



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2017 – 12:16 PM EDT

PDB ID : 5IM6
Title : Crystal structure of designed two-component self-assembling icosahedral cage I32-28
Authors : Liu, Y.A.; Cascio, D.; Sawaya, M.R.; Bale, J.B.; Collazo, M.J.; Thomas, C.; Sheffler, W.; King, N.P.; Baker, D.; Yeates, T.O.
Deposited on : unknown
Resolution : 5.59 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

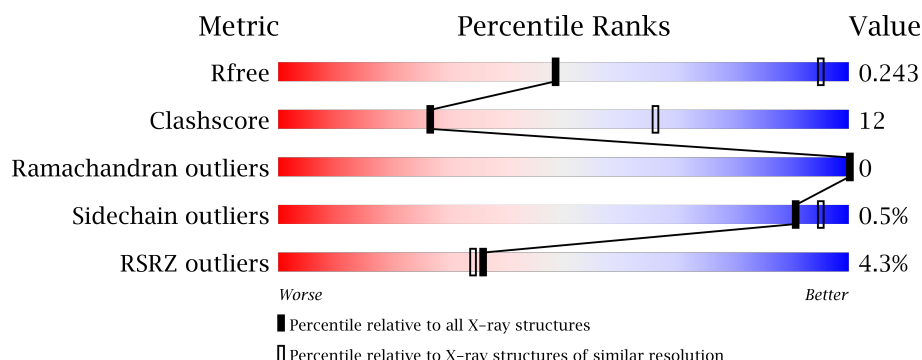
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.59 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.





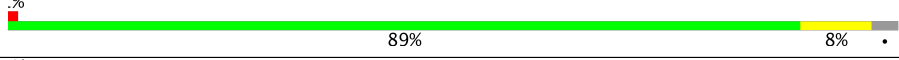
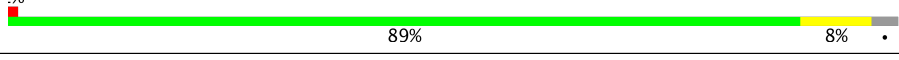

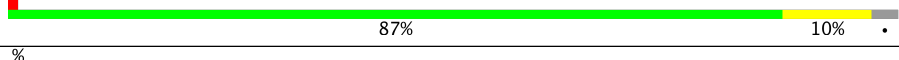
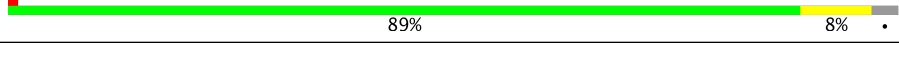
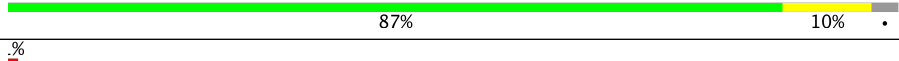

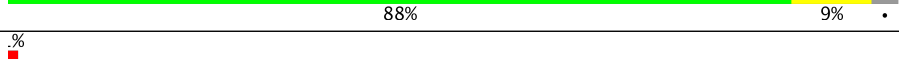
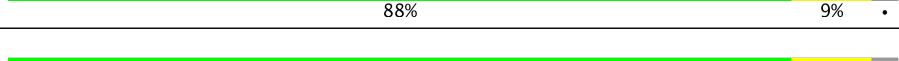
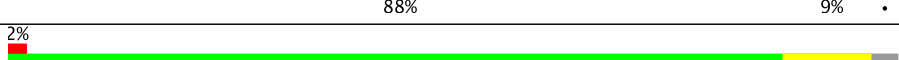
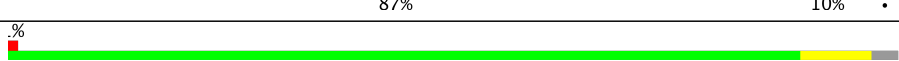
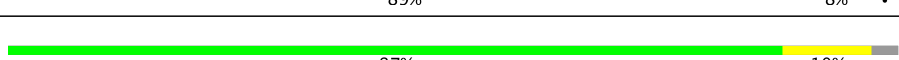
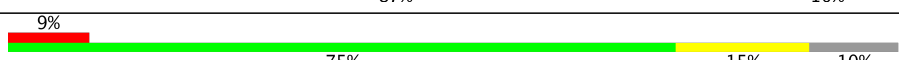
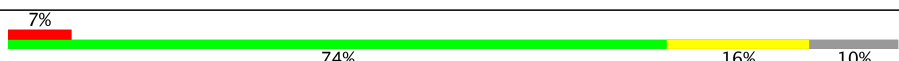
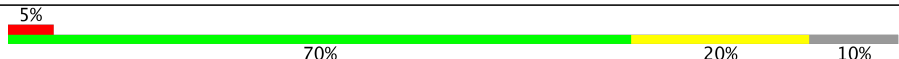
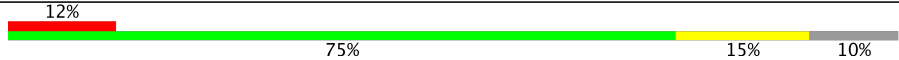


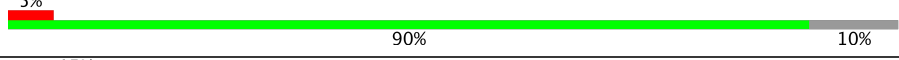
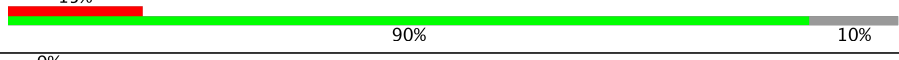
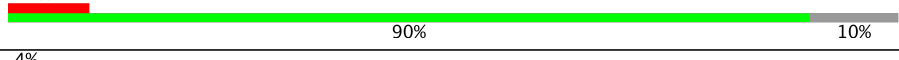
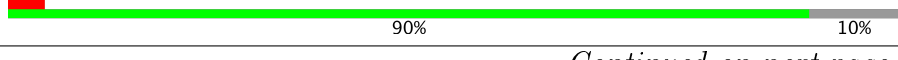

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1056 (7.40-3.70)
Clashscore	112137	1001 (7.38-3.78)
Ramachandran outliers	110173	1086 (7.40-3.70)
Sidechain outliers	110143	1059 (7.40-3.70)
RSRZ outliers	101464	1065 (7.40-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	157	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>.</div> </div> </div>
1	B	157	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>.</div> </div> </div>
1	C	157	<div> <div></div> <div> <div></div> <div>85%</div> <div>11%</div> <div>.</div> </div> </div>
1	D	157	<div> <div></div> <div> <div></div> <div>83%</div> <div>14%</div> <div>.</div> </div> </div>
1	E	157	<div> <div>3%</div> <div> <div></div> <div>84%</div> <div>13%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	157	
1	G	157	
1	H	157	
1	I	157	
1	J	157	
1	K	157	
1	L	157	
1	M	157	
1	N	157	
1	O	157	
1	P	157	
1	Q	157	
1	R	157	
1	S	157	
1	T	157	
2	U	165	
2	V	165	
2	W	165	
2	X	165	
2	Y	165	
2	Z	165	
2	a	165	
2	b	165	
2	c	165	
2	d	165	

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Mol	Chain	Length	Quality of chain
2	e	165	
2	f	165	
2	g	165	
2	h	165	
2	i	165	
2	j	165	
2	k	165	
2	l	165	
2	m	165	
2	n	165	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 44220 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 Designed self-assembling icosahedral cage I32-28 trimeric sub-unit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	B	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	C	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	D	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	E	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	F	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	G	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	H	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	I	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	J	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	K	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	L	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	M	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	N	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	O	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	P	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	R	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	S	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			
1	T	152	Total	C	N	O	S	0	0	0
			1134	719	203	209	3			

There are 260 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	expression tag	UNP Q2SZ09
A	28	GLY	-	expression tag	UNP Q2SZ09
A	86	GLU	ASP	engineered mutation	UNP Q2SZ09
A	87	ASP	ALA	engineered mutation	UNP Q2SZ09
A	90	LEU	ALA	engineered mutation	UNP Q2SZ09
A	93	ALA	ASP	engineered mutation	UNP Q2SZ09
A	94	LEU	GLY	engineered mutation	UNP Q2SZ09
A	97	VAL	ALA	engineered mutation	UNP Q2SZ09
A	136	LYS	VAL	engineered mutation	UNP Q2SZ09
A	146	ILE	ALA	engineered mutation	UNP Q2SZ09
A	149	ALA	ARG	engineered mutation	UNP Q2SZ09
A	150	ALA	ARG	engineered mutation	UNP Q2SZ09
A	154	LEU	ARG	engineered mutation	UNP Q2SZ09
B	27	MET	-	expression tag	UNP Q2SZ09
B	28	GLY	-	expression tag	UNP Q2SZ09
B	86	GLU	ASP	engineered mutation	UNP Q2SZ09
B	87	ASP	ALA	engineered mutation	UNP Q2SZ09
B	90	LEU	ALA	engineered mutation	UNP Q2SZ09
B	93	ALA	ASP	engineered mutation	UNP Q2SZ09
B	94	LEU	GLY	engineered mutation	UNP Q2SZ09
B	97	VAL	ALA	engineered mutation	UNP Q2SZ09
B	136	LYS	VAL	engineered mutation	UNP Q2SZ09
B	146	ILE	ALA	engineered mutation	UNP Q2SZ09
B	149	ALA	ARG	engineered mutation	UNP Q2SZ09
B	150	ALA	ARG	engineered mutation	UNP Q2SZ09
B	154	LEU	ARG	engineered mutation	UNP Q2SZ09
C	27	MET	-	expression tag	UNP Q2SZ09
C	28	GLY	-	expression tag	UNP Q2SZ09
C	86	GLU	ASP	engineered mutation	UNP Q2SZ09
C	87	ASP	ALA	engineered mutation	UNP Q2SZ09
C	90	LEU	ALA	engineered mutation	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
C	93	ALA	ASP	engineered mutation	UNP Q2SZ09
C	94	LEU	GLY	engineered mutation	UNP Q2SZ09
C	97	VAL	ALA	engineered mutation	UNP Q2SZ09
C	136	LYS	VAL	engineered mutation	UNP Q2SZ09
C	146	ILE	ALA	engineered mutation	UNP Q2SZ09
C	149	ALA	ARG	engineered mutation	UNP Q2SZ09
C	150	ALA	ARG	engineered mutation	UNP Q2SZ09
C	154	LEU	ARG	engineered mutation	UNP Q2SZ09
D	27	MET	-	expression tag	UNP Q2SZ09
D	28	GLY	-	expression tag	UNP Q2SZ09
D	86	GLU	ASP	engineered mutation	UNP Q2SZ09
D	87	ASP	ALA	engineered mutation	UNP Q2SZ09
D	90	LEU	ALA	engineered mutation	UNP Q2SZ09
D	93	ALA	ASP	engineered mutation	UNP Q2SZ09
D	94	LEU	GLY	engineered mutation	UNP Q2SZ09
D	97	VAL	ALA	engineered mutation	UNP Q2SZ09
D	136	LYS	VAL	engineered mutation	UNP Q2SZ09
D	146	ILE	ALA	engineered mutation	UNP Q2SZ09
D	149	ALA	ARG	engineered mutation	UNP Q2SZ09
D	150	ALA	ARG	engineered mutation	UNP Q2SZ09
D	154	LEU	ARG	engineered mutation	UNP Q2SZ09
E	27	MET	-	expression tag	UNP Q2SZ09
E	28	GLY	-	expression tag	UNP Q2SZ09
E	86	GLU	ASP	engineered mutation	UNP Q2SZ09
E	87	ASP	ALA	engineered mutation	UNP Q2SZ09
E	90	LEU	ALA	engineered mutation	UNP Q2SZ09
E	93	ALA	ASP	engineered mutation	UNP Q2SZ09
E	94	LEU	GLY	engineered mutation	UNP Q2SZ09
E	97	VAL	ALA	engineered mutation	UNP Q2SZ09
E	136	LYS	VAL	engineered mutation	UNP Q2SZ09
E	146	ILE	ALA	engineered mutation	UNP Q2SZ09
E	149	ALA	ARG	engineered mutation	UNP Q2SZ09
E	150	ALA	ARG	engineered mutation	UNP Q2SZ09
E	154	LEU	ARG	engineered mutation	UNP Q2SZ09
F	27	MET	-	expression tag	UNP Q2SZ09
F	28	GLY	-	expression tag	UNP Q2SZ09
F	86	GLU	ASP	engineered mutation	UNP Q2SZ09
F	87	ASP	ALA	engineered mutation	UNP Q2SZ09
F	90	LEU	ALA	engineered mutation	UNP Q2SZ09
F	93	ALA	ASP	engineered mutation	UNP Q2SZ09
F	94	LEU	GLY	engineered mutation	UNP Q2SZ09
F	97	VAL	ALA	engineered mutation	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
F	136	LYS	VAL	engineered mutation	UNP Q2SZ09
F	146	ILE	ALA	engineered mutation	UNP Q2SZ09
F	149	ALA	ARG	engineered mutation	UNP Q2SZ09
F	150	ALA	ARG	engineered mutation	UNP Q2SZ09
F	154	LEU	ARG	engineered mutation	UNP Q2SZ09
G	27	MET	-	expression tag	UNP Q2SZ09
G	28	GLY	-	expression tag	UNP Q2SZ09
G	86	GLU	ASP	engineered mutation	UNP Q2SZ09
G	87	ASP	ALA	engineered mutation	UNP Q2SZ09
G	90	LEU	ALA	engineered mutation	UNP Q2SZ09
G	93	ALA	ASP	engineered mutation	UNP Q2SZ09
G	94	LEU	GLY	engineered mutation	UNP Q2SZ09
G	97	VAL	ALA	engineered mutation	UNP Q2SZ09
G	136	LYS	VAL	engineered mutation	UNP Q2SZ09
G	146	ILE	ALA	engineered mutation	UNP Q2SZ09
G	149	ALA	ARG	engineered mutation	UNP Q2SZ09
G	150	ALA	ARG	engineered mutation	UNP Q2SZ09
G	154	LEU	ARG	engineered mutation	UNP Q2SZ09
H	27	MET	-	expression tag	UNP Q2SZ09
H	28	GLY	-	expression tag	UNP Q2SZ09
H	86	GLU	ASP	engineered mutation	UNP Q2SZ09
H	87	ASP	ALA	engineered mutation	UNP Q2SZ09
H	90	LEU	ALA	engineered mutation	UNP Q2SZ09
H	93	ALA	ASP	engineered mutation	UNP Q2SZ09
H	94	LEU	GLY	engineered mutation	UNP Q2SZ09
H	97	VAL	ALA	engineered mutation	UNP Q2SZ09
H	136	LYS	VAL	engineered mutation	UNP Q2SZ09
H	146	ILE	ALA	engineered mutation	UNP Q2SZ09
H	149	ALA	ARG	engineered mutation	UNP Q2SZ09
H	150	ALA	ARG	engineered mutation	UNP Q2SZ09
H	154	LEU	ARG	engineered mutation	UNP Q2SZ09
I	27	MET	-	expression tag	UNP Q2SZ09
I	28	GLY	-	expression tag	UNP Q2SZ09
I	86	GLU	ASP	engineered mutation	UNP Q2SZ09
I	87	ASP	ALA	engineered mutation	UNP Q2SZ09
I	90	LEU	ALA	engineered mutation	UNP Q2SZ09
I	93	ALA	ASP	engineered mutation	UNP Q2SZ09
I	94	LEU	GLY	engineered mutation	UNP Q2SZ09
I	97	VAL	ALA	engineered mutation	UNP Q2SZ09
I	136	LYS	VAL	engineered mutation	UNP Q2SZ09
I	146	ILE	ALA	engineered mutation	UNP Q2SZ09
I	149	ALA	ARG	engineered mutation	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
I	150	ALA	ARG	engineered mutation	UNP Q2SZ09
I	154	LEU	ARG	engineered mutation	UNP Q2SZ09
J	27	MET	-	expression tag	UNP Q2SZ09
J	28	GLY	-	expression tag	UNP Q2SZ09
J	86	GLU	ASP	engineered mutation	UNP Q2SZ09
J	87	ASP	ALA	engineered mutation	UNP Q2SZ09
J	90	LEU	ALA	engineered mutation	UNP Q2SZ09
J	93	ALA	ASP	engineered mutation	UNP Q2SZ09
J	94	LEU	GLY	engineered mutation	UNP Q2SZ09
J	97	VAL	ALA	engineered mutation	UNP Q2SZ09
J	136	LYS	VAL	engineered mutation	UNP Q2SZ09
J	146	ILE	ALA	engineered mutation	UNP Q2SZ09
J	149	ALA	ARG	engineered mutation	UNP Q2SZ09
J	150	ALA	ARG	engineered mutation	UNP Q2SZ09
J	154	LEU	ARG	engineered mutation	UNP Q2SZ09
K	27	MET	-	expression tag	UNP Q2SZ09
K	28	GLY	-	expression tag	UNP Q2SZ09
K	86	GLU	ASP	engineered mutation	UNP Q2SZ09
K	87	ASP	ALA	engineered mutation	UNP Q2SZ09
K	90	LEU	ALA	engineered mutation	UNP Q2SZ09
K	93	ALA	ASP	engineered mutation	UNP Q2SZ09
K	94	LEU	GLY	engineered mutation	UNP Q2SZ09
K	97	VAL	ALA	engineered mutation	UNP Q2SZ09
K	136	LYS	VAL	engineered mutation	UNP Q2SZ09
K	146	ILE	ALA	engineered mutation	UNP Q2SZ09
K	149	ALA	ARG	engineered mutation	UNP Q2SZ09
K	150	ALA	ARG	engineered mutation	UNP Q2SZ09
K	154	LEU	ARG	engineered mutation	UNP Q2SZ09
L	27	MET	-	expression tag	UNP Q2SZ09
L	28	GLY	-	expression tag	UNP Q2SZ09
L	86	GLU	ASP	engineered mutation	UNP Q2SZ09
L	87	ASP	ALA	engineered mutation	UNP Q2SZ09
L	90	LEU	ALA	engineered mutation	UNP Q2SZ09
L	93	ALA	ASP	engineered mutation	UNP Q2SZ09
L	94	LEU	GLY	engineered mutation	UNP Q2SZ09
L	97	VAL	ALA	engineered mutation	UNP Q2SZ09
L	136	LYS	VAL	engineered mutation	UNP Q2SZ09
L	146	ILE	ALA	engineered mutation	UNP Q2SZ09
L	149	ALA	ARG	engineered mutation	UNP Q2SZ09
L	150	ALA	ARG	engineered mutation	UNP Q2SZ09
L	154	LEU	ARG	engineered mutation	UNP Q2SZ09
M	27	MET	-	expression tag	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
M	28	GLY	-	expression tag	UNP Q2SZ09
M	86	GLU	ASP	engineered mutation	UNP Q2SZ09
M	87	ASP	ALA	engineered mutation	UNP Q2SZ09
M	90	LEU	ALA	engineered mutation	UNP Q2SZ09
M	93	ALA	ASP	engineered mutation	UNP Q2SZ09
M	94	LEU	GLY	engineered mutation	UNP Q2SZ09
M	97	VAL	ALA	engineered mutation	UNP Q2SZ09
M	136	LYS	VAL	engineered mutation	UNP Q2SZ09
M	146	ILE	ALA	engineered mutation	UNP Q2SZ09
M	149	ALA	ARG	engineered mutation	UNP Q2SZ09
M	150	ALA	ARG	engineered mutation	UNP Q2SZ09
M	154	LEU	ARG	engineered mutation	UNP Q2SZ09
N	27	MET	-	expression tag	UNP Q2SZ09
N	28	GLY	-	expression tag	UNP Q2SZ09
N	86	GLU	ASP	engineered mutation	UNP Q2SZ09
N	87	ASP	ALA	engineered mutation	UNP Q2SZ09
N	90	LEU	ALA	engineered mutation	UNP Q2SZ09
N	93	ALA	ASP	engineered mutation	UNP Q2SZ09
N	94	LEU	GLY	engineered mutation	UNP Q2SZ09
N	97	VAL	ALA	engineered mutation	UNP Q2SZ09
N	136	LYS	VAL	engineered mutation	UNP Q2SZ09
N	146	ILE	ALA	engineered mutation	UNP Q2SZ09
N	149	ALA	ARG	engineered mutation	UNP Q2SZ09
N	150	ALA	ARG	engineered mutation	UNP Q2SZ09
N	154	LEU	ARG	engineered mutation	UNP Q2SZ09
O	27	MET	-	expression tag	UNP Q2SZ09
O	28	GLY	-	expression tag	UNP Q2SZ09
O	86	GLU	ASP	engineered mutation	UNP Q2SZ09
O	87	ASP	ALA	engineered mutation	UNP Q2SZ09
O	90	LEU	ALA	engineered mutation	UNP Q2SZ09
O	93	ALA	ASP	engineered mutation	UNP Q2SZ09
O	94	LEU	GLY	engineered mutation	UNP Q2SZ09
O	97	VAL	ALA	engineered mutation	UNP Q2SZ09
O	136	LYS	VAL	engineered mutation	UNP Q2SZ09
O	146	ILE	ALA	engineered mutation	UNP Q2SZ09
O	149	ALA	ARG	engineered mutation	UNP Q2SZ09
O	150	ALA	ARG	engineered mutation	UNP Q2SZ09
O	154	LEU	ARG	engineered mutation	UNP Q2SZ09
P	27	MET	-	expression tag	UNP Q2SZ09
P	28	GLY	-	expression tag	UNP Q2SZ09
P	86	GLU	ASP	engineered mutation	UNP Q2SZ09
P	87	ASP	ALA	engineered mutation	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
P	90	LEU	ALA	engineered mutation	UNP Q2SZ09
P	93	ALA	ASP	engineered mutation	UNP Q2SZ09
P	94	LEU	GLY	engineered mutation	UNP Q2SZ09
P	97	VAL	ALA	engineered mutation	UNP Q2SZ09
P	136	LYS	VAL	engineered mutation	UNP Q2SZ09
P	146	ILE	ALA	engineered mutation	UNP Q2SZ09
P	149	ALA	ARG	engineered mutation	UNP Q2SZ09
P	150	ALA	ARG	engineered mutation	UNP Q2SZ09
P	154	LEU	ARG	engineered mutation	UNP Q2SZ09
Q	27	MET	-	expression tag	UNP Q2SZ09
Q	28	GLY	-	expression tag	UNP Q2SZ09
Q	86	GLU	ASP	engineered mutation	UNP Q2SZ09
Q	87	ASP	ALA	engineered mutation	UNP Q2SZ09
Q	90	LEU	ALA	engineered mutation	UNP Q2SZ09
Q	93	ALA	ASP	engineered mutation	UNP Q2SZ09
Q	94	LEU	GLY	engineered mutation	UNP Q2SZ09
Q	97	VAL	ALA	engineered mutation	UNP Q2SZ09
Q	136	LYS	VAL	engineered mutation	UNP Q2SZ09
Q	146	ILE	ALA	engineered mutation	UNP Q2SZ09
Q	149	ALA	ARG	engineered mutation	UNP Q2SZ09
Q	150	ALA	ARG	engineered mutation	UNP Q2SZ09
Q	154	LEU	ARG	engineered mutation	UNP Q2SZ09
R	27	MET	-	expression tag	UNP Q2SZ09
R	28	GLY	-	expression tag	UNP Q2SZ09
R	86	GLU	ASP	engineered mutation	UNP Q2SZ09
R	87	ASP	ALA	engineered mutation	UNP Q2SZ09
R	90	LEU	ALA	engineered mutation	UNP Q2SZ09
R	93	ALA	ASP	engineered mutation	UNP Q2SZ09
R	94	LEU	GLY	engineered mutation	UNP Q2SZ09
R	97	VAL	ALA	engineered mutation	UNP Q2SZ09
R	136	LYS	VAL	engineered mutation	UNP Q2SZ09
R	146	ILE	ALA	engineered mutation	UNP Q2SZ09
R	149	ALA	ARG	engineered mutation	UNP Q2SZ09
R	150	ALA	ARG	engineered mutation	UNP Q2SZ09
R	154	LEU	ARG	engineered mutation	UNP Q2SZ09
S	27	MET	-	expression tag	UNP Q2SZ09
S	28	GLY	-	expression tag	UNP Q2SZ09
S	86	GLU	ASP	engineered mutation	UNP Q2SZ09
S	87	ASP	ALA	engineered mutation	UNP Q2SZ09
S	90	LEU	ALA	engineered mutation	UNP Q2SZ09
S	93	ALA	ASP	engineered mutation	UNP Q2SZ09
S	94	LEU	GLY	engineered mutation	UNP Q2SZ09

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Chain	Residue	Modelled	Actual	Comment	Reference
S	97	VAL	ALA	engineered mutation	UNP Q2SZ09
S	136	LYS	VAL	engineered mutation	UNP Q2SZ09
S	146	ILE	ALA	engineered mutation	UNP Q2SZ09
S	149	ALA	ARG	engineered mutation	UNP Q2SZ09
S	150	ALA	ARG	engineered mutation	UNP Q2SZ09
S	154	LEU	ARG	engineered mutation	UNP Q2SZ09
T	27	MET	-	expression tag	UNP Q2SZ09
T	28	GLY	-	expression tag	UNP Q2SZ09
T	86	GLU	ASP	engineered mutation	UNP Q2SZ09
T	87	ASP	ALA	engineered mutation	UNP Q2SZ09
T	90	LEU	ALA	engineered mutation	UNP Q2SZ09
T	93	ALA	ASP	engineered mutation	UNP Q2SZ09
T	94	LEU	GLY	engineered mutation	UNP Q2SZ09
T	97	VAL	ALA	engineered mutation	UNP Q2SZ09
T	136	LYS	VAL	engineered mutation	UNP Q2SZ09
T	146	ILE	ALA	engineered mutation	UNP Q2SZ09
T	149	ALA	ARG	engineered mutation	UNP Q2SZ09
T	150	ALA	ARG	engineered mutation	UNP Q2SZ09
T	154	LEU	ARG	engineered mutation	UNP Q2SZ09

- Molecule 2 is a protein called Designed self-assembling icosahedral cage I32-28 dimeric sub-unit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	U	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	V	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	W	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	X	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	Y	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	Z	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	a	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	b	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	c	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	d	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	e	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	f	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	g	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	h	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	i	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	j	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	k	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	l	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	m	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			
2	n	148	Total	C	N	O	S	0	0	0
			1077	684	193	197	3			

There are 360 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	35	GLN	ARG	engineered mutation	UNP Q9RSW5
U	36	ARG	PHE	engineered mutation	UNP Q9RSW5
U	54	ARG	THR	engineered mutation	UNP Q9RSW5
U	122	GLU	TRP	engineered mutation	UNP Q9RSW5
U	129	VAL	LYS	engineered mutation	UNP Q9RSW5
U	137	VAL	ARG	engineered mutation	UNP Q9RSW5
U	140	LEU	GLU	engineered mutation	UNP Q9RSW5
U	141	LEU	ARG	engineered mutation	UNP Q9RSW5
U	144	MET	LYS	engineered mutation	UNP Q9RSW5
U	148	GLN	GLU	engineered mutation	UNP Q9RSW5
U	158	LEU	-	expression tag	UNP Q9RSW5
U	159	GLU	-	expression tag	UNP Q9RSW5
U	160	HIS	-	expression tag	UNP Q9RSW5
U	161	HIS	-	expression tag	UNP Q9RSW5
U	162	HIS	-	expression tag	UNP Q9RSW5
U	163	HIS	-	expression tag	UNP Q9RSW5
U	164	HIS	-	expression tag	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
U	165	HIS	-	expression tag	UNP Q9RSW5
V	35	GLN	ARG	engineered mutation	UNP Q9RSW5
V	36	ARG	PHE	engineered mutation	UNP Q9RSW5
V	54	ARG	THR	engineered mutation	UNP Q9RSW5
V	122	GLU	TRP	engineered mutation	UNP Q9RSW5
V	129	VAL	LYS	engineered mutation	UNP Q9RSW5
V	137	VAL	ARG	engineered mutation	UNP Q9RSW5
V	140	LEU	GLU	engineered mutation	UNP Q9RSW5
V	141	LEU	ARG	engineered mutation	UNP Q9RSW5
V	144	MET	LYS	engineered mutation	UNP Q9RSW5
V	148	GLN	GLU	engineered mutation	UNP Q9RSW5
V	158	LEU	-	expression tag	UNP Q9RSW5
V	159	GLU	-	expression tag	UNP Q9RSW5
V	160	HIS	-	expression tag	UNP Q9RSW5
V	161	HIS	-	expression tag	UNP Q9RSW5
V	162	HIS	-	expression tag	UNP Q9RSW5
V	163	HIS	-	expression tag	UNP Q9RSW5
V	164	HIS	-	expression tag	UNP Q9RSW5
V	165	HIS	-	expression tag	UNP Q9RSW5
W	35	GLN	ARG	engineered mutation	UNP Q9RSW5
W	36	ARG	PHE	engineered mutation	UNP Q9RSW5
W	54	ARG	THR	engineered mutation	UNP Q9RSW5
W	122	GLU	TRP	engineered mutation	UNP Q9RSW5
W	129	VAL	LYS	engineered mutation	UNP Q9RSW5
W	137	VAL	ARG	engineered mutation	UNP Q9RSW5
W	140	LEU	GLU	engineered mutation	UNP Q9RSW5
W	141	LEU	ARG	engineered mutation	UNP Q9RSW5
W	144	MET	LYS	engineered mutation	UNP Q9RSW5
W	148	GLN	GLU	engineered mutation	UNP Q9RSW5
W	158	LEU	-	expression tag	UNP Q9RSW5
W	159	GLU	-	expression tag	UNP Q9RSW5
W	160	HIS	-	expression tag	UNP Q9RSW5
W	161	HIS	-	expression tag	UNP Q9RSW5
W	162	HIS	-	expression tag	UNP Q9RSW5
W	163	HIS	-	expression tag	UNP Q9RSW5
W	164	HIS	-	expression tag	UNP Q9RSW5
W	165	HIS	-	expression tag	UNP Q9RSW5
X	35	GLN	ARG	engineered mutation	UNP Q9RSW5
X	36	ARG	PHE	engineered mutation	UNP Q9RSW5
X	54	ARG	THR	engineered mutation	UNP Q9RSW5
X	122	GLU	TRP	engineered mutation	UNP Q9RSW5
X	129	VAL	LYS	engineered mutation	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
X	137	VAL	ARG	engineered mutation	UNP Q9RSW5
X	140	LEU	GLU	engineered mutation	UNP Q9RSW5
X	141	LEU	ARG	engineered mutation	UNP Q9RSW5
X	144	MET	LYS	engineered mutation	UNP Q9RSW5
X	148	GLN	GLU	engineered mutation	UNP Q9RSW5
X	158	LEU	-	expression tag	UNP Q9RSW5
X	159	GLU	-	expression tag	UNP Q9RSW5
X	160	HIS	-	expression tag	UNP Q9RSW5
X	161	HIS	-	expression tag	UNP Q9RSW5
X	162	HIS	-	expression tag	UNP Q9RSW5
X	163	HIS	-	expression tag	UNP Q9RSW5
X	164	HIS	-	expression tag	UNP Q9RSW5
X	165	HIS	-	expression tag	UNP Q9RSW5
Y	35	GLN	ARG	engineered mutation	UNP Q9RSW5
Y	36	ARG	PHE	engineered mutation	UNP Q9RSW5
Y	54	ARG	THR	engineered mutation	UNP Q9RSW5
Y	122	GLU	TRP	engineered mutation	UNP Q9RSW5
Y	129	VAL	LYS	engineered mutation	UNP Q9RSW5
Y	137	VAL	ARG	engineered mutation	UNP Q9RSW5
Y	140	LEU	GLU	engineered mutation	UNP Q9RSW5
Y	141	LEU	ARG	engineered mutation	UNP Q9RSW5
Y	144	MET	LYS	engineered mutation	UNP Q9RSW5
Y	148	GLN	GLU	engineered mutation	UNP Q9RSW5
Y	158	LEU	-	expression tag	UNP Q9RSW5
Y	159	GLU	-	expression tag	UNP Q9RSW5
Y	160	HIS	-	expression tag	UNP Q9RSW5
Y	161	HIS	-	expression tag	UNP Q9RSW5
Y	162	HIS	-	expression tag	UNP Q9RSW5
Y	163	HIS	-	expression tag	UNP Q9RSW5
Y	164	HIS	-	expression tag	UNP Q9RSW5
Y	165	HIS	-	expression tag	UNP Q9RSW5
Z	35	GLN	ARG	engineered mutation	UNP Q9RSW5
Z	36	ARG	PHE	engineered mutation	UNP Q9RSW5
Z	54	ARG	THR	engineered mutation	UNP Q9RSW5
Z	122	GLU	TRP	engineered mutation	UNP Q9RSW5
Z	129	VAL	LYS	engineered mutation	UNP Q9RSW5
Z	137	VAL	ARG	engineered mutation	UNP Q9RSW5
Z	140	LEU	GLU	engineered mutation	UNP Q9RSW5
Z	141	LEU	ARG	engineered mutation	UNP Q9RSW5
Z	144	MET	LYS	engineered mutation	UNP Q9RSW5
Z	148	GLN	GLU	engineered mutation	UNP Q9RSW5
Z	158	LEU	-	expression tag	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	159	GLU	-	expression tag	UNP Q9RSW5
Z	160	HIS	-	expression tag	UNP Q9RSW5
Z	161	HIS	-	expression tag	UNP Q9RSW5
Z	162	HIS	-	expression tag	UNP Q9RSW5
Z	163	HIS	-	expression tag	UNP Q9RSW5
Z	164	HIS	-	expression tag	UNP Q9RSW5
Z	165	HIS	-	expression tag	UNP Q9RSW5
a	35	GLN	ARG	engineered mutation	UNP Q9RSW5
a	36	ARG	PHE	engineered mutation	UNP Q9RSW5
a	54	ARG	THR	engineered mutation	UNP Q9RSW5
a	122	GLU	TRP	engineered mutation	UNP Q9RSW5
a	129	VAL	LYS	engineered mutation	UNP Q9RSW5
a	137	VAL	ARG	engineered mutation	UNP Q9RSW5
a	140	LEU	GLU	engineered mutation	UNP Q9RSW5
a	141	LEU	ARG	engineered mutation	UNP Q9RSW5
a	144	MET	LYS	engineered mutation	UNP Q9RSW5
a	148	GLN	GLU	engineered mutation	UNP Q9RSW5
a	158	LEU	-	expression tag	UNP Q9RSW5
a	159	GLU	-	expression tag	UNP Q9RSW5
a	160	HIS	-	expression tag	UNP Q9RSW5
a	161	HIS	-	expression tag	UNP Q9RSW5
a	162	HIS	-	expression tag	UNP Q9RSW5
a	163	HIS	-	expression tag	UNP Q9RSW5
a	164	HIS	-	expression tag	UNP Q9RSW5
a	165	HIS	-	expression tag	UNP Q9RSW5
b	35	GLN	ARG	engineered mutation	UNP Q9RSW5
b	36	ARG	PHE	engineered mutation	UNP Q9RSW5
b	54	ARG	THR	engineered mutation	UNP Q9RSW5
b	122	GLU	TRP	engineered mutation	UNP Q9RSW5
b	129	VAL	LYS	engineered mutation	UNP Q9RSW5
b	137	VAL	ARG	engineered mutation	UNP Q9RSW5
b	140	LEU	GLU	engineered mutation	UNP Q9RSW5
b	141	LEU	ARG	engineered mutation	UNP Q9RSW5
b	144	MET	LYS	engineered mutation	UNP Q9RSW5
b	148	GLN	GLU	engineered mutation	UNP Q9RSW5
b	158	LEU	-	expression tag	UNP Q9RSW5
b	159	GLU	-	expression tag	UNP Q9RSW5
b	160	HIS	-	expression tag	UNP Q9RSW5
b	161	HIS	-	expression tag	UNP Q9RSW5
b	162	HIS	-	expression tag	UNP Q9RSW5
b	163	HIS	-	expression tag	UNP Q9RSW5
b	164	HIS	-	expression tag	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
b	165	HIS	-	expression tag	UNP Q9RSW5
c	35	GLN	ARG	engineered mutation	UNP Q9RSW5
c	36	ARG	PHE	engineered mutation	UNP Q9RSW5
c	54	ARG	THR	engineered mutation	UNP Q9RSW5
c	122	GLU	TRP	engineered mutation	UNP Q9RSW5
c	129	VAL	LYS	engineered mutation	UNP Q9RSW5
c	137	VAL	ARG	engineered mutation	UNP Q9RSW5
c	140	LEU	GLU	engineered mutation	UNP Q9RSW5
c	141	LEU	ARG	engineered mutation	UNP Q9RSW5
c	144	MET	LYS	engineered mutation	UNP Q9RSW5
c	148	GLN	GLU	engineered mutation	UNP Q9RSW5
c	158	LEU	-	expression tag	UNP Q9RSW5
c	159	GLU	-	expression tag	UNP Q9RSW5
c	160	HIS	-	expression tag	UNP Q9RSW5
c	161	HIS	-	expression tag	UNP Q9RSW5
c	162	HIS	-	expression tag	UNP Q9RSW5
c	163	HIS	-	expression tag	UNP Q9RSW5
c	164	HIS	-	expression tag	UNP Q9RSW5
c	165	HIS	-	expression tag	UNP Q9RSW5
d	35	GLN	ARG	engineered mutation	UNP Q9RSW5
d	36	ARG	PHE	engineered mutation	UNP Q9RSW5
d	54	ARG	THR	engineered mutation	UNP Q9RSW5
d	122	GLU	TRP	engineered mutation	UNP Q9RSW5
d	129	VAL	LYS	engineered mutation	UNP Q9RSW5
d	137	VAL	ARG	engineered mutation	UNP Q9RSW5
d	140	LEU	GLU	engineered mutation	UNP Q9RSW5
d	141	LEU	ARG	engineered mutation	UNP Q9RSW5
d	144	MET	LYS	engineered mutation	UNP Q9RSW5
d	148	GLN	GLU	engineered mutation	UNP Q9RSW5
d	158	LEU	-	expression tag	UNP Q9RSW5
d	159	GLU	-	expression tag	UNP Q9RSW5
d	160	HIS	-	expression tag	UNP Q9RSW5
d	161	HIS	-	expression tag	UNP Q9RSW5
d	162	HIS	-	expression tag	UNP Q9RSW5
d	163	HIS	-	expression tag	UNP Q9RSW5
d	164	HIS	-	expression tag	UNP Q9RSW5
d	165	HIS	-	expression tag	UNP Q9RSW5
e	35	GLN	ARG	engineered mutation	UNP Q9RSW5
e	36	ARG	PHE	engineered mutation	UNP Q9RSW5
e	54	ARG	THR	engineered mutation	UNP Q9RSW5
e	122	GLU	TRP	engineered mutation	UNP Q9RSW5
e	129	VAL	LYS	engineered mutation	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
e	137	VAL	ARG	engineered mutation	UNP Q9RSW5
e	140	LEU	GLU	engineered mutation	UNP Q9RSW5
e	141	LEU	ARG	engineered mutation	UNP Q9RSW5
e	144	MET	LYS	engineered mutation	UNP Q9RSW5
e	148	GLN	GLU	engineered mutation	UNP Q9RSW5
e	158	LEU	-	expression tag	UNP Q9RSW5
e	159	GLU	-	expression tag	UNP Q9RSW5
e	160	HIS	-	expression tag	UNP Q9RSW5
e	161	HIS	-	expression tag	UNP Q9RSW5
e	162	HIS	-	expression tag	UNP Q9RSW5
e	163	HIS	-	expression tag	UNP Q9RSW5
e	164	HIS	-	expression tag	UNP Q9RSW5
e	165	HIS	-	expression tag	UNP Q9RSW5
f	35	GLN	ARG	engineered mutation	UNP Q9RSW5
f	36	ARG	PHE	engineered mutation	UNP Q9RSW5
f	54	ARG	THR	engineered mutation	UNP Q9RSW5
f	122	GLU	TRP	engineered mutation	UNP Q9RSW5
f	129	VAL	LYS	engineered mutation	UNP Q9RSW5
f	137	VAL	ARG	engineered mutation	UNP Q9RSW5
f	140	LEU	GLU	engineered mutation	UNP Q9RSW5
f	141	LEU	ARG	engineered mutation	UNP Q9RSW5
f	144	MET	LYS	engineered mutation	UNP Q9RSW5
f	148	GLN	GLU	engineered mutation	UNP Q9RSW5
f	158	LEU	-	expression tag	UNP Q9RSW5
f	159	GLU	-	expression tag	UNP Q9RSW5
f	160	HIS	-	expression tag	UNP Q9RSW5
f	161	HIS	-	expression tag	UNP Q9RSW5
f	162	HIS	-	expression tag	UNP Q9RSW5
f	163	HIS	-	expression tag	UNP Q9RSW5
f	164	HIS	-	expression tag	UNP Q9RSW5
f	165	HIS	-	expression tag	UNP Q9RSW5
g	35	GLN	ARG	engineered mutation	UNP Q9RSW5
g	36	ARG	PHE	engineered mutation	UNP Q9RSW5
g	54	ARG	THR	engineered mutation	UNP Q9RSW5
g	122	GLU	TRP	engineered mutation	UNP Q9RSW5
g	129	VAL	LYS	engineered mutation	UNP Q9RSW5
g	137	VAL	ARG	engineered mutation	UNP Q9RSW5
g	140	LEU	GLU	engineered mutation	UNP Q9RSW5
g	141	LEU	ARG	engineered mutation	UNP Q9RSW5
g	144	MET	LYS	engineered mutation	UNP Q9RSW5
g	148	GLN	GLU	engineered mutation	UNP Q9RSW5
g	158	LEU	-	expression tag	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
g	159	GLU	-	expression tag	UNP Q9RSW5
g	160	HIS	-	expression tag	UNP Q9RSW5
g	161	HIS	-	expression tag	UNP Q9RSW5
g	162	HIS	-	expression tag	UNP Q9RSW5
g	163	HIS	-	expression tag	UNP Q9RSW5
g	164	HIS	-	expression tag	UNP Q9RSW5
g	165	HIS	-	expression tag	UNP Q9RSW5
h	35	GLN	ARG	engineered mutation	UNP Q9RSW5
h	36	ARG	PHE	engineered mutation	UNP Q9RSW5
h	54	ARG	THR	engineered mutation	UNP Q9RSW5
h	122	GLU	TRP	engineered mutation	UNP Q9RSW5
h	129	VAL	LYS	engineered mutation	UNP Q9RSW5
h	137	VAL	ARG	engineered mutation	UNP Q9RSW5
h	140	LEU	GLU	engineered mutation	UNP Q9RSW5
h	141	LEU	ARG	engineered mutation	UNP Q9RSW5
h	144	MET	LYS	engineered mutation	UNP Q9RSW5
h	148	GLN	GLU	engineered mutation	UNP Q9RSW5
h	158	LEU	-	expression tag	UNP Q9RSW5
h	159	GLU	-	expression tag	UNP Q9RSW5
h	160	HIS	-	expression tag	UNP Q9RSW5
h	161	HIS	-	expression tag	UNP Q9RSW5
h	162	HIS	-	expression tag	UNP Q9RSW5
h	163	HIS	-	expression tag	UNP Q9RSW5
h	164	HIS	-	expression tag	UNP Q9RSW5
h	165	HIS	-	expression tag	UNP Q9RSW5
i	35	GLN	ARG	engineered mutation	UNP Q9RSW5
i	36	ARG	PHE	engineered mutation	UNP Q9RSW5
i	54	ARG	THR	engineered mutation	UNP Q9RSW5
i	122	GLU	TRP	engineered mutation	UNP Q9RSW5
i	129	VAL	LYS	engineered mutation	UNP Q9RSW5
i	137	VAL	ARG	engineered mutation	UNP Q9RSW5
i	140	LEU	GLU	engineered mutation	UNP Q9RSW5
i	141	LEU	ARG	engineered mutation	UNP Q9RSW5
i	144	MET	LYS	engineered mutation	UNP Q9RSW5
i	148	GLN	GLU	engineered mutation	UNP Q9RSW5
i	158	LEU	-	expression tag	UNP Q9RSW5
i	159	GLU	-	expression tag	UNP Q9RSW5
i	160	HIS	-	expression tag	UNP Q9RSW5
i	161	HIS	-	expression tag	UNP Q9RSW5
i	162	HIS	-	expression tag	UNP Q9RSW5
i	163	HIS	-	expression tag	UNP Q9RSW5
i	164	HIS	-	expression tag	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
i	165	HIS	-	expression tag	UNP Q9RSW5
j	35	GLN	ARG	engineered mutation	UNP Q9RSW5
j	36	ARG	PHE	engineered mutation	UNP Q9RSW5
j	54	ARG	THR	engineered mutation	UNP Q9RSW5
j	122	GLU	TRP	engineered mutation	UNP Q9RSW5
j	129	VAL	LYS	engineered mutation	UNP Q9RSW5
j	137	VAL	ARG	engineered mutation	UNP Q9RSW5
j	140	LEU	GLU	engineered mutation	UNP Q9RSW5
j	141	LEU	ARG	engineered mutation	UNP Q9RSW5
j	144	MET	LYS	engineered mutation	UNP Q9RSW5
j	148	GLN	GLU	engineered mutation	UNP Q9RSW5
j	158	LEU	-	expression tag	UNP Q9RSW5
j	159	GLU	-	expression tag	UNP Q9RSW5
j	160	HIS	-	expression tag	UNP Q9RSW5
j	161	HIS	-	expression tag	UNP Q9RSW5
j	162	HIS	-	expression tag	UNP Q9RSW5
j	163	HIS	-	expression tag	UNP Q9RSW5
j	164	HIS	-	expression tag	UNP Q9RSW5
j	165	HIS	-	expression tag	UNP Q9RSW5
k	35	GLN	ARG	engineered mutation	UNP Q9RSW5
k	36	ARG	PHE	engineered mutation	UNP Q9RSW5
k	54	ARG	THR	engineered mutation	UNP Q9RSW5
k	122	GLU	TRP	engineered mutation	UNP Q9RSW5
k	129	VAL	LYS	engineered mutation	UNP Q9RSW5
k	137	VAL	ARG	engineered mutation	UNP Q9RSW5
k	140	LEU	GLU	engineered mutation	UNP Q9RSW5
k	141	LEU	ARG	engineered mutation	UNP Q9RSW5
k	144	MET	LYS	engineered mutation	UNP Q9RSW5
k	148	GLN	GLU	engineered mutation	UNP Q9RSW5
k	158	LEU	-	expression tag	UNP Q9RSW5
k	159	GLU	-	expression tag	UNP Q9RSW5
k	160	HIS	-	expression tag	UNP Q9RSW5
k	161	HIS	-	expression tag	UNP Q9RSW5
k	162	HIS	-	expression tag	UNP Q9RSW5
k	163	HIS	-	expression tag	UNP Q9RSW5
k	164	HIS	-	expression tag	UNP Q9RSW5
k	165	HIS	-	expression tag	UNP Q9RSW5
l	35	GLN	ARG	engineered mutation	UNP Q9RSW5
l	36	ARG	PHE	engineered mutation	UNP Q9RSW5
l	54	ARG	THR	engineered mutation	UNP Q9RSW5
l	122	GLU	TRP	engineered mutation	UNP Q9RSW5
l	129	VAL	LYS	engineered mutation	UNP Q9RSW5

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Chain	Residue	Modelled	Actual	Comment	Reference
l	137	VAL	ARG	engineered mutation	UNP Q9RSW5
l	140	LEU	GLU	engineered mutation	UNP Q9RSW5
l	141	LEU	ARG	engineered mutation	UNP Q9RSW5
l	144	MET	LYS	engineered mutation	UNP Q9RSW5
l	148	GLN	GLU	engineered mutation	UNP Q9RSW5
l	158	LEU	-	expression tag	UNP Q9RSW5
l	159	GLU	-	expression tag	UNP Q9RSW5
l	160	HIS	-	expression tag	UNP Q9RSW5
l	161	HIS	-	expression tag	UNP Q9RSW5
l	162	HIS	-	expression tag	UNP Q9RSW5
l	163	HIS	-	expression tag	UNP Q9RSW5
l	164	HIS	-	expression tag	UNP Q9RSW5
l	165	HIS	-	expression tag	UNP Q9RSW5
m	35	GLN	ARG	engineered mutation	UNP Q9RSW5
m	36	ARG	PHE	engineered mutation	UNP Q9RSW5
m	54	ARG	THR	engineered mutation	UNP Q9RSW5
m	122	GLU	TRP	engineered mutation	UNP Q9RSW5
m	129	VAL	LYS	engineered mutation	UNP Q9RSW5
m	137	VAL	ARG	engineered mutation	UNP Q9RSW5
m	140	LEU	GLU	engineered mutation	UNP Q9RSW5
m	141	LEU	ARG	engineered mutation	UNP Q9RSW5
m	144	MET	LYS	engineered mutation	UNP Q9RSW5
m	148	GLN	GLU	engineered mutation	UNP Q9RSW5
m	158	LEU	-	expression tag	UNP Q9RSW5
m	159	GLU	-	expression tag	UNP Q9RSW5
m	160	HIS	-	expression tag	UNP Q9RSW5
m	161	HIS	-	expression tag	UNP Q9RSW5
m	162	HIS	-	expression tag	UNP Q9RSW5
m	163	HIS	-	expression tag	UNP Q9RSW5
m	164	HIS	-	expression tag	UNP Q9RSW5
m	165	HIS	-	expression tag	UNP Q9RSW5
n	35	GLN	ARG	engineered mutation	UNP Q9RSW5
n	36	ARG	PHE	engineered mutation	UNP Q9RSW5
n	54	ARG	THR	engineered mutation	UNP Q9RSW5
n	122	GLU	TRP	engineered mutation	UNP Q9RSW5
n	129	VAL	LYS	engineered mutation	UNP Q9RSW5
n	137	VAL	ARG	engineered mutation	UNP Q9RSW5
n	140	LEU	GLU	engineered mutation	UNP Q9RSW5
n	141	LEU	ARG	engineered mutation	UNP Q9RSW5
n	144	MET	LYS	engineered mutation	UNP Q9RSW5
n	148	GLN	GLU	engineered mutation	UNP Q9RSW5
n	158	LEU	-	expression tag	UNP Q9RSW5

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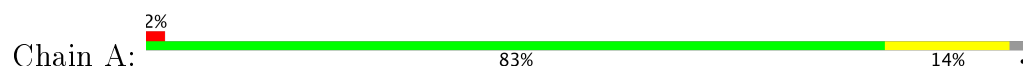
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Chain	Residue	Modelled	Actual	Comment	Reference
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n	160	HIS	-	expression tag	UNP Q9RSW5
n	161	HIS	-	expression tag	UNP Q9RSW5
n	162	HIS	-	expression tag	UNP Q9RSW5
n	163	HIS	-	expression tag	UNP Q9RSW5
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n	165	HIS	-	expression tag	UNP Q9RSW5

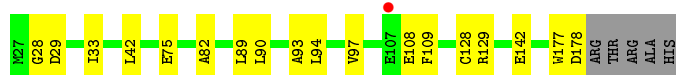
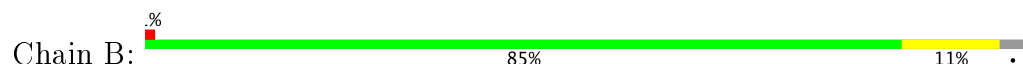
3 Residue-property plots [i](#)

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.

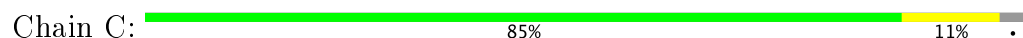
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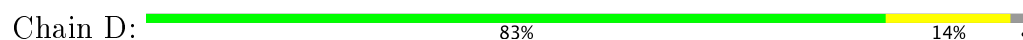
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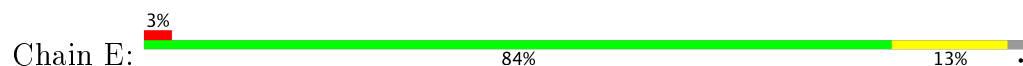
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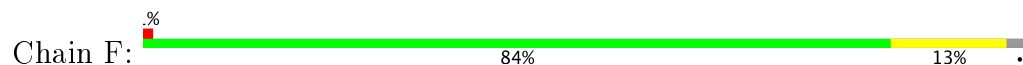
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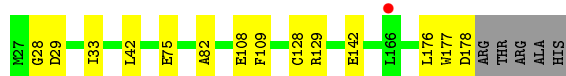
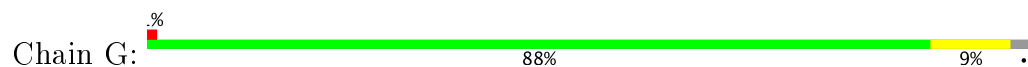


- Molecule 1: Designed self-assembling icosahedral cage I32-28 trimeric subunit

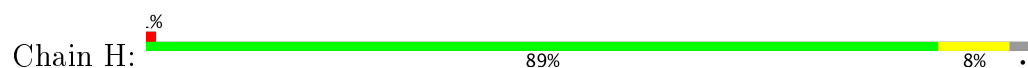




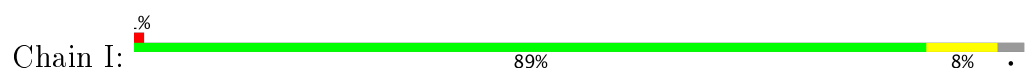
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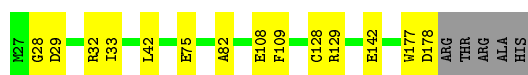
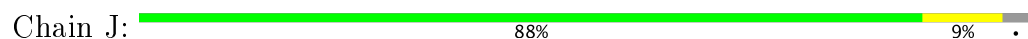
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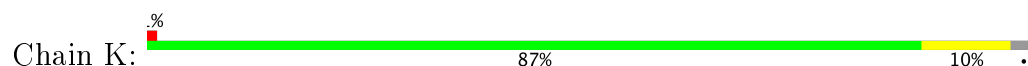
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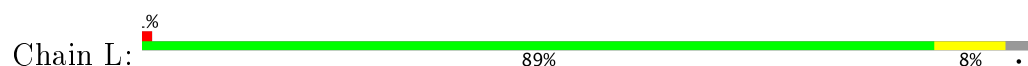
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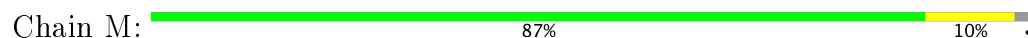
- Molecule 1: Designed self-assembling icosahedral cage I32-28 trimeric subunit



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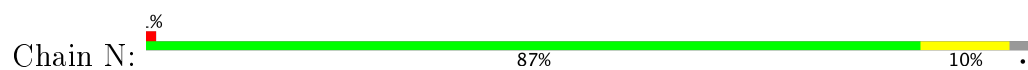


- Molecule 1: Designed self-assembling icosahedral cage I32-28 trimeric subunit

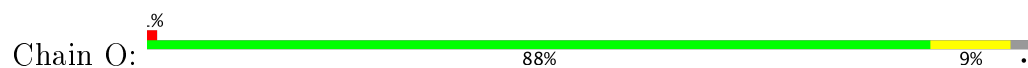




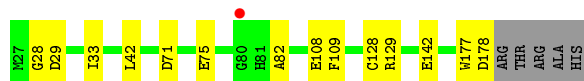
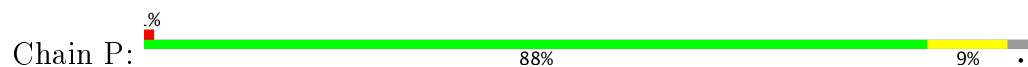
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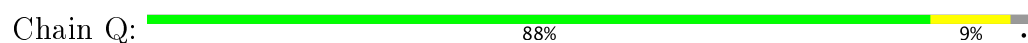
- Molecule 1: Designed self-assembling icosahedral cage I32-28 trimeric subunit



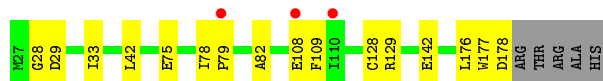
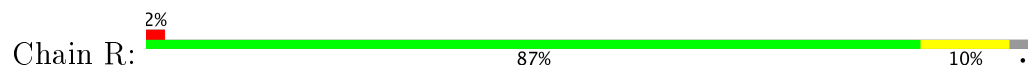
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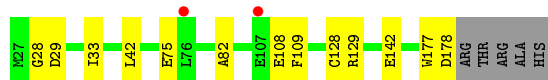
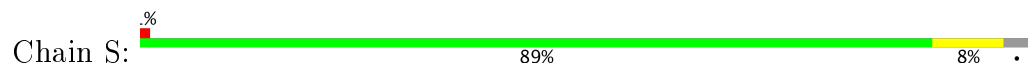
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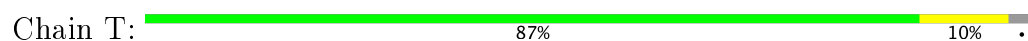
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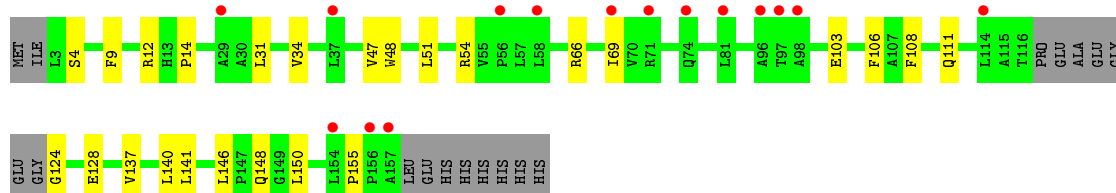
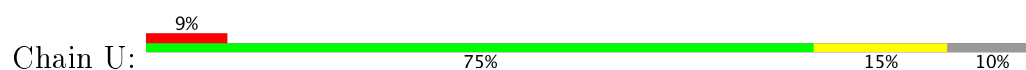


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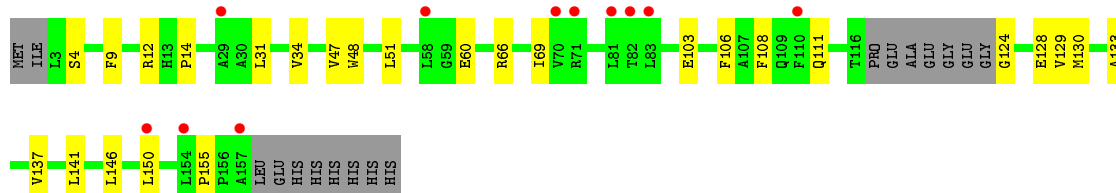




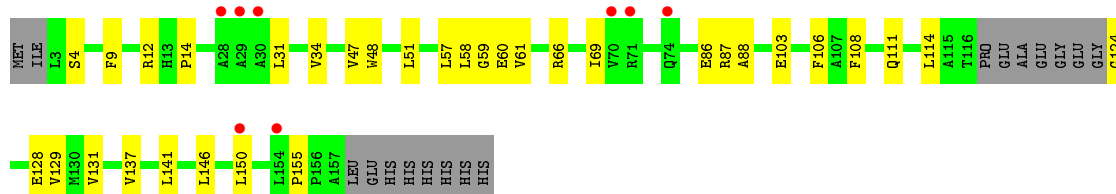
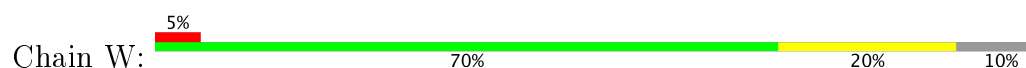
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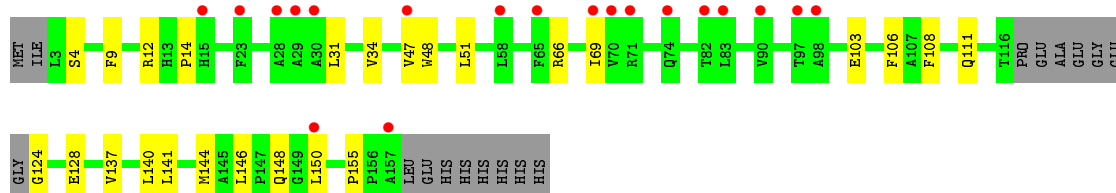
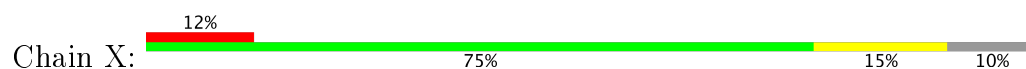
- Molecule 2: Designed self-assembling icosahedral cage I32-28 dimeric subunit



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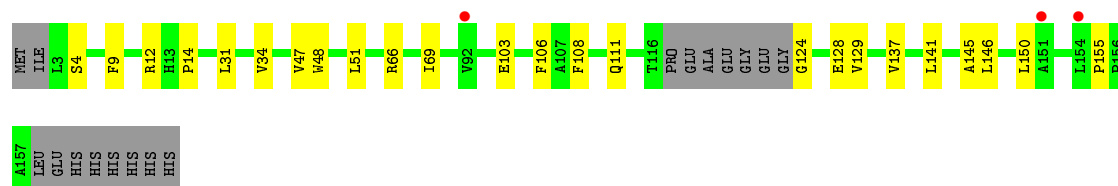
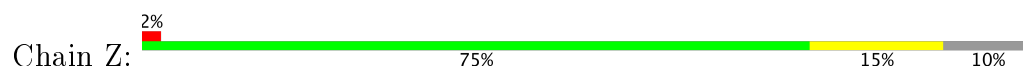
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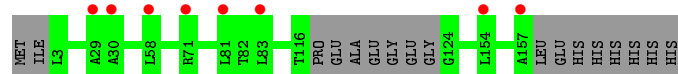
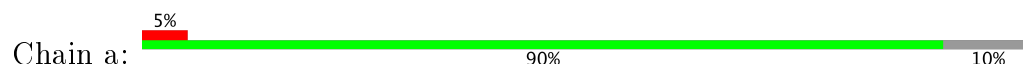
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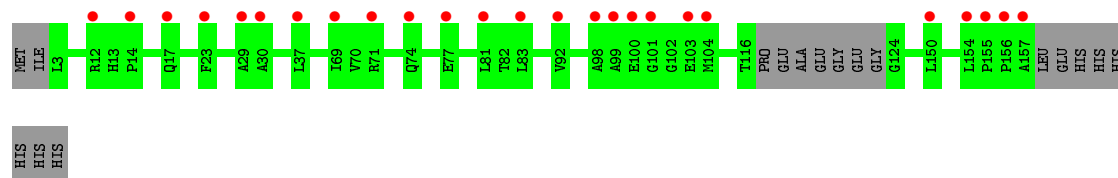
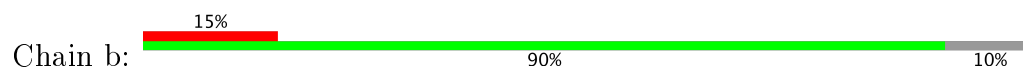
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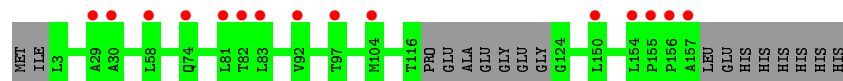
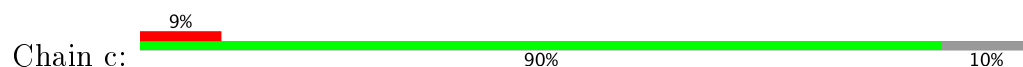
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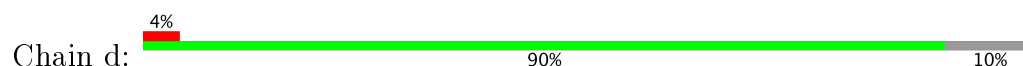
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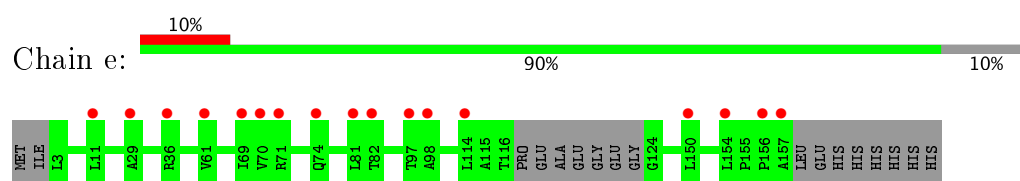
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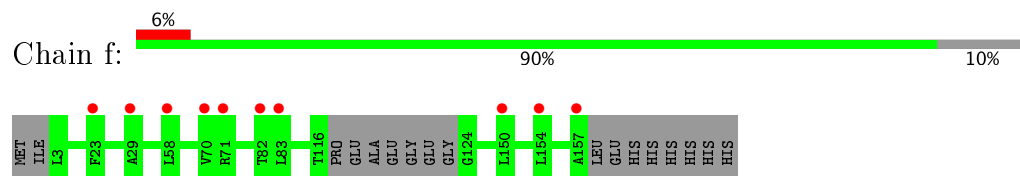
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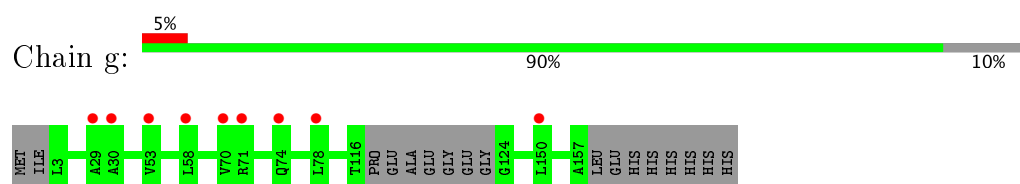
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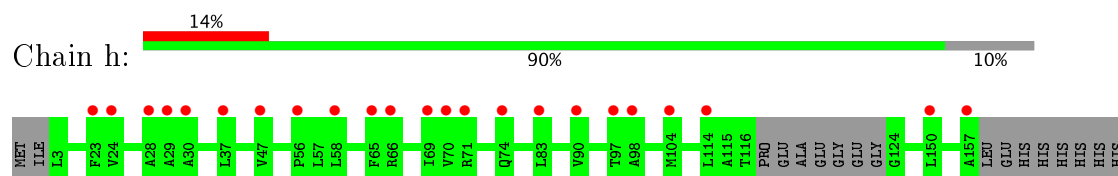
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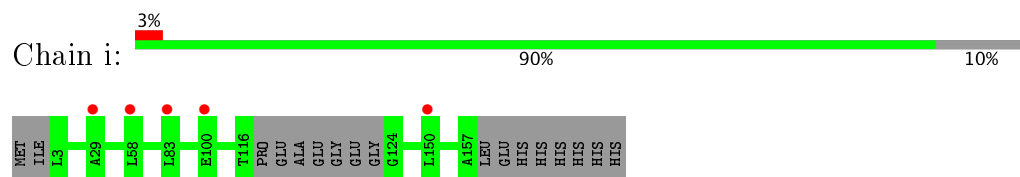
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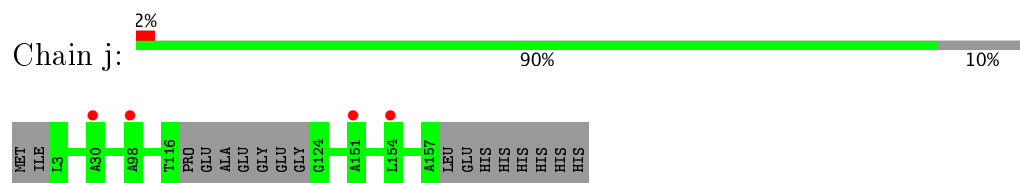
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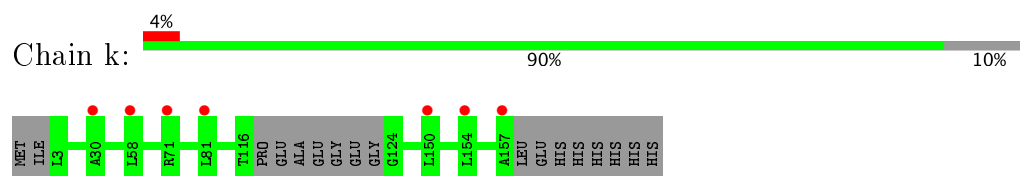
- Molecule 2: Designed self-assembling icosahedral cage I32-28 dimeric subunit



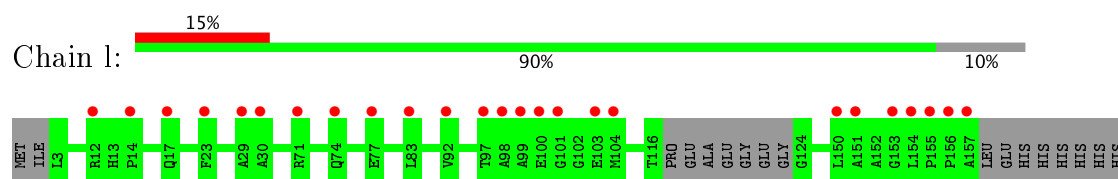
- Molecule 2: Designed self-assembling icosahedral cage I32-28 dimeric subunit



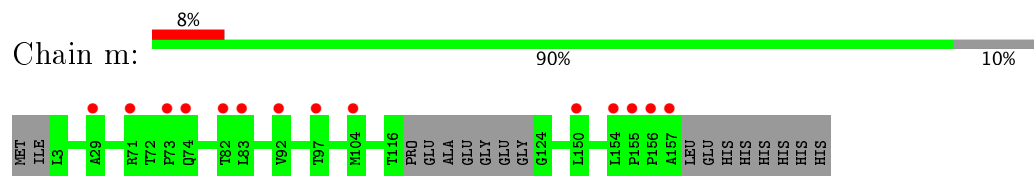
- Molecule 2: Designed self-assembling icosahedral cage I32-28 dimeric subunit



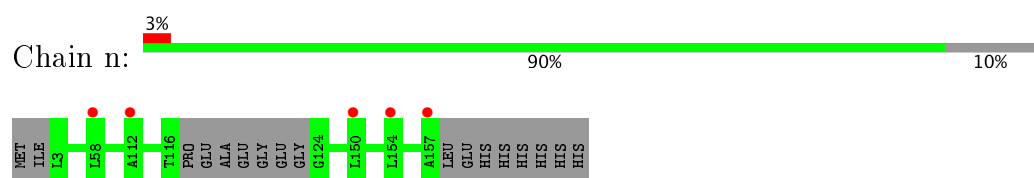
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- Molecule 2: Designed self-assembling icosahedral cage I32-28 dimeric subunit



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	284.17Å 284.17Å 640.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	213.20 – 5.59 213.49 – 5.59	Depositor EDS
% Data completeness (in resolution range)	90.0 (213.20-5.59) 90.3 (213.49-5.59)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 5.42Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.226 , 0.240 0.230 , 0.243	Depositor DCC
R_{free} test set	5385 reflections (10.01%)	DCC
Wilson B-factor (Å ²)	317.4	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 246.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.440 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	44220	wwPDB-VP
Average B, all atoms (Å ²)	327.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.34	0/1155	0.51	0/1577
1	B	0.35	0/1155	0.51	0/1577
1	C	0.34	0/1155	0.50	0/1577
1	D	0.34	0/1155	0.51	0/1577
1	E	0.34	0/1155	0.50	0/1577
1	F	0.34	0/1155	0.50	0/1577
1	G	0.34	0/1155	0.51	0/1577
1	H	0.34	0/1155	0.50	0/1577
1	I	0.34	0/1155	0.50	0/1577
1	J	0.34	0/1155	0.51	0/1577
1	K	0.35	0/1155	0.51	0/1577
1	L	0.35	0/1155	0.50	0/1577
1	M	0.35	0/1155	0.51	0/1577
1	N	0.34	0/1155	0.51	0/1577
1	O	0.35	0/1155	0.50	0/1577
1	P	0.34	0/1155	0.50	0/1577
1	Q	0.35	0/1155	0.51	0/1577
1	R	0.34	0/1155	0.51	0/1577
1	S	0.34	0/1155	0.51	0/1577
1	T	0.34	0/1155	0.51	0/1577
2	U	0.62	0/1097	0.54	0/1494
2	V	0.62	0/1097	0.55	0/1494
2	W	0.62	0/1097	0.55	0/1494
2	X	0.62	0/1097	0.55	0/1494
2	Y	0.62	0/1097	0.55	0/1494
2	Z	0.62	0/1097	0.55	0/1494
2	a	0.63	0/1097	0.55	0/1494
2	b	0.62	0/1097	0.55	0/1494
2	c	0.62	0/1097	0.54	0/1494
2	d	0.62	0/1097	0.55	0/1494
2	e	0.62	0/1097	0.55	0/1494
2	f	0.62	0/1097	0.55	0/1494
2	g	0.62	0/1097	0.55	0/1494
2	h	0.62	0/1097	0.55	0/1494

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	0.62	0/1097	0.55	0/1494
2	j	0.62	0/1097	0.55	0/1494
2	k	0.62	0/1097	0.55	0/1494
2	l	0.62	0/1097	0.55	0/1494
2	m	0.62	0/1097	0.55	0/1494
2	n	0.62	0/1097	0.55	0/1494
All	All	0.50	0/45040	0.53	0/61420

There are no bond length outliers.

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	1134	0	1138	44	0
1	B	1134	0	1138	25	0
1	C	1134	0	1138	21	0
1	D	1134	0	1138	45	0
1	E	1134	0	1138	28	0
1	F	1134	0	1138	26	0
1	G	1134	0	1138	14	0
1	H	1134	0	1138	14	0
1	I	1134	0	1138	14	0
1	J	1134	0	1138	15	0
1	K	1134	0	1138	16	0
1	L	1134	0	1138	17	0
1	M	1134	0	1138	16	0
1	N	1134	0	1138	16	0
1	O	1134	0	1138	16	0
1	P	1134	0	1138	15	0
1	Q	1134	0	1138	14	0
1	R	1134	0	1138	15	0
1	S	1134	0	1138	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	1134	0	1138	16	0
2	U	1077	0	1078	43	0
2	V	1077	0	1078	24	0
2	W	1077	0	1078	55	0
2	X	1077	0	1078	41	0
2	Y	1077	0	1078	63	0
2	Z	1077	0	1078	23	0
2	a	1077	0	1078	0	0
2	b	1077	0	1078	0	0
2	c	1077	0	1078	0	0
2	d	1077	0	1078	0	0
2	e	1077	0	1078	0	0
2	f	1077	0	1078	0	0
2	g	1077	0	1078	0	0
2	h	1077	0	1078	0	0
2	i	1077	0	1078	0	0
2	j	1077	0	1078	0	0
2	k	1077	0	1078	0	0
2	l	1077	0	1078	0	0
2	m	1077	0	1078	0	0
2	n	1077	0	1078	0	0
All	All	44220	0	44320	512	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 12.

All (512) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:LEU:CD1	2:X:141:LEU:HD21	1.53	1.39
1:A:89:LEU:CD1	2:U:141:LEU:HD21	1.59	1.31
1:A:89:LEU:HD13	2:U:141:LEU:HD21	1.19	1.14
2:W:57:LEU:HD13	2:Y:114:LEU:HD13	1.30	1.13
1:D:154:LEU:CD2	2:X:140:LEU:CD2	2.33	1.06
1:D:89:LEU:HD13	2:X:141:LEU:HD21	1.09	1.06
1:D:154:LEU:CD2	2:X:140:LEU:HD22	1.86	1.05
2:W:114:LEU:HD13	2:Y:57:LEU:HB3	1.37	1.01
1:D:154:LEU:HD21	2:X:140:LEU:HD22	1.42	1.01
1:D:154:LEU:HD21	2:X:140:LEU:CD2	1.91	1.01
1:D:93:ALA:HB2	2:X:137:VAL:CG2	1.91	0.99
1:E:97:VAL:HG12	2:Y:129:VAL:HG13	1.45	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:LEU:HD13	2:X:141:LEU:CD2	1.93	0.98
1:C:97:VAL:HG12	2:W:129:VAL:HG13	1.46	0.97
1:D:146:ILE:HG22	2:X:148:GLN:OE1	1.62	0.96
2:W:57:LEU:HD13	2:Y:114:LEU:CD1	1.97	0.94
1:D:93:ALA:CB	2:X:137:VAL:HG23	1.98	0.93
1:A:93:ALA:HB2	2:U:137:VAL:CG2	2.00	0.92
1:D:154:LEU:HG	2:X:140:LEU:CD2	2.03	0.89
1:D:93:ALA:CB	2:X:137:VAL:CG2	2.51	0.88
1:A:154:LEU:CD2	2:U:140:LEU:CD2	2.52	0.88
1:L:29:ASP:HB3	1:L:33:ILE:HD12	1.55	0.86
1:N:29:ASP:HB3	1:N:33:ILE:HD12	1.58	0.85
1:C:97:VAL:CG1	2:W:129:VAL:HG13	2.06	0.85
1:A:89:LEU:HD13	2:U:141:LEU:CD2	2.05	0.85
1:A:29:ASP:HB3	1:A:33:ILE:HD12	1.59	0.85
1:C:29:ASP:HB3	1:C:33:ILE:HD12	1.59	0.85
1:I:29:ASP:HB3	1:I:33:ILE:HD12	1.59	0.85
1:D:89:LEU:CD1	2:X:141:LEU:CD2	2.48	0.84
1:A:154:LEU:CD2	2:U:140:LEU:HD22	2.07	0.84
1:B:97:VAL:HG12	2:V:129:VAL:HG13	1.58	0.84
1:T:29:ASP:HB3	1:T:33:ILE:HD12	1.59	0.84
1:G:29:ASP:HB3	1:G:33:ILE:HD12	1.59	0.84
1:K:29:ASP:HB3	1:K:33:ILE:HD12	1.59	0.84
1:R:29:ASP:HB3	1:R:33:ILE:HD12	1.59	0.84
1:S:29:ASP:HB3	1:S:33:ILE:HD12	1.59	0.84
1:M:29:ASP:HB3	1:M:33:ILE:HD12	1.59	0.84
1:B:29:ASP:HB3	1:B:33:ILE:HD12	1.59	0.84
1:J:29:ASP:HB3	1:J:33:ILE:HD12	1.59	0.84
1:O:29:ASP:HB3	1:O:33:ILE:HD12	1.59	0.83
1:A:154:LEU:HD21	2:U:140:LEU:CD2	2.09	0.83
1:H:29:ASP:HB3	1:H:33:ILE:HD12	1.59	0.83
1:P:29:ASP:HB3	1:P:33:ILE:HD12	1.59	0.83
1:F:29:ASP:HB3	1:F:33:ILE:HD12	1.59	0.83
1:D:29:ASP:HB3	1:D:33:ILE:HD12	1.59	0.83
1:D:154:LEU:CG	2:X:140:LEU:CD2	2.56	0.83
1:E:29:ASP:HB3	1:E:33:ILE:HD12	1.59	0.82
1:Q:29:ASP:HB3	1:Q:33:ILE:HD12	1.59	0.82
1:A:89:LEU:HD11	2:U:141:LEU:HD21	1.61	0.81
1:A:154:LEU:HD21	2:U:140:LEU:HD22	1.61	0.81
1:L:29:ASP:HB3	1:L:33:ILE:CD1	2.10	0.81
2:W:114:LEU:HD13	2:Y:57:LEU:CB	2.11	0.81
1:D:93:ALA:HB2	2:X:137:VAL:HG22	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:VAL:HG12	2:Z:129:VAL:HG13	1.64	0.80
1:A:93:ALA:CB	2:U:137:VAL:HG23	2.11	0.79
1:E:97:VAL:CG1	2:Y:129:VAL:HG13	2.12	0.79
2:W:57:LEU:CD1	2:Y:114:LEU:HD13	2.11	0.78
1:D:153:ASN:OD1	2:X:140:LEU:HD11	1.84	0.78
2:W:57:LEU:O	2:Y:88:ALA:HB2	1.83	0.77
2:W:114:LEU:HB3	2:Y:57:LEU:HA	1.67	0.77
1:D:154:LEU:CG	2:X:140:LEU:HD23	2.16	0.76
1:A:93:ALA:CB	2:U:137:VAL:CG2	2.65	0.75
1:D:93:ALA:HB2	2:X:137:VAL:HG23	1.63	0.75
1:F:89:LEU:CD1	2:Z:141:LEU:HD21	2.17	0.75
1:A:93:ALA:HB2	2:U:137:VAL:HG23	1.67	0.75
1:E:89:LEU:CD1	2:Y:141:LEU:HD21	2.18	0.74
1:O:29:ASP:HB3	1:O:33:ILE:CD1	2.18	0.74
1:B:29:ASP:HB3	1:B:33:ILE:CD1	2.18	0.74
2:U:124:GLY:O	2:U:128:GLU:HG3	1.88	0.74
2:W:59:GLY:HA3	2:Y:87:ARG:HA	1.68	0.74
1:F:29:ASP:HB3	1:F:33:ILE:CD1	2.18	0.74
1:S:29:ASP:HB3	1:S:33:ILE:CD1	2.18	0.74
2:W:124:GLY:O	2:W:128:GLU:HG3	1.88	0.74
1:A:146:ILE:HG22	2:U:148:GLN:OE1	1.88	0.73
1:T:29:ASP:HB3	1:T:33:ILE:CD1	2.18	0.73
2:Y:124:GLY:O	2:Y:128:GLU:HG3	1.88	0.73
1:F:97:VAL:CG1	2:Z:129:VAL:HG13	2.19	0.73
1:N:29:ASP:HB3	1:N:33:ILE:CD1	2.18	0.73
1:E:29:ASP:HB3	1:E:33:ILE:CD1	2.18	0.73
1:K:29:ASP:HB3	1:K:33:ILE:CD1	2.19	0.73
1:Q:29:ASP:HB3	1:Q:33:ILE:CD1	2.18	0.73
1:R:29:ASP:HB3	1:R:33:ILE:CD1	2.18	0.73
1:M:29:ASP:HB3	1:M:33:ILE:CD1	2.18	0.73
1:I:29:ASP:HB3	1:I:33:ILE:CD1	2.18	0.72
2:V:124:GLY:O	2:V:128:GLU:HG3	1.88	0.72
1:H:29:ASP:HB3	1:H:33:ILE:CD1	2.18	0.72
1:J:29:ASP:HB3	1:J:33:ILE:CD1	2.18	0.72
2:Z:124:GLY:O	2:Z:128:GLU:HG3	1.88	0.72
1:D:29:ASP:HB3	1:D:33:ILE:CD1	2.18	0.72
1:G:29:ASP:HB3	1:G:33:ILE:CD1	2.18	0.72
1:P:29:ASP:HB3	1:P:33:ILE:CD1	2.18	0.72
2:X:124:GLY:O	2:X:128:GLU:HG3	1.88	0.72
1:A:29:ASP:HB3	1:A:33:ILE:CD1	2.18	0.72
1:C:29:ASP:HB3	1:C:33:ILE:CD1	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:HG	2:U:140:LEU:CD2	2.19	0.72
1:D:154:LEU:HG	2:X:140:LEU:HD21	1.72	0.71
1:D:154:LEU:HG	2:X:140:LEU:HD23	1.72	0.71
2:W:114:LEU:HD13	2:Y:57:LEU:HD13	1.73	0.71
2:W:114:LEU:CD1	2:Y:57:LEU:HD13	2.23	0.69
1:D:154:LEU:HD23	2:X:140:LEU:HD22	1.73	0.69
1:A:153:ASN:OD1	2:U:140:LEU:HD11	1.92	0.69
1:D:154:LEU:CD2	2:X:140:LEU:HD23	2.22	0.68
2:W:57:LEU:HB3	2:Y:114:LEU:HD13	1.76	0.68
1:L:29:ASP:O	1:L:33:ILE:HB	1.96	0.65
1:A:93:ALA:HB2	2:U:137:VAL:HG22	1.77	0.65
1:A:154:LEU:CG	2:U:140:LEU:CD2	2.76	0.64
1:B:97:VAL:CG1	2:V:129:VAL:HG13	2.27	0.64
1:B:97:VAL:HG11	2:V:129:VAL:HA	1.78	0.64
1:D:154:LEU:HD21	2:X:140:LEU:HD23	1.73	0.63
1:D:89:LEU:HD11	2:X:141:LEU:HD21	1.69	0.63
1:E:93:ALA:HB2	2:Y:137:VAL:HG23	1.80	0.63
2:W:86:GLU:O	2:Y:60:GLU:HG3	1.99	0.63
2:W:114:LEU:HD22	2:Y:57:LEU:O	1.99	0.62
1:B:93:ALA:HB2	2:V:137:VAL:HG23	1.80	0.62
1:A:154:LEU:HG	2:U:140:LEU:HD23	1.80	0.62
1:C:97:VAL:HG11	2:W:129:VAL:HA	1.80	0.62
1:A:154:LEU:CG	2:U:140:LEU:HD23	2.30	0.61
2:W:57:LEU:HD22	2:Y:114:LEU:HB3	1.82	0.61
2:W:61:VAL:HG22	2:Y:61:VAL:CG1	2.30	0.61
1:E:93:ALA:HB2	2:Y:137:VAL:CG2	2.31	0.61
2:W:61:VAL:HG11	2:Y:61:VAL:HG22	1.82	0.60
1:L:29:ASP:O	1:L:33:ILE:CB	2.50	0.60
2:W:131:VAL:HG11	2:Y:57:LEU:HB2	1.84	0.60
2:Y:9:PHE:CZ	2:Y:150:LEU:HD22	2.38	0.59
1:E:93:ALA:CB	2:Y:137:VAL:HG23	2.32	0.59
1:R:29:ASP:O	1:R:33:ILE:HB	2.03	0.59
2:X:9:PHE:CZ	2:X:150:LEU:HD22	2.38	0.59
2:W:57:LEU:HD22	2:Y:114:LEU:CB	2.32	0.59
1:P:29:ASP:O	1:P:33:ILE:HB	2.03	0.59
1:N:29:ASP:O	1:N:33:ILE:HB	2.02	0.59
1:O:29:ASP:O	1:O:33:ILE:HB	2.03	0.59
1:B:29:ASP:O	1:B:33:ILE:HB	2.02	0.59
1:J:29:ASP:O	1:J:33:ILE:HB	2.02	0.59
2:W:9:PHE:CZ	2:W:150:LEU:HD22	2.37	0.59
1:S:29:ASP:O	1:S:33:ILE:HB	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:29:ASP:O	1:H:33:ILE:HB	2.03	0.59
1:A:29:ASP:O	1:A:33:ILE:HB	2.02	0.58
1:A:86:GLU:CB	2:U:54:ARG:HH21	2.16	0.58
1:D:29:ASP:O	1:D:33:ILE:HB	2.03	0.58
1:E:29:ASP:O	1:E:33:ILE:HB	2.02	0.58
1:F:29:ASP:O	1:F:33:ILE:HB	2.03	0.58
2:U:9:PHE:CZ	2:U:150:LEU:HD22	2.37	0.58
1:C:29:ASP:O	1:C:33:ILE:HB	2.03	0.58
1:I:29:ASP:O	1:I:33:ILE:HB	2.03	0.58
2:Z:9:PHE:CZ	2:Z:150:LEU:HD22	2.38	0.58
2:V:9:PHE:CZ	2:V:150:LEU:HD22	2.38	0.58
1:K:29:ASP:O	1:K:33:ILE:HB	2.03	0.58
1:Q:29:ASP:O	1:Q:33:ILE:HB	2.03	0.58
1:A:154:LEU:HD21	2:U:140:LEU:HD23	1.86	0.58
1:T:29:ASP:O	1:T:33:ILE:HB	2.03	0.58
1:G:29:ASP:O	1:G:33:ILE:HB	2.03	0.58
1:O:177:TRP:CZ2	1:P:71:ASP:OD1	2.57	0.57
1:L:28:GLY:HA2	1:L:142:GLU:OE2	2.04	0.57
1:R:177:TRP:CG	1:R:178:ASP:N	2.73	0.57
1:D:177:TRP:CG	1:D:178:ASP:N	2.73	0.57
1:J:177:TRP:CG	1:J:178:ASP:N	2.73	0.57
1:K:177:TRP:CG	1:K:178:ASP:N	2.73	0.57
1:Q:177:TRP:CG	1:Q:178:ASP:N	2.73	0.57
1:S:177:TRP:CG	1:S:178:ASP:N	2.73	0.57
1:A:177:TRP:CG	1:A:178:ASP:N	2.73	0.57
1:F:177:TRP:CG	1:F:178:ASP:N	2.73	0.57
1:T:177:TRP:CG	1:T:178:ASP:N	2.73	0.57
1:L:177:TRP:CG	1:L:178:ASP:N	2.73	0.57
1:M:29:ASP:O	1:M:33:ILE:HB	2.03	0.57
1:B:177:TRP:CG	1:B:178:ASP:N	2.73	0.56
1:I:177:TRP:CG	1:I:178:ASP:N	2.73	0.56
1:E:177:TRP:CG	1:E:178:ASP:N	2.73	0.56
1:O:177:TRP:CG	1:O:178:ASP:N	2.73	0.56
1:G:177:TRP:CG	1:G:178:ASP:N	2.73	0.56
1:M:177:TRP:CG	1:M:178:ASP:N	2.73	0.56
1:N:177:TRP:CG	1:N:178:ASP:N	2.73	0.56
1:P:177:TRP:CG	1:P:178:ASP:N	2.73	0.56
2:W:114:LEU:HD13	2:Y:57:LEU:CG	2.35	0.56
1:B:93:ALA:CB	2:V:137:VAL:HG23	2.35	0.56
1:G:28:GLY:HA2	1:G:142:GLU:OE2	2.06	0.56
1:C:177:TRP:CG	1:C:178:ASP:N	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:177:TRP:CG	1:H:178:ASP:N	2.73	0.56
1:D:90:LEU:HA	2:X:137:VAL:HG21	1.88	0.55
1:B:93:ALA:HB2	2:V:137:VAL:CG2	2.36	0.55
1:A:177:TRP:CD2	1:A:178:ASP:N	2.75	0.55
1:B:28:GLY:HA2	1:B:142:GLU:OE2	2.06	0.55
1:C:28:GLY:HA2	1:C:142:GLU:OE2	2.07	0.55
1:E:28:GLY:HA2	1:E:142:GLU:OE2	2.07	0.55
1:F:28:GLY:HA2	1:F:142:GLU:OE2	2.07	0.55
1:D:28:GLY:HA2	1:D:142:GLU:OE2	2.07	0.55
1:K:28:GLY:HA2	1:K:142:GLU:OE2	2.06	0.55
1:Q:177:TRP:CD2	1:Q:178:ASP:N	2.75	0.55
1:B:177:TRP:CD2	1:B:178:ASP:N	2.75	0.55
1:D:177:TRP:CD2	1:D:178:ASP:N	2.75	0.55
1:G:177:TRP:CD2	1:G:178:ASP:N	2.75	0.55
1:N:28:GLY:HA2	1:N:142:GLU:OE2	2.06	0.55
1:P:28:GLY:HA2	1:P:142:GLU:OE2	2.06	0.55
1:A:28:GLY:HA2	1:A:142:GLU:OE2	2.07	0.55
1:I:28:GLY:HA2	1:I:142:GLU:OE2	2.06	0.55
1:E:94:LEU:HD21	2:Y:130:MET:SD	2.46	0.55
1:M:177:TRP:CD2	1:M:178:ASP:N	2.75	0.55
1:L:177:TRP:CD2	1:L:178:ASP:N	2.75	0.55
1:O:177:TRP:CD2	1:O:178:ASP:N	2.75	0.55
1:H:28:GLY:HA2	1:H:142:GLU:OE2	2.06	0.55
1:J:177:TRP:CD2	1:J:178:ASP:N	2.75	0.55
1:P:177:TRP:CD2	1:P:178:ASP:N	2.75	0.55
1:T:177:TRP:CD2	1:T:178:ASP:N	2.75	0.55
1:A:86:GLU:HB3	2:U:54:ARG:HH21	1.72	0.55
1:F:177:TRP:CD2	1:F:178:ASP:N	2.75	0.55
1:O:28:GLY:HA2	1:O:142:GLU:OE2	2.06	0.55
1:R:28:GLY:HA2	1:R:142:GLU:OE2	2.06	0.55
1:T:28:GLY:HA2	1:T:142:GLU:OE2	2.06	0.55
1:C:177:TRP:CD2	1:C:178:ASP:N	2.75	0.55
1:G:108:GLU:HG3	1:G:109:PHE:N	2.22	0.55
1:H:177:TRP:CD2	1:H:178:ASP:N	2.75	0.55
1:K:177:TRP:CD2	1:K:178:ASP:N	2.75	0.55
1:M:28:GLY:HA2	1:M:142:GLU:OE2	2.06	0.55
1:Q:28:GLY:HA2	1:Q:142:GLU:OE2	2.07	0.55
1:J:108:GLU:HG3	1:J:109:PHE:N	2.22	0.54
1:E:108:GLU:HG3	1:E:109:PHE:N	2.23	0.54
1:E:177:TRP:CD2	1:E:178:ASP:N	2.75	0.54
1:I:177:TRP:CD2	1:I:178:ASP:N	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:177:TRP:CD2	1:N:178:ASP:N	2.75	0.54
1:P:108:GLU:HG3	1:P:109:PHE:N	2.23	0.54
1:R:177:TRP:CD2	1:R:178:ASP:N	2.75	0.54
1:S:177:TRP:CD2	1:S:178:ASP:N	2.75	0.54
1:T:108:GLU:HG3	1:T:109:PHE:N	2.23	0.54
2:W:61:VAL:HG22	2:Y:61:VAL:HG11	1.88	0.54
1:S:28:GLY:HA2	1:S:142:GLU:OE2	2.07	0.54
1:H:108:GLU:HG3	1:H:109:PHE:N	2.22	0.54
1:N:108:GLU:HG3	1:N:109:PHE:N	2.23	0.54
1:K:108:GLU:HG3	1:K:109:PHE:N	2.23	0.54
1:M:108:GLU:HG3	1:M:109:PHE:N	2.23	0.54
1:Q:108:GLU:HG3	1:Q:109:PHE:N	2.22	0.54
1:J:28:GLY:HA2	1:J:142:GLU:OE2	2.07	0.54
1:O:108:GLU:HG3	1:O:109:PHE:N	2.23	0.54
1:S:108:GLU:HG3	1:S:109:PHE:N	2.23	0.54
1:B:89:LEU:CD1	2:V:141:LEU:HD21	2.39	0.53
1:L:108:GLU:HG3	1:L:109:PHE:N	2.23	0.53
1:A:108:GLU:HG3	1:A:109:PHE:N	2.22	0.53
1:F:108:GLU:HG3	1:F:109:PHE:N	2.23	0.53
2:W:87:ARG:HB3	2:Y:60:GLU:HB2	1.90	0.53
1:C:108:GLU:HG3	1:C:109:PHE:N	2.22	0.53
1:I:108:GLU:HG3	1:I:109:PHE:N	2.22	0.53
1:B:108:GLU:HG3	1:B:109:PHE:N	2.23	0.53
1:K:75:GLU:HG3	1:K:82:ALA:HA	1.91	0.53
1:L:75:GLU:HG3	1:L:82:ALA:HA	1.91	0.53
1:R:108:GLU:HG3	1:R:109:PHE:N	2.23	0.53
1:E:177:TRP:CZ2	1:F:71:ASP:OD1	2.62	0.53
1:C:75:GLU:HG3	1:C:82:ALA:HA	1.91	0.52
1:D:108:GLU:HG3	1:D:109:PHE:N	2.23	0.52
1:T:75:GLU:HG3	1:T:82:ALA:HA	1.91	0.52
2:W:114:LEU:HD13	2:Y:57:LEU:CD1	2.36	0.52
1:P:75:GLU:HG3	1:P:82:ALA:HA	1.91	0.52
2:W:114:LEU:CD1	2:Y:57:LEU:HD22	2.39	0.52
1:J:75:GLU:HG3	1:J:82:ALA:HA	1.91	0.52
1:R:75:GLU:HG3	1:R:82:ALA:HA	1.92	0.52
1:A:75:GLU:HG3	1:A:82:ALA:HA	1.91	0.52
1:E:75:GLU:HG3	1:E:82:ALA:HA	1.92	0.52
1:M:75:GLU:HG3	1:M:82:ALA:HA	1.92	0.52
1:B:75:GLU:HG3	1:B:82:ALA:HA	1.91	0.52
1:D:75:GLU:HG3	1:D:82:ALA:HA	1.92	0.51
1:F:75:GLU:HG3	1:F:82:ALA:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:75:GLU:HG3	1:N:82:ALA:HA	1.92	0.51
2:W:61:VAL:CG1	2:Y:61:VAL:HG22	2.40	0.51
2:U:106:PHE:CD1	2:U:150:LEU:HD21	2.46	0.51
2:W:106:PHE:CD1	2:W:150:LEU:HD21	2.46	0.51
1:S:75:GLU:HG3	1:S:82:ALA:HA	1.91	0.51
1:B:29:ASP:O	1:B:33:ILE:CB	2.59	0.51
1:E:29:ASP:O	1:E:33:ILE:CB	2.59	0.51
1:N:29:ASP:O	1:N:33:ILE:CB	2.59	0.51
1:O:75:GLU:HG3	1:O:82:ALA:HA	1.92	0.51
1:G:75:GLU:HG3	1:G:82:ALA:HA	1.92	0.51
1:H:75:GLU:HG3	1:H:82:ALA:HA	1.92	0.51
1:I:75:GLU:HG3	1:I:82:ALA:HA	1.92	0.51
1:R:29:ASP:O	1:R:33:ILE:CB	2.59	0.51
2:Y:106:PHE:CD1	2:Y:150:LEU:HD21	2.46	0.51
1:Q:75:GLU:HG3	1:Q:82:ALA:HA	1.91	0.51
1:F:93:ALA:HB2	2:Z:137:VAL:HG23	1.93	0.51
1:A:29:ASP:O	1:A:33:ILE:CB	2.59	0.50
1:D:29:ASP:O	1:D:33:ILE:CB	2.60	0.50
1:O:29:ASP:O	1:O:33:ILE:CB	2.59	0.50
1:F:29:ASP:O	1:F:33:ILE:CB	2.59	0.50
1:A:154:LEU:HG	2:U:140:LEU:HD21	1.93	0.50
1:G:29:ASP:O	1:G:33:ILE:CB	2.59	0.50
2:W:114:LEU:CD1	2:Y:57:LEU:HB3	2.26	0.50
1:M:29:ASP:O	1:M:33:ILE:CB	2.60	0.50
2:U:108:PHE:CD2	2:U:146:LEU:HD13	2.47	0.50
2:X:106:PHE:CZ	2:X:150:LEU:HD23	2.47	0.50
1:C:29:ASP:O	1:C:33:ILE:CB	2.59	0.50
1:H:29:ASP:O	1:H:33:ILE:CB	2.59	0.50
1:T:29:ASP:O	1:T:33:ILE:CB	2.59	0.50
2:W:108:PHE:CD2	2:W:146:LEU:HD13	2.47	0.50
2:X:106:PHE:CD1	2:X:150:LEU:HD21	2.46	0.50
2:Y:4:SER:OG	2:Y:111:GLN:OE1	2.30	0.50
2:Z:106:PHE:CD1	2:Z:150:LEU:HD21	2.46	0.50
1:I:29:ASP:O	1:I:33:ILE:CB	2.59	0.50
2:V:106:PHE:CZ	2:V:150:LEU:HD23	2.47	0.50
2:Z:106:PHE:CZ	2:Z:150:LEU:HD23	2.47	0.50
1:J:29:ASP:O	1:J:33:ILE:CB	2.59	0.50
2:U:4:SER:OG	2:U:111:GLN:OE1	2.30	0.50
2:V:106:PHE:CD1	2:V:150:LEU:HD21	2.46	0.50
2:V:108:PHE:CD2	2:V:146:LEU:HD13	2.47	0.50
2:Y:106:PHE:CZ	2:Y:150:LEU:HD23	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:ILE:HD13	2:Z:145:ALA:HB2	1.93	0.50
1:Q:29:ASP:O	1:Q:33:ILE:CB	2.59	0.50
2:Y:108:PHE:CD2	2:Y:146:LEU:HD13	2.47	0.50
1:L:29:ASP:HB3	1:L:33:ILE:HD11	1.91	0.49
1:P:29:ASP:O	1:P:33:ILE:CB	2.59	0.49
2:W:106:PHE:CZ	2:W:150:LEU:HD23	2.47	0.49
2:Z:108:PHE:CD2	2:Z:146:LEU:HD13	2.47	0.49
2:V:4:SER:OG	2:V:111:GLN:OE1	2.30	0.49
2:Y:12:ARG:HD2	2:Y:103:GLU:OE2	2.13	0.49
1:S:29:ASP:O	1:S:33:ILE:CB	2.60	0.49
2:X:108:PHE:CD2	2:X:146:LEU:HD13	2.47	0.49
2:V:12:ARG:HD2	2:V:103:GLU:OE2	2.13	0.49
2:Z:12:ARG:HD2	2:Z:103:GLU:OE2	2.13	0.49
2:Z:4:SER:OG	2:Z:111:GLN:OE1	2.30	0.49
2:X:4:SER:OG	2:X:111:GLN:OE1	2.30	0.49
2:W:87:ARG:HA	2:Y:59:GLY:HA3	1.95	0.49
2:W:4:SER:OG	2:W:111:GLN:OE1	2.30	0.49
1:K:29:ASP:O	1:K:33:ILE:CB	2.59	0.49
1:E:146:ILE:HD13	2:Y:145:ALA:HB2	1.95	0.49
2:W:12:ARG:HD2	2:W:103:GLU:OE2	2.13	0.49
1:E:97:VAL:HG11	2:Y:129:VAL:HA	1.94	0.49
2:Y:31:LEU:HA	2:Y:34:VAL:HG23	1.95	0.49
1:A:90:LEU:HA	2:U:137:VAL:HG21	1.95	0.48
2:Z:31:LEU:HA	2:Z:34:VAL:HG23	1.95	0.48
2:X:31:LEU:HA	2:X:34:VAL:HG23	1.95	0.48
1:A:154:LEU:HD23	2:U:140:LEU:HD22	1.90	0.48
2:U:31:LEU:HA	2:U:34:VAL:HG23	1.95	0.48
1:E:90:LEU:HA	2:Y:137:VAL:HG21	1.95	0.48
2:U:12:ARG:HD2	2:U:103:GLU:OE2	2.13	0.48
2:X:12:ARG:HD2	2:X:103:GLU:OE2	2.13	0.48
2:W:131:VAL:HG13	2:Y:58:LEU:HG	1.96	0.48
2:U:106:PHE:CZ	2:U:150:LEU:HD23	2.47	0.48
2:V:31:LEU:HA	2:V:34:VAL:HG23	1.95	0.48
2:W:61:VAL:HG22	2:Y:61:VAL:HG13	1.94	0.48
1:B:93:ALA:HB1	2:V:133:ALA:O	2.14	0.48
1:L:177:TRP:CE3	1:L:178:ASP:C	2.88	0.47
2:X:51:LEU:N	2:X:51:LEU:HD12	2.29	0.47
2:Y:51:LEU:HD12	2:Y:51:LEU:N	2.29	0.47
2:W:51:LEU:N	2:W:51:LEU:HD12	2.29	0.47
1:O:177:TRP:CE3	1:O:178:ASP:C	2.88	0.47
1:M:177:TRP:CE3	1:M:178:ASP:C	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:177:TRP:CE3	1:N:178:ASP:C	2.88	0.47
2:W:88:ALA:HB2	2:Y:57:LEU:O	2.15	0.47
1:B:29:ASP:O	1:B:33:ILE:N	2.43	0.47
1:E:177:TRP:CE3	1:E:178:ASP:C	2.88	0.47
2:U:51:LEU:N	2:U:51:LEU:HD12	2.29	0.47
1:I:177:TRP:CE3	1:I:178:ASP:C	2.88	0.47
1:P:177:TRP:CE3	1:P:178:ASP:C	2.88	0.47
1:B:177:TRP:CE3	1:B:178:ASP:C	2.88	0.47
1:K:177:TRP:CE3	1:K:178:ASP:C	2.88	0.47
1:G:177:TRP:CE3	1:G:178:ASP:C	2.88	0.47
1:R:177:TRP:CE3	1:R:178:ASP:C	2.88	0.47
1:T:177:TRP:CE3	1:T:178:ASP:C	2.88	0.47
1:D:177:TRP:CZ2	1:E:71:ASP:OD1	2.68	0.47
1:F:177:TRP:CE3	1:F:178:ASP:C	2.88	0.47
1:Q:177:TRP:CE3	1:Q:178:ASP:C	2.88	0.47
2:Z:51:LEU:N	2:Z:51:LEU:HD12	2.29	0.47
1:C:177:TRP:CE3	1:C:178:ASP:C	2.88	0.46
1:D:177:TRP:CE3	1:D:178:ASP:C	2.88	0.46
2:W:31:LEU:HA	2:W:34:VAL:HG23	1.95	0.46
1:S:177:TRP:CE3	1:S:178:ASP:C	2.88	0.46
1:A:177:TRP:CE3	1:A:178:ASP:C	2.88	0.46
1:H:177:TRP:CE3	1:H:178:ASP:C	2.88	0.46
1:J:177:TRP:CE3	1:J:178:ASP:C	2.88	0.46
2:V:51:LEU:N	2:V:51:LEU:HD12	2.29	0.46
1:K:28:GLY:CA	1:K:142:GLU:OE2	2.64	0.46
1:N:28:GLY:CA	1:N:142:GLU:OE2	2.64	0.46
1:F:90:LEU:HA	2:Z:137:VAL:HG21	1.96	0.46
1:J:29:ASP:O	1:J:33:ILE:N	2.43	0.46
1:M:28:GLY:CA	1:M:142:GLU:OE2	2.64	0.46
2:W:9:PHE:CE2	2:W:150:LEU:HD22	2.51	0.46
2:Y:9:PHE:CE2	2:Y:150:LEU:HD22	2.51	0.46
1:F:93:ALA:HB2	2:Z:137:VAL:CG2	2.46	0.46
1:D:28:GLY:CA	1:D:142:GLU:OE2	2.64	0.46
1:G:28:GLY:CA	1:G:142:GLU:OE2	2.64	0.46
1:L:29:ASP:O	1:L:33:ILE:CG1	2.63	0.46
1:O:28:GLY:CA	1:O:142:GLU:OE2	2.64	0.46
1:S:28:GLY:CA	1:S:142:GLU:OE2	2.64	0.46
1:A:28:GLY:CA	1:A:142:GLU:OE2	2.64	0.45
1:F:28:GLY:CA	1:F:142:GLU:OE2	2.64	0.45
1:B:28:GLY:CA	1:B:142:GLU:OE2	2.64	0.45
1:H:28:GLY:CA	1:H:142:GLU:OE2	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:28:GLY:CA	1:J:142:GLU:OE2	2.64	0.45
2:U:9:PHE:CE2	2:U:150:LEU:HD22	2.51	0.45
2:W:57:LEU:HB2	2:Y:131:VAL:HG11	1.99	0.45
1:F:29:ASP:O	1:F:33:ILE:N	2.43	0.45
1:N:177:TRP:CZ2	1:O:71:ASP:OD1	2.69	0.45
1:D:86:GLU:O	2:V:60:GLU:HG3	132.65	0.45
2:W:58:LEU:HA	2:Y:88:ALA:HB2	1.98	0.45
1:I:28:GLY:CA	1:I:142:GLU:OE2	2.64	0.45
1:L:29:ASP:O	1:L:33:ILE:N	2.38	0.45
1:T:28:GLY:CA	1:T:142:GLU:OE2	2.64	0.45
1:L:28:GLY:CA	1:L:142:GLU:OE2	2.65	0.45
1:R:28:GLY:CA	1:R:142:GLU:OE2	2.64	0.45
1:P:28:GLY:CA	1:P:142:GLU:OE2	2.64	0.45
2:Z:9:PHE:CE2	2:Z:150:LEU:HD22	2.51	0.45
1:C:28:GLY:CA	1:C:142:GLU:OE2	2.64	0.45
1:D:177:TRP:CZ3	1:D:178:ASP:O	2.70	0.45
1:B:177:TRP:CZ3	1:B:178:ASP:O	2.70	0.44
1:E:28:GLY:CA	1:E:142:GLU:OE2	2.64	0.44
1:J:177:TRP:CZ3	1:J:178:ASP:O	2.71	0.44
1:O:29:ASP:O	1:O:33:ILE:N	2.43	0.44
1:A:154:LEU:CD2	2:U:140:LEU:HD23	2.35	0.44
1:I:29:ASP:O	1:I:33:ILE:N	2.43	0.44
1:P:29:ASP:O	1:P:33:ILE:N	2.43	0.44
1:N:177:TRP:CZ3	1:N:178:ASP:O	2.70	0.44
1:O:177:TRP:CZ3	1:O:178:ASP:O	2.70	0.44
2:U:14:PRO:HG2	2:U:155:PRO:O	2.18	0.44
2:X:9:PHE:CE2	2:X:150:LEU:HD22	2.51	0.44
1:E:177:TRP:CZ3	1:E:178:ASP:O	2.70	0.44
1:F:93:ALA:CB	2:Z:137:VAL:HG23	2.48	0.44
2:V:9:PHE:CE2	2:V:150:LEU:HD22	2.51	0.44
1:I:177:TRP:CZ3	1:I:178:ASP:O	2.70	0.44
1:R:177:TRP:CZ3	1:R:178:ASP:O	2.71	0.44
2:W:14:PRO:HG2	2:W:155:PRO:O	2.18	0.44
1:G:177:TRP:CZ3	1:G:178:ASP:O	2.71	0.44
2:V:47:VAL:HG23	2:V:69:ILE:HD11	2.00	0.44
1:H:29:ASP:O	1:H:33:ILE:N	2.43	0.44
1:M:177:TRP:CZ3	1:M:178:ASP:O	2.71	0.44
2:Y:14:PRO:HG2	2:Y:155:PRO:O	2.18	0.44
1:A:177:TRP:CZ3	1:A:178:ASP:O	2.71	0.44
1:E:42:LEU:HD22	1:E:128:CYS:HA	2.00	0.43
2:X:47:VAL:HG23	2:X:69:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:177:TRP:CZ3	1:F:178:ASP:O	2.71	0.43
1:H:177:TRP:CZ3	1:H:178:ASP:O	2.70	0.43
1:K:42:LEU:HD22	1:K:128:CYS:HA	2.00	0.43
1:L:177:TRP:CZ3	1:L:178:ASP:O	2.70	0.43
1:P:177:TRP:CZ3	1:P:178:ASP:O	2.70	0.43
1:C:177:TRP:CZ3	1:C:178:ASP:O	2.71	0.43
1:C:89:LEU:CD1	2:W:141:LEU:HD21	2.48	0.43
1:Q:28:GLY:CA	1:Q:142:GLU:OE2	2.64	0.43
2:W:114:LEU:HB3	2:Y:57:LEU:CA	2.44	0.43
1:D:71:ASP:OD1	1:F:177:TRP:CZ2	2.72	0.43
1:K:177:TRP:CZ3	1:K:178:ASP:O	2.70	0.43
1:N:42:LEU:HD22	1:N:128:CYS:HA	2.01	0.43
1:S:42:LEU:HD22	1:S:128:CYS:HA	2.01	0.43
1:T:177:TRP:CZ3	1:T:178:ASP:O	2.71	0.43
1:T:42:LEU:HD22	1:T:128:CYS:HA	2.01	0.43
1:A:86:GLU:HB2	2:U:54:ARG:HH21	1.82	0.43
1:D:93:ALA:HB3	2:X:137:VAL:CG2	2.46	0.43
1:E:29:ASP:O	1:E:33:ILE:N	2.43	0.43
1:Q:177:TRP:CZ3	1:Q:178:ASP:O	2.71	0.43
2:W:47:VAL:HG23	2:W:69:ILE:HD11	2.00	0.43
1:D:132:GLU:OE2	2:X:144:MET:HE1	2.18	0.43
2:Z:14:PRO:HG2	2:Z:155:PRO:O	2.18	0.43
1:Q:42:LEU:HD22	1:Q:128:CYS:HA	2.01	0.43
2:Z:48:TRP:HB3	2:Z:66:ARG:HG3	2.01	0.43
1:C:42:LEU:HD22	1:C:128:CYS:HA	2.01	0.43
1:I:42:LEU:HD22	1:I:128:CYS:HA	2.01	0.43
1:P:42:LEU:HD22	1:P:128:CYS:HA	2.00	0.43
2:X:48:TRP:HB3	2:X:66:ARG:HG3	2.01	0.43
2:Y:47:VAL:HG23	2:Y:69:ILE:HD11	2.00	0.43
1:F:42:LEU:HD22	1:F:128:CYS:HA	2.00	0.43
1:L:42:LEU:HD22	1:L:128:CYS:HA	2.01	0.43
2:V:14:PRO:HG2	2:V:155:PRO:O	2.18	0.43
1:H:42:LEU:HD22	1:H:128:CYS:HA	2.01	0.43
1:J:42:LEU:HD22	1:J:128:CYS:HA	2.01	0.43
1:S:177:TRP:CZ3	1:S:178:ASP:O	2.71	0.43
1:B:177:TRP:CZ2	1:C:71:ASP:OD1	2.72	0.43
1:D:42:LEU:HD22	1:D:128:CYS:HA	2.00	0.43
2:U:47:VAL:HG23	2:U:69:ILE:HD11	2.00	0.43
2:X:14:PRO:HG2	2:X:155:PRO:O	2.18	0.43
2:Z:47:VAL:HG23	2:Z:69:ILE:HD11	2.00	0.43
1:E:89:LEU:HD13	2:Y:141:LEU:HD21	1.95	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:42:LEU:HD22	1:G:128:CYS:HA	2.01	0.42
1:B:94:LEU:HD21	2:V:130:MET:SD	2.59	0.42
1:A:42:LEU:HD22	1:A:128:CYS:HA	2.01	0.42
1:A:29:ASP:O	1:A:33:ILE:N	2.43	0.42
1:M:42:LEU:HD22	1:M:128:CYS:HA	2.01	0.42
2:W:60:GLU:H	2:Y:87:ARG:HB3	1.84	0.42
1:E:97:VAL:CG1	2:Y:129:VAL:CG1	2.92	0.42
2:W:57:LEU:CB	2:Y:114:LEU:HD13	2.47	0.42
1:C:93:ALA:HB2	2:W:137:VAL:HG23	2.01	0.42
1:K:29:ASP:O	1:K:33:ILE:N	2.43	0.42
1:L:177:TRP:CZ2	1:M:71:ASP:OD1	2.73	0.42
2:U:48:TRP:HB3	2:U:66:ARG:HG3	2.01	0.42
2:Y:48:TRP:HB3	2:Y:66:ARG:HG3	2.01	0.42
1:B:42:LEU:HD22	1:B:128:CYS:HA	2.01	0.42
1:O:42:LEU:HD22	1:O:128:CYS:HA	2.01	0.42
1:R:78:ILE:HA	1:R:79:PRO:HD2	1.94	0.42
2:W:58:LEU:HA	2:Y:88:ALA:CB	2.49	0.42
1:N:78:ILE:HA	1:N:79:PRO:HD2	1.94	0.42
1:S:29:ASP:O	1:S:33:ILE:N	2.43	0.42
2:W:48:TRP:HB3	2:W:66:ARG:HG3	2.01	0.42
2:W:57:LEU:CD2	2:Y:114:LEU:HB3	2.48	0.42
1:B:90:LEU:HA	2:V:137:VAL:HG21	2.02	0.41
1:A:28:GLY:O	1:A:32:ARG:N	2.40	0.41
1:K:28:GLY:O	1:K:32:ARG:N	2.40	0.41
1:T:29:ASP:O	1:T:33:ILE:N	2.43	0.41
1:M:29:ASP:O	1:M:33:ILE:N	2.43	0.41
2:V:48:TRP:HB3	2:V:66:ARG:HG3	2.01	0.41
1:A:71:ASP:OD1	1:C:177:TRP:CZ2	2.73	0.41
1:R:42:LEU:HD22	1:R:128:CYS:HA	2.01	0.41
2:Z:9:PHE:HZ	2:Z:150:LEU:HD22	1.85	0.41
1:J:28:GLY:O	1:J:32:ARG:N	2.40	0.41
1:S:177:TRP:CZ2	1:T:71:ASP:OD1	2.74	0.41
1:F:89:LEU:HD13	2:Z:141:LEU:HD21	2.00	0.41
1:F:28:GLY:O	1:F:32:ARG:N	2.40	0.41
2:U:9:PHE:HZ	2:U:150:LEU:HD22	1.85	0.41
1:C:108:GLU:HB3	1:C:176:LEU:HD22	2.03	0.41
1:N:108:GLU:HB3	1:N:176:LEU:HD22	2.03	0.41
1:G:108:GLU:HB3	1:G:176:LEU:HD22	2.03	0.40
2:W:57:LEU:HA	2:Y:114:LEU:HB3	2.02	0.40
1:K:108:GLU:HB3	1:K:176:LEU:HD22	2.04	0.40
1:T:108:GLU:HB3	1:T:176:LEU:HD22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:108:GLU:HB3	1:M:176:LEU:HD22	2.04	0.40
2:U:106:PHE:CE1	2:U:150:LEU:HD21	2.57	0.40
1:D:89:LEU:HD12	2:X:141:LEU:HD21	1.76	0.40
2:Y:9:PHE:HZ	2:Y:150:LEU:HD22	1.85	0.40
1:A:89:LEU:CD1	2:U:141:LEU:CD2	2.56	0.40
1:D:29:ASP:O	1:D:33:ILE:N	2.43	0.40
1:Q:108:GLU:HB3	1:Q:176:LEU:HD22	2.04	0.40
1:R:108:GLU:HB3	1:R:176:LEU:HD22	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	B	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	C	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	D	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	E	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	F	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	G	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	H	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	I	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	J	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	K	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	L	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	M	150/157 (96%)	149 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	O	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	P	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	Q	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	R	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	S	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
1	T	150/157 (96%)	149 (99%)	1 (1%)	0	100	100
2	U	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	V	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	W	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	X	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	Y	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	Z	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	a	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	b	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	c	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	d	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	e	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	f	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	g	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	h	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	i	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	j	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	k	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	l	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	m	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
2	n	144/165 (87%)	142 (99%)	2 (1%)	0	100	100
All	All	5880/6440 (91%)	5820 (99%)	60 (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	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	B	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	C	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	D	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	E	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	F	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	G	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	H	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	I	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	J	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	K	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	L	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	M	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	N	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	O	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	P	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	Q	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	R	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	S	114/119 (96%)	113 (99%)	1 (1%)	82	91
1	T	114/119 (96%)	113 (99%)	1 (1%)	82	91
2	U	102/118 (86%)	102 (100%)	0	100	100
2	V	102/118 (86%)	102 (100%)	0	100	100
2	W	102/118 (86%)	102 (100%)	0	100	100
2	X	102/118 (86%)	102 (100%)	0	100	100
2	Y	102/118 (86%)	102 (100%)	0	100	100
2	Z	102/118 (86%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	a	102/118 (86%)	102 (100%)	0	100	100
2	b	102/118 (86%)	102 (100%)	0	100	100
2	c	102/118 (86%)	102 (100%)	0	100	100
2	d	102/118 (86%)	102 (100%)	0	100	100
2	e	102/118 (86%)	102 (100%)	0	100	100
2	f	102/118 (86%)	102 (100%)	0	100	100
2	g	102/118 (86%)	102 (100%)	0	100	100
2	h	102/118 (86%)	102 (100%)	0	100	100
2	i	102/118 (86%)	102 (100%)	0	100	100
2	j	102/118 (86%)	102 (100%)	0	100	100
2	k	102/118 (86%)	102 (100%)	0	100	100
2	l	102/118 (86%)	102 (100%)	0	100	100
2	m	102/118 (86%)	102 (100%)	0	100	100
2	n	102/118 (86%)	102 (100%)	0	100	100
All	All	4320/4740 (91%)	4300 (100%)	20 (0%)	91	95

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	ARG
1	B	129	ARG
1	C	129	ARG
1	D	129	ARG
1	E	129	ARG
1	F	129	ARG
1	G	129	ARG
1	H	129	ARG
1	I	129	ARG
1	J	129	ARG
1	K	129	ARG
1	L	129	ARG
1	M	129	ARG
1	N	129	ARG
1	O	129	ARG
1	P	129	ARG
1	Q	129	ARG
1	R	129	ARG

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Mol	Chain	Res	Type
1	S	129	ARG
1	T	129	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates 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	152/157 (96%)	0.20	3 (1%) 65 61	270, 310, 365, 448	0
1	B	152/157 (96%)	0.13	1 (0%) 87 84	255, 299, 357, 413	0
1	C	152/157 (96%)	0.03	0 100 100	261, 303, 346, 387	0
1	D	152/157 (96%)	0.11	0 100 100	268, 317, 350, 408	0
1	E	152/157 (96%)	0.14	4 (2%) 56 52	271, 308, 369, 416	0
1	F	152/157 (96%)	0.01	2 (1%) 77 71	273, 318, 363, 405	0
1	G	152/157 (96%)	0.18	1 (0%) 87 84	236, 294, 343, 395	0
1	H	152/157 (96%)	0.32	1 (0%) 87 84	232, 277, 335, 401	0
1	I	152/157 (96%)	0.14	2 (1%) 77 71	238, 283, 333, 382	0
1	J	152/157 (96%)	0.18	0 100 100	241, 283, 348, 416	0
1	K	152/157 (96%)	0.20	2 (1%) 77 71	267, 305, 357, 442	0
1	L	152/157 (96%)	0.13	1 (0%) 87 84	249, 295, 350, 403	0
1	M	152/157 (96%)	0.03	0 100 100	273, 303, 357, 406	0
1	N	152/157 (96%)	0.11	1 (0%) 87 84	275, 313, 348, 413	0
1	O	152/157 (96%)	0.13	1 (0%) 87 84	261, 307, 361, 413	0
1	P	152/157 (96%)	0.01	1 (0%) 87 84	271, 314, 364, 404	0
1	Q	152/157 (96%)	0.20	0 100 100	238, 293, 343, 392	0
1	R	152/157 (96%)	0.35	3 (1%) 65 61	234, 280, 339, 403	0
1	S	152/157 (96%)	0.13	2 (1%) 77 71	234, 286, 333, 404	0
1	T	152/157 (96%)	0.14	0 100 100	239, 283, 341, 397	0
2	U	148/165 (89%)	0.72	15 (10%) 8 12	318, 375, 453, 476	0
2	V	148/165 (89%)	0.45	11 (7%) 15 18	293, 336, 392, 440	0
2	W	148/165 (89%)	0.32	8 (5%) 26 28	294, 360, 407, 437	0
2	X	148/165 (89%)	0.74	19 (12%) 4 9	313, 374, 446, 482	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	Y	148/165 (89%)	0.19	5 (3%) 46 43	302, 348, 391, 448	0
2	Z	148/165 (89%)	0.19	3 (2%) 65 61	332, 373, 427, 456	0
2	a	148/165 (89%)	0.49	8 (5%) 26 28	271, 337, 394, 444	0
2	b	148/165 (89%)	0.84	25 (16%) 2 7	270, 323, 394, 435	0
2	c	148/165 (89%)	0.56	15 (10%) 8 12	266, 322, 378, 431	0
2	d	148/165 (89%)	0.28	6 (4%) 38 35	285, 347, 409, 440	0
2	e	148/165 (89%)	0.72	17 (11%) 5 10	307, 370, 445, 476	0
2	f	148/165 (89%)	0.40	10 (6%) 18 21	287, 339, 391, 431	0
2	g	148/165 (89%)	0.32	9 (6%) 22 23	289, 359, 414, 441	0
2	h	148/165 (89%)	0.75	23 (15%) 2 7	318, 376, 441, 482	0
2	i	148/165 (89%)	0.23	5 (3%) 46 43	306, 349, 391, 443	0
2	j	148/165 (89%)	0.19	4 (2%) 55 50	323, 372, 421, 445	0
2	k	148/165 (89%)	0.51	7 (4%) 32 32	268, 334, 395, 446	0
2	l	148/165 (89%)	0.84	25 (16%) 2 7	271, 322, 379, 426	0
2	m	148/165 (89%)	0.58	14 (9%) 9 13	273, 320, 378, 432	0
2	n	148/165 (89%)	0.24	5 (3%) 46 43	283, 349, 411, 458	0
All	All	6000/6440 (93%)	0.31	259 (4%) 36 34	232, 324, 409, 482	0

All (259) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	b	157	ALA	7.5
2	l	157	ALA	7.1
2	g	71	ARG	6.1
2	W	71	ARG	5.7
2	l	154	LEU	5.7
2	h	157	ALA	5.7
2	b	154	LEU	5.6
2	n	157	ALA	5.6
2	l	156	PRO	5.5
2	X	157	ALA	5.5
1	K	79	PRO	5.4
2	a	157	ALA	5.4
1	A	79	PRO	5.4
2	b	100	GLU	5.2
2	b	156	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
2	l	100	GLU	4.9
2	b	155	PRO	4.9
2	k	30	ALA	4.7
2	U	97	THR	4.7
2	a	30	ALA	4.5
2	d	157	ALA	4.5
2	l	98	ALA	4.3
2	l	155	PRO	4.3
2	W	30	ALA	4.2
2	b	99	ALA	4.2
2	b	30	ALA	4.0
2	m	154	LEU	3.9
2	U	74	GLN	3.9
2	l	30	ALA	3.8
1	K	80	GLY	3.8
2	m	157	ALA	3.8
2	b	98	ALA	3.8
2	c	82	THR	3.8
1	A	80	GLY	3.8
2	c	154	LEU	3.7
2	X	69	ILE	3.7
2	k	157	ALA	3.7
2	l	99	ALA	3.7
2	V	71	ARG	3.6
2	a	71	ARG	3.6
2	Z	151	ALA	3.6
2	l	29	ALA	3.6
1	R	79	PRO	3.6
2	c	157	ALA	3.6
2	V	154	LEU	3.6
2	V	157	ALA	3.6
2	f	157	ALA	3.5
2	e	97	THR	3.5
2	g	29	ALA	3.5
2	k	81	LEU	3.5
2	m	82	THR	3.4
2	b	23	PHE	3.4
2	e	74	GLN	3.3
2	c	81	LEU	3.3
2	h	29	ALA	3.3
2	b	150	LEU	3.3
2	l	23	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
2	g	30	ALA	3.2
2	U	157	ALA	3.2
2	b	29	ALA	3.2
2	X	74	GLN	3.2
2	h	74	GLN	3.2
2	i	29	ALA	3.2
2	h	47	VAL	3.2
2	b	17	GLN	3.1
2	b	104	MET	3.1
2	h	71	ARG	3.1
2	f	71	ARG	3.1
2	l	150	LEU	3.1
2	k	71	ARG	3.1
2	l	103	GLU	3.0
2	l	74	GLN	3.0
2	V	82	THR	3.0
2	m	83	LEU	3.0
2	k	58	LEU	3.0
2	h	98	ALA	3.0
2	e	154	LEU	3.0
2	b	103	GLU	3.0
2	c	83	LEU	3.0
2	X	98	ALA	3.0
2	m	155	PRO	3.0
2	X	97	THR	2.9
2	l	83	LEU	2.9
2	U	71	ARG	2.9
2	l	104	MET	2.9
1	B	107	GLU	2.9
2	e	29	ALA	2.9
2	Y	58	LEU	2.9
2	g	74	GLN	2.9
2	h	28	ALA	2.9
2	c	74	GLN	2.9
2	d	154	LEU	2.9
2	Y	29	ALA	2.8
2	a	81	LEU	2.8
2	j	151	ALA	2.8
2	f	150	LEU	2.8
2	h	97	THR	2.8
2	U	154	LEU	2.8
2	e	157	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
2	e	69	ILE	2.8
2	W	29	ALA	2.8
2	X	29	ALA	2.8
1	L	107	GLU	2.8
2	U	81	LEU	2.8
2	W	70	VAL	2.8
2	X	47	VAL	2.8
2	Z	154	LEU	2.8
2	g	70	VAL	2.8
2	m	97	THR	2.7
2	l	151	ALA	2.7
2	l	14	PRO	2.7
2	e	98	ALA	2.7
2	h	70	VAL	2.7
2	c	30	ALA	2.7
2	W	150	LEU	2.7
2	X	28	ALA	2.7
2	e	71	ARG	2.7
2	k	150	LEU	2.7
2	c	92	VAL	2.7
2	l	77	GLU	2.7
2	m	92	VAL	2.7
2	b	77	GLU	2.7
2	a	58	LEU	2.6
2	f	82	THR	2.6
1	H	79	PRO	2.6
2	W	74	GLN	2.6
2	e	81	LEU	2.6
2	h	150	LEU	2.6
2	X	15	HIS	2.6
2	b	74	GLN	2.6
2	m	74	GLN	2.6
2	h	83	LEU	2.6
2	f	83	LEU	2.6
2	b	12	ARG	2.6
2	d	150	LEU	2.6
2	h	23	PHE	2.6
2	j	154	LEU	2.6
2	h	56	PRO	2.5
2	n	154	LEU	2.5
1	I	76	LEU	2.5
2	b	14	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
2	k	154	LEU	2.5
2	l	12	ARG	2.5
2	f	29	ALA	2.5
2	g	150	LEU	2.5
2	f	154	LEU	2.5
2	U	29	ALA	2.5
2	W	154	LEU	2.5
2	b	71	ARG	2.5
2	X	82	THR	2.5
2	m	156	PRO	2.5
2	U	114	LEU	2.5
2	e	11	LEU	2.5
2	V	29	ALA	2.4
2	m	71	ARG	2.4
2	a	29	ALA	2.4
2	b	101	GLY	2.4
2	Z	92	VAL	2.4
2	h	69	ILE	2.4
2	V	83	LEU	2.4
1	E	110	ILE	2.4
2	V	150	LEU	2.4
2	Y	100	GLU	2.4
2	d	30	ALA	2.4
2	i	100	GLU	2.4
2	b	83	LEU	2.4
2	d	23	PHE	2.4
1	I	79	PRO	2.3
2	X	71	ARG	2.3
2	c	155	PRO	2.3
2	e	114	LEU	2.3
2	a	83	LEU	2.3
2	l	71	ARG	2.3
2	Y	83	LEU	2.3
2	h	58	LEU	2.3
2	n	150	LEU	2.3
2	c	156	PRO	2.3
2	l	92	VAL	2.3
2	X	23	PHE	2.3
2	U	98	ALA	2.3
2	U	58	LEU	2.3
2	e	156	PRO	2.3
2	U	96	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	X	83	LEU	2.2
2	i	58	LEU	2.2
2	U	156	PRO	2.2
2	e	61	VAL	2.2
2	X	58	LEU	2.2
2	c	104	MET	2.2
2	U	69	ILE	2.2
2	X	90	VAL	2.2
2	a	154	LEU	2.2
2	X	30	ALA	2.2
2	e	70	VAL	2.2
2	g	58	LEU	2.2
2	h	30	ALA	2.2
1	N	144	LEU	2.2
2	i	83	LEU	2.2
2	V	110	PHE	2.2
2	j	98	ALA	2.2
1	R	110	ILE	2.2
2	V	70	VAL	2.2
2	f	58	LEU	2.2
2	Y	71	ARG	2.2
2	j	30	ALA	2.2
2	g	78	LEU	2.2
2	f	70	VAL	2.1
2	h	37	LEU	2.1
2	c	58	LEU	2.1
2	c	150	LEU	2.1
2	e	150	LEU	2.1
2	e	82	THR	2.1
2	X	65	PHE	2.1
2	n	58	LEU	2.1
2	h	104	MET	2.1
2	l	17	GLN	2.1
2	h	66	ARG	2.1
2	l	101	GLY	2.1
1	G	166	LEU	2.1
2	h	90	VAL	2.1
2	l	153	GLY	2.1
2	X	150	LEU	2.1
1	A	135	ILE	2.1
2	U	37	LEU	2.1
2	b	69	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
2	b	92	VAL	2.1
2	h	65	PHE	2.1
2	m	73	PRO	2.1
2	i	150	LEU	2.1
2	c	97	THR	2.1
2	f	23	PHE	2.1
2	h	24	VAL	2.1
1	E	107	GLU	2.1
2	d	58	LEU	2.1
1	F	80	GLY	2.1
1	R	108	GLU	2.1
1	P	80	GLY	2.1
2	V	58	LEU	2.1
1	S	76	LEU	2.1
2	g	53	VAL	2.1
1	S	107	GLU	2.1
2	l	97	THR	2.1
2	U	56	PRO	2.0
1	E	108	GLU	2.0
2	n	112	ALA	2.0
1	F	144	LEU	2.0
2	b	81	LEU	2.0
2	c	29	ALA	2.0
2	b	37	LEU	2.0
2	m	104	MET	2.0
1	O	79	PRO	2.0
2	W	28	ALA	2.0
2	e	36	ARG	2.0
2	V	81	LEU	2.0
2	m	150	LEU	2.0
2	h	114	LEU	2.0
2	m	29	ALA	2.0
1	E	79	PRO	2.0
2	X	70	VAL	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.