1	L	58/105 (55%)	-0.10	3 (5%) 27 26	19, 25, 43, 50	0
1	M	58/105 (55%)	-0.06	3 (5%) 27 26	19, 26, 44, 50	0
1	N	58/105 (55%)	-0.03	2 (3%) 45 43	18, 26, 44, 50	0
1	O	58/105 (55%)	-0.22	1 (1%) 70 68	21, 28, 44, 50	0
1	P	58/105 (55%)	-0.01	2 (3%) 45 43	18, 25, 43, 49	0
1	Q	58/105 (55%)	-0.15	2 (3%) 45 43	19, 25, 43, 49	0
1	R	58/105 (55%)	0.04	6 (10%) 6 5	20, 27, 46, 52	0
1	T	58/105 (55%)	-0.01	4 (6%) 16 15	22, 27, 45, 52	0
1	U	58/105 (55%)	-0.17	1 (1%) 70 68	21, 28, 45, 50	0
1	V	58/105 (55%)	-0.20	1 (1%) 70 68	20, 27, 43, 50	0
1	W	58/105 (55%)	0.05	4 (6%) 16 15	18, 24, 43, 49	0
1	X	58/105 (55%)	-0.23	2 (3%) 45 43	20, 26, 44, 50	0
1	Y	58/105 (55%)	0.13	1 (1%) 70 68	18, 25, 43, 49	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	1392/2520 (55%)	-0.05	53 (3%) 40 38	17, 26, 45, 52	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	68	TYR	5.6
1	M	68	TYR	5.3
1	D	68	TYR	5.0
1	G	68	TYR	4.3
1	L	68	TYR	3.5
1	J	28	HIS	3.4
1	D	28	HIS	3.2
1	V	71	ILE	3.2
1	X	28	HIS	3.1
1	W	28	HIS	3.0
1	U	28	HIS	3.0
1	Q	28	HIS	2.9
1	K	35	TYR	2.9
1	W	70	ARG	2.9
1	K	28	HIS	2.8
1	E	34	ASN	2.7
1	B	28	HIS	2.7
1	M	28	HIS	2.7
1	I	70	ARG	2.6
1	N	28	HIS	2.6
1	R	28	HIS	2.6
1	X	70	ARG	2.6
1	R	71	ILE	2.6
1	I	28	HIS	2.5
1	T	68	TYR	2.5
1	R	13	ARG	2.5
1	K	34	ASN	2.5
1	M	71	ILE	2.5
1	R	34	ASN	2.5
1	P	28	HIS	2.4
1	J	70	ARG	2.4
1	R	70	ARG	2.4
1	T	34	ASN	2.4
1	W	34	ASN	2.4
1	Q	70	ARG	2.3
1	E	28	HIS	2.3
1	K	68	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	28	HIS	2.2
1	G	28	HIS	2.2
1	R	12	GLY	2.2
1	L	70	ARG	2.2
1	T	12	GLY	2.2
1	B	35	TYR	2.1
1	T	35	TYR	2.1
1	O	70	ARG	2.1
1	H	41	ARG	2.1
1	W	35	TYR	2.1
1	Y	68	TYR	2.1
1	A	31	ASN	2.1
1	D	71	ILE	2.0
1	C	34	ASN	2.0
1	L	28	HIS	2.0
1	P	68	TYR	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.