



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 02:21 AM UTC

PDB ID : 5IM4 / pdb\_00005im4  
Title : Crystal structure of designed two-component self-assembling icosahedral cage I52-32  
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 : 2016-03-05  
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

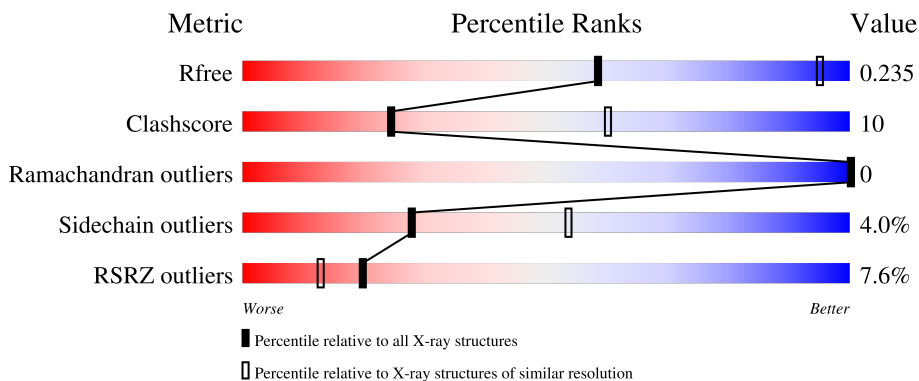
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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

Mol	Chain	Length	Quality of chain
1	A	162	 11% 69% 14% 17%
1	B	162	 10% 69% 15% 15%
1	C	162	 10% 65% 17% 15%
1	D	162	 10% 64% 16% 19%
1	E	162	 9% 67% 15% 18%

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Mol	Chain	Length	Quality of chain
1	K	162	11% 64% 19% • 17%
1	L	162	9% 67% 15% • 16%
1	M	162	12% 64% 20% • 14%
1	N	162	11% 67% 14% • 17%
1	O	162	9% 65% 14% • 20%
1	U	162	11% 65% 16% • 17%
1	V	162	12% 65% 17% • 16%
1	W	162	12% 65% 15% • 19%
1	X	162	9% 63% 18% • 19%
1	Y	162	10% 66% 16% • 17%
1	e	162	9% 65% 17% • 18%
1	f	162	8% 66% 16% • 17%
1	g	162	10% 64% 16% • 20%
1	h	162	10% 66% 14% • 18%
1	i	162	10% 67% 14% • 17%
2	F	138	4% 75% 18% • 5%
2	G	138	2% 79% 14% • 5%
2	H	138	3% 78% 15% • 5%
2	I	138	% 81% 12% • 5%
2	J	138	2% 77% 17% • 5%
2	P	138	4% 78% 15% • 5%
2	Q	138	3% 80% 13% • 5%
2	R	138	3% 78% 15% • 5%
2	S	138	3% 78% 15% • 5%
2	T	138	% 80% 14% • 5%

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Mol	Chain	Length	Quality of chain
2	Z	138	<p>4% 78% 16% • 5%</p>
2	a	138	<p>3% 81% 12% • 5%</p>
2	b	138	<p>3% 78% 14% • 5%</p>
2	c	138	<p>2% 80% 13% • 5%</p>
2	d	138	<p>1% 78% 14% • 5%</p>
2	j	138	<p>2% 78% 16% • 5%</p>
2	k	138	<p>2% 80% 13% • 5%</p>
2	l	138	<p>3% 80% 14% • 5%</p>
2	m	138	<p>3% 79% 14% • 5%</p>
2	n	138	<p>4% 80% 12% • 5%</p>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 40538 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 6,7-dimethyl-8-ribityllumazine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	135	1031	670	172	185	4	0	0	0
1	E	133	1016	662	169	181	4	0	0	0
1	C	137	1051	680	177	190	4	0	0	0
1	B	137	1051	682	179	186	4	0	0	0
1	D	132	1013	660	171	178	4	0	0	0
1	K	135	1032	670	174	184	4	0	0	0
1	L	136	1045	677	175	189	4	0	0	0
1	N	134	1023	664	172	183	4	0	0	0
1	M	139	1072	693	181	194	4	0	0	0
1	O	130	993	648	166	175	4	0	0	0
1	U	134	1018	661	171	182	4	0	0	0
1	V	136	1036	672	175	185	4	0	0	0
1	X	132	1013	659	170	180	4	0	0	0
1	W	132	1009	657	170	178	4	0	0	0
1	Y	135	1017	659	170	184	4	0	0	0
1	e	133	1018	662	171	181	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	f	134	1027	667	172	184	4	0	0	0
1	h	133	1008	657	168	179	4	0	0	0
1	g	130	995	648	168	175	4	0	0	0
1	i	135	1026	666	170	186	4	0	0	0

There are 280 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	expression tag	UNP A0A0A3CUI3
A	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
A	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
A	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
A	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
A	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
A	165	LEU	-	expression tag	UNP A0A0A3CUI3
A	166	GLU	-	expression tag	UNP A0A0A3CUI3
A	167	HIS	-	expression tag	UNP A0A0A3CUI3
A	168	HIS	-	expression tag	UNP A0A0A3CUI3
A	169	HIS	-	expression tag	UNP A0A0A3CUI3
A	170	HIS	-	expression tag	UNP A0A0A3CUI3
A	171	HIS	-	expression tag	UNP A0A0A3CUI3
A	172	HIS	-	expression tag	UNP A0A0A3CUI3
E	11	MET	-	expression tag	UNP A0A0A3CUI3
E	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
E	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
E	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
E	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
E	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
E	165	LEU	-	expression tag	UNP A0A0A3CUI3
E	166	GLU	-	expression tag	UNP A0A0A3CUI3
E	167	HIS	-	expression tag	UNP A0A0A3CUI3
E	168	HIS	-	expression tag	UNP A0A0A3CUI3
E	169	HIS	-	expression tag	UNP A0A0A3CUI3
E	170	HIS	-	expression tag	UNP A0A0A3CUI3
E	171	HIS	-	expression tag	UNP A0A0A3CUI3
E	172	HIS	-	expression tag	UNP A0A0A3CUI3
C	11	MET	-	expression tag	UNP A0A0A3CUI3
C	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
C	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
C	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
C	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
C	165	LEU	-	expression tag	UNP A0A0A3CUI3
C	166	GLU	-	expression tag	UNP A0A0A3CUI3
C	167	HIS	-	expression tag	UNP A0A0A3CUI3
C	168	HIS	-	expression tag	UNP A0A0A3CUI3
C	169	HIS	-	expression tag	UNP A0A0A3CUI3
C	170	HIS	-	expression tag	UNP A0A0A3CUI3
C	171	HIS	-	expression tag	UNP A0A0A3CUI3
C	172	HIS	-	expression tag	UNP A0A0A3CUI3
B	11	MET	-	expression tag	UNP A0A0A3CUI3
B	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
B	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
B	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
B	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
B	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
B	165	LEU	-	expression tag	UNP A0A0A3CUI3
B	166	GLU	-	expression tag	UNP A0A0A3CUI3
B	167	HIS	-	expression tag	UNP A0A0A3CUI3
B	168	HIS	-	expression tag	UNP A0A0A3CUI3
B	169	HIS	-	expression tag	UNP A0A0A3CUI3
B	170	HIS	-	expression tag	UNP A0A0A3CUI3
B	171	HIS	-	expression tag	UNP A0A0A3CUI3
B	172	HIS	-	expression tag	UNP A0A0A3CUI3
D	11	MET	-	expression tag	UNP A0A0A3CUI3
D	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
D	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
D	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
D	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
D	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
D	165	LEU	-	expression tag	UNP A0A0A3CUI3
D	166	GLU	-	expression tag	UNP A0A0A3CUI3
D	167	HIS	-	expression tag	UNP A0A0A3CUI3
D	168	HIS	-	expression tag	UNP A0A0A3CUI3
D	169	HIS	-	expression tag	UNP A0A0A3CUI3
D	170	HIS	-	expression tag	UNP A0A0A3CUI3
D	171	HIS	-	expression tag	UNP A0A0A3CUI3
D	172	HIS	-	expression tag	UNP A0A0A3CUI3
K	11	MET	-	expression tag	UNP A0A0A3CUI3
K	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
K	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
K	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
K	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
K	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
K	165	LEU	-	expression tag	UNP A0A0A3CUI3
K	166	GLU	-	expression tag	UNP A0A0A3CUI3
K	167	HIS	-	expression tag	UNP A0A0A3CUI3
K	168	HIS	-	expression tag	UNP A0A0A3CUI3
K	169	HIS	-	expression tag	UNP A0A0A3CUI3
K	170	HIS	-	expression tag	UNP A0A0A3CUI3
K	171	HIS	-	expression tag	UNP A0A0A3CUI3
K	172	HIS	-	expression tag	UNP A0A0A3CUI3
L	11	MET	-	expression tag	UNP A0A0A3CUI3
L	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
L	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
L	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
L	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
L	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
L	165	LEU	-	expression tag	UNP A0A0A3CUI3
L	166	GLU	-	expression tag	UNP A0A0A3CUI3
L	167	HIS	-	expression tag	UNP A0A0A3CUI3
L	168	HIS	-	expression tag	UNP A0A0A3CUI3
L	169	HIS	-	expression tag	UNP A0A0A3CUI3
L	170	HIS	-	expression tag	UNP A0A0A3CUI3
L	171	HIS	-	expression tag	UNP A0A0A3CUI3
L	172	HIS	-	expression tag	UNP A0A0A3CUI3
N	11	MET	-	expression tag	UNP A0A0A3CUI3
N	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
N	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
N	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
N	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
N	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
N	165	LEU	-	expression tag	UNP A0A0A3CUI3
N	166	GLU	-	expression tag	UNP A0A0A3CUI3
N	167	HIS	-	expression tag	UNP A0A0A3CUI3
N	168	HIS	-	expression tag	UNP A0A0A3CUI3
N	169	HIS	-	expression tag	UNP A0A0A3CUI3
N	170	HIS	-	expression tag	UNP A0A0A3CUI3
N	171	HIS	-	expression tag	UNP A0A0A3CUI3
N	172	HIS	-	expression tag	UNP A0A0A3CUI3
M	11	MET	-	expression tag	UNP A0A0A3CUI3
M	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
M	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
M	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
M	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
M	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
M	165	LEU	-	expression tag	UNP A0A0A3CUI3
M	166	GLU	-	expression tag	UNP A0A0A3CUI3
M	167	HIS	-	expression tag	UNP A0A0A3CUI3
M	168	HIS	-	expression tag	UNP A0A0A3CUI3
M	169	HIS	-	expression tag	UNP A0A0A3CUI3
M	170	HIS	-	expression tag	UNP A0A0A3CUI3
M	171	HIS	-	expression tag	UNP A0A0A3CUI3
M	172	HIS	-	expression tag	UNP A0A0A3CUI3
O	11	MET	-	expression tag	UNP A0A0A3CUI3
O	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
O	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
O	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
O	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
O	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
O	165	LEU	-	expression tag	UNP A0A0A3CUI3
O	166	GLU	-	expression tag	UNP A0A0A3CUI3
O	167	HIS	-	expression tag	UNP A0A0A3CUI3
O	168	HIS	-	expression tag	UNP A0A0A3CUI3
O	169	HIS	-	expression tag	UNP A0A0A3CUI3
O	170	HIS	-	expression tag	UNP A0A0A3CUI3
O	171	HIS	-	expression tag	UNP A0A0A3CUI3
O	172	HIS	-	expression tag	UNP A0A0A3CUI3
U	11	MET	-	expression tag	UNP A0A0A3CUI3
U	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
U	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
U	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
U	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
U	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
U	165	LEU	-	expression tag	UNP A0A0A3CUI3
U	166	GLU	-	expression tag	UNP A0A0A3CUI3
U	167	HIS	-	expression tag	UNP A0A0A3CUI3
U	168	HIS	-	expression tag	UNP A0A0A3CUI3
U	169	HIS	-	expression tag	UNP A0A0A3CUI3
U	170	HIS	-	expression tag	UNP A0A0A3CUI3
U	171	HIS	-	expression tag	UNP A0A0A3CUI3
U	172	HIS	-	expression tag	UNP A0A0A3CUI3
V	11	MET	-	expression tag	UNP A0A0A3CUI3
V	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
V	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
V	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
V	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
V	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
V	165	LEU	-	expression tag	UNP A0A0A3CUI3
V	166	GLU	-	expression tag	UNP A0A0A3CUI3
V	167	HIS	-	expression tag	UNP A0A0A3CUI3
V	168	HIS	-	expression tag	UNP A0A0A3CUI3
V	169	HIS	-	expression tag	UNP A0A0A3CUI3
V	170	HIS	-	expression tag	UNP A0A0A3CUI3
V	171	HIS	-	expression tag	UNP A0A0A3CUI3
V	172	HIS	-	expression tag	UNP A0A0A3CUI3
X	11	MET	-	expression tag	UNP A0A0A3CUI3
X	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
X	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
X	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
X	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
X	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
X	165	LEU	-	expression tag	UNP A0A0A3CUI3
X	166	GLU	-	expression tag	UNP A0A0A3CUI3
X	167	HIS	-	expression tag	UNP A0A0A3CUI3
X	168	HIS	-	expression tag	UNP A0A0A3CUI3
X	169	HIS	-	expression tag	UNP A0A0A3CUI3
X	170	HIS	-	expression tag	UNP A0A0A3CUI3
X	171	HIS	-	expression tag	UNP A0A0A3CUI3
X	172	HIS	-	expression tag	UNP A0A0A3CUI3
W	11	MET	-	expression tag	UNP A0A0A3CUI3
W	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
W	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
W	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
W	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
W	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
W	165	LEU	-	expression tag	UNP A0A0A3CUI3
W	166	GLU	-	expression tag	UNP A0A0A3CUI3
W	167	HIS	-	expression tag	UNP A0A0A3CUI3
W	168	HIS	-	expression tag	UNP A0A0A3CUI3
W	169	HIS	-	expression tag	UNP A0A0A3CUI3
W	170	HIS	-	expression tag	UNP A0A0A3CUI3
W	171	HIS	-	expression tag	UNP A0A0A3CUI3
W	172	HIS	-	expression tag	UNP A0A0A3CUI3
Y	11	MET	-	expression tag	UNP A0A0A3CUI3
Y	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
Y	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
Y	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
Y	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
Y	165	LEU	-	expression tag	UNP A0A0A3CUI3
Y	166	GLU	-	expression tag	UNP A0A0A3CUI3
Y	167	HIS	-	expression tag	UNP A0A0A3CUI3
Y	168	HIS	-	expression tag	UNP A0A0A3CUI3
Y	169	HIS	-	expression tag	UNP A0A0A3CUI3
Y	170	HIS	-	expression tag	UNP A0A0A3CUI3
Y	171	HIS	-	expression tag	UNP A0A0A3CUI3
Y	172	HIS	-	expression tag	UNP A0A0A3CUI3
e	11	MET	-	expression tag	UNP A0A0A3CUI3
e	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
e	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
e	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
e	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
e	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
e	165	LEU	-	expression tag	UNP A0A0A3CUI3
e	166	GLU	-	expression tag	UNP A0A0A3CUI3
e	167	HIS	-	expression tag	UNP A0A0A3CUI3
e	168	HIS	-	expression tag	UNP A0A0A3CUI3
e	169	HIS	-	expression tag	UNP A0A0A3CUI3
e	170	HIS	-	expression tag	UNP A0A0A3CUI3
e	171	HIS	-	expression tag	UNP A0A0A3CUI3
e	172	HIS	-	expression tag	UNP A0A0A3CUI3
f	11	MET	-	expression tag	UNP A0A0A3CUI3
f	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
f	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
f	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
f	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
f	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
f	165	LEU	-	expression tag	UNP A0A0A3CUI3
f	166	GLU	-	expression tag	UNP A0A0A3CUI3
f	167	HIS	-	expression tag	UNP A0A0A3CUI3
f	168	HIS	-	expression tag	UNP A0A0A3CUI3
f	169	HIS	-	expression tag	UNP A0A0A3CUI3
f	170	HIS	-	expression tag	UNP A0A0A3CUI3
f	171	HIS	-	expression tag	UNP A0A0A3CUI3
f	172	HIS	-	expression tag	UNP A0A0A3CUI3
h	11	MET	-	expression tag	UNP A0A0A3CUI3
h	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
h	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3

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Chain	Residue	Modelled	Actual	Comment	Reference
h	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
h	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
h	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
h	165	LEU	-	expression tag	UNP A0A0A3CUI3
h	166	GLU	-	expression tag	UNP A0A0A3CUI3
h	167	HIS	-	expression tag	UNP A0A0A3CUI3
h	168	HIS	-	expression tag	UNP A0A0A3CUI3
h	169	HIS	-	expression tag	UNP A0A0A3CUI3
h	170	HIS	-	expression tag	UNP A0A0A3CUI3
h	171	HIS	-	expression tag	UNP A0A0A3CUI3
h	172	HIS	-	expression tag	UNP A0A0A3CUI3
g	11	MET	-	expression tag	UNP A0A0A3CUI3
g	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
g	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
g	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
g	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
g	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
g	165	LEU	-	expression tag	UNP A0A0A3CUI3
g	166	GLU	-	expression tag	UNP A0A0A3CUI3
g	167	HIS	-	expression tag	UNP A0A0A3CUI3
g	168	HIS	-	expression tag	UNP A0A0A3CUI3
g	169	HIS	-	expression tag	UNP A0A0A3CUI3
g	170	HIS	-	expression tag	UNP A0A0A3CUI3
g	171	HIS	-	expression tag	UNP A0A0A3CUI3
g	172	HIS	-	expression tag	UNP A0A0A3CUI3
i	11	MET	-	expression tag	UNP A0A0A3CUI3
i	29	LEU	ARG	engineered mutation	UNP A0A0A3CUI3
i	30	GLU	LYS	engineered mutation	UNP A0A0A3CUI3
i	33	ALA	ASP	engineered mutation	UNP A0A0A3CUI3
i	40	ILE	VAL	engineered mutation	UNP A0A0A3CUI3
i	50	ALA	GLU	engineered mutation	UNP A0A0A3CUI3
i	165	LEU	-	expression tag	UNP A0A0A3CUI3
i	166	GLU	-	expression tag	UNP A0A0A3CUI3
i	167	HIS	-	expression tag	UNP A0A0A3CUI3
i	168	HIS	-	expression tag	UNP A0A0A3CUI3
i	169	HIS	-	expression tag	UNP A0A0A3CUI3
i	170	HIS	-	expression tag	UNP A0A0A3CUI3
i	171	HIS	-	expression tag	UNP A0A0A3CUI3
i	172	HIS	-	expression tag	UNP A0A0A3CUI3

- Molecule 2 is a protein called Phosphotransferase system, mannose/fructose-specific component IIA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	H	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	G	131	Total	C	N	O	S	0	0	0
			996	646	159	185	6			
2	I	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	J	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	P	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	Q	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	S	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	R	131	Total	C	N	O	S	0	0	0
			1008	653	160	189	6			
2	T	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	b	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	d	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	c	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	Z	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	a	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	j	131	Total	C	N	O	S	0	0	0
			1004	651	160	187	6			
2	k	131	Total	C	N	O	S	0	0	0
			1008	653	160	189	6			
2	m	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			
2	l	131	Total	C	N	O	S	0	0	0
			996	647	160	183	6			
2	n	131	Total	C	N	O	S	0	0	0
			1000	649	160	185	6			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	MET	-	expression tag	UNP Q8RD55
F	0	GLY	-	expression tag	UNP Q8RD55
F	45	LYS	VAL	engineered mutation	UNP Q8RD55
F	47	ALA	ARG	engineered mutation	UNP Q8RD55
F	51	MET	GLU	engineered mutation	UNP Q8RD55
F	52	ARG	LYS	engineered mutation	UNP Q8RD55
F	55	ILE	LYS	engineered mutation	UNP Q8RD55
F	56	ALA	GLU	engineered mutation	UNP Q8RD55
F	59	ALA	GLN	engineered mutation	UNP Q8RD55
F	81	GLU	SER	engineered mutation	UNP Q8RD55
F	85	THR	GLU	engineered mutation	UNP Q8RD55
F	86	PHE	TYR	engineered mutation	UNP Q8RD55
H	-1	MET	-	expression tag	UNP Q8RD55
H	0	GLY	-	expression tag	UNP Q8RD55
H	45	LYS	VAL	engineered mutation	UNP Q8RD55
H	47	ALA	ARG	engineered mutation	UNP Q8RD55
H	51	MET	GLU	engineered mutation	UNP Q8RD55
H	52	ARG	LYS	engineered mutation	UNP Q8RD55
H	55	ILE	LYS	engineered mutation	UNP Q8RD55
H	56	ALA	GLU	engineered mutation	UNP Q8RD55
H	59	ALA	GLN	engineered mutation	UNP Q8RD55
H	81	GLU	SER	engineered mutation	UNP Q8RD55
H	85	THR	GLU	engineered mutation	UNP Q8RD55
H	86	PHE	TYR	engineered mutation	UNP Q8RD55
G	-1	MET	-	expression tag	UNP Q8RD55
G	0	GLY	-	expression tag	UNP Q8RD55
G	45	LYS	VAL	engineered mutation	UNP Q8RD55
G	47	ALA	ARG	engineered mutation	UNP Q8RD55
G	51	MET	GLU	engineered mutation	UNP Q8RD55
G	52	ARG	LYS	engineered mutation	UNP Q8RD55
G	55	ILE	LYS	engineered mutation	UNP Q8RD55
G	56	ALA	GLU	engineered mutation	UNP Q8RD55
G	59	ALA	GLN	engineered mutation	UNP Q8RD55
G	81	GLU	SER	engineered mutation	UNP Q8RD55
G	85	THR	GLU	engineered mutation	UNP Q8RD55
G	86	PHE	TYR	engineered mutation	UNP Q8RD55
I	-1	MET	-	expression tag	UNP Q8RD55
I	0	GLY	-	expression tag	UNP Q8RD55
I	45	LYS	VAL	engineered mutation	UNP Q8RD55
I	47	ALA	ARG	engineered mutation	UNP Q8RD55
I	51	MET	GLU	engineered mutation	UNP Q8RD55
I	52	ARG	LYS	engineered mutation	UNP Q8RD55
I	55	ILE	LYS	engineered mutation	UNP Q8RD55

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Chain	Residue	Modelled	Actual	Comment	Reference
I	56	ALA	GLU	engineered mutation	UNP Q8RD55
I	59	ALA	GLN	engineered mutation	UNP Q8RD55
I	81	GLU	SER	engineered mutation	UNP Q8RD55
I	85	THR	GLU	engineered mutation	UNP Q8RD55
I	86	PHE	TYR	engineered mutation	UNP Q8RD55
J	-1	MET	-	expression tag	UNP Q8RD55
J	0	GLY	-	expression tag	UNP Q8RD55
J	45	LYS	VAL	engineered mutation	UNP Q8RD55
J	47	ALA	ARG	engineered mutation	UNP Q8RD55
J	51	MET	GLU	engineered mutation	UNP Q8RD55
J	52	ARG	LYS	engineered mutation	UNP Q8RD55
J	55	ILE	LYS	engineered mutation	UNP Q8RD55
J	56	ALA	GLU	engineered mutation	UNP Q8RD55
J	59	ALA	GLN	engineered mutation	UNP Q8RD55
J	81	GLU	SER	engineered mutation	UNP Q8RD55
J	85	THR	GLU	engineered mutation	UNP Q8RD55
J	86	PHE	TYR	engineered mutation	UNP Q8RD55
P	-1	MET	-	expression tag	UNP Q8RD55
P	0	GLY	-	expression tag	UNP Q8RD55
P	45	LYS	VAL	engineered mutation	UNP Q8RD55
P	47	ALA	ARG	engineered mutation	UNP Q8RD55
P	51	MET	GLU	engineered mutation	UNP Q8RD55
P	52	ARG	LYS	engineered mutation	UNP Q8RD55
P	55	ILE	LYS	engineered mutation	UNP Q8RD55
P	56	ALA	GLU	engineered mutation	UNP Q8RD55
P	59	ALA	GLN	engineered mutation	UNP Q8RD55
P	81	GLU	SER	engineered mutation	UNP Q8RD55
P	85	THR	GLU	engineered mutation	UNP Q8RD55
P	86	PHE	TYR	engineered mutation	UNP Q8RD55
Q	-1	MET	-	expression tag	UNP Q8RD55
Q	0	GLY	-	expression tag	UNP Q8RD55
Q	45	LYS	VAL	engineered mutation	UNP Q8RD55
Q	47	ALA	ARG	engineered mutation	UNP Q8RD55
Q	51	MET	GLU	engineered mutation	UNP Q8RD55
Q	52	ARG	LYS	engineered mutation	UNP Q8RD55
Q	55	ILE	LYS	engineered mutation	UNP Q8RD55
Q	56	ALA	GLU	engineered mutation	UNP Q8RD55
Q	59	ALA	GLN	engineered mutation	UNP Q8RD55
Q	81	GLU	SER	engineered mutation	UNP Q8RD55
Q	85	THR	GLU	engineered mutation	UNP Q8RD55
Q	86	PHE	TYR	engineered mutation	UNP Q8RD55
S	-1	MET	-	expression tag	UNP Q8RD55

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Chain	Residue	Modelled	Actual	Comment	Reference
S	0	GLY	-	expression tag	UNP Q8RD55
S	45	LYS	VAL	engineered mutation	UNP Q8RD55
S	47	ALA	ARG	engineered mutation	UNP Q8RD55
S	51	MET	GLU	engineered mutation	UNP Q8RD55
S	52	ARG	LYS	engineered mutation	UNP Q8RD55
S	55	ILE	LYS	engineered mutation	UNP Q8RD55
S	56	ALA	GLU	engineered mutation	UNP Q8RD55
S	59	ALA	GLN	engineered mutation	UNP Q8RD55
S	81	GLU	SER	engineered mutation	UNP Q8RD55
S	85	THR	GLU	engineered mutation	UNP Q8RD55
S	86	PHE	TYR	engineered mutation	UNP Q8RD55
R	-1	MET	-	expression tag	UNP Q8RD55
R	0	GLY	-	expression tag	UNP Q8RD55
R	45	LYS	VAL	engineered mutation	UNP Q8RD55
R	47	ALA	ARG	engineered mutation	UNP Q8RD55
R	51	MET	GLU	engineered mutation	UNP Q8RD55
R	52	ARG	LYS	engineered mutation	UNP Q8RD55
R	55	ILE	LYS	engineered mutation	UNP Q8RD55
R	56	ALA	GLU	engineered mutation	UNP Q8RD55
R	59	ALA	GLN	engineered mutation	UNP Q8RD55
R	81	GLU	SER	engineered mutation	UNP Q8RD55
R	85	THR	GLU	engineered mutation	UNP Q8RD55
R	86	PHE	TYR	engineered mutation	UNP Q8RD55
T	-1	MET	-	expression tag	UNP Q8RD55
T	0	GLY	-	expression tag	UNP Q8RD55
T	45	LYS	VAL	engineered mutation	UNP Q8RD55
T	47	ALA	ARG	engineered mutation	UNP Q8RD55
T	51	MET	GLU	engineered mutation	UNP Q8RD55
T	52	ARG	LYS	engineered mutation	UNP Q8RD55
T	55	ILE	LYS	engineered mutation	UNP Q8RD55
T	56	ALA	GLU	engineered mutation	UNP Q8RD55
T	59	ALA	GLN	engineered mutation	UNP Q8RD55
T	81	GLU	SER	engineered mutation	UNP Q8RD55
T	85	THR	GLU	engineered mutation	UNP Q8RD55
T	86	PHE	TYR	engineered mutation	UNP Q8RD55
b	-1	MET	-	expression tag	UNP Q8RD55
b	0	GLY	-	expression tag	UNP Q8RD55
b	45	LYS	VAL	engineered mutation	UNP Q8RD55
b	47	ALA	ARG	engineered mutation	UNP Q8RD55
b	51	MET	GLU	engineered mutation	UNP Q8RD55
b	52	ARG	LYS	engineered mutation	UNP Q8RD55
b	55	ILE	LYS	engineered mutation	UNP Q8RD55

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Chain	Residue	Modelled	Actual	Comment	Reference
b	56	ALA	GLU	engineered mutation	UNP Q8RD55
b	59	ALA	GLN	engineered mutation	UNP Q8RD55
b	81	GLU	SER	engineered mutation	UNP Q8RD55
b	85	THR	GLU	engineered mutation	UNP Q8RD55
b	86	PHE	TYR	engineered mutation	UNP Q8RD55
d	-1	MET	-	expression tag	UNP Q8RD55
d	0	GLY	-	expression tag	UNP Q8RD55
d	45	LYS	VAL	engineered mutation	UNP Q8RD55
d	47	ALA	ARG	engineered mutation	UNP Q8RD55
d	51	MET	GLU	engineered mutation	UNP Q8RD55
d	52	ARG	LYS	engineered mutation	UNP Q8RD55
d	55	ILE	LYS	engineered mutation	UNP Q8RD55
d	56	ALA	GLU	engineered mutation	UNP Q8RD55
d	59	ALA	GLN	engineered mutation	UNP Q8RD55
d	81	GLU	SER	engineered mutation	UNP Q8RD55
d	85	THR	GLU	engineered mutation	UNP Q8RD55
d	86	PHE	TYR	engineered mutation	UNP Q8RD55
c	-1	MET	-	expression tag	UNP Q8RD55
c	0	GLY	-	expression tag	UNP Q8RD55
c	45	LYS	VAL	engineered mutation	UNP Q8RD55
c	47	ALA	ARG	engineered mutation	UNP Q8RD55
c	51	MET	GLU	engineered mutation	UNP Q8RD55
c	52	ARG	LYS	engineered mutation	UNP Q8RD55
c	55	ILE	LYS	engineered mutation	UNP Q8RD55
c	56	ALA	GLU	engineered mutation	UNP Q8RD55
c	59	ALA	GLN	engineered mutation	UNP Q8RD55
c	81	GLU	SER	engineered mutation	UNP Q8RD55
c	85	THR	GLU	engineered mutation	UNP Q8RD55
c	86	PHE	TYR	engineered mutation	UNP Q8RD55
Z	-1	MET	-	expression tag	UNP Q8RD55
Z	0	GLY	-	expression tag	UNP Q8RD55
Z	45	LYS	VAL	engineered mutation	UNP Q8RD55
Z	47	ALA	ARG	engineered mutation	UNP Q8RD55
Z	51	MET	GLU	engineered mutation	UNP Q8RD55
Z	52	ARG	LYS	engineered mutation	UNP Q8RD55
Z	55	ILE	LYS	engineered mutation	UNP Q8RD55
Z	56	ALA	GLU	engineered mutation	UNP Q8RD55
Z	59	ALA	GLN	engineered mutation	UNP Q8RD55
Z	81	GLU	SER	engineered mutation	UNP Q8RD55
Z	85	THR	GLU	engineered mutation	UNP Q8RD55
Z	86	PHE	TYR	engineered mutation	UNP Q8RD55
a	-1	MET	-	expression tag	UNP Q8RD55

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Chain	Residue	Modelled	Actual	Comment	Reference
a	0	GLY	-	expression tag	UNP Q8RD55
a	45	LYS	VAL	engineered mutation	UNP Q8RD55
a	47	ALA	ARG	engineered mutation	UNP Q8RD55
a	51	MET	GLU	engineered mutation	UNP Q8RD55
a	52	ARG	LYS	engineered mutation	UNP Q8RD55
a	55	ILE	LYS	engineered mutation	UNP Q8RD55
a	56	ALA	GLU	engineered mutation	UNP Q8RD55
a	59	ALA	GLN	engineered mutation	UNP Q8RD55
a	81	GLU	SER	engineered mutation	UNP Q8RD55
a	85	THR	GLU	engineered mutation	UNP Q8RD55
a	86	PHE	TYR	engineered mutation	UNP Q8RD55
j	-1	MET	-	expression tag	UNP Q8RD55
j	0	GLY	-	expression tag	UNP Q8RD55
j	45	LYS	VAL	engineered mutation	UNP Q8RD55
j	47	ALA	ARG	engineered mutation	UNP Q8RD55
j	51	MET	GLU	engineered mutation	UNP Q8RD55
j	52	ARG	LYS	engineered mutation	UNP Q8RD55
j	55	ILE	LYS	engineered mutation	UNP Q8RD55
j	56	ALA	GLU	engineered mutation	UNP Q8RD55
j	59	ALA	GLN	engineered mutation	UNP Q8RD55
j	81	GLU	SER	engineered mutation	UNP Q8RD55
j	85	THR	GLU	engineered mutation	UNP Q8RD55
j	86	PHE	TYR	engineered mutation	UNP Q8RD55
k	-1	MET	-	expression tag	UNP Q8RD55
k	0	GLY	-	expression tag	UNP Q8RD55
k	45	LYS	VAL	engineered mutation	UNP Q8RD55
k	47	ALA	ARG	engineered mutation	UNP Q8RD55
k	51	MET	GLU	engineered mutation	UNP Q8RD55
k	52	ARG	LYS	engineered mutation	UNP Q8RD55
k	55	ILE	LYS	engineered mutation	UNP Q8RD55
k	56	ALA	GLU	engineered mutation	UNP Q8RD55
k	59	ALA	GLN	engineered mutation	UNP Q8RD55
k	81	GLU	SER	engineered mutation	UNP Q8RD55
k	85	THR	GLU	engineered mutation	UNP Q8RD55
k	86	PHE	TYR	engineered mutation	UNP Q8RD55
m	-1	MET	-	expression tag	UNP Q8RD55
m	0	GLY	-	expression tag	UNP Q8RD55
m	45	LYS	VAL	engineered mutation	UNP Q8RD55
m	47	ALA	ARG	engineered mutation	UNP Q8RD55
m	51	MET	GLU	engineered mutation	UNP Q8RD55
m	52	ARG	LYS	engineered mutation	UNP Q8RD55
m	55	ILE	LYS	engineered mutation	UNP Q8RD55

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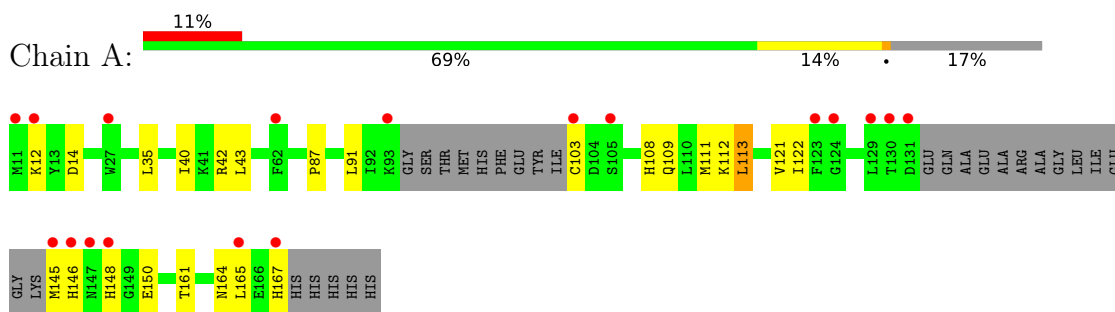
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Chain	Residue	Modelled	Actual	Comment	Reference
m	56	ALA	GLU	engineered mutation	UNP Q8RD55
m	59	ALA	GLN	engineered mutation	UNP Q8RD55
m	81	GLU	SER	engineered mutation	UNP Q8RD55
m	85	THR	GLU	engineered mutation	UNP Q8RD55
m	86	PHE	TYR	engineered mutation	UNP Q8RD55
l	-1	MET	-	expression tag	UNP Q8RD55
l	0	GLY	-	expression tag	UNP Q8RD55
l	45	LYS	VAL	engineered mutation	UNP Q8RD55
l	47	ALA	ARG	engineered mutation	UNP Q8RD55
l	51	MET	GLU	engineered mutation	UNP Q8RD55
l	52	ARG	LYS	engineered mutation	UNP Q8RD55
l	55	ILE	LYS	engineered mutation	UNP Q8RD55
l	56	ALA	GLU	engineered mutation	UNP Q8RD55
l	59	ALA	GLN	engineered mutation	UNP Q8RD55
l	81	GLU	SER	engineered mutation	UNP Q8RD55
l	85	THR	GLU	engineered mutation	UNP Q8RD55
l	86	PHE	TYR	engineered mutation	UNP Q8RD55
n	-1	MET	-	expression tag	UNP Q8RD55
n	0	GLY	-	expression tag	UNP Q8RD55
n	45	LYS	VAL	engineered mutation	UNP Q8RD55
n	47	ALA	ARG	engineered mutation	UNP Q8RD55
n	51	MET	GLU	engineered mutation	UNP Q8RD55
n	52	ARG	LYS	engineered mutation	UNP Q8RD55
n	55	ILE	LYS	engineered mutation	UNP Q8RD55
n	56	ALA	GLU	engineered mutation	UNP Q8RD55
n	59	ALA	GLN	engineered mutation	UNP Q8RD55
n	81	GLU	SER	engineered mutation	UNP Q8RD55
n	85	THR	GLU	engineered mutation	UNP Q8RD55
n	86	PHE	TYR	engineered mutation	UNP Q8RD55

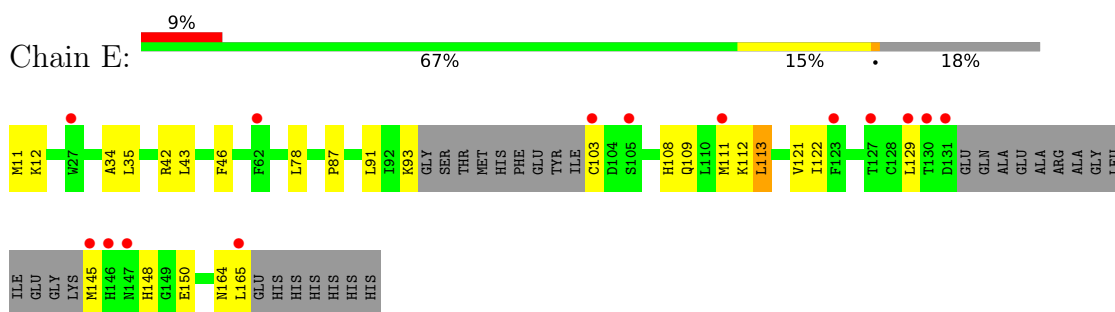
### 3 Residue-property plots [i](#)

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

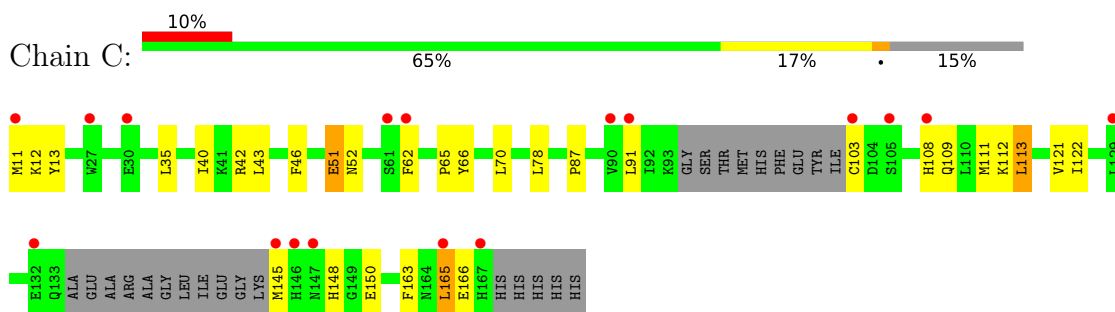
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

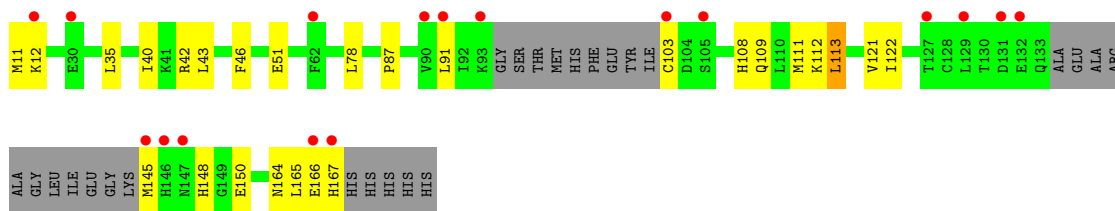


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

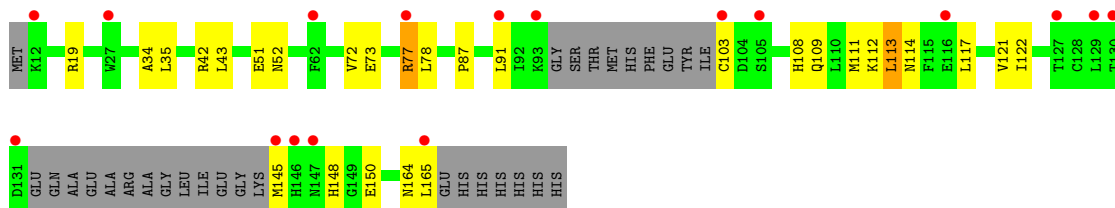


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

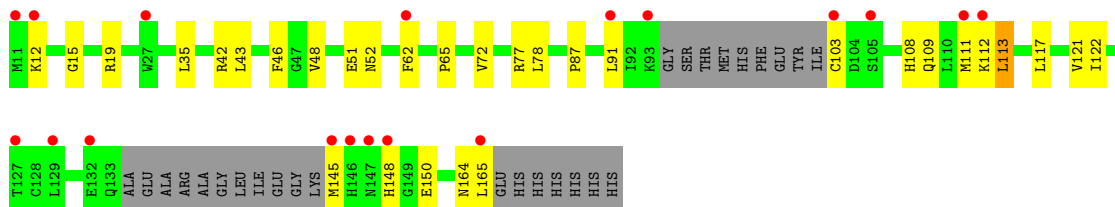




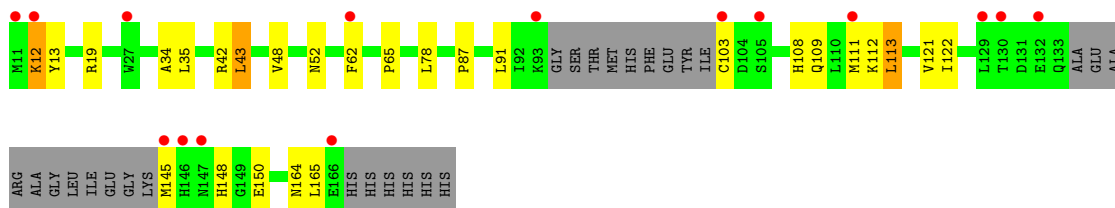
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



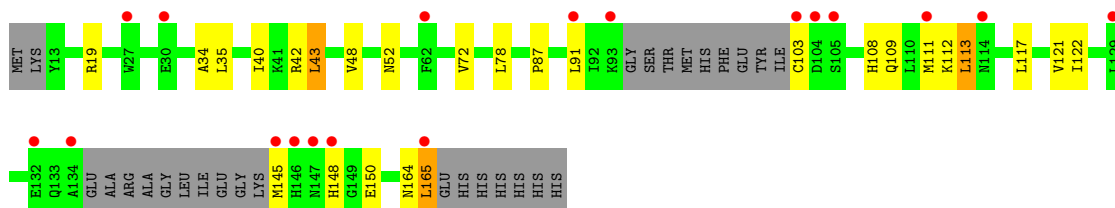
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



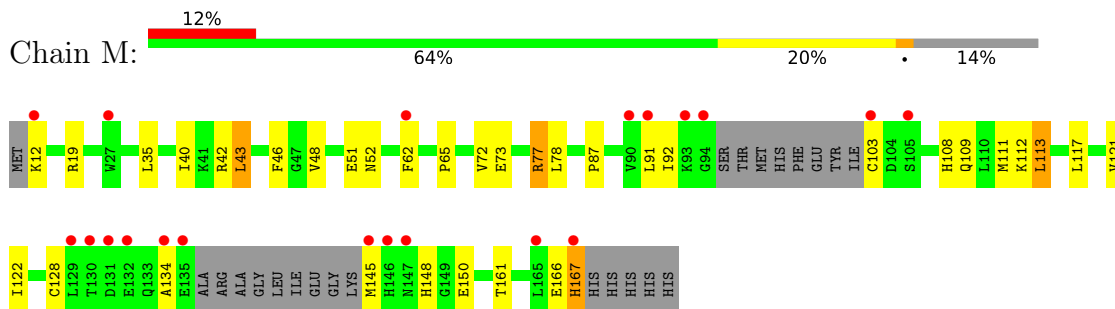
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



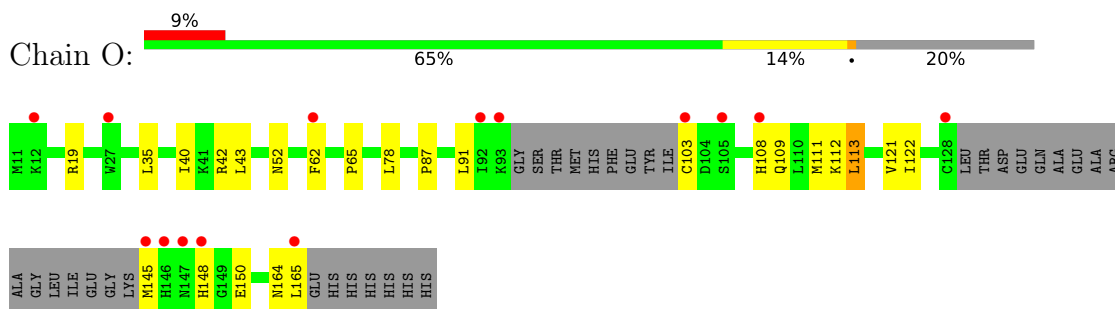
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



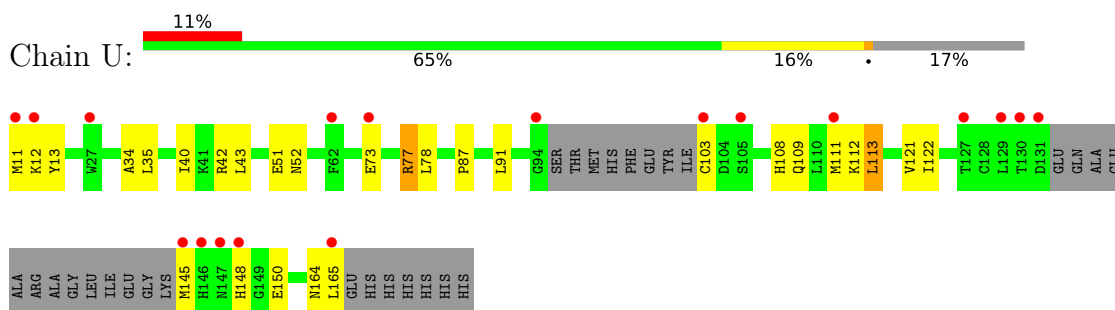
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



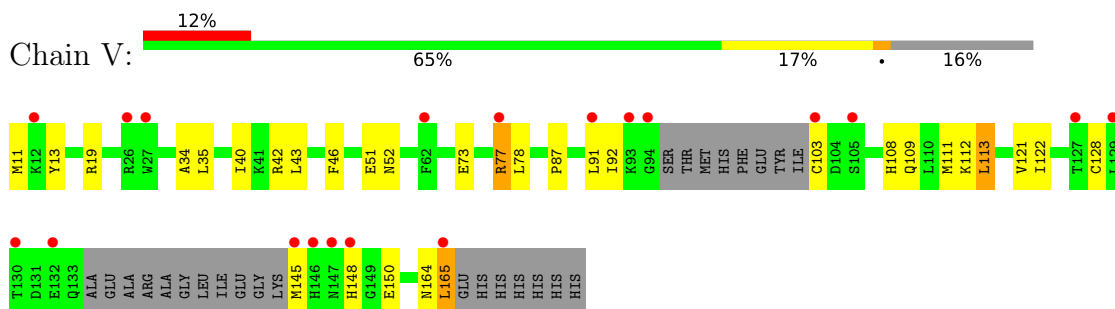
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



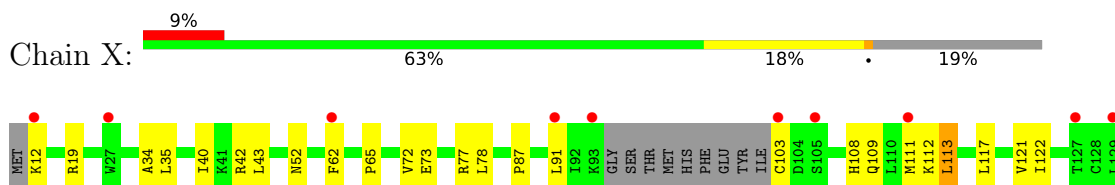
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

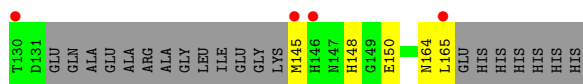


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

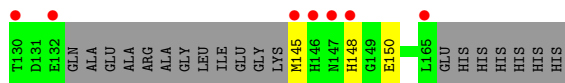
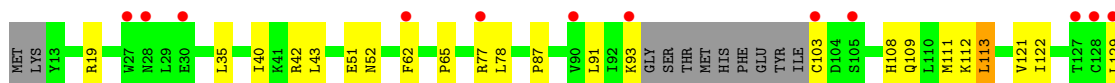


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

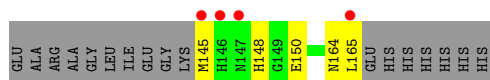
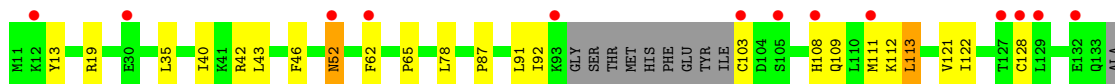




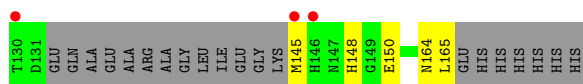
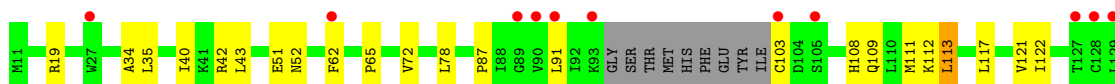
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



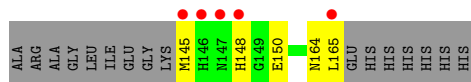
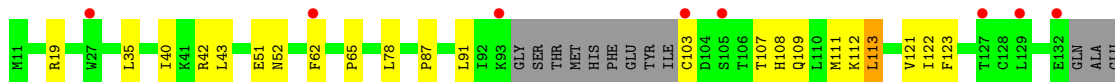
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



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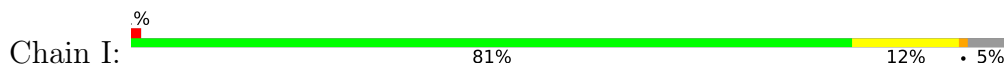
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase







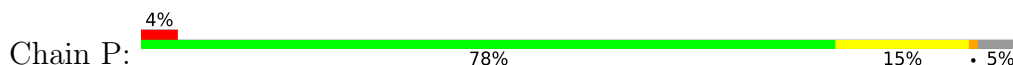
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



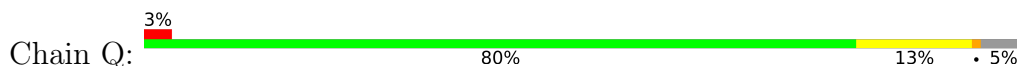
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



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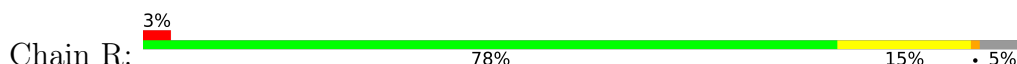
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



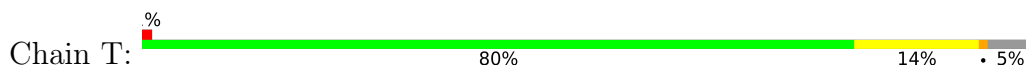
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



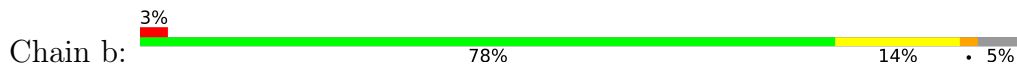
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



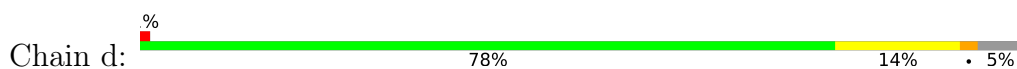
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



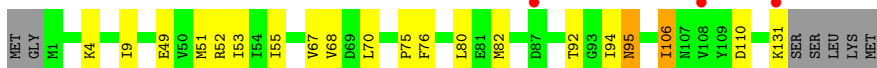
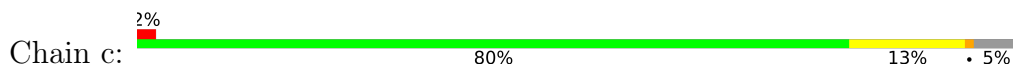
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



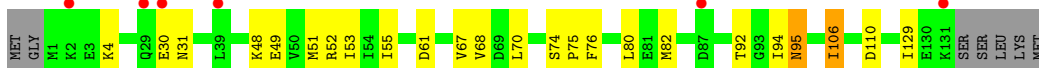
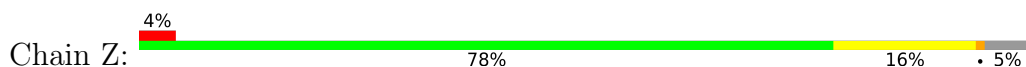
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



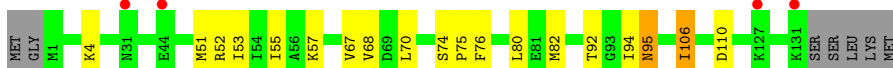
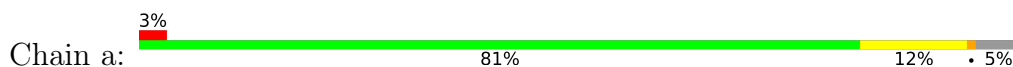
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA



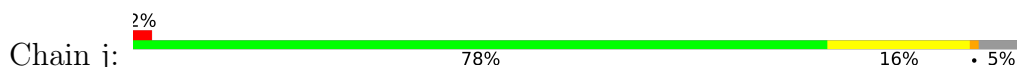
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA




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Chain k: 




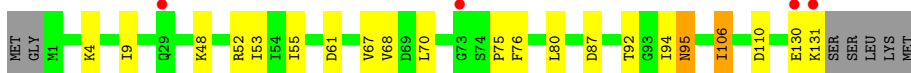
- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA

Chain m: 




- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA

Chain l: 



- Molecule 2: Phosphotransferase system, mannose/fructose-specific component IIA

Chain n: 



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	258.82Å 258.82Å 641.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	110.72 – 3.50 110.72 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (110.72-3.50) 99.1 (110.72-3.50)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 3.49Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.227 , 0.233 0.229 , 0.235	Depositor DCC
$R_{free}$ test set	20042 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	104.8	Xtrriage
Anisotropy	0.073	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 68.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for $-1/3^*h+1/3^*k+1/3^*l,-k,8/3^*h+4/3^*k+1/3^*l$ 0.000 for $-2/3^*h-1/3^*k-1/3^*l,-1/3^*h-2/3^*k+1/3^*l,-4/3^*h+4/3^*k+1/3^*l$ 0.000 for $-h,1/3^*h-1/3^*k-1/3^*l,-4/3^*h-8/3^*k+1/3^*l$ 0.000 for $-h,2/3^*h+1/3^*k+1/3^*l,4/3^*h+8/3^*k-1/3^*l$ 0.000 for $1/3^*h+2/3^*k-1/3^*l,-k,-8/3^*h-4/3^*k-1/3^*l$ 0.000 for $-1/3^*h-2/3^*k+1/3^*l,-2/3^*h-1/3^*k-1/3^*l,4/3^*h-4/3^*k-1/3^*l$ 0.000 for $-h-k,k,-l$	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	40538	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	103.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.91% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.52	0/1049	0.80	0/1417
1	B	0.49	0/1069	0.83	0/1442
1	C	0.52	0/1069	0.88	4/1444 (0.3%)
1	D	0.56	0/1030	0.83	0/1389
1	E	0.54	0/1033	0.83	0/1394
1	K	0.50	0/1049	0.83	0/1416
1	L	0.57	0/1062	0.87	2/1433 (0.1%)
1	M	0.50	0/1090	0.87	0/1469
1	N	0.55	0/1040	0.84	0/1405
1	O	0.54	0/1010	0.83	0/1362
1	U	0.50	0/1035	0.88	2/1398 (0.1%)
1	V	0.56	0/1053	0.84	0/1421
1	W	0.53	0/1026	0.84	0/1385
1	X	0.54	0/1030	0.83	0/1390
1	Y	0.47	0/1032	0.85	1/1393 (0.1%)
1	e	0.54	0/1035	0.83	0/1397
1	f	0.54	0/1044	0.84	0/1409
1	g	0.52	0/1012	0.84	0/1365
1	h	0.52	0/1025	0.85	1/1384 (0.1%)
1	i	0.52	0/1043	0.87	1/1410 (0.1%)
2	F	0.53	0/1009	0.82	1/1356 (0.1%)
2	G	0.55	0/1005	0.83	1/1352 (0.1%)
2	H	0.53	0/1013	0.82	1/1361 (0.1%)
2	I	0.52	0/1009	0.81	0/1356
2	J	0.53	0/1013	0.83	1/1361 (0.1%)
2	P	0.54	0/1013	0.81	1/1361 (0.1%)
2	Q	0.54	0/1013	0.80	0/1361
2	R	0.52	0/1017	0.81	1/1366 (0.1%)
2	S	0.55	0/1009	0.82	1/1356 (0.1%)
2	T	0.53	0/1013	0.83	1/1361 (0.1%)
2	Z	0.53	0/1013	0.85	2/1361 (0.1%)
2	a	0.53	0/1013	0.82	1/1361 (0.1%)
2	b	0.54	0/1009	0.85	2/1356 (0.1%)
2	c	0.53	0/1009	0.83	1/1356 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	d	0.55	0/1013	0.83	0/1361
2	j	0.54	0/1013	0.83	1/1361 (0.1%)
2	k	0.54	0/1017	0.84	1/1366 (0.1%)
2	l	0.54	0/1005	0.83	1/1351 (0.1%)
2	m	0.56	0/1009	0.83	1/1356 (0.1%)
2	n	0.53	0/1009	0.86	3/1356 (0.2%)
All	All	0.53	0/41060	0.84	32/55299 (0.1%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	n	53	ILE	N-CA-C	8.24	119.03	110.62
2	b	53	ILE	N-CA-C	8.11	118.89	110.62
1	C	163	PHE	N-CA-C	7.89	121.72	112.72
2	G	53	ILE	N-CA-C	6.74	117.49	110.62
2	c	53	ILE	N-CA-C	6.58	117.34	110.62

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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	1031	0	1048	33	0
1	B	1051	0	1076	30	0
1	C	1051	0	1062	35	0
1	D	1013	0	1051	37	0
1	E	1016	0	1046	35	0
1	K	1032	0	1056	45	0
1	L	1045	0	1066	38	0
1	M	1072	0	1096	43	0
1	N	1023	0	1046	33	0
1	O	993	0	1024	31	0
1	U	1018	0	1038	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	1036	0	1059	39	0
1	W	1009	0	1040	30	0
1	X	1013	0	1044	33	0
1	Y	1017	0	1037	34	0
1	e	1018	0	1046	31	0
1	f	1027	0	1052	30	0
1	g	995	0	1024	32	0
1	h	1008	0	1034	32	0
1	i	1026	0	1041	34	0
2	F	1000	0	1074	28	0
2	G	996	0	1063	16	0
2	H	1004	0	1078	18	0
2	I	1000	0	1074	16	0
2	J	1004	0	1078	17	0
2	P	1004	0	1078	15	0
2	Q	1004	0	1078	24	0
2	R	1008	0	1082	14	0
2	S	1000	0	1074	27	0
2	T	1004	0	1078	17	0
2	Z	1004	0	1078	18	0
2	a	1004	0	1078	15	0
2	b	1000	0	1074	17	0
2	c	1000	0	1074	12	0
2	d	1004	0	1078	18	0
2	j	1004	0	1078	17	0
2	k	1008	0	1082	21	0
2	l	996	0	1070	14	0
2	m	1000	0	1074	23	0
2	n	1000	0	1074	13	0
All	All	40538	0	42503	823	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 10.

The worst 5 of 823 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:M:12:LYS:HB2	1:M:46:PHE:HE2	1.32	0.94
2:F:14:PHE:HE1	2:S:14:PHE:HE1	1.11	0.93
2:Q:14:PHE:HE1	2:k:14:PHE:HE1	1.14	0.91
2:Q:129:ILE:HD11	2:k:76:PHE:HE1	1.37	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:52:ARG:NH1	2:Q:52:ARG:HB2	1.85	0.90

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	129/162 (80%)	127 (98%)	2 (2%)	0	100	100
1	B	131/162 (81%)	129 (98%)	2 (2%)	0	100	100
1	C	131/162 (81%)	128 (98%)	3 (2%)	0	100	100
1	D	126/162 (78%)	124 (98%)	2 (2%)	0	100	100
1	E	127/162 (78%)	125 (98%)	2 (2%)	0	100	100
1	K	129/162 (80%)	127 (98%)	2 (2%)	0	100	100
1	L	130/162 (80%)	127 (98%)	3 (2%)	0	100	100
1	M	133/162 (82%)	131 (98%)	2 (2%)	0	100	100
1	N	128/162 (79%)	126 (98%)	2 (2%)	0	100	100
1	O	124/162 (76%)	121 (98%)	3 (2%)	0	100	100
1	U	128/162 (79%)	125 (98%)	3 (2%)	0	100	100
1	V	130/162 (80%)	127 (98%)	3 (2%)	0	100	100
1	W	126/162 (78%)	124 (98%)	2 (2%)	0	100	100
1	X	126/162 (78%)	124 (98%)	2 (2%)	0	100	100
1	Y	129/162 (80%)	126 (98%)	3 (2%)	0	100	100
1	e	127/162 (78%)	125 (98%)	2 (2%)	0	100	100
1	f	128/162 (79%)	126 (98%)	2 (2%)	0	100	100
1	g	124/162 (76%)	122 (98%)	2 (2%)	0	100	100
1	h	127/162 (78%)	124 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	i	129/162 (80%)	125 (97%)	4 (3%)	0	100	100
2	F	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	G	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	H	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	I	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	J	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	P	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	Q	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	R	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	S	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	T	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	Z	129/138 (94%)	127 (98%)	2 (2%)	0	100	100
2	a	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	b	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	c	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	d	129/138 (94%)	127 (98%)	2 (2%)	0	100	100
2	j	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	k	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	l	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	m	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
2	n	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
All	All	5142/6000 (86%)	5071 (99%)	71 (1%)	0	100	100

There are no Ramachandran outliers to report.

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	107/133 (80%)	104 (97%)	3 (3%)	38	61
1	B	109/133 (82%)	104 (95%)	5 (5%)	24	50
1	C	109/133 (82%)	104 (95%)	5 (5%)	24	50
1	D	106/133 (80%)	100 (94%)	6 (6%)	18	45
1	E	106/133 (80%)	102 (96%)	4 (4%)	29	55
1	K	107/133 (80%)	102 (95%)	5 (5%)	23	49
1	L	109/133 (82%)	104 (95%)	5 (5%)	24	50
1	M	112/133 (84%)	105 (94%)	7 (6%)	16	42
1	N	106/133 (80%)	101 (95%)	5 (5%)	23	49
1	O	103/133 (77%)	99 (96%)	4 (4%)	28	54
1	U	105/133 (79%)	100 (95%)	5 (5%)	23	49
1	V	107/133 (80%)	100 (94%)	7 (6%)	15	42
1	W	105/133 (79%)	99 (94%)	6 (6%)	18	45
1	X	106/133 (80%)	102 (96%)	4 (4%)	29	55
1	Y	105/133 (79%)	101 (96%)	4 (4%)	29	55
1	e	106/133 (80%)	101 (95%)	5 (5%)	23	49
1	f	107/133 (80%)	102 (95%)	5 (5%)	23	49
1	g	103/133 (77%)	99 (96%)	4 (4%)	28	54
1	h	104/133 (78%)	98 (94%)	6 (6%)	18	44
1	i	106/133 (80%)	100 (94%)	6 (6%)	18	45
2	F	112/120 (93%)	109 (97%)	3 (3%)	39	62
2	G	111/120 (92%)	108 (97%)	3 (3%)	39	62
2	H	113/120 (94%)	108 (96%)	5 (4%)	25	51
2	I	112/120 (93%)	107 (96%)	5 (4%)	24	50
2	J	113/120 (94%)	108 (96%)	5 (4%)	25	51
2	P	113/120 (94%)	110 (97%)	3 (3%)	39	62
2	Q	113/120 (94%)	110 (97%)	3 (3%)	39	62
2	R	114/120 (95%)	109 (96%)	5 (4%)	25	51
2	S	112/120 (93%)	109 (97%)	3 (3%)	39	62
2	T	113/120 (94%)	109 (96%)	4 (4%)	32	57
2	Z	113/120 (94%)	110 (97%)	3 (3%)	39	62
2	a	113/120 (94%)	110 (97%)	3 (3%)	39	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	112/120 (93%)	109 (97%)	3 (3%)	39	62
2	c	112/120 (93%)	108 (96%)	4 (4%)	31	57
2	d	113/120 (94%)	109 (96%)	4 (4%)	32	57
2	j	113/120 (94%)	110 (97%)	3 (3%)	39	62
2	k	114/120 (95%)	110 (96%)	4 (4%)	32	57
2	l	111/120 (92%)	107 (96%)	4 (4%)	31	57
2	m	112/120 (93%)	108 (96%)	4 (4%)	31	57
2	n	112/120 (93%)	109 (97%)	3 (3%)	39	62
All	All	4379/5060 (86%)	4204 (96%)	175 (4%)	28	54

5 of 175 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	95	ASN
1	h	78	LEU
2	d	106	ILE
2	a	106	ILE
1	g	148	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
2	R	95	ASN
2	m	33	HIS
1	Y	108	HIS
2	k	95	ASN
2	n	33	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	135/162 (83%)	0.69	18 (13%) 7 6	66, 93, 176, 231	0
1	B	137/162 (84%)	0.71	17 (12%) 8 6	55, 92, 168, 243	0
1	C	137/162 (84%)	0.70	17 (12%) 8 6	47, 73, 170, 239	0
1	D	132/162 (81%)	0.66	17 (12%) 7 6	47, 77, 158, 225	0
1	E	133/162 (82%)	0.61	14 (10%) 11 8	56, 86, 159, 236	0
1	K	135/162 (83%)	0.62	18 (13%) 7 6	55, 90, 167, 250	0
1	L	136/162 (83%)	0.60	15 (11%) 10 7	59, 89, 171, 245	0
1	M	139/162 (85%)	0.68	20 (14%) 6 5	58, 96, 192, 231	0
1	N	134/162 (82%)	0.64	18 (13%) 7 6	69, 98, 174, 256	0
1	O	130/162 (80%)	0.55	14 (10%) 11 8	64, 94, 154, 219	0
1	U	134/162 (82%)	0.67	18 (13%) 7 6	48, 77, 169, 229	0
1	V	136/162 (83%)	0.68	19 (13%) 6 5	44, 79, 178, 246	0
1	W	132/162 (81%)	0.60	19 (14%) 6 5	52, 82, 170, 226	0
1	X	132/162 (81%)	0.57	14 (10%) 11 8	61, 94, 168, 210	0
1	Y	135/162 (83%)	0.71	17 (12%) 8 6	58, 90, 179, 244	0
1	e	133/162 (82%)	0.57	14 (10%) 11 8	58, 91, 165, 222	0
1	f	134/162 (82%)	0.53	13 (9%) 13 9	64, 96, 173, 221	0
1	g	130/162 (80%)	0.67	16 (12%) 8 6	68, 96, 170, 203	0
1	h	133/162 (82%)	0.71	17 (12%) 7 6	60, 93, 161, 242	0
1	i	135/162 (83%)	0.65	16 (11%) 9 6	59, 87, 167, 245	0
2	F	131/138 (94%)	0.26	6 (4%) 37 20	78, 107, 158, 174	0
2	G	131/138 (94%)	0.24	3 (2%) 61 37	66, 92, 146, 184	0
2	H	131/138 (94%)	0.27	4 (3%) 51 29	55, 88, 149, 172	0
2	I	131/138 (94%)	0.24	1 (0%) 82 60	64, 97, 145, 176	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
2	J	131/138 (94%)	0.28	3 (2%) 61 37	73, 101, 146, 177	0
2	P	131/138 (94%)	0.20	6 (4%) 37 20	69, 101, 146, 168	0
2	Q	131/138 (94%)	0.26	4 (3%) 51 29	72, 96, 140, 166	0
2	R	131/138 (94%)	0.24	4 (3%) 51 29	75, 102, 150, 170	0
2	S	131/138 (94%)	0.24	4 (3%) 51 29	80, 109, 156, 174	0
2	T	131/138 (94%)	0.21	1 (0%) 82 60	65, 93, 146, 167	0
2	Z	131/138 (94%)	0.32	6 (4%) 37 20	72, 101, 152, 193	0
2	a	131/138 (94%)	0.17	4 (3%) 51 29	65, 92, 149, 166	0
2	b	131/138 (94%)	0.26	4 (3%) 51 29	62, 91, 142, 165	0
2	c	131/138 (94%)	0.17	3 (2%) 61 37	66, 93, 146, 181	0
2	d	131/138 (94%)	0.24	2 (1%) 72 47	78, 107, 157, 178	0
2	j	131/138 (94%)	0.30	3 (2%) 61 37	73, 99, 148, 163	0
2	k	131/138 (94%)	0.27	3 (2%) 61 37	76, 103, 154, 183	0
2	l	131/138 (94%)	0.22	4 (3%) 51 29	80, 108, 151, 190	0
2	m	131/138 (94%)	0.27	4 (3%) 51 29	66, 98, 151, 162	0
2	n	131/138 (94%)	0.19	5 (3%) 44 24	66, 88, 132, 147	0
All	All	5302/6000 (88%)	0.44	405 (7%) 20 13	44, 95, 160, 256	0

The worst 5 of 405 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	146	HIS	6.8
1	f	146	HIS	6.7
1	X	146	HIS	6.6
1	C	27	TRP	6.3
1	i	146	HIS	6.3

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.