



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2016 – 05:03 AM EDT

PDB ID : 5EC5
Title : Crystal structure of lysenin pore
Authors : Podobnik, M.; Savory, P.; Rojko, N.; Kisovec, M.; Bruce, M.; Jayasinghe, L.;
Anderluh, G.
Deposited on : 2015-10-20
Resolution : 3.10 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : **FAILED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

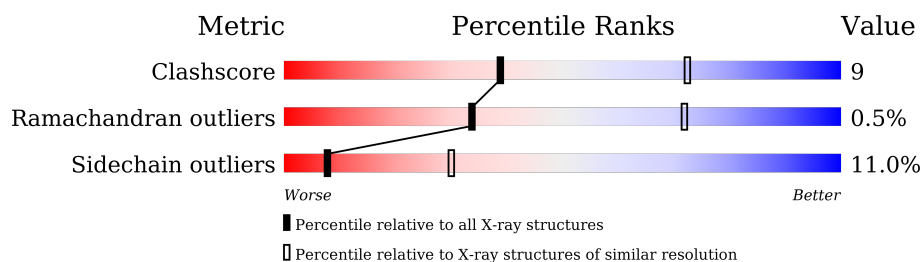
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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))
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)

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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	298	
1	B	298	
1	C	298	
1	D	298	
1	E	298	
1	F	298	
1	G	298	

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Mol	Chain	Length	Quality of chain
1	H	298	 70% 22% • 5%
1	I	298	 73% 19% • 5%
1	J	298	 75% 20% • •
1	K	298	 74% 20% • •
1	L	298	 74% 18% • 5%
1	M	298	 72% 22% • •
1	N	298	 76% 18% • •
1	O	298	 74% 21% • •
1	P	298	 72% 24% • •
1	R	298	 74% 18% • 5%
1	S	298	 73% 20% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MBO	A	302	-	-	X	-
2	MBO	B	301	-	-	X	-
2	MBO	C	301	-	-	X	-
2	MBO	D	301	-	-	X	-
2	MBO	E	301	-	-	X	-
2	MBO	F	302	-	-	X	-
2	MBO	G	301	-	-	X	-
2	MBO	H	301	-	-	X	-
2	MBO	H	302	-	-	X	-
2	MBO	I	302	-	-	X	-
2	MBO	K	301	-	-	X	-
2	MBO	K	302	-	-	X	-
2	MBO	L	301	-	-	X	-
2	MBO	L	302	-	-	X	-
2	MBO	M	301	-	-	X	-
2	MBO	O	301	-	-	X	-
2	MBO	P	302	-	-	X	-
2	MBO	R	301	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MBO	S	301	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 41248 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 Lysenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	0	0	0
			2301	1459	390	444	8			
1	B	284	Total	C	N	O	S	0	0	0
			2260	1432	384	436	8			
1	C	286	Total	C	N	O	S	0	0	0
			2268	1436	386	438	8			
1	D	285	Total	C	N	O	S	0	0	0
			2265	1435	385	437	8			
1	E	283	Total	C	N	O	S	0	0	0
			2252	1428	383	433	8			
1	F	283	Total	C	N	O	S	0	0	0
			2252	1428	383	433	8			
1	G	290	Total	C	N	O	S	0	0	0
			2301	1459	390	444	8			
1	H	283	Total	C	N	O	S	0	0	0
			2252	1428	383	433	8			
1	I	282	Total	C	N	O	S	0	0	0
			2248	1426	382	432	8			
1	J	290	Total	C	N	O	S	0	0	0
			2301	1459	390	444	8			
1	K	290	Total	C	N	O	S	0	0	0
			2301	1459	390	444	8			
1	L	284	Total	C	N	O	S	0	0	0
			2260	1434	384	434	8			
1	M	289	Total	C	N	O	S	0	0	0
			2297	1457	389	443	8			
1	N	289	Total	C	N	O	S	0	0	0
			2297	1457	389	443	8			
1	O	289	Total	C	N	O	S	0	0	0
			2297	1457	389	443	8			
1	P	289	Total	C	N	O	S	0	0	0
			2297	1457	389	443	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	283	Total	C	N	O	S	0	0	0
			2252	1428	383	433	8			
1	S	283	Total	C	N	O	S	0	0	0
			2252	1428	383	433	8			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP O18423
A	84	GLN	GLU	engineered mutation	UNP O18423
A	85	LYS	GLU	engineered mutation	UNP O18423
A	92	GLN	GLU	engineered mutation	UNP O18423
A	97	SER	GLU	engineered mutation	UNP O18423
A	126	GLY	ASP	engineered mutation	UNP O18423
B	0	GLY	-	expression tag	UNP O18423
B	84	GLN	GLU	engineered mutation	UNP O18423
B	85	LYS	GLU	engineered mutation	UNP O18423
B	92	GLN	GLU	engineered mutation	UNP O18423
B	97	SER	GLU	engineered mutation	UNP O18423
B	126	GLY	ASP	engineered mutation	UNP O18423
C	0	GLY	-	expression tag	UNP O18423
C	84	GLN	GLU	engineered mutation	UNP O18423
C	85	LYS	GLU	engineered mutation	UNP O18423
C	92	GLN	GLU	engineered mutation	UNP O18423
C	97	SER	GLU	engineered mutation	UNP O18423
C	126	GLY	ASP	engineered mutation	UNP O18423
D	0	GLY	-	expression tag	UNP O18423
D	84	GLN	GLU	engineered mutation	UNP O18423
D	85	LYS	GLU	engineered mutation	UNP O18423
D	92	GLN	GLU	engineered mutation	UNP O18423
D	97	SER	GLU	engineered mutation	UNP O18423
D	126	GLY	ASP	engineered mutation	UNP O18423
E	0	GLY	-	expression tag	UNP O18423
E	84	GLN	GLU	engineered mutation	UNP O18423
E	85	LYS	GLU	engineered mutation	UNP O18423
E	92	GLN	GLU	engineered mutation	UNP O18423
E	97	SER	GLU	engineered mutation	UNP O18423
E	126	GLY	ASP	engineered mutation	UNP O18423
F	0	GLY	-	expression tag	UNP O18423
F	84	GLN	GLU	engineered mutation	UNP O18423
F	85	LYS	GLU	engineered mutation	UNP O18423
F	92	GLN	GLU	engineered mutation	UNP O18423

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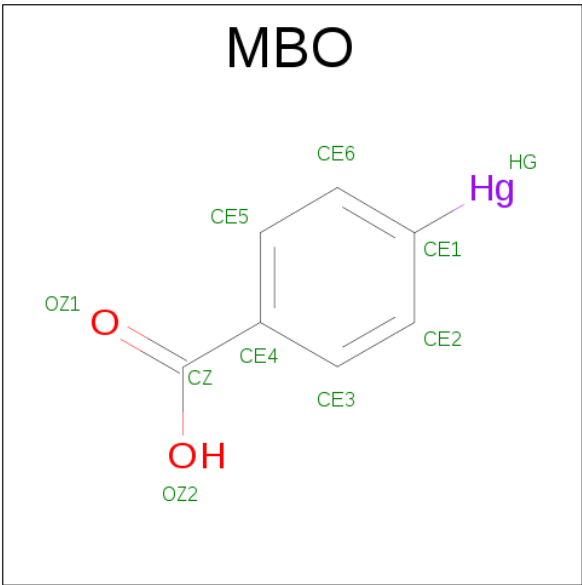
Chain	Residue	Modelled	Actual	Comment	Reference
F	97	SER	GLU	engineered mutation	UNP O18423
F	126	GLY	ASP	engineered mutation	UNP O18423
G	0	GLY	-	expression tag	UNP O18423
G	84	GLN	GLU	engineered mutation	UNP O18423
G	85	LYS	GLU	engineered mutation	UNP O18423
G	92	GLN	GLU	engineered mutation	UNP O18423
G	97	SER	GLU	engineered mutation	UNP O18423
G	126	GLY	ASP	engineered mutation	UNP O18423
H	0	GLY	-	expression tag	UNP O18423
H	84	GLN	GLU	engineered mutation	UNP O18423
H	85	LYS	GLU	engineered mutation	UNP O18423
H	92	GLN	GLU	engineered mutation	UNP O18423
H	97	SER	GLU	engineered mutation	UNP O18423
H	126	GLY	ASP	engineered mutation	UNP O18423
I	0	GLY	-	expression tag	UNP O18423
I	84	GLN	GLU	engineered mutation	UNP O18423
I	85	LYS	GLU	engineered mutation	UNP O18423
I	92	GLN	GLU	engineered mutation	UNP O18423
I	97	SER	GLU	engineered mutation	UNP O18423
I	126	GLY	ASP	engineered mutation	UNP O18423
J	0	GLY	-	expression tag	UNP O18423
J	84	GLN	GLU	engineered mutation	UNP O18423
J	85	LYS	GLU	engineered mutation	UNP O18423
J	92	GLN	GLU	engineered mutation	UNP O18423
J	97	SER	GLU	engineered mutation	UNP O18423
J	126	GLY	ASP	engineered mutation	UNP O18423
K	0	GLY	-	expression tag	UNP O18423
K	84	GLN	GLU	engineered mutation	UNP O18423
K	85	LYS	GLU	engineered mutation	UNP O18423
K	92	GLN	GLU	engineered mutation	UNP O18423
K	97	SER	GLU	engineered mutation	UNP O18423
K	126	GLY	ASP	engineered mutation	UNP O18423
L	0	GLY	-	expression tag	UNP O18423
L	84	GLN	GLU	engineered mutation	UNP O18423
L	85	LYS	GLU	engineered mutation	UNP O18423
L	92	GLN	GLU	engineered mutation	UNP O18423
L	97	SER	GLU	engineered mutation	UNP O18423
L	126	GLY	ASP	engineered mutation	UNP O18423
M	0	GLY	-	expression tag	UNP O18423
M	84	GLN	GLU	engineered mutation	UNP O18423
M	85	LYS	GLU	engineered mutation	UNP O18423
M	92	GLN	GLU	engineered mutation	UNP O18423

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Chain	Residue	Modelled	Actual	Comment	Reference
M	97	SER	GLU	engineered mutation	UNP O18423
M	126	GLY	ASP	engineered mutation	UNP O18423
N	0	GLY	-	expression tag	UNP O18423
N	84	GLN	GLU	engineered mutation	UNP O18423
N	85	LYS	GLU	engineered mutation	UNP O18423
N	92	GLN	GLU	engineered mutation	UNP O18423
N	97	SER	GLU	engineered mutation	UNP O18423
N	126	GLY	ASP	engineered mutation	UNP O18423
O	0	GLY	-	expression tag	UNP O18423
O	84	GLN	GLU	engineered mutation	UNP O18423
O	85	LYS	GLU	engineered mutation	UNP O18423
O	92	GLN	GLU	engineered mutation	UNP O18423
O	97	SER	GLU	engineered mutation	UNP O18423
O	126	GLY	ASP	engineered mutation	UNP O18423
P	0	GLY	-	expression tag	UNP O18423
P	84	GLN	GLU	engineered mutation	UNP O18423
P	85	LYS	GLU	engineered mutation	UNP O18423
P	92	GLN	GLU	engineered mutation	UNP O18423
P	97	SER	GLU	engineered mutation	UNP O18423
P	126	GLY	ASP	engineered mutation	UNP O18423
R	0	GLY	-	expression tag	UNP O18423
R	84	GLN	GLU	engineered mutation	UNP O18423
R	85	LYS	GLU	engineered mutation	UNP O18423
R	92	GLN	GLU	engineered mutation	UNP O18423
R	97	SER	GLU	engineered mutation	UNP O18423
R	126	GLY	ASP	engineered mutation	UNP O18423
S	0	GLY	-	expression tag	UNP O18423
S	84	GLN	GLU	engineered mutation	UNP O18423
S	85	LYS	GLU	engineered mutation	UNP O18423
S	92	GLN	GLU	engineered mutation	UNP O18423
S	97	SER	GLU	engineered mutation	UNP O18423
S	126	GLY	ASP	engineered mutation	UNP O18423

- Molecule 2 is MERCURIBENZOIC ACID (three-letter code: MBO) (formula: C₇H₅HgO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	A	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	B	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	B	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	C	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	D	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	E	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	F	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	G	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	H	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	H	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	I	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	K	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	K	1	Total	C	Hg	O	0	0
			10	7	1	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	L	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	L	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	M	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	M	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	O	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	P	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	R	1	Total	C	Hg	O	0	0
			10	7	1	2		
2	S	1	Total	C	Hg	O	0	0
			10	7	1	2		

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total	Hg	0	0
			1	1		
3	G	1	Total	Hg	0	0
			1	1		
3	J	2	Total	Hg	0	0
			2	2		
3	D	1	Total	Hg	0	0
			1	1		
3	E	1	Total	Hg	0	0
			1	1		
3	I	1	Total	Hg	0	0
			1	1		
3	C	1	Total	Hg	0	0
			1	1		
3	N	2	Total	Hg	0	0
			2	2		
3	O	1	Total	Hg	0	0
			1	1		
3	R	1	Total	Hg	0	0
			1	1		
3	S	1	Total	Hg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	1	Total	Hg	0	0
			1	1		

- Molecule 4 is water.

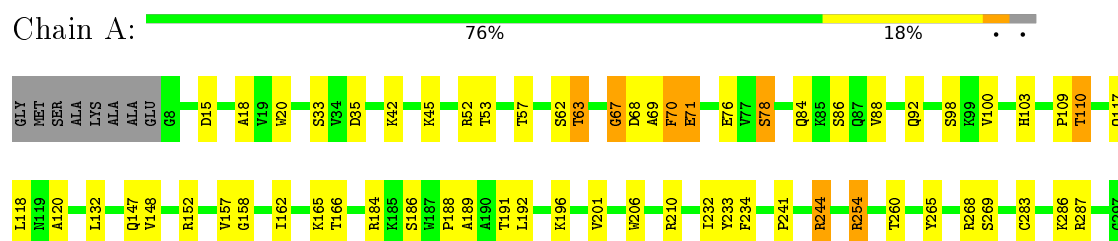
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	O	0	0
			7	7		
4	B	2	Total	O	0	0
			2	2		
4	C	2	Total	O	0	0
			2	2		
4	D	7	Total	O	0	0
			7	7		
4	E	5	Total	O	0	0
			5	5		
4	F	5	Total	O	0	0
			5	5		
4	G	2	Total	O	0	0
			2	2		
4	H	2	Total	O	0	0
			2	2		
4	I	4	Total	O	0	0
			4	4		
4	J	4	Total	O	0	0
			4	4		
4	K	8	Total	O	0	0
			8	8		
4	L	2	Total	O	0	0
			2	2		
4	M	2	Total	O	0	0
			2	2		
4	N	2	Total	O	0	0
			2	2		
4	O	2	Total	O	0	0
			2	2		
4	P	1	Total	O	0	0
			1	1		
4	R	3	Total	O	0	0
			3	3		
4	S	1	Total	O	0	0
			1	1		

3 Residue-property plots [i](#)

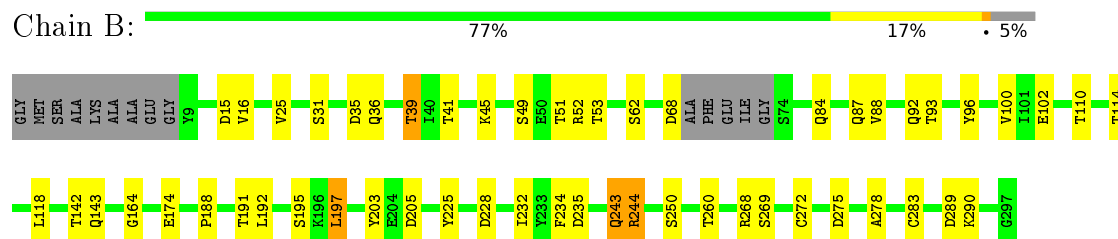
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS failed to run properly.

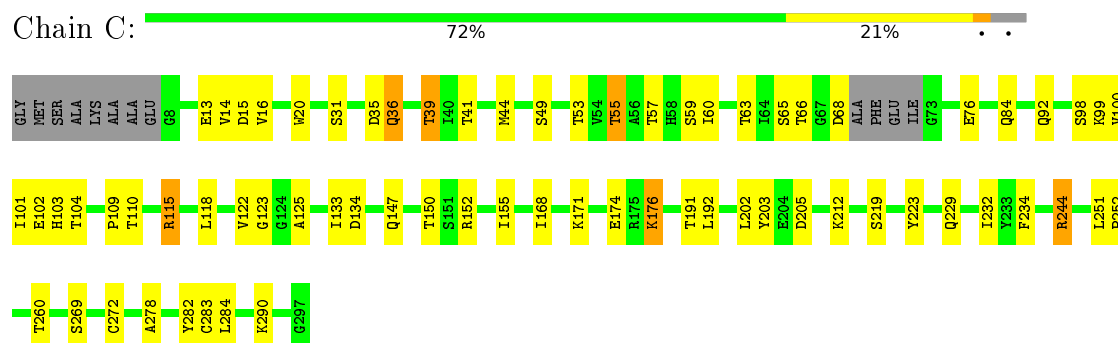
• Molecule 1: Lysenin



• Molecule 1: Lysenin

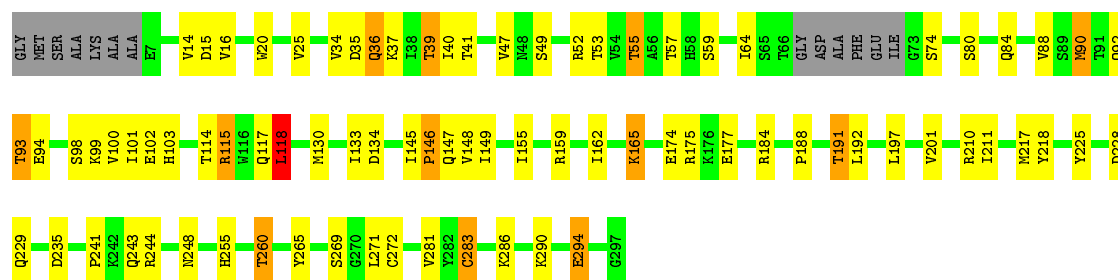


• Molecule 1: Lysenin



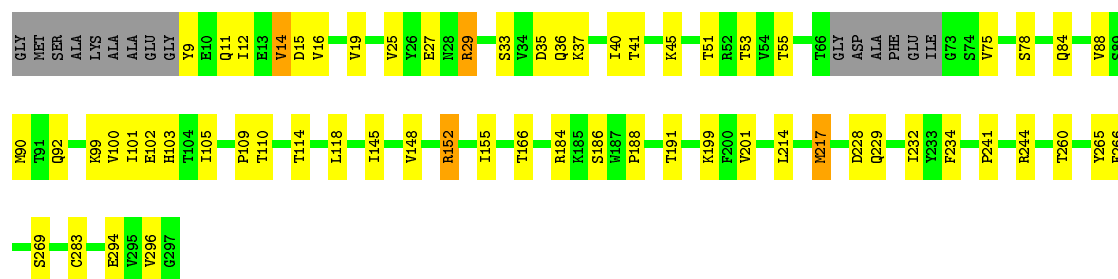
• Molecule 1: Lysenin





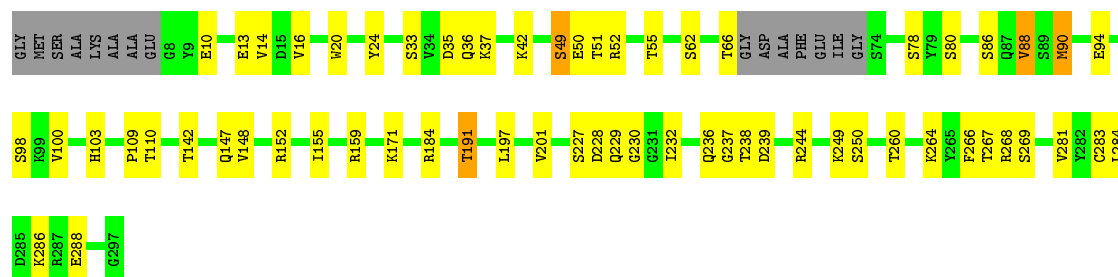
• Molecule 1: Lysenin

Chain E: 74% 19% 5%



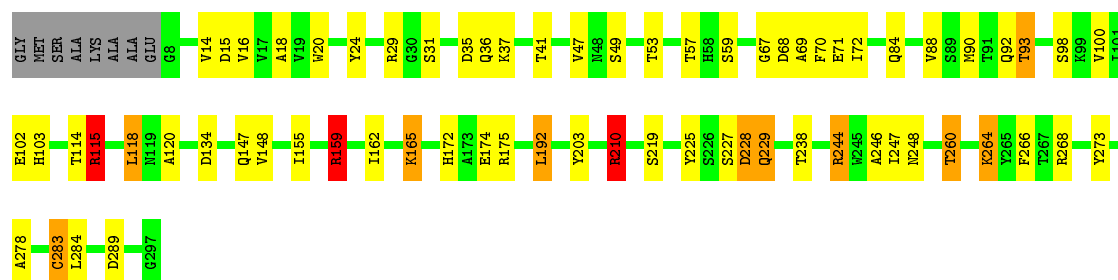
• Molecule 1: Lysenin

Chain F: 74% 20% 5%



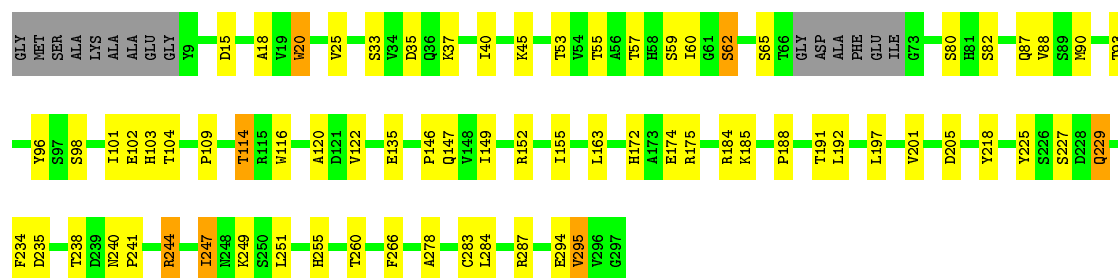
• Molecule 1: Lysenin

Chain G: 74% 18% 5%



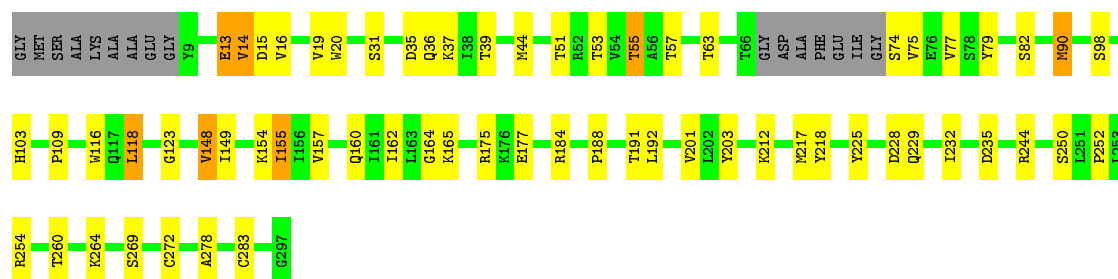
• Molecule 1: Lysenin

Chain H: 70% 22% 5%



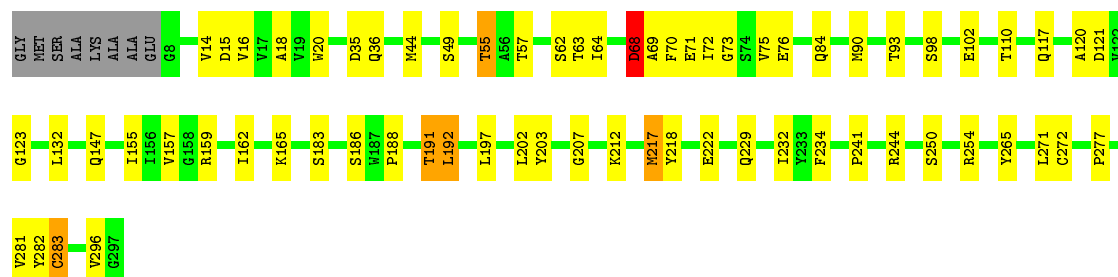
• Molecule 1: Lysenin

Chain I: 73% 19% • 5%



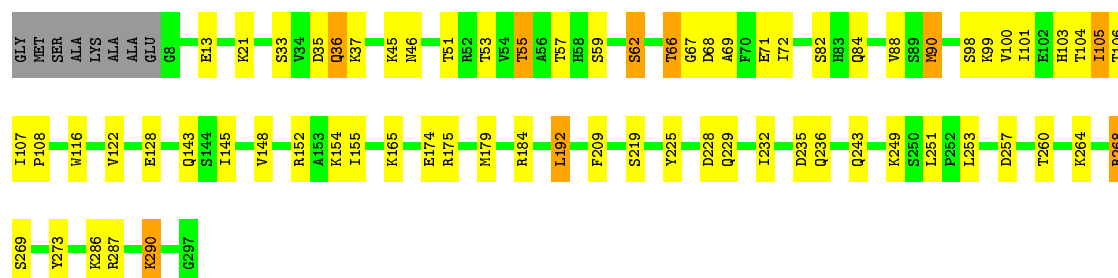
• Molecule 1: Lysenin

Chain J: 75% 20% • •



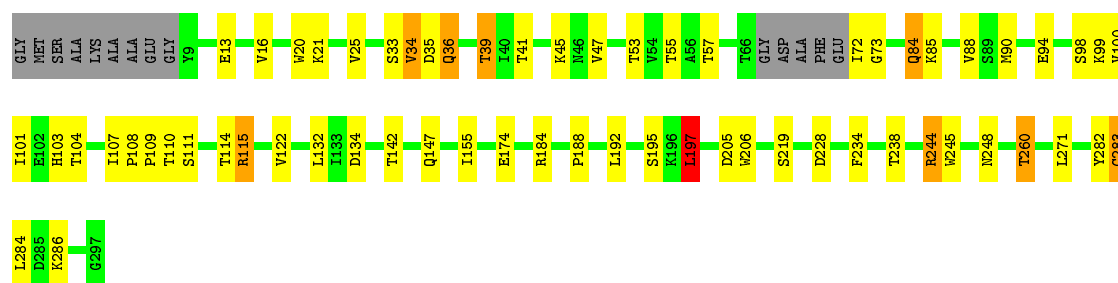
• Molecule 1: Lysenin

Chain K: 74% 20% • •



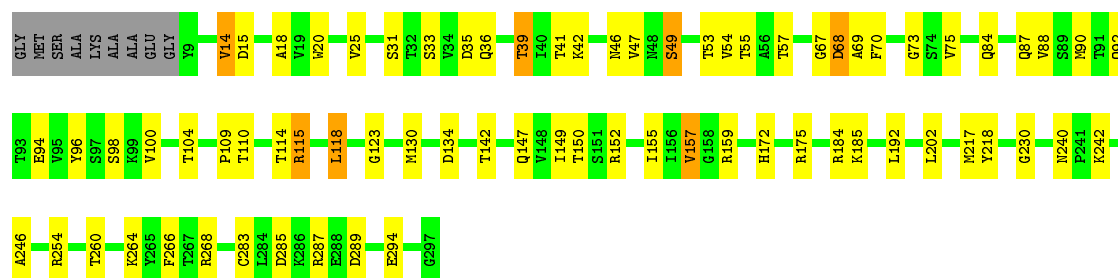
• Molecule 1: Lysenin

Chain L: 74% 18% • 5%



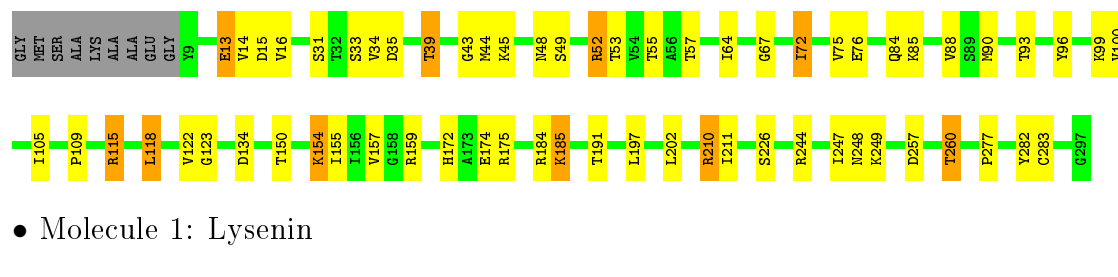
• Molecule 1: Lysenin

Chain M: 72% 22%



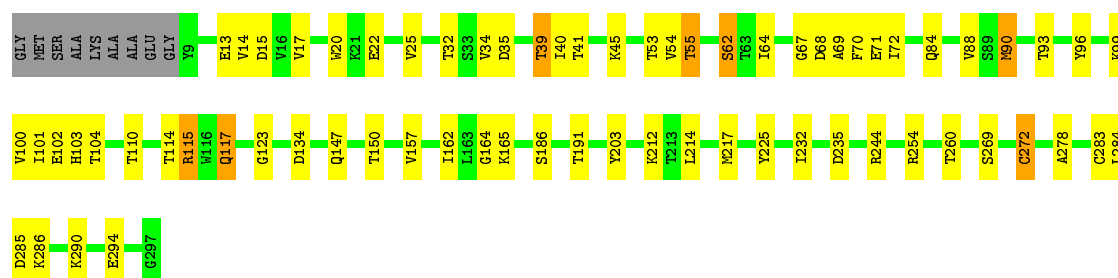
• Molecule 1: Lysenin

Chain N: 76% 18%



• Molecule 1: Lysenin

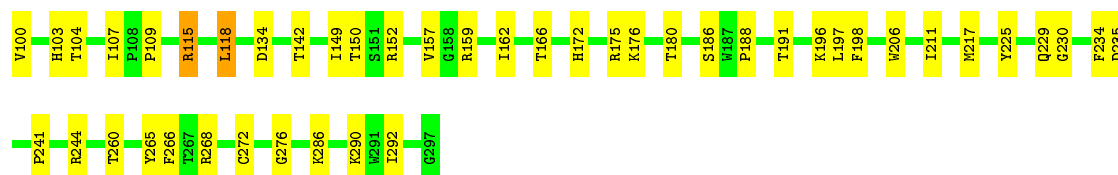
Chain O: 74% 21%



• Molecule 1: Lysenin

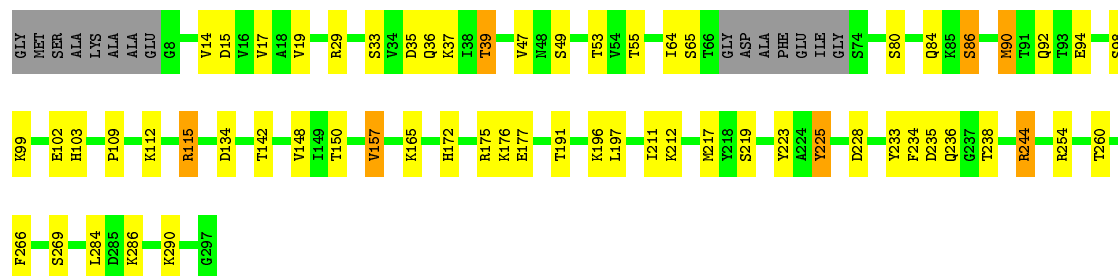
Chain P: 72% 24%





• Molecule 1: Lysenin

Chain R: 74% 18% • 5%



• Molecule 1: Lysenin

Chain S: 73% 20% • 5%



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	192.99Å 192.99Å 493.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.10 – 3.10	Depositor
% Data completeness (in resolution range)	99.9 (49.10-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.214 , 0.258	Depositor
Wilson B-factor (Å ²)	57.6	Xtriage
Anisotropy	0.541	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	41248	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MBO, HG

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	0.49	0/2352	0.73	0/3186
1	B	0.48	0/2309	0.70	0/3127
1	C	0.49	0/2317	0.69	0/3137
1	D	0.49	0/2314	0.73	1/3133 (0.0%)
1	E	0.50	0/2301	0.73	0/3116
1	F	0.55	0/2301	0.77	0/3116
1	G	0.56	0/2352	0.81	4/3186 (0.1%)
1	H	0.51	0/2301	0.75	0/3116
1	I	0.50	0/2297	0.73	1/3111 (0.0%)
1	J	0.49	0/2352	0.69	0/3186
1	K	0.51	0/2352	0.75	0/3186
1	L	0.48	0/2309	0.71	1/3127 (0.0%)
1	M	0.49	0/2348	0.70	0/3181
1	N	0.50	0/2348	0.72	1/3181 (0.0%)
1	O	0.50	0/2348	0.72	0/3181
1	P	0.51	0/2348	0.72	0/3181
1	R	0.49	0/2301	0.72	0/3116
1	S	0.49	0/2301	0.71	1/3116 (0.0%)
All	All	0.50	0/41851	0.73	9/56683 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	S	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	118	LEU	CA-CB-CG	7.35	132.21	115.30
1	N	118	LEU	CA-CB-CG	6.95	131.29	115.30
1	G	115	ARG	NE-CZ-NH1	6.37	123.49	120.30
1	G	210	ARG	NE-CZ-NH1	6.13	123.37	120.30
1	G	118	LEU	CA-CB-CG	6.00	129.11	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	67	GLY	Peptide
1	S	221	TYR	Peptide

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	2301	0	2264	32	0
1	B	2260	0	2226	26	0
1	C	2268	0	2233	31	0
1	D	2265	0	2232	42	0
1	E	2252	0	2222	33	0
1	F	2252	0	2222	35	1
1	G	2301	0	2265	53	0
1	H	2252	0	2223	49	0
1	I	2248	0	2219	30	0
1	J	2301	0	2265	26	0
1	K	2301	0	2265	32	0
1	L	2260	0	2234	39	0
1	M	2297	0	2262	45	0
1	N	2297	0	2262	37	0
1	O	2297	0	2262	39	0
1	P	2297	0	2261	36	0
1	R	2252	0	2222	35	1
1	S	2252	0	2223	33	0
2	A	20	0	8	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	20	0	8	16	0
2	C	10	0	4	9	0
2	D	10	0	4	17	0
2	E	10	0	4	5	0
2	F	10	0	4	19	0
2	G	10	0	4	13	0
2	H	20	0	8	29	0
2	I	10	0	4	6	0
2	K	20	0	8	29	0
2	L	20	0	8	25	0
2	M	20	0	8	18	0
2	O	10	0	4	12	0
2	P	10	0	4	20	0
2	R	10	0	4	7	0
2	S	10	0	4	15	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
3	J	2	0	0	0	0
3	N	2	0	0	0	0
3	O	1	0	0	1	0
3	P	1	0	0	0	0
3	R	1	0	0	0	0
3	S	1	0	0	0	0
4	A	7	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	7	0	0	0	0
4	E	5	0	0	0	0
4	F	5	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	I	4	0	0	0	0
4	J	4	0	0	0	0
4	K	8	0	0	0	0
4	L	2	0	0	0	0
4	M	2	0	0	0	0
4	N	2	0	0	0	0
4	O	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	P	1	0	0	0	0
4	R	3	0	0	0	0
4	S	1	0	0	0	0
All	All	41248	0	40450	735	1

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 9.

The worst 5 of 735 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)
2:H:301:MBO:HE6	2:H:301:MBO:CE1	2.06	1.24
2:S:301:MBO:HE2	2:S:301:MBO:CE3	2.06	1.24
2:L:302:MBO:CE5	2:L:302:MBO:HE6	2.06	1.24
2:B:301:MBO:CE4	2:B:301:MBO:HE3	2.06	1.24
2:O:301:MBO:HE6	2:O:301:MBO:CE1	2.06	1.24

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:239:ASP:OD2	1:R:236:GLN:OE1[7_556]	1.52	0.68

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	288/298 (97%)	273 (95%)	12 (4%)	3 (1%)	19	58
1	B	280/298 (94%)	269 (96%)	11 (4%)	0	100	100
1	C	282/298 (95%)	269 (95%)	13 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	281/298 (94%)	272 (97%)	8 (3%)	1 (0%)	39	75
1	E	279/298 (94%)	267 (96%)	12 (4%)	0	100	100
1	F	279/298 (94%)	259 (93%)	18 (6%)	2 (1%)	26	65
1	G	288/298 (97%)	273 (95%)	11 (4%)	4 (1%)	14	48
1	H	279/298 (94%)	272 (98%)	7 (2%)	0	100	100
1	I	278/298 (93%)	269 (97%)	9 (3%)	0	100	100
1	J	288/298 (97%)	274 (95%)	11 (4%)	3 (1%)	19	58
1	K	288/298 (97%)	272 (94%)	13 (4%)	3 (1%)	19	58
1	L	280/298 (94%)	268 (96%)	12 (4%)	0	100	100
1	M	287/298 (96%)	265 (92%)	20 (7%)	2 (1%)	26	65
1	N	287/298 (96%)	270 (94%)	16 (6%)	1 (0%)	46	80
1	O	287/298 (96%)	274 (96%)	10 (4%)	3 (1%)	19	58
1	P	287/298 (96%)	270 (94%)	15 (5%)	2 (1%)	26	65
1	R	279/298 (94%)	270 (97%)	9 (3%)	0	100	100
1	S	279/298 (94%)	263 (94%)	15 (5%)	1 (0%)	39	75
All	All	5096/5364 (95%)	4849 (95%)	222 (4%)	25 (0%)	34	72

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	ASP
1	A	70	PHE
1	A	71	GLU
1	G	68	ASP
1	G	72	ILE

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	253/257 (98%)	225 (89%)	28 (11%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	250/257 (97%)	228 (91%)	22 (9%)	12	43
1	C	250/257 (97%)	222 (89%)	28 (11%)	7	29
1	D	250/257 (97%)	212 (85%)	38 (15%)	3	14
1	E	249/257 (97%)	224 (90%)	25 (10%)	9	34
1	F	249/257 (97%)	216 (87%)	33 (13%)	5	20
1	G	253/257 (98%)	227 (90%)	26 (10%)	9	32
1	H	249/257 (97%)	222 (89%)	27 (11%)	8	30
1	I	249/257 (97%)	221 (89%)	28 (11%)	7	29
1	J	253/257 (98%)	223 (88%)	30 (12%)	6	25
1	K	253/257 (98%)	220 (87%)	33 (13%)	5	21
1	L	250/257 (97%)	227 (91%)	23 (9%)	11	40
1	M	253/257 (98%)	231 (91%)	22 (9%)	13	44
1	N	253/257 (98%)	226 (89%)	27 (11%)	8	31
1	O	253/257 (98%)	230 (91%)	23 (9%)	12	40
1	P	253/257 (98%)	222 (88%)	31 (12%)	6	23
1	R	249/257 (97%)	224 (90%)	25 (10%)	9	34
1	S	249/257 (97%)	223 (90%)	26 (10%)	9	32
All	All	4518/4626 (98%)	4023 (89%)	495 (11%)	8	30

5 of 495 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	283	CYS
1	J	202	LEU
1	R	165	LYS
1	I	16	VAL
1	I	250	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	194	HIS
1	K	58	HIS
1	R	92	GLN
1	I	11	GLN

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Mol	Chain	Res	Type
1	I	160	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 36 ligands modelled in this entry, 14 are monoatomic - leaving 22 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MBO	A	301	1	4,10,10	0.75	0	8,13,13	0.81	0
2	MBO	A	302	1	4,10,10	0.92	0	8,13,13	1.14	0
2	MBO	B	301	1	4,10,10	0.73	0	8,13,13	1.25	1 (12%)
2	MBO	B	302	1	4,10,10	0.70	0	8,13,13	0.93	0
2	MBO	C	301	1	4,10,10	0.74	0	8,13,13	0.85	0
2	MBO	D	301	1	4,10,10	0.56	0	8,13,13	1.29	0
2	MBO	E	301	1	4,10,10	0.57	0	8,13,13	1.06	0
2	MBO	F	302	1	4,10,10	0.82	0	8,13,13	1.30	1 (12%)
2	MBO	G	301	1	4,10,10	0.64	0	8,13,13	1.02	0
2	MBO	H	301	1	4,10,10	0.69	0	8,13,13	1.08	0
2	MBO	H	302	1	4,10,10	0.71	0	8,13,13	1.37	1 (12%)
2	MBO	I	302	1	4,10,10	0.71	0	8,13,13	0.93	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MBO	K	301	1	4,10,10	0.78	0	8,13,13	1.39	1 (12%)
2	MBO	K	302	1	4,10,10	0.55	0	8,13,13	1.00	0
2	MBO	L	301	1	4,10,10	0.59	0	8,13,13	0.85	0
2	MBO	L	302	1	4,10,10	0.72	0	8,13,13	0.98	0
2	MBO	M	301	1	4,10,10	0.62	0	8,13,13	1.10	0
2	MBO	M	302	1	4,10,10	0.70	0	8,13,13	1.82	2 (25%)
2	MBO	O	301	1	4,10,10	0.72	0	8,13,13	1.42	1 (12%)
2	MBO	P	302	1	4,10,10	0.78	0	8,13,13	0.69	0
2	MBO	R	301	1	4,10,10	0.62	0	8,13,13	1.12	0
2	MBO	S	301	1	4,10,10	0.54	0	8,13,13	1.14	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MBO	A	301	1	-	0/0/4/4	0/1/1/1
2	MBO	A	302	1	-	0/0/4/4	0/1/1/1
2	MBO	B	301	1	-	0/0/4/4	0/1/1/1
2	MBO	B	302	1	-	0/0/4/4	0/1/1/1
2	MBO	C	301	1	-	0/0/4/4	0/1/1/1
2	MBO	D	301	1	-	0/0/4/4	0/1/1/1
2	MBO	E	301	1	-	0/0/4/4	0/1/1/1
2	MBO	F	302	1	-	0/0/4/4	0/1/1/1
2	MBO	G	301	1	-	0/0/4/4	0/1/1/1
2	MBO	H	301	1	-	0/0/4/4	0/1/1/1
2	MBO	H	302	1	-	0/0/4/4	0/1/1/1
2	MBO	I	302	1	-	0/0/4/4	0/1/1/1
2	MBO	K	301	1	-	0/0/4/4	0/1/1/1
2	MBO	K	302	1	-	0/0/4/4	0/1/1/1
2	MBO	L	301	1	-	0/0/4/4	0/1/1/1
2	MBO	L	302	1	-	0/0/4/4	0/1/1/1
2	MBO	M	301	1	-	0/0/4/4	0/1/1/1
2	MBO	M	302	1	-	0/0/4/4	0/1/1/1
2	MBO	O	301	1	-	0/0/4/4	0/1/1/1
2	MBO	P	302	1	-	0/0/4/4	0/1/1/1
2	MBO	R	301	1	-	0/0/4/4	0/1/1/1
2	MBO	S	301	1	-	0/0/4/4	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	302	MBO	CE5-CE4-CZ	-3.44	115.90	120.43
2	O	301	MBO	CE5-CE4-CZ	-2.54	117.09	120.43
2	H	302	MBO	CE5-CE4-CZ	-2.17	117.57	120.43
2	B	301	MBO	CE3-CE4-CZ	-2.10	117.67	120.43
2	F	302	MBO	CE3-CE4-CZ	-2.09	117.67	120.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

22 monomers are involved in 249 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	MBO	1	0
2	A	302	MBO	8	0
2	B	301	MBO	13	0
2	B	302	MBO	3	0
2	C	301	MBO	9	0
2	D	301	MBO	17	0
2	E	301	MBO	5	0
2	F	302	MBO	19	0
2	G	301	MBO	13	0
2	H	301	MBO	15	0
2	H	302	MBO	14	0
2	I	302	MBO	6	0
2	K	301	MBO	15	0
2	K	302	MBO	14	0
2	L	301	MBO	17	0
2	L	302	MBO	8	0
2	M	301	MBO	17	0
2	M	302	MBO	1	0
2	O	301	MBO	12	0
2	P	302	MBO	20	0
2	R	301	MBO	7	0
2	S	301	MBO	15	0

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.