



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2022 – 04:09 PM JST

PDB ID : 7VPU  
Title : Crystal structure of the ligand-binding domain of L. thermotolerans Upc2 in complex with ergosterol  
Authors : Tan, L.; Im, Y.J.  
Deposited on : 2021-10-18  
Resolution : 2.59 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](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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.29

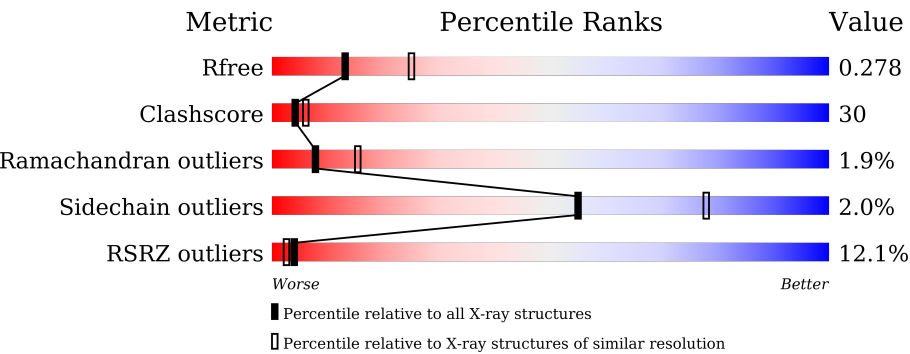
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	332	<div><div>10%</div><div><div></div><div>46%</div><div>33%</div><div>..</div><div>17%</div></div></div>
1	B	332	<div><div>10%</div><div><div></div><div>45%</div><div>32%</div><div>.</div><div>20%</div></div></div>
1	C	332	<div><div>8%</div><div><div></div><div>39%</div><div>37%</div><div>..</div><div>19%</div></div></div>
1	D	332	<div><div>11%</div><div><div></div><div>45%</div><div>32%</div><div>..</div><div>20%</div></div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8804 atoms, of which 176 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 Sterol uptake control protein 2 (Upc2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2168	1408	352	397	11			
1	B	266	Total	C	N	O	S	0	0	0
			2110	1372	343	384	11			
1	C	269	Total	C	N	O	S	0	0	0
			2128	1381	346	390	11			
1	D	266	Total	C	N	O	S	0	0	0
			2106	1368	343	384	11			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	MET	-	initiating methionine	UNP C5DKV6
A	446	SER	-	expression tag	UNP C5DKV6
A	447	TYR	-	expression tag	UNP C5DKV6
A	448	TYR	-	expression tag	UNP C5DKV6
A	449	HIS	-	expression tag	UNP C5DKV6
A	450	HIS	-	expression tag	UNP C5DKV6
A	451	HIS	-	expression tag	UNP C5DKV6
A	452	HIS	-	expression tag	UNP C5DKV6
A	453	HIS	-	expression tag	UNP C5DKV6
A	454	HIS	-	expression tag	UNP C5DKV6
A	455	ASP	-	expression tag	UNP C5DKV6
A	456	TYR	-	expression tag	UNP C5DKV6
A	457	ASP	-	expression tag	UNP C5DKV6
A	458	ILE	-	expression tag	UNP C5DKV6
A	459	PRO	-	expression tag	UNP C5DKV6
A	460	THR	-	expression tag	UNP C5DKV6
A	461	LEU	-	expression tag	UNP C5DKV6
A	462	VAL	-	expression tag	UNP C5DKV6
A	463	PRO	-	expression tag	UNP C5DKV6
A	464	ARG	-	expression tag	UNP C5DKV6
A	465	GLY	-	expression tag	UNP C5DKV6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	466	SER	-	expression tag	UNP C5DKV6
A	467	ALA	-	expression tag	UNP C5DKV6
A	468	MET	-	expression tag	UNP C5DKV6
A	469	GLY	-	expression tag	UNP C5DKV6
A	470	SER	-	expression tag	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	?	-	ALA	deletion	UNP C5DKV6
A	?	-	VAL	deletion	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	?	-	GLU	deletion	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	?	-	LEU	deletion	UNP C5DKV6
A	?	-	ALA	deletion	UNP C5DKV6
A	?	-	ALA	deletion	UNP C5DKV6
A	?	-	SER	deletion	UNP C5DKV6
A	599	VAL	SER	engineered mutation	UNP C5DKV6
A	600	ASP	MET	engineered mutation	UNP C5DKV6
B	445	MET	-	initiating methionine	UNP C5DKV6
B	446	SER	-	expression tag	UNP C5DKV6
B	447	TYR	-	expression tag	UNP C5DKV6
B	448	TYR	-	expression tag	UNP C5DKV6
B	449	HIS	-	expression tag	UNP C5DKV6
B	450	HIS	-	expression tag	UNP C5DKV6
B	451	HIS	-	expression tag	UNP C5DKV6
B	452	HIS	-	expression tag	UNP C5DKV6
B	453	HIS	-	expression tag	UNP C5DKV6
B	454	HIS	-	expression tag	UNP C5DKV6
B	455	ASP	-	expression tag	UNP C5DKV6
B	456	TYR	-	expression tag	UNP C5DKV6
B	457	ASP	-	expression tag	UNP C5DKV6
B	458	ILE	-	expression tag	UNP C5DKV6
B	459	PRO	-	expression tag	UNP C5DKV6
B	460	THR	-	expression tag	UNP C5DKV6
B	461	LEU	-	expression tag	UNP C5DKV6
B	462	VAL	-	expression tag	UNP C5DKV6
B	463	PRO	-	expression tag	UNP C5DKV6
B	464	ARG	-	expression tag	UNP C5DKV6
B	465	GLY	-	expression tag	UNP C5DKV6
B	466	SER	-	expression tag	UNP C5DKV6
B	467	ALA	-	expression tag	UNP C5DKV6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	468	MET	-	expression tag	UNP C5DKV6
B	469	GLY	-	expression tag	UNP C5DKV6
B	470	SER	-	expression tag	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	?	-	ALA	deletion	UNP C5DKV6
B	?	-	VAL	deletion	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	?	-	GLU	deletion	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	?	-	LEU	deletion	UNP C5DKV6
B	?	-	ALA	deletion	UNP C5DKV6
B	?	-	ALA	deletion	UNP C5DKV6
B	?	-	SER	deletion	UNP C5DKV6
B	599	VAL	SER	engineered mutation	UNP C5DKV6
B	600	ASP	MET	engineered mutation	UNP C5DKV6
C	445	MET	-	initiating methionine	UNP C5DKV6
C	446	SER	-	expression tag	UNP C5DKV6
C	447	TYR	-	expression tag	UNP C5DKV6
C	448	TYR	-	expression tag	UNP C5DKV6
C	449	HIS	-	expression tag	UNP C5DKV6
C	450	HIS	-	expression tag	UNP C5DKV6
C	451	HIS	-	expression tag	UNP C5DKV6
C	452	HIS	-	expression tag	UNP C5DKV6
C	453	HIS	-	expression tag	UNP C5DKV6
C	454	HIS	-	expression tag	UNP C5DKV6
C	455	ASP	-	expression tag	UNP C5DKV6
C	456	TYR	-	expression tag	UNP C5DKV6
C	457	ASP	-	expression tag	UNP C5DKV6
C	458	ILE	-	expression tag	UNP C5DKV6
C	459	PRO	-	expression tag	UNP C5DKV6
C	460	THR	-	expression tag	UNP C5DKV6
C	461	LEU	-	expression tag	UNP C5DKV6
C	462	VAL	-	expression tag	UNP C5DKV6
C	463	PRO	-	expression tag	UNP C5DKV6
C	464	ARG	-	expression tag	UNP C5DKV6
C	465	GLY	-	expression tag	UNP C5DKV6
C	466	SER	-	expression tag	UNP C5DKV6
C	467	ALA	-	expression tag	UNP C5DKV6
C	468	MET	-	expression tag	UNP C5DKV6
C	469	GLY	-	expression tag	UNP C5DKV6

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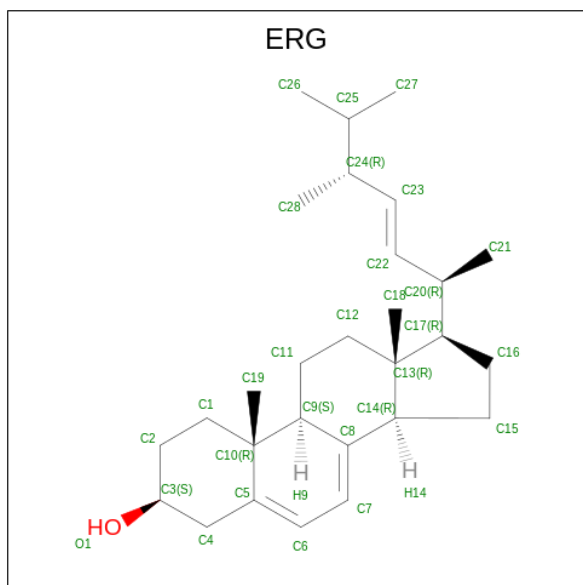
Chain	Residue	Modelled	Actual	Comment	Reference
C	470	SER	-	expression tag	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	?	-	ALA	deletion	UNP C5DKV6
C	?	-	VAL	deletion	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	?	-	GLU	deletion	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	?	-	LEU	deletion	UNP C5DKV6
C	?	-	ALA	deletion	UNP C5DKV6
C	?	-	ALA	deletion	UNP C5DKV6
C	?	-	SER	deletion	UNP C5DKV6
C	599	VAL	SER	engineered mutation	UNP C5DKV6
C	600	ASP	MET	engineered mutation	UNP C5DKV6
D	445	MET	-	initiating methionine	UNP C5DKV6
D	446	SER	-	expression tag	UNP C5DKV6
D	447	TYR	-	expression tag	UNP C5DKV6
D	448	TYR	-	expression tag	UNP C5DKV6
D	449	HIS	-	expression tag	UNP C5DKV6
D	450	HIS	-	expression tag	UNP C5DKV6
D	451	HIS	-	expression tag	UNP C5DKV6
D	452	HIS	-	expression tag	UNP C5DKV6
D	453	HIS	-	expression tag	UNP C5DKV6
D	454	HIS	-	expression tag	UNP C5DKV6
D	455	ASP	-	expression tag	UNP C5DKV6
D	456	TYR	-	expression tag	UNP C5DKV6
D	457	ASP	-	expression tag	UNP C5DKV6
D	458	ILE	-	expression tag	UNP C5DKV6
D	459	PRO	-	expression tag	UNP C5DKV6
D	460	THR	-	expression tag	UNP C5DKV6
D	461	LEU	-	expression tag	UNP C5DKV6
D	462	VAL	-	expression tag	UNP C5DKV6
D	463	PRO	-	expression tag	UNP C5DKV6
D	464	ARG	-	expression tag	UNP C5DKV6
D	465	GLY	-	expression tag	UNP C5DKV6
D	466	SER	-	expression tag	UNP C5DKV6
D	467	ALA	-	expression tag	UNP C5DKV6
D	468	MET	-	expression tag	UNP C5DKV6
D	469	GLY	-	expression tag	UNP C5DKV6
D	470	SER	-	expression tag	UNP C5DKV6
D	?	-	SER	deletion	UNP C5DKV6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	SER	deletion	UNP C5DKV6
D	?	-	SER	deletion	UNP C5DKV6
D	?	-	ALA	deletion	UNP C5DKV6
D	?	-	VAL	deletion	UNP C5DKV6
D	?	-	SER	deletion	UNP C5DKV6
D	?	-	GLU	deletion	UNP C5DKV6
D	?	-	SER	deletion	UNP C5DKV6
D	?	-	LEU	deletion	UNP C5DKV6
D	?	-	ALA	deletion	UNP C5DKV6
D	?	-	ALA	deletion	UNP C5DKV6
D	?	-	SER	deletion	UNP C5DKV6
D	599	VAL	SER	engineered mutation	UNP C5DKV6
D	600	ASP	MET	engineered mutation	UNP C5DKV6

- Molecule 2 is ERGOSTEROL (three-letter code: ERG) (formula:  $C_{28}H_{44}O$ ) (labeled as "Ligand of Interest" by depositor).

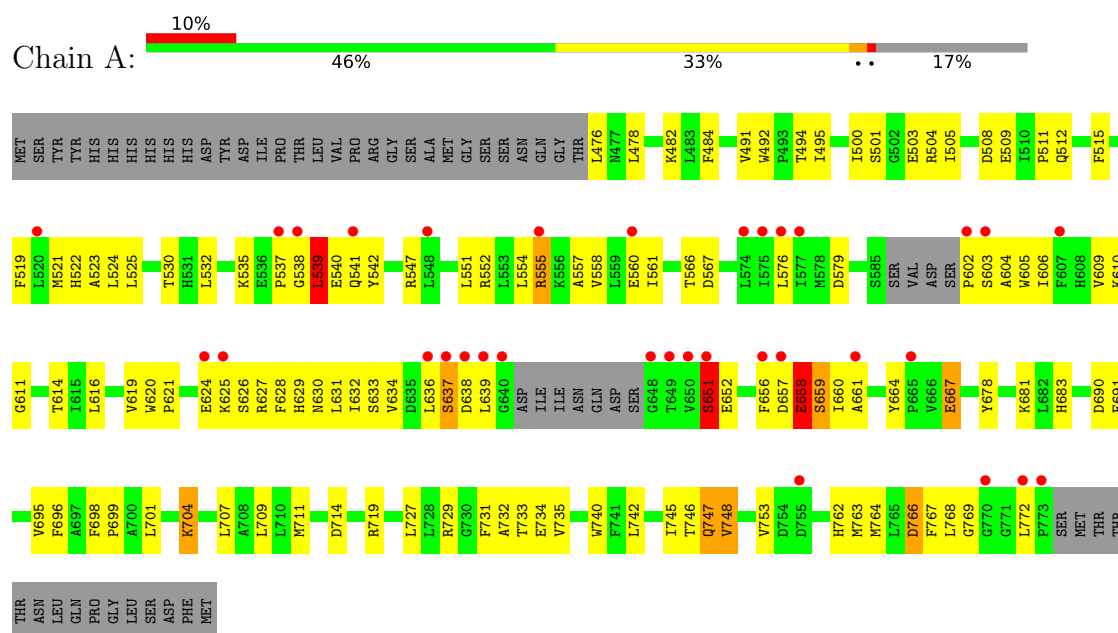


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			73	28	44	1		
2	B	1	Total	C	H	O	0	0
			73	28	44	1		
2	C	1	Total	C	H	O	0	0
			73	28	44	1		
2	D	1	Total	C	H	O	0	0
			73	28	44	1		

### 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: Sterol uptake control protein 2 (Upc2)

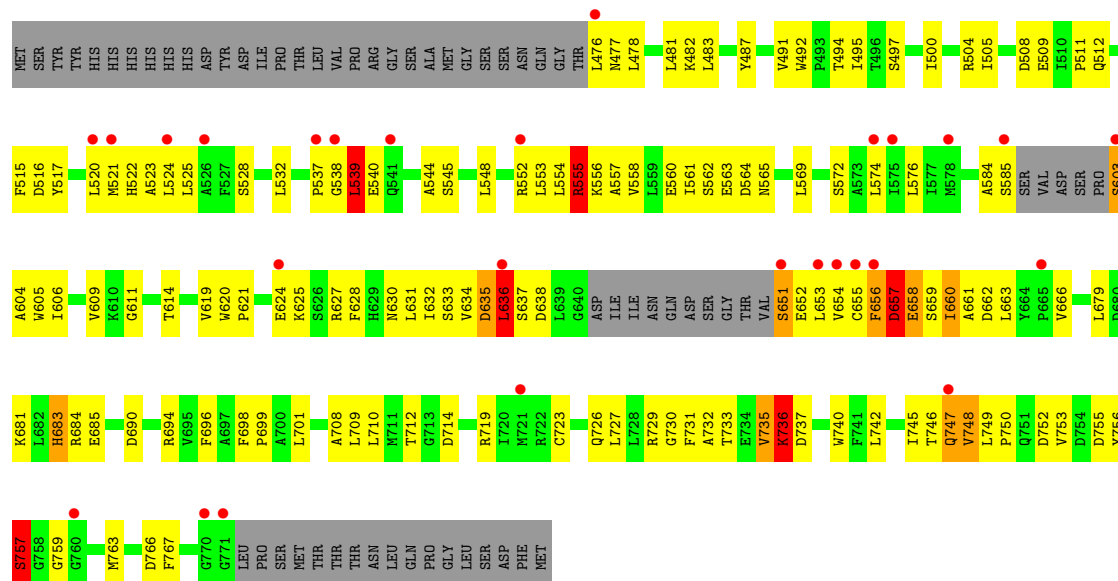




ASN  
LEU  
GLN  
PRO  
GLY  
LEU  
SER  
ASP  
PHE  
MET

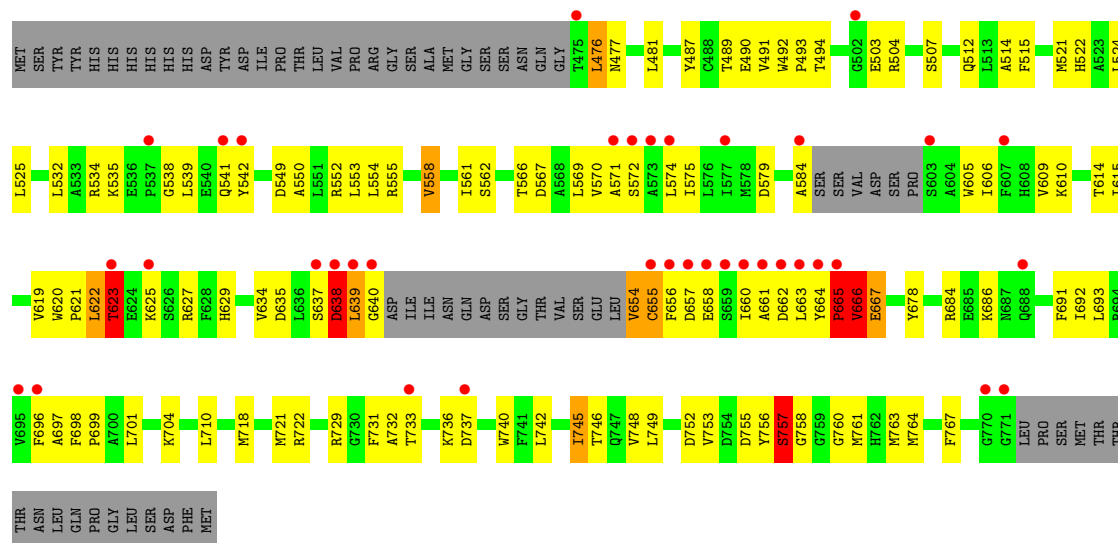
• Molecule 1: Sterol uptake control protein 2 (Upc2)

Chain C: 8% 39% 37% 19%



• Molecule 1: Sterol uptake control protein 2 (Upc2)

Chain D: 11% 45% 32% 20%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.38Å 147.13Å 90.95Å 90.00° 108.33° 90.00°	Depositor
Resolution (Å)	24.31 – 2.59 24.31 – 2.59	Depositor EDS
% Data completeness (in resolution range)	98.5 (24.31-2.59) 98.5 (24.31-2.59)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.97 (at 2.60Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.229 , 0.279 0.229 , 0.278	Depositor DCC
$R_{free}$ test set	2485 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.9	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8804	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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

### 5.1 Standard geometry

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

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	0.53	1/2218 (0.0%)	0.91	12/3012 (0.4%)
1	B	0.58	1/2158 (0.0%)	0.93	11/2930 (0.4%)
1	C	0.57	1/2176 (0.0%)	1.19	29/2953 (1.0%)
1	D	0.64	5/2154 (0.2%)	1.10	18/2924 (0.6%)
All	All	0.58	8/8706 (0.1%)	1.04	70/11819 (0.6%)

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	4
1	B	0	1
1	C	0	8
1	D	0	7
All	All	0	20

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	639	LEU	C-N	7.31	1.46	1.33
1	B	667	GLU	CD-OE1	-6.52	1.18	1.25
1	D	640	GLY	N-CA	6.17	1.55	1.46
1	D	666	VAL	CB-CG1	-5.29	1.41	1.52
1	D	667	GLU	CB-CG	-5.20	1.42	1.52
1	C	757	SER	CB-OG	-5.17	1.35	1.42
1	A	667	GLU	CD-OE1	-5.13	1.20	1.25
1	D	757	SER	CB-OG	-5.07	1.35	1.42

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	656	PHE	C-N-CA	-17.29	78.47	121.70
1	C	657	ASP	CA-C-N	-12.20	90.36	117.20
1	C	756	TYR	C-N-CA	-11.09	93.99	121.70
1	C	584	ALA	C-N-CA	-11.01	94.17	121.70
1	D	756	TYR	C-N-CA	-10.83	94.63	121.70
1	C	539	LEU	CB-CG-CD1	-10.12	93.80	111.00
1	A	539	LEU	CB-CG-CD1	-10.10	93.83	111.00
1	C	757	SER	C-N-CA	-9.87	101.57	122.30
1	C	757	SER	O-C-N	-9.21	107.54	123.20
1	C	757	SER	CA-C-N	9.16	134.53	116.20
1	D	757	SER	C-N-CA	-8.91	103.60	122.30
1	A	766	ASP	CB-CG-OD1	8.79	126.21	118.30
1	B	756	TYR	C-N-CA	-8.27	101.02	121.70
1	D	666	VAL	N-CA-CB	-8.01	93.88	111.50
1	A	766	ASP	CB-CG-OD2	-7.84	111.24	118.30
1	C	651	SER	O-C-N	-7.80	110.23	122.70
1	A	478	LEU	CB-CG-CD1	7.74	124.16	111.00
1	C	652	GLU	C-N-CA	-7.46	103.04	121.70
1	D	757	SER	O-C-N	-7.25	110.87	123.20
1	B	757	SER	C-N-CA	-7.25	107.08	122.30
1	D	579	ASP	C-N-CA	-7.03	104.12	121.70
1	C	766	ASP	CB-CG-OD1	7.01	124.61	118.30
1	D	745	ILE	C-N-CA	6.79	138.67	121.70
1	D	666	VAL	CA-CB-CG1	6.74	121.02	110.90
1	D	665	PRO	O-C-N	6.72	133.45	122.70
1	A	537	PRO	C-N-CA	-6.69	108.24	122.30
1	C	537	PRO	C-N-CA	-6.69	108.25	122.30
1	C	636	LEU	O-C-N	-6.63	112.08	122.70
1	D	757	SER	CA-C-N	6.61	129.43	116.20
1	C	757	SER	CB-CA-C	6.57	122.58	110.10
1	D	558	VAL	C-N-CA	-6.54	105.34	121.70
1	C	478	LEU	CB-CG-CD1	6.53	122.10	111.00
1	B	666	VAL	CA-CB-CG2	6.41	120.52	110.90
1	D	623	THR	O-C-N	-6.39	112.48	122.70
1	D	654	VAL	O-C-N	6.21	132.63	122.70
1	A	602	PRO	C-N-CA	-6.04	106.60	121.70
1	C	635	ASP	C-N-CA	-5.96	106.79	121.70
1	B	757	SER	CA-C-N	5.86	127.93	116.20
1	B	761	MET	CB-CG-SD	-5.86	94.83	112.40
1	C	563	GLU	C-N-CA	-5.85	107.07	121.70
1	D	761	MET	CB-CG-SD	-5.84	94.89	112.40
1	B	757	SER	O-C-N	-5.80	113.34	123.20
1	C	735	VAL	C-N-CA	5.76	136.10	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	657	ASP	O-C-N	5.75	131.91	122.70
1	C	661	ALA	C-N-CA	5.73	136.03	121.70
1	C	736	LYS	CA-C-N	-5.72	104.62	117.20
1	C	660	ILE	C-N-CA	5.66	135.85	121.70
1	D	629	HIS	C-N-CA	-5.65	107.58	121.70
1	C	657	ASP	C-N-CA	5.63	135.79	121.70
1	A	769	GLY	N-CA-C	5.63	127.18	113.10
1	C	736	LYS	CB-CA-C	-5.60	99.20	110.40
1	B	665	PRO	O-C-N	5.60	131.66	122.70
1	A	660	ILE	C-N-CA	5.59	135.67	121.70
1	A	539	LEU	CA-CB-CG	-5.58	102.47	115.30
1	B	667	GLU	OE1-CD-OE2	-5.57	116.62	123.30
1	C	539	LEU	CA-CB-CG	-5.53	102.58	115.30
1	A	478	LEU	CA-CB-CG	5.46	127.86	115.30
1	B	666	VAL	CB-CA-C	-5.46	101.03	111.40
1	C	651	SER	CA-C-N	5.45	129.19	117.20
1	C	658	GLU	N-CA-C	-5.44	96.31	111.00
1	D	665	PRO	CA-C-N	-5.41	105.30	117.20
1	D	655	CYS	CA-C-N	-5.35	105.43	117.20
1	A	667	GLU	OE1-CD-OE2	-5.33	116.90	123.30
1	D	489	THR	C-N-CA	-5.25	108.57	121.70
1	B	637	SER	O-C-N	-5.21	114.37	122.70
1	C	666	VAL	C-N-CA	-5.14	108.86	121.70
1	C	683	HIS	C-N-CA	-5.11	108.94	121.70
1	D	666	VAL	CA-CB-CG2	5.08	118.51	110.90
1	B	736	LYS	C-N-CA	5.06	134.35	121.70
1	A	658	GLU	N-CA-C	-5.01	97.46	111.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	603	SER	Mainchain
1	A	651	SER	Mainchain
1	A	657	ASP	Mainchain
1	A	747	GLN	Mainchain
1	B	665	PRO	Peptide
1	C	604	ALA	Mainchain
1	C	636	LEU	Mainchain
1	C	651	SER	Mainchain
1	C	657	ASP	Mainchain
1	C	662	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	C	736	LYS	Mainchain
1	C	747	GLN	Mainchain
1	C	757	SER	Mainchain
1	D	490	GLU	Mainchain
1	D	541	GLN	Mainchain
1	D	622	LEU	Peptide
1	D	637	SER	Mainchain
1	D	638	ASP	Mainchain
1	D	665	PRO	Peptide
1	D	757	SER	Mainchain

## 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	2168	0	2166	123	0
1	B	2110	0	2109	121	1
1	C	2128	0	2123	133	2
1	D	2106	0	2103	159	1
2	A	29	44	44	5	0
2	B	29	44	44	6	0
2	C	29	44	44	3	0
2	D	29	44	44	15	0
All	All	8628	176	8677	513	2

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 30.

All (513) 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:B:509:GLU:CD	1:B:627:ARG:HH22	1.29	1.36
1:B:509:GLU:CD	1:B:627:ARG:NH2	1.86	1.27
1:C:494:THR:HG21	1:C:740:TRP:NE1	1.47	1.27
1:D:491:VAL:O	1:D:494:THR:HG22	1.34	1.25
1:B:491:VAL:O	1:B:494:THR:HG22	1.34	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:509:GLU:OE2	1:B:627:ARG:NH2	1.74	1.18
1:B:639:LEU:HD13	1:B:639:LEU:O	1.42	1.17
1:D:554:LEU:HG	1:D:615:ILE:HD11	1.28	1.09
1:C:624:GLU:HG3	1:C:625:LYS:HD3	1.13	1.09
1:C:747:GLN:O	1:C:748:VAL:HG23	1.50	1.09
1:A:494:THR:HG21	1:A:740:TRP:NE1	1.65	1.08
1:C:494:THR:CG2	1:C:740:TRP:HE1	1.66	1.08
1:A:494:THR:HG21	1:A:740:TRP:HE1	1.09	1.07
1:A:733:THR:HG22	1:A:746:THR:CG2	1.86	1.04
1:D:665:PRO:HA	1:D:666:VAL:HG22	1.39	1.03
1:A:733:THR:HG22	1:A:746:THR:HG22	1.39	1.02
1:B:660:ILE:HB	1:B:663:LEU:HD12	1.45	0.99
1:D:623:THR:HG22	1:D:625:LYS:H	1.29	0.98
1:D:554:LEU:HG	1:D:615:ILE:CD1	1.93	0.97
1:B:554:LEU:O	1:B:558:VAL:HG23	1.66	0.95
1:A:747:GLN:O	1:A:748:VAL:HG23	1.66	0.94
1:B:555:ARG:HA	1:B:558:VAL:CG2	1.98	0.94
1:D:764:MET:HG3	2:D:801:ERG:C6	1.98	0.94
1:D:665:PRO:CA	1:D:666:VAL:HG22	1.97	0.94
1:C:494:THR:HG21	1:C:740:TRP:HE1	0.81	0.93
1:D:623:THR:HG22	1:D:625:LYS:N	1.83	0.92
1:C:660:ILE:HB	1:C:663:LEU:HD12	1.50	0.92
1:C:605:TRP:CZ2	1:C:748:VAL:CG1	2.52	0.91
1:C:624:GLU:CG	1:C:625:LYS:HD3	2.00	0.91
1:D:605:TRP:CZ2	1:D:748:VAL:CG1	2.53	0.91
1:C:656:PHE:O	1:C:657:ASP:HB3	1.70	0.91
1:D:491:VAL:O	1:D:494:THR:CG2	2.18	0.90
1:B:753:VAL:CG2	1:B:763:MET:SD	2.59	0.90
1:B:491:VAL:O	1:B:494:THR:CG2	2.19	0.89
1:B:605:TRP:O	1:B:609:VAL:HG23	1.71	0.89
1:A:729:ARG:O	1:A:733:THR:HG23	1.73	0.89
1:B:539:LEU:HA	1:B:542:TYR:HD2	1.36	0.89
1:D:487:TYR:CG	1:D:524:LEU:HD21	2.10	0.87
1:C:655:CYS:HB2	1:C:723:CYS:SG	2.16	0.86
1:B:639:LEU:O	1:B:639:LEU:CD1	2.24	0.85
1:C:729:ARG:O	1:C:733:THR:HG22	1.76	0.85
1:C:476:LEU:HD22	1:D:522:HIS:CD2	2.11	0.84
1:D:539:LEU:HA	1:D:542:TYR:HD2	1.40	0.84
1:A:734:GLU:O	1:C:497:SER:HA	1.77	0.84
1:A:659:SER:O	1:A:719:ARG:NH1	2.10	0.83
1:A:494:THR:HG21	1:A:740:TRP:CD1	2.13	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:764:MET:HB2	2:D:801:ERG:C5	2.08	0.83
1:C:494:THR:CG2	1:C:740:TRP:NE1	2.30	0.83
1:D:487:TYR:CB	1:D:524:LEU:HD21	2.10	0.82
1:D:692:ILE:HG23	1:D:693:LEU:HG	1.59	0.82
1:D:745:ILE:HG23	1:D:746:THR:N	1.94	0.82
1:A:753:VAL:HG23	1:A:763:MET:SD	2.20	0.82
1:D:606:ILE:HG23	1:D:767:PHE:CE2	2.15	0.81
1:C:476:LEU:HB2	1:D:522:HIS:CE1	2.15	0.81
1:D:562:SER:O	1:D:566:THR:HG23	1.80	0.80
1:B:562:SER:O	1:B:566:THR:HG23	1.81	0.80
1:A:691:PHE:CZ	1:A:695:VAL:HG21	2.16	0.80
1:C:656:PHE:O	1:C:657:ASP:CB	2.10	0.79
1:A:558:VAL:HG23	1:A:561:ILE:HD11	1.65	0.79
1:A:566:THR:HG23	1:A:619:VAL:CG2	2.13	0.79
1:C:494:THR:HG21	1:C:740:TRP:CD1	2.17	0.79
1:A:624:GLU:HG2	1:A:629:HIS:ND1	1.99	0.78
1:A:566:THR:HG23	1:A:619:VAL:HG21	1.66	0.78
1:D:729:ARG:O	1:D:733:THR:HG23	1.84	0.78
1:D:606:ILE:HD13	1:D:767:PHE:CZ	2.18	0.78
1:B:606:ILE:HD13	1:B:767:PHE:CZ	2.19	0.77
1:B:736:LYS:O	1:B:743:GLU:HG2	1.85	0.77
1:C:656:PHE:CD2	1:C:657:ASP:N	2.53	0.77
1:A:494:THR:CG2	1:A:740:TRP:HE1	1.94	0.77
1:C:747:GLN:O	1:C:748:VAL:CG2	2.31	0.77
1:C:552:ARG:HH11	1:C:552:ARG:HG2	1.49	0.77
1:B:509:GLU:OE1	1:B:627:ARG:NH2	2.18	0.76
1:C:660:ILE:HB	1:C:663:LEU:CD1	2.15	0.76
1:B:554:LEU:C	1:B:558:VAL:HG23	2.05	0.76
1:C:532:LEU:HD23	1:C:539:LEU:HD11	1.68	0.76
1:D:654:VAL:HG12	1:D:655:CYS:N	1.99	0.76
1:B:547:ARG:NH2	1:B:576:LEU:HG	2.02	0.75
1:B:764:MET:HB2	2:B:801:ERG:C5	2.16	0.75
1:B:764:MET:HG3	2:B:801:ERG:C6	2.17	0.75
1:C:605:TRP:CZ2	1:C:748:VAL:HG12	2.22	0.75
1:C:558:VAL:HG23	1:C:561:ILE:HD11	1.67	0.75
1:D:745:ILE:CG2	1:D:746:THR:N	2.49	0.74
1:B:555:ARG:HA	1:B:558:VAL:HG23	1.67	0.74
1:D:605:TRP:CE2	1:D:748:VAL:CG1	2.70	0.74
1:A:532:LEU:HD23	1:A:539:LEU:HD11	1.68	0.73
1:C:656:PHE:CZ	1:C:726:GLN:HB3	2.23	0.73
1:D:764:MET:HA	2:D:801:ERG:H9	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:554:LEU:HD22	1:B:615:ILE:HD13	1.69	0.73
1:C:494:THR:CG2	1:C:740:TRP:CD1	2.71	0.73
1:D:610:LYS:O	1:D:614:THR:HG23	1.89	0.72
1:B:539:LEU:HA	1:B:542:TYR:CD2	2.24	0.72
1:A:733:THR:HG22	1:A:746:THR:HG21	1.72	0.71
1:C:656:PHE:HZ	1:C:726:GLN:HB3	1.54	0.71
1:A:541:GLN:NE2	1:A:542:TYR:CE1	2.59	0.71
1:B:692:ILE:HD13	1:B:731:PHE:CE2	2.25	0.71
1:B:753:VAL:HG22	1:B:763:MET:SD	2.31	0.70
1:C:476:LEU:HD11	1:D:521:MET:HG3	1.72	0.70
1:D:550:ALA:O	1:D:554:LEU:HB2	1.92	0.70
1:C:477:ASN:O	1:C:481:LEU:HD12	1.90	0.70
1:D:494:THR:OG1	1:D:740:TRP:NE1	2.24	0.70
1:D:558:VAL:HG23	1:D:561:ILE:HD11	1.72	0.70
1:C:683:HIS:CD2	1:C:727:LEU:HD22	2.26	0.70
1:D:538:GLY:O	1:D:539:LEU:HB2	1.91	0.69
1:B:605:TRP:CE2	1:B:748:VAL:HG11	2.28	0.69
1:A:494:THR:CG2	1:A:740:TRP:CD1	2.75	0.69
1:C:684:ARG:HH11	1:C:684:ARG:HG2	1.58	0.69
1:A:541:GLN:NE2	1:A:542:TYR:CZ	2.61	0.68
1:B:555:ARG:HA	1:B:558:VAL:HG21	1.73	0.68
1:D:753:VAL:HG23	1:D:763:MET:SD	2.32	0.68
1:D:539:LEU:HA	1:D:542:TYR:CD2	2.27	0.68
1:A:707:LEU:HD23	1:A:772:LEU:HD21	1.73	0.68
1:C:683:HIS:NE2	1:C:727:LEU:HD22	2.09	0.68
1:A:634:VAL:HG22	1:A:636:LEU:HB3	1.74	0.68
1:C:635:ASP:O	1:C:636:LEU:HD23	1.93	0.68
1:C:657:ASP:OD1	1:C:657:ASP:O	2.11	0.68
1:A:624:GLU:HG2	1:A:629:HIS:CE1	2.30	0.67
1:C:763:MET:SD	2:C:801:ERG:H112	2.34	0.67
1:B:532:LEU:HD23	1:B:539:LEU:HD11	1.76	0.67
1:B:605:TRP:CZ2	1:B:748:VAL:CG1	2.77	0.67
1:B:753:VAL:HG23	1:B:763:MET:SD	2.34	0.67
1:A:772:LEU:N	1:A:772:LEU:HD22	2.10	0.67
1:B:666:VAL:HG13	1:B:666:VAL:O	1.95	0.67
1:B:606:ILE:CD1	1:B:767:PHE:CZ	2.78	0.67
1:B:692:ILE:HD13	1:B:731:PHE:HE2	1.58	0.67
1:B:685:GLU:OE1	1:B:688:GLN:HG3	1.95	0.67
1:D:696:PHE:CD1	2:D:801:ERG:H261	2.29	0.67
1:D:619:VAL:CG1	1:D:622:LEU:HD21	2.26	0.66
1:A:494:THR:CG2	1:A:740:TRP:NE1	2.50	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:LEU:CD2	1:A:772:LEU:HD21	2.25	0.66
1:B:605:TRP:CE3	1:B:609:VAL:HG21	2.31	0.66
1:C:476:LEU:HD22	1:D:522:HIS:NE2	2.10	0.66
1:D:745:ILE:CG2	1:D:746:THR:H	2.09	0.66
1:A:505:ILE:HA	1:A:509:GLU:HB2	1.78	0.66
1:C:505:ILE:HA	1:C:509:GLU:HB2	1.78	0.66
1:B:605:TRP:CZ2	1:B:748:VAL:HG11	2.31	0.65
1:C:605:TRP:CZ2	1:C:748:VAL:HG11	2.30	0.65
1:D:605:TRP:NE1	1:D:748:VAL:HG13	2.11	0.65
1:D:555:ARG:O	1:D:558:VAL:HG12	1.96	0.65
1:D:605:TRP:CZ2	1:D:748:VAL:HG11	2.29	0.65
1:D:554:LEU:CG	1:D:615:ILE:CD1	2.72	0.65
1:D:606:ILE:O	1:D:609:VAL:HG12	1.96	0.65
1:D:549:ASP:O	1:D:553:LEU:HD12	1.96	0.65
1:C:696:PHE:CD1	2:C:801:ERG:H261	2.33	0.64
1:D:764:MET:CG	2:D:801:ERG:C6	2.74	0.64
1:D:605:TRP:CZ2	1:D:748:VAL:HG12	2.33	0.64
1:C:606:ILE:HG23	1:C:767:PHE:CE1	2.32	0.63
1:D:532:LEU:HD23	1:D:539:LEU:HD11	1.79	0.63
1:C:605:TRP:CE2	1:C:748:VAL:HG11	2.33	0.63
1:A:620:TRP:CD2	1:A:621:PRO:HA	2.35	0.62
1:A:652:GLU:HG3	1:A:664:TYR:CE2	2.34	0.62
1:C:620:TRP:CD2	1:C:621:PRO:HA	2.35	0.62
1:D:622:LEU:O	1:D:623:THR:O	2.17	0.62
1:A:634:VAL:CG2	1:A:636:LEU:HB3	2.29	0.62
1:A:772:LEU:HD22	1:A:772:LEU:H	1.65	0.62
1:B:737:ASP:HB3	1:B:738:LYS:HD2	1.81	0.62
1:D:665:PRO:CB	1:D:666:VAL:HG22	2.29	0.61
1:B:538:GLY:O	1:B:539:LEU:HB2	2.00	0.61
1:B:764:MET:HA	2:B:801:ERG:H9	1.82	0.61
1:C:522:HIS:CE1	1:D:476:LEU:HD22	2.35	0.61
1:A:639:LEU:CD2	1:A:651:SER:HB3	2.31	0.61
1:C:558:VAL:O	1:C:561:ILE:HG13	2.00	0.61
1:C:495:ILE:HG23	1:C:500:ILE:HD12	1.82	0.61
1:C:605:TRP:HH2	1:C:749:LEU:HD11	1.66	0.60
1:A:495:ILE:HG23	1:A:500:ILE:HD12	1.81	0.60
1:D:605:TRP:CE2	1:D:748:VAL:HG11	2.36	0.60
1:A:634:VAL:HG22	1:A:636:LEU:CB	2.31	0.60
1:B:547:ARG:HH22	1:B:576:LEU:HG	1.65	0.60
1:D:487:TYR:CD2	1:D:524:LEU:HD11	2.36	0.60
1:B:554:LEU:HD22	1:B:615:ILE:CD1	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:605:TRP:HZ2	1:C:748:VAL:CG1	2.09	0.60
1:C:757:SER:O	1:C:759:GLY:N	2.34	0.60
1:C:482:LYS:NZ	1:D:512:GLN:HE21	2.00	0.59
1:A:753:VAL:HG21	2:A:801:ERG:H11	1.83	0.59
1:D:605:TRP:CE2	1:D:748:VAL:HG13	2.37	0.59
1:B:555:ARG:CA	1:B:558:VAL:HG23	2.32	0.59
1:B:606:ILE:HD13	1:B:767:PHE:CE1	2.37	0.59
1:D:620:TRP:CD2	1:D:621:PRO:HA	2.38	0.59
1:D:732:ALA:HB1	1:D:745:ILE:HG12	1.83	0.59
1:A:605:TRP:CZ3	1:A:609:VAL:HG21	2.38	0.59
1:A:652:GLU:HG3	1:A:664:TYR:CD2	2.38	0.58
1:D:571:ALA:O	1:D:575:ILE:HG12	2.04	0.58
1:B:620:TRP:CD2	1:B:621:PRO:HA	2.38	0.58
1:C:520:LEU:HD12	1:C:572:SER:HB3	1.84	0.58
1:D:692:ILE:HG23	1:D:693:LEU:N	2.19	0.58
1:B:571:ALA:O	1:B:575:ILE:HG12	2.04	0.57
1:A:492:TRP:CZ3	1:A:503:GLU:HG3	2.39	0.57
1:B:512:GLN:HA	1:B:515:PHE:CD2	2.40	0.57
1:B:556:LYS:HE2	1:B:560:GLU:OE2	2.04	0.57
1:B:698:PHE:HB3	1:B:699:PRO:HD3	1.87	0.57
1:D:698:PHE:HB3	1:D:699:PRO:HD3	1.87	0.57
1:C:552:ARG:HG2	1:C:552:ARG:NH1	2.14	0.56
1:D:692:ILE:HD12	1:D:731:PHE:HE2	1.69	0.56
1:B:696:PHE:HZ	1:B:742:LEU:HD21	1.69	0.56
1:C:476:LEU:CD1	1:D:525:LEU:HD12	2.36	0.56
1:B:486:HIS:NE2	1:B:531:HIS:HD2	2.04	0.56
1:D:696:PHE:HZ	1:D:742:LEU:HD21	1.70	0.56
1:C:512:GLN:HA	1:C:515:PHE:CD2	2.40	0.56
1:C:561:ILE:HD13	1:C:619:VAL:HG12	1.88	0.56
1:D:661:ALA:C	1:D:663:LEU:H	2.09	0.56
1:D:606:ILE:HG23	1:D:767:PHE:CZ	2.40	0.56
1:A:625:LYS:C	1:A:625:LYS:HD3	2.26	0.56
1:D:554:LEU:CG	1:D:615:ILE:HD11	2.20	0.56
1:C:605:TRP:CE2	1:C:748:VAL:CG1	2.87	0.56
1:C:605:TRP:HZ2	1:C:748:VAL:HG12	1.66	0.55
1:C:552:ARG:HH12	1:C:555:ARG:CD	2.20	0.55
1:A:482:LYS:NZ	1:B:512:GLN:HE22	2.05	0.55
1:A:709:LEU:HG	1:A:714:ASP:CB	2.37	0.55
1:D:660:ILE:O	1:D:663:LEU:HB2	2.07	0.55
1:A:560:GLU:O	1:A:560:GLU:HG3	2.07	0.55
1:C:494:THR:HG23	1:C:740:TRP:CD1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:555:ARG:HA	1:D:558:VAL:HG12	1.88	0.55
1:A:567:ASP:OD2	1:A:627:ARG:HG3	2.07	0.55
1:A:632:ILE:HG13	1:A:633:SER:O	2.07	0.55
1:A:747:GLN:O	1:A:748:VAL:CG2	2.48	0.55
1:C:603:SER:O	1:C:603:SER:OG	2.13	0.55
1:D:665:PRO:HA	1:D:666:VAL:CG2	2.26	0.55
1:A:519:PHE:HB2	1:A:554:LEU:HG	1.88	0.55
1:A:772:LEU:H	1:A:772:LEU:CD2	2.20	0.55
1:C:516:ASP:HB2	1:C:517:TYR:CE1	2.42	0.55
1:A:476:LEU:HD22	1:B:522:HIS:NE2	2.22	0.54
1:A:492:TRP:HA	1:A:495:ILE:HD12	1.89	0.54
1:A:696:PHE:HZ	1:A:742:LEU:HD21	1.73	0.54
1:C:660:ILE:O	1:C:663:LEU:HB2	2.06	0.54
1:C:491:VAL:O	1:C:494:THR:HB	2.07	0.54
1:C:679:LEU:O	1:C:683:HIS:HD2	1.89	0.54
1:C:708:ALA:O	1:C:712:THR:HG23	2.07	0.54
1:C:709:LEU:HG	1:C:714:ASP:CB	2.37	0.54
1:B:540:GLU:CD	1:B:540:GLU:H	2.11	0.54
1:D:623:THR:HG22	1:D:625:LYS:CA	2.38	0.54
1:C:632:ILE:HG13	1:C:633:SER:O	2.07	0.54
1:C:696:PHE:HZ	1:C:742:LEU:HD21	1.73	0.54
1:D:666:VAL:O	1:D:666:VAL:HG23	2.08	0.54
1:A:551:LEU:O	1:A:555:ARG:HG2	2.08	0.53
1:C:521:MET:HE2	1:C:525:LEU:HD21	1.89	0.53
1:A:691:PHE:CZ	1:A:695:VAL:CG2	2.88	0.53
1:B:737:ASP:HB3	1:B:738:LYS:CD	2.38	0.53
1:C:624:GLU:HG3	1:C:625:LYS:CD	2.08	0.53
1:C:681:LYS:O	1:C:685:GLU:HG2	2.08	0.53
1:C:487:TYR:CE1	1:C:524:LEU:HD11	2.43	0.53
1:A:535:LYS:HE2	1:D:504:ARG:CZ	2.39	0.53
1:B:504:ARG:HA	1:B:507:SER:HB3	1.91	0.53
1:C:492:TRP:HA	1:C:495:ILE:HD12	1.89	0.53
1:C:656:PHE:CG	1:C:657:ASP:N	2.75	0.53
1:C:659:SER:O	1:C:719:ARG:NH2	2.41	0.53
1:D:764:MET:SD	2:D:801:ERG:H41	2.49	0.53
1:D:569:LEU:O	1:D:572:SER:HB2	2.09	0.53
1:D:609:VAL:HG13	1:D:610:LYS:N	2.24	0.53
1:C:476:LEU:CB	1:D:522:HIS:CE1	2.90	0.52
1:A:482:LYS:HZ1	1:B:512:GLN:HE22	1.57	0.52
1:B:620:TRP:CZ3	1:B:622:LEU:HD23	2.44	0.52
1:B:734:GLU:O	1:B:734:GLU:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:760:GLY:O	2:B:801:ERG:H12	2.09	0.52
1:C:476:LEU:CD1	1:D:525:LEU:CD1	2.87	0.52
1:A:637:SER:O	1:A:638:ASP:OD1	2.27	0.52
1:A:764:MET:HB2	2:A:801:ERG:C5	2.40	0.52
1:B:567:ASP:OD2	1:B:627:ARG:HG3	2.10	0.52
1:B:605:TRP:CZ3	1:B:609:VAL:HG21	2.45	0.52
1:C:522:HIS:NE2	1:D:476:LEU:HD22	2.24	0.52
1:C:554:LEU:CD2	1:C:569:LEU:HD23	2.39	0.52
1:D:757:SER:O	1:D:758:GLY:C	2.44	0.52
1:A:558:VAL:O	1:A:561:ILE:HG13	2.09	0.51
1:B:494:THR:OG1	1:B:740:TRP:NE1	2.44	0.51
1:C:555:ARG:NH1	1:C:555:ARG:HG3	2.24	0.51
1:D:736:LYS:HG3	1:D:737:ASP:N	2.25	0.51
1:A:633:SER:HB3	1:A:681:LYS:HG2	1.92	0.51
1:B:696:PHE:CD1	2:B:801:ERG:H261	2.45	0.51
1:D:487:TYR:CE2	1:D:524:LEU:HD11	2.45	0.51
1:A:707:LEU:HD11	1:A:711:MET:HE2	1.92	0.51
1:A:639:LEU:HD23	1:A:651:SER:HB3	1.93	0.50
1:B:736:LYS:HG3	1:B:737:ASP:N	2.26	0.50
1:B:605:TRP:CE2	1:B:748:VAL:CG1	2.93	0.50
1:D:606:ILE:C	1:D:609:VAL:HG12	2.32	0.50
1:B:507:SER:OG	1:B:508:ASP:OD2	2.30	0.50
1:D:764:MET:HB2	2:D:801:ERG:H3	1.93	0.50
1:A:630:ASN:OD1	1:A:631:LEU:HD12	2.12	0.50
1:D:492:TRP:CZ3	1:D:503:GLU:CG	2.95	0.50
1:D:558:VAL:O	1:D:558:VAL:HG22	2.10	0.50
1:A:567:ASP:OD1	1:A:626:SER:OG	2.25	0.50
1:B:710:LEU:HD22	1:B:764:MET:SD	2.52	0.50
1:B:661:ALA:C	1:B:663:LEU:H	2.14	0.49
1:C:482:LYS:NZ	1:D:512:GLN:NE2	2.60	0.49
1:C:574:LEU:HD11	1:C:631:LEU:HD11	1.92	0.49
1:A:691:PHE:CE1	1:A:695:VAL:HG23	2.46	0.49
1:B:711:MET:CE	1:B:768:LEU:HB3	2.41	0.49
1:C:476:LEU:HD11	1:D:521:MET:CG	2.42	0.49
1:B:692:ILE:CD1	1:B:731:PHE:CZ	2.95	0.49
1:D:686:LYS:HA	1:D:691:PHE:CE1	2.47	0.49
1:A:683:HIS:CE1	1:A:727:LEU:HD22	2.48	0.49
1:B:718:MET:O	1:B:722:ARG:HG3	2.13	0.49
1:D:552:ARG:NH2	1:D:553:LEU:HD11	2.27	0.49
1:D:760:GLY:O	2:D:801:ERG:H12	2.11	0.49
1:B:620:TRP:CE3	1:B:622:LEU:HD23	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:494:THR:OG1	1:D:740:TRP:CD1	2.66	0.49
1:D:606:ILE:O	1:D:609:VAL:CG1	2.60	0.49
1:D:710:LEU:HD22	1:D:764:MET:SD	2.52	0.49
1:D:764:MET:CB	2:D:801:ERG:C5	2.88	0.49
1:A:772:LEU:N	1:A:772:LEU:CD2	2.76	0.49
1:D:606:ILE:HD13	1:D:767:PHE:CE1	2.48	0.49
1:A:530:THR:OG1	1:A:579:ASP:OD1	2.21	0.49
1:D:561:ILE:HG12	1:D:569:LEU:HD13	1.94	0.49
1:A:521:MET:HE2	1:A:525:LEU:HD21	1.95	0.49
1:D:492:TRP:CZ3	1:D:503:GLU:HG3	2.48	0.48
1:A:631:LEU:HD12	1:A:631:LEU:N	2.29	0.48
1:D:698:PHE:CE2	1:D:721:MET:HE1	2.48	0.48
1:B:737:ASP:CB	1:B:738:LYS:CD	2.91	0.48
1:D:664:TYR:CD2	1:D:666:VAL:HG13	2.49	0.48
1:A:535:LYS:HE2	1:D:504:ARG:NH2	2.29	0.48
1:C:553:LEU:HD23	1:C:556:LYS:HZ3	1.79	0.48
1:A:605:TRP:CZ2	1:A:606:ILE:HG12	2.48	0.48
1:A:636:LEU:C	1:A:636:LEU:HD23	2.34	0.48
1:C:512:GLN:HA	1:C:515:PHE:CE2	2.48	0.48
1:D:606:ILE:HA	1:D:609:VAL:HG12	1.94	0.48
1:D:692:ILE:HD11	1:D:742:LEU:HD11	1.95	0.48
1:D:718:MET:O	1:D:722:ARG:HG3	2.13	0.48
1:A:634:VAL:CG2	1:A:636:LEU:CB	2.91	0.48
1:B:698:PHE:CE2	1:B:721:MET:HE1	2.48	0.48
1:B:660:ILE:O	1:B:660:ILE:HG13	2.14	0.48
1:B:686:LYS:HA	1:B:691:PHE:CE1	2.48	0.48
1:C:482:LYS:HD2	1:D:515:PHE:CD2	2.48	0.48
1:D:622:LEU:C	1:D:623:THR:O	2.50	0.48
1:A:558:VAL:O	1:A:558:VAL:HG22	2.14	0.47
1:A:491:VAL:O	1:A:494:THR:HB	2.14	0.47
1:B:737:ASP:HB2	1:B:738:LYS:HD3	1.95	0.47
1:C:558:VAL:O	1:C:558:VAL:HG22	2.14	0.47
1:A:762:HIS:HE1	1:A:766:ASP:OD1	1.98	0.47
1:D:753:VAL:CG2	1:D:763:MET:SD	3.00	0.47
1:B:639:LEU:HD13	1:B:639:LEU:C	2.27	0.47
1:A:522:HIS:CE1	1:B:476:LEU:HD22	2.49	0.47
1:A:634:VAL:HG22	1:A:636:LEU:H	1.80	0.47
1:C:544:ALA:O	1:C:548:LEU:HG	2.14	0.47
1:D:620:TRP:CG	1:D:701:LEU:HD22	2.50	0.47
1:D:748:VAL:HG12	1:D:749:LEU:HD23	1.96	0.47
1:A:605:TRP:CE2	1:A:606:ILE:HG12	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:SER:OG	1:A:661:ALA:HB3	2.15	0.47
1:A:707:LEU:HD11	1:A:711:MET:CE	2.45	0.47
1:B:752:ASP:O	1:B:755:ASP:HB2	2.15	0.47
1:A:691:PHE:CE1	1:A:695:VAL:CG2	2.98	0.46
1:B:538:GLY:O	1:B:540:GLU:OE2	2.34	0.46
1:C:487:TYR:HA	1:C:491:VAL:HB	1.97	0.46
1:D:504:ARG:HA	1:D:507:SER:OG	2.15	0.46
1:D:584:ALA:HB1	1:D:748:VAL:CG2	2.46	0.46
1:A:625:LYS:HD3	1:A:625:LYS:O	2.14	0.46
1:B:683:HIS:O	1:B:686:LYS:HB2	2.15	0.46
1:D:657:ASP:OD1	1:D:658:GLU:HG3	2.16	0.46
1:A:733:THR:CG2	1:A:746:THR:HG21	2.45	0.46
1:D:698:PHE:HE2	1:D:721:MET:HE1	1.81	0.46
1:C:482:LYS:HZ1	1:D:512:GLN:HE21	1.63	0.46
1:C:562:SER:HB3	1:C:565:ASN:OD1	2.16	0.46
1:D:549:ASP:OD1	1:D:552:ARG:NH2	2.45	0.46
1:D:692:ILE:CG2	1:D:693:LEU:N	2.79	0.46
1:A:609:VAL:CG1	2:A:801:ERG:H25	2.46	0.46
1:A:611:GLY:O	1:A:614:THR:HB	2.16	0.46
1:C:698:PHE:HB3	1:C:699:PRO:HD3	1.97	0.46
1:C:730:GLY:HA2	1:C:733:THR:CG2	2.46	0.46
1:B:764:MET:CG	2:B:801:ERG:C6	2.89	0.46
1:D:634:VAL:HG22	1:D:678:TYR:CE1	2.51	0.46
1:B:567:ASP:OD1	1:B:626:SER:OG	2.31	0.46
1:C:605:TRP:O	1:C:609:VAL:HG23	2.16	0.46
1:D:620:TRP:CE3	1:D:621:PRO:HA	2.51	0.46
1:C:553:LEU:HD23	1:C:556:LYS:NZ	2.31	0.46
1:B:620:TRP:CE3	1:B:621:PRO:HA	2.51	0.45
1:C:710:LEU:HD23	1:C:710:LEU:HA	1.73	0.45
1:B:698:PHE:HE2	1:B:721:MET:HE1	1.81	0.45
1:D:654:VAL:HG12	1:D:655:CYS:CA	2.46	0.45
1:B:502:GLY:HA3	1:B:505:ILE:HG13	1.97	0.45
1:B:556:LYS:HA	1:B:559:LEU:HD12	1.99	0.45
1:D:760:GLY:O	2:D:801:ERG:H21	2.15	0.45
1:D:606:ILE:HG23	1:D:767:PHE:CD2	2.51	0.45
1:A:698:PHE:HB3	1:A:699:PRO:HD3	1.97	0.45
1:B:762:HIS:CE1	1:B:766:ASP:OD2	2.70	0.45
1:C:611:GLY:O	1:C:614:THR:HB	2.16	0.45
1:C:624:GLU:OE2	1:C:625:LYS:NZ	2.49	0.45
1:D:561:ILE:HG12	1:D:569:LEU:CD1	2.46	0.45
1:B:494:THR:OG1	1:B:740:TRP:CD1	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:GLY:O	1:B:505:ILE:CG1	2.65	0.45
1:D:477:ASN:O	1:D:481:LEU:HD12	2.17	0.45
1:A:512:GLN:HA	1:A:515:PHE:CD2	2.52	0.45
1:A:659:SER:OG	1:A:661:ALA:CB	2.65	0.45
1:A:764:MET:HA	2:A:801:ERG:H9	1.98	0.45
1:B:477:ASN:O	1:B:481:LEU:HD12	2.17	0.45
1:C:552:ARG:NH1	1:C:555:ARG:CD	2.80	0.45
1:B:711:MET:HE3	1:B:765:LEU:HD23	1.99	0.44
1:C:552:ARG:NH1	1:C:552:ARG:CG	2.79	0.44
1:D:764:MET:HG3	2:D:801:ERG:H6	1.93	0.44
1:A:610:LYS:HD3	1:A:768:LEU:O	2.18	0.44
1:C:750:PRO:HD2	1:C:763:MET:CE	2.47	0.44
1:D:764:MET:HG3	2:D:801:ERG:C7	2.46	0.44
1:B:620:TRP:CE3	1:B:620:TRP:HA	2.52	0.44
1:C:508:ASP:C	1:C:511:PRO:HD2	2.37	0.44
1:C:538:GLY:O	1:C:540:GLU:N	2.48	0.44
1:B:492:TRP:CG	1:B:493:PRO:HD3	2.53	0.44
1:D:514:ALA:HB1	1:D:521:MET:HB2	2.00	0.44
1:D:620:TRP:CE3	1:D:620:TRP:HA	2.52	0.44
1:C:731:PHE:CE1	1:C:735:VAL:HG11	2.52	0.44
1:A:501:SER:N	1:A:690:ASP:OD1	2.31	0.44
1:A:605:TRP:CE3	1:A:609:VAL:HG21	2.53	0.44
1:B:508:ASP:O	1:B:511:PRO:HD2	2.18	0.44
1:C:516:ASP:HB2	1:C:517:TYR:CD1	2.53	0.44
1:C:736:LYS:CD	1:C:736:LYS:O	2.66	0.44
1:A:521:MET:HE3	1:A:525:LEU:HG	2.00	0.43
1:A:632:ILE:HD12	1:A:678:TYR:CE1	2.53	0.43
1:C:562:SER:OG	1:C:564:ASP:N	2.49	0.43
1:A:492:TRP:HH2	1:A:503:GLU:OE2	2.02	0.43
1:B:554:LEU:O	1:B:557:ALA:N	2.52	0.43
1:C:730:GLY:O	1:C:733:THR:HG23	2.18	0.43
1:A:729:ARG:NH2	1:A:746:THR:HB	2.33	0.43
1:C:653:LEU:HD12	1:C:654:VAL:H	1.83	0.43
1:C:763:MET:O	1:C:763:MET:HG2	2.18	0.43
1:D:492:TRP:CG	1:D:493:PRO:HD3	2.53	0.43
1:D:567:ASP:OD2	1:D:627:ARG:NH2	2.41	0.43
1:D:606:ILE:CA	1:D:609:VAL:HG12	2.49	0.43
1:C:752:ASP:O	1:C:755:ASP:HB2	2.19	0.43
1:D:570:VAL:O	1:D:574:LEU:HG	2.19	0.43
1:A:552:ARG:HA	1:A:552:ARG:HD3	1.73	0.43
1:B:547:ARG:NH1	1:B:580:SER:OG	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:524:LEU:HD12	1:C:524:LEU:HA	1.88	0.43
1:C:637:SER:O	1:C:638:ASP:OD2	2.36	0.43
1:D:664:TYR:CD2	1:D:666:VAL:CG1	3.02	0.43
1:B:662:ASP:OD1	1:B:719:ARG:NH2	2.48	0.43
1:B:664:TYR:HA	1:B:666:VAL:H	1.84	0.43
1:C:532:LEU:O	1:C:532:LEU:HG	2.19	0.43
1:C:555:ARG:CG	1:C:555:ARG:HH11	2.32	0.43
1:D:535:LYS:HB2	1:D:535:LYS:HE3	1.91	0.43
1:D:623:THR:CG2	1:D:625:LYS:HB2	2.49	0.43
1:D:760:GLY:O	2:D:801:ERG:C2	2.67	0.43
1:A:605:TRP:CG	1:A:606:ILE:N	2.87	0.43
1:A:605:TRP:HZ3	1:A:609:VAL:HG21	1.82	0.43
1:C:729:ARG:NH2	1:C:746:THR:HB	2.33	0.43
1:D:733:THR:O	1:D:736:LYS:HD2	2.19	0.43
1:A:524:LEU:HD23	1:A:524:LEU:HA	1.84	0.42
1:B:634:VAL:HG22	1:B:678:TYR:CE1	2.54	0.42
1:A:767:PHE:CD1	2:A:801:ERG:H22	2.53	0.42
1:B:544:ALA:O	1:B:548:LEU:HD23	2.19	0.42
1:D:763:MET:O	1:D:767:PHE:HD1	2.02	0.42
1:B:584:ALA:HB1	1:B:748:VAL:CG2	2.50	0.42
1:D:704:LYS:HD2	1:D:704:LYS:N	2.34	0.42
1:A:616:LEU:O	1:A:619:VAL:HG12	2.19	0.42
1:A:637:SER:OG	1:A:638:ASP:N	2.50	0.42
1:A:667:GLU:H	1:A:667:GLU:CD	2.23	0.42
1:C:690:ASP:O	1:C:694:ARG:HG3	2.19	0.42
1:D:492:TRP:HZ3	1:D:503:GLU:HG3	1.84	0.42
1:D:745:ILE:O	1:D:748:VAL:HB	2.19	0.42
1:B:627:ARG:HG3	1:B:627:ARG:H	1.59	0.42
1:D:606:ILE:HA	1:D:609:VAL:CG1	2.50	0.42
1:A:628:PHE:C	1:A:630:ASN:H	2.22	0.42
1:B:763:MET:O	1:B:767:PHE:HD1	2.02	0.42
1:C:730:GLY:O	1:C:733:THR:CG2	2.68	0.42
1:A:508:ASP:C	1:A:511:PRO:HD2	2.40	0.42
1:A:554:LEU:O	1:A:557:ALA:N	2.52	0.42
1:B:681:LYS:NZ	1:B:684:ARG:CZ	2.83	0.42
1:D:605:TRP:CE2	1:D:606:ILE:HG12	2.55	0.42
1:D:697:ALA:O	1:D:701:LEU:HG	2.20	0.42
1:A:532:LEU:O	1:A:532:LEU:HG	2.19	0.42
1:B:486:HIS:CE1	1:B:490:GLU:HB2	2.55	0.42
1:B:656:PHE:O	1:B:657:ASP:C	2.58	0.42
1:D:752:ASP:OD1	1:D:752:ASP:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:TRP:CG	1:A:701:LEU:HD22	2.54	0.42
1:B:692:ILE:CD1	1:B:731:PHE:HZ	2.33	0.42
1:C:509:GLU:OE1	1:C:627:ARG:HD3	2.20	0.42
1:C:628:PHE:C	1:C:630:ASN:H	2.22	0.42
1:D:752:ASP:O	1:D:755:ASP:HB2	2.19	0.42
1:A:482:LYS:NZ	1:B:512:GLN:NE2	2.67	0.42
1:A:501:SER:OG	1:A:690:ASP:OD1	2.38	0.42
1:A:731:PHE:O	1:A:735:VAL:HG22	2.20	0.42
1:B:556:LYS:O	1:B:557:ALA:C	2.58	0.41
1:B:624:GLU:CG	1:B:624:GLU:O	2.68	0.41
1:B:697:ALA:O	1:B:701:LEU:HG	2.20	0.41
1:C:553:LEU:CD2	1:C:556:LYS:NZ	2.83	0.41
1:C:636:LEU:HD23	1:C:636:LEU:HA	1.85	0.41
1:A:632:ILE:HD12	1:A:633:SER:H	1.86	0.41
1:B:570:VAL:O	1:B:574:LEU:HG	2.19	0.41
1:B:662:ASP:OD1	1:B:719:ARG:NH1	2.48	0.41
1:C:605:TRP:CH2	1:C:749:LEU:HD11	2.51	0.41
1:D:476:LEU:HD12	1:D:477:ASN:N	2.35	0.41
1:D:639:LEU:HD23	1:D:684:ARG:HH22	1.85	0.41
1:D:764:MET:HB2	2:D:801:ERG:C3	2.50	0.41
1:D:487:TYR:HB2	1:D:524:LEU:HD21	1.96	0.41
1:D:732:ALA:HB1	1:D:745:ILE:HG21	2.02	0.41
1:D:764:MET:HB2	2:D:801:ERG:C4	2.49	0.41
1:B:512:GLN:HA	1:B:515:PHE:CE2	2.56	0.41
1:D:554:LEU:O	1:D:558:VAL:HG12	2.21	0.41
1:D:692:ILE:HD12	1:D:731:PHE:CE2	2.53	0.41
1:A:484:PHE:CE2	1:B:485:HIS:HB2	2.56	0.41
1:C:732:ALA:HB1	1:C:745:ILE:HG21	2.03	0.41
1:D:655:CYS:SG	1:D:656:PHE:N	2.94	0.41
1:A:732:ALA:HB1	1:A:745:ILE:HG21	2.03	0.41
1:B:605:TRP:CZ2	1:B:748:VAL:HG12	2.54	0.41
1:B:715:LEU:HD23	1:B:715:LEU:HA	1.81	0.41
1:C:504:ARG:CZ	1:C:508:ASP:OD2	2.68	0.41
1:C:634:VAL:O	1:C:681:LYS:NZ	2.52	0.41
1:D:627:ARG:H	1:D:627:ARG:HG3	1.61	0.41
1:D:639:LEU:HD23	1:D:684:ARG:NH2	2.35	0.41
1:D:661:ALA:C	1:D:663:LEU:N	2.73	0.41
1:A:523:ALA:HB1	1:A:576:LEU:HD13	2.03	0.41
1:A:538:GLY:O	1:A:540:GLU:N	2.50	0.41
1:A:704:LYS:H	1:A:704:LYS:HG3	1.69	0.41
1:C:552:ARG:NH1	1:C:555:ARG:HD2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:684:ARG:HG2	1:C:684:ARG:NH1	2.31	0.41
1:D:512:GLN:HA	1:D:515:PHE:CD2	2.56	0.41
1:C:753:VAL:HG21	2:C:801:ERG:H11	2.02	0.40
1:D:555:ARG:HA	1:D:558:VAL:CG1	2.51	0.40
1:D:732:ALA:CB	1:D:745:ILE:HG12	2.49	0.40
1:C:483:LEU:HD23	1:C:483:LEU:HA	1.90	0.40
1:C:523:ALA:HB1	1:C:576:LEU:HD13	2.03	0.40
1:A:620:TRP:CG	1:A:621:PRO:HA	2.56	0.40
1:A:656:PHE:O	1:A:658:GLU:N	2.50	0.40
1:B:508:ASP:C	1:B:511:PRO:HD2	2.41	0.40
1:C:554:LEU:O	1:C:557:ALA:N	2.54	0.40
1:C:620:TRP:CG	1:C:701:LEU:HD22	2.55	0.40
1:C:753:VAL:HG23	1:C:763:MET:SD	2.61	0.40
1:A:745:ILE:HD12	1:A:745:ILE:HA	1.84	0.40
1:A:753:VAL:CG2	1:A:763:MET:SD	3.00	0.40
1:D:532:LEU:C	1:D:534:ARG:H	2.25	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:736:LYS:NZ	1:C:560:GLU:OE1[2_544]	1.85	0.35
1:C:636:LEU:CD2	1:D:667:GLU:CG[1_656]	2.19	0.01

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	269/332 (81%)	246 (91%)	16 (6%)	7 (3%)	5	9
1	B	260/332 (78%)	242 (93%)	14 (5%)	4 (2%)	10	21
1	C	263/332 (79%)	243 (92%)	15 (6%)	5 (2%)	8	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	260/332 (78%)	240 (92%)	16 (6%)	4 (2%)	10	21
All	All	1052/1328 (79%)	971 (92%)	61 (6%)	20 (2%)	8	15

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	539	LEU
1	A	658	GLU
1	B	666	VAL
1	C	539	LEU
1	C	555	ARG
1	C	658	GLU
1	D	623	THR
1	D	666	VAL
1	A	555	ARG
1	A	637	SER
1	A	651	SER
1	A	748	VAL
1	C	736	LYS
1	C	748	VAL
1	B	476	LEU
1	B	638	ASP
1	D	638	ASP
1	B	686	LYS
1	A	604	ALA
1	D	476	LEU

### 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	234/286 (82%)	230 (98%)	4 (2%)	60	81
1	B	227/286 (79%)	222 (98%)	5 (2%)	52	76
1	C	229/286 (80%)	223 (97%)	6 (3%)	46	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	226/286 (79%)	223 (99%)	3 (1%)	69	86
All	All	916/1144 (80%)	898 (98%)	18 (2%)	55	78

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	504	ARG
1	A	547	ARG
1	A	659	SER
1	A	704	LYS
1	B	555	ARG
1	B	638	ASP
1	B	656	PHE
1	B	659	SER
1	B	662	ASP
1	C	528	SER
1	C	545	SER
1	C	555	ARG
1	C	585	SER
1	C	603	SER
1	C	737	ASP
1	D	635	ASP
1	D	638	ASP
1	D	662	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	747	GLN
1	A	762	HIS
1	B	512	GLN
1	B	531	HIS
1	B	762	HIS
1	C	485	HIS
1	C	683	HIS
1	C	687	ASN
1	D	512	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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

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	ERG	C	801	-	31,32,32	1.93	7 (22%)	47,50,50	1.48	9 (19%)
2	ERG	A	801	-	31,32,32	1.93	7 (22%)	47,50,50	1.48	9 (19%)
2	ERG	D	801	-	31,32,32	1.93	7 (22%)	47,50,50	1.48	9 (19%)
2	ERG	B	801	-	31,32,32	1.93	7 (22%)	47,50,50	1.49	9 (19%)

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	ERG	C	801	-	-	0/13/71/71	0/4/4/4
2	ERG	A	801	-	-	0/13/71/71	0/4/4/4
2	ERG	D	801	-	-	0/13/71/71	0/4/4/4
2	ERG	B	801	-	-	0/13/71/71	0/4/4/4

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	801	ERG	C23-C22	5.96	1.50	1.32
2	A	801	ERG	C23-C22	5.94	1.50	1.32
2	B	801	ERG	C23-C22	5.92	1.50	1.32
2	C	801	ERG	C23-C22	5.91	1.50	1.32
2	D	801	ERG	C10-C5	-5.38	1.42	1.52
2	A	801	ERG	C10-C5	-5.36	1.42	1.52
2	C	801	ERG	C10-C5	-5.36	1.42	1.52
2	B	801	ERG	C10-C5	-5.32	1.42	1.52
2	C	801	ERG	C4-C5	-3.52	1.44	1.51
2	B	801	ERG	C4-C5	-3.52	1.44	1.51
2	D	801	ERG	C4-C5	-3.48	1.44	1.51
2	A	801	ERG	C4-C5	-3.46	1.44	1.51
2	B	801	ERG	C9-C8	-3.27	1.43	1.51
2	C	801	ERG	C9-C8	-3.25	1.43	1.51
2	A	801	ERG	C9-C8	-3.24	1.43	1.51
2	D	801	ERG	C9-C8	-3.24	1.43	1.51
2	A	801	ERG	C11-C9	3.04	1.59	1.53
2	C	801	ERG	C11-C9	3.01	1.59	1.53
2	B	801	ERG	C11-C9	3.00	1.59	1.53
2	D	801	ERG	C11-C9	3.00	1.59	1.53
2	A	801	ERG	C14-C8	-2.44	1.45	1.51
2	D	801	ERG	C14-C8	-2.44	1.45	1.51
2	B	801	ERG	C14-C8	-2.43	1.45	1.51
2	C	801	ERG	C14-C8	-2.43	1.45	1.51
2	B	801	ERG	C6-C5	2.39	1.39	1.33
2	D	801	ERG	C6-C5	2.38	1.39	1.33
2	C	801	ERG	C6-C5	2.37	1.39	1.33
2	A	801	ERG	C6-C5	2.34	1.39	1.33

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	ERG	C19-C10-C5	-3.38	102.88	108.34
2	C	801	ERG	C19-C10-C5	-3.35	102.92	108.34
2	D	801	ERG	C19-C10-C5	-3.32	102.97	108.34
2	A	801	ERG	C19-C10-C5	-3.32	102.97	108.34
2	C	801	ERG	C4-C5-C10	3.11	120.55	116.42
2	B	801	ERG	C4-C5-C10	3.10	120.54	116.42
2	A	801	ERG	C4-C5-C10	3.09	120.53	116.42
2	D	801	ERG	C4-C5-C10	3.08	120.50	116.42
2	B	801	ERG	C15-C14-C13	-2.73	101.78	104.21
2	D	801	ERG	C15-C14-C13	-2.71	101.79	104.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	ERG	C15-C14-C13	-2.69	101.81	104.21
2	A	801	ERG	C11-C12-C13	-2.68	108.19	112.78
2	D	801	ERG	C11-C12-C13	-2.68	108.19	112.78
2	C	801	ERG	C11-C12-C13	-2.67	108.20	112.78
2	C	801	ERG	C15-C14-C13	-2.67	101.83	104.21
2	B	801	ERG	C11-C12-C13	-2.66	108.22	112.78
2	C	801	ERG	C19-C10-C9	-2.54	106.77	111.03
2	B	801	ERG	C19-C10-C9	-2.50	106.83	111.03
2	D	801	ERG	C19-C10-C9	-2.48	106.86	111.03
2	A	801	ERG	C19-C10-C9	-2.46	106.89	111.03
2	A	801	ERG	C1-C2-C3	-2.41	107.37	110.47
2	C	801	ERG	C1-C2-C3	-2.41	107.38	110.47
2	B	801	ERG	C1-C2-C3	-2.40	107.39	110.47
2	D	801	ERG	C1-C2-C3	-2.39	107.40	110.47
2	D	801	ERG	C17-C20-C22	-2.30	105.89	110.27
2	A	801	ERG	C17-C20-C22	-2.29	105.90	110.27
2	B	801	ERG	C14-C8-C9	2.29	118.10	114.66
2	C	801	ERG	C14-C8-C9	2.29	118.10	114.66
2	D	801	ERG	C14-C8-C9	2.28	118.09	114.66
2	D	801	ERG	C18-C13-C14	2.28	113.93	110.24
2	A	801	ERG	C18-C13-C14	2.27	113.92	110.24
2	B	801	ERG	C17-C20-C22	-2.26	105.96	110.27
2	B	801	ERG	C18-C13-C14	2.26	113.91	110.24
2	C	801	ERG	C17-C20-C22	-2.26	105.97	110.27
2	A	801	ERG	C14-C8-C9	2.25	118.05	114.66
2	C	801	ERG	C18-C13-C14	2.23	113.86	110.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

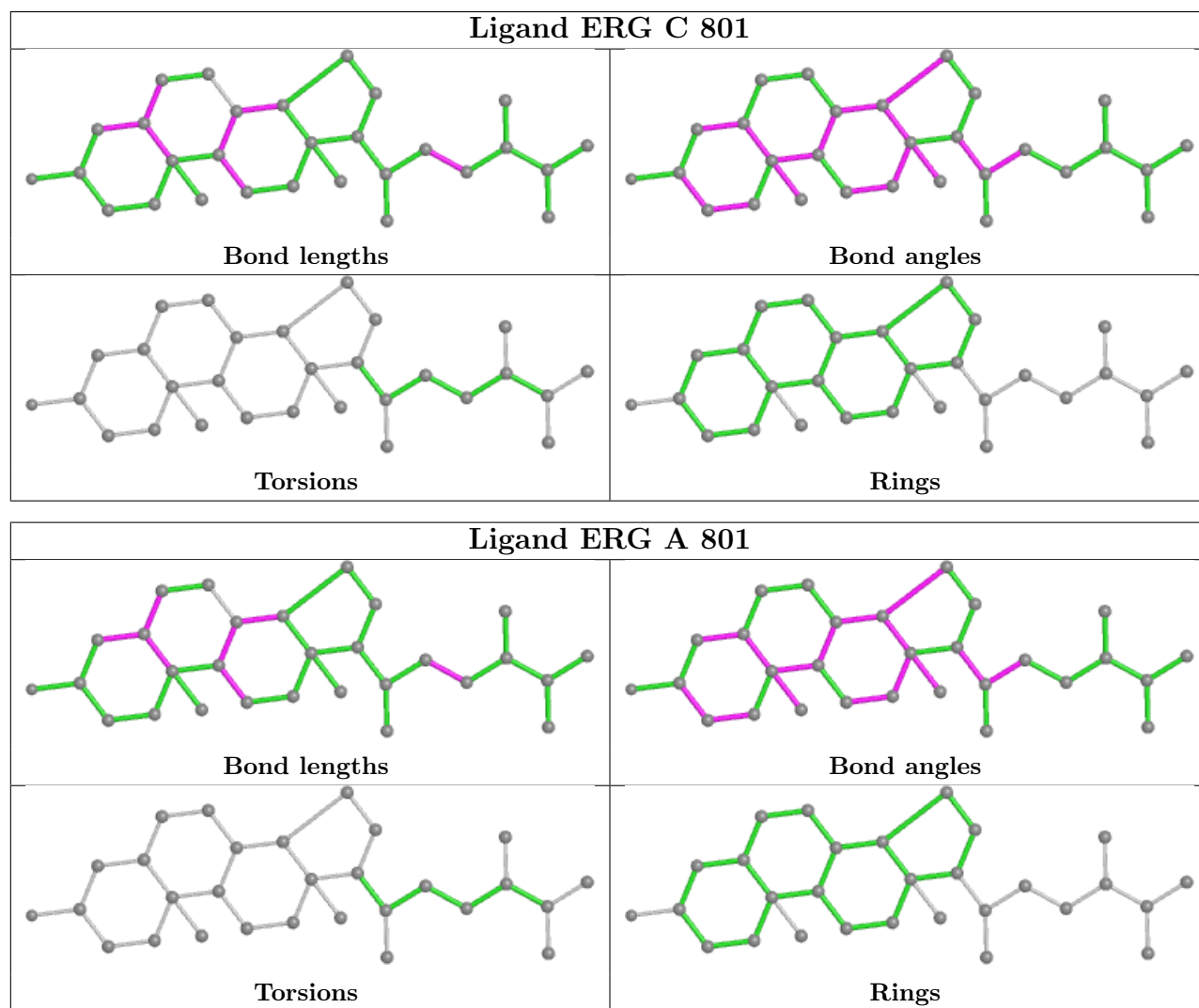
4 monomers are involved in 29 short contacts:

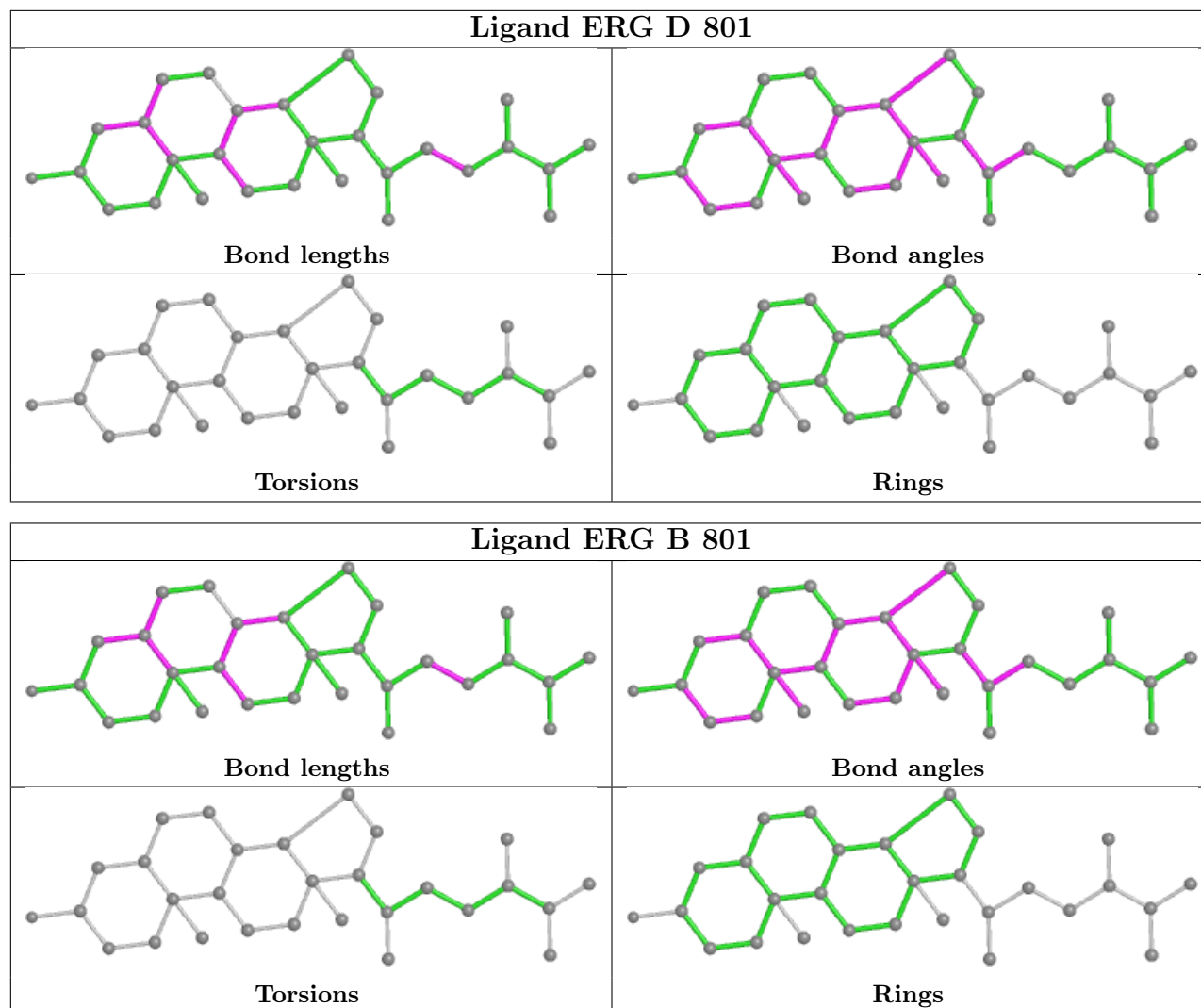
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	ERG	3	0
2	A	801	ERG	5	0
2	D	801	ERG	15	0
2	B	801	ERG	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will



also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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

### 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, 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	275/332 (82%)	0.59	33 (12%) 4 2	44, 65, 103, 147	0
1	B	266/332 (80%)	0.71	33 (12%) 4 2	48, 70, 110, 133	0
1	C	269/332 (81%)	0.77	27 (10%) 7 4	40, 63, 110, 138	0
1	D	266/332 (80%)	0.86	37 (13%) 2 1	48, 71, 108, 140	0
All	All	1076/1328 (81%)	0.73	130 (12%) 4 2	40, 67, 109, 147	0

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	771	GLY	16.7
1	A	649	THR	8.5
1	C	771	GLY	7.7
1	B	771	GLY	7.0
1	C	770	GLY	6.8
1	B	772	LEU	6.7
1	D	770	GLY	6.6
1	D	603	SER	6.2
1	A	640	GLY	5.9
1	A	639	LEU	5.6
1	C	656	PHE	5.2
1	D	584	ALA	5.2
1	C	636	LEU	5.2
1	C	665	PRO	5.0
1	B	770	GLY	5.0
1	D	665	PRO	4.8
1	A	636	LEU	4.8
1	C	655	CYS	4.6
1	D	655	CYS	4.5
1	A	773	PRO	4.5
1	D	607	PHE	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	656	PHE	4.4
1	A	650	VAL	4.3
1	A	602	PRO	4.3
1	B	657	ASP	4.2
1	B	665	PRO	4.0
1	D	660	ILE	4.0
1	C	721	MET	4.0
1	D	542	TYR	3.9
1	B	475	THR	3.9
1	D	475	THR	3.9
1	A	603	SER	3.7
1	B	656	PHE	3.7
1	C	575	ILE	3.6
1	C	537	PRO	3.5
1	C	747	GLN	3.5
1	B	574	LEU	3.4
1	D	657	ASP	3.3
1	B	604	ALA	3.3
1	B	520	LEU	3.2
1	C	552	ARG	3.2
1	B	684	ARG	3.2
1	C	524	LEU	3.2
1	D	572	SER	3.1
1	C	654	VAL	3.1
1	A	651	SER	3.1
1	A	656	PHE	3.1
1	B	603	SER	3.0
1	D	639	LEU	3.0
1	D	688	GLN	3.0
1	A	648	GLY	3.0
1	D	625	LYS	2.9
1	D	661	ALA	2.9
1	C	760	GLY	2.9
1	C	538	GLY	2.9
1	B	607	PHE	2.9
1	B	625	LYS	2.8
1	C	585	SER	2.8
1	D	574	LEU	2.8
1	D	623	THR	2.8
1	D	637	SER	2.8
1	B	655	CYS	2.8
1	A	575	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	538	GLY	2.8
1	B	537	PRO	2.8
1	C	651	SER	2.7
1	C	653	LEU	2.7
1	B	661	ALA	2.7
1	B	572	SER	2.7
1	C	603	SER	2.7
1	D	541	GLN	2.7
1	B	695	VAL	2.6
1	A	555	ARG	2.6
1	D	577	ILE	2.6
1	A	538	GLY	2.6
1	A	638	ASP	2.6
1	B	624	GLU	2.6
1	A	574	LEU	2.6
1	A	665	PRO	2.6
1	D	663	LEU	2.5
1	B	575	ILE	2.5
1	B	623	THR	2.5
1	D	571	ALA	2.5
1	D	640	GLY	2.4
1	C	476	LEU	2.4
1	D	737	ASP	2.4
1	A	607	PHE	2.4
1	C	574	LEU	2.4
1	A	560	GLU	2.3
1	D	659	SER	2.3
1	A	576	LEU	2.3
1	A	770	GLY	2.3
1	C	541	GLN	2.3
1	A	637	SER	2.3
1	B	573	ALA	2.3
1	D	662	ASP	2.3
1	B	762	HIS	2.3
1	B	560	GLU	2.3
1	D	638	ASP	2.3
1	B	535	LYS	2.2
1	A	755	ASP	2.2
1	D	696	PHE	2.2
1	C	521	MET	2.2
1	A	661	ALA	2.2
1	D	573	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	520	LEU	2.2
1	B	540	GLU	2.2
1	D	658	GLU	2.2
1	D	695	VAL	2.2
1	C	578	MET	2.2
1	B	581	LEU	2.2
1	A	625	LYS	2.1
1	B	629	HIS	2.1
1	A	541	GLN	2.1
1	C	526	ALA	2.1
1	D	733	THR	2.1
1	D	537	PRO	2.1
1	D	664	TYR	2.1
1	A	537	PRO	2.1
1	A	520	LEU	2.0
1	A	548	LEU	2.0
1	A	657	ASP	2.0
1	B	542	TYR	2.0
1	D	502	GLY	2.0
1	A	624	GLU	2.0
1	A	577	ILE	2.0
1	A	772	LEU	2.0
1	B	639	LEU	2.0
1	B	638	ASP	2.0
1	C	624	GLU	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 ⓘ

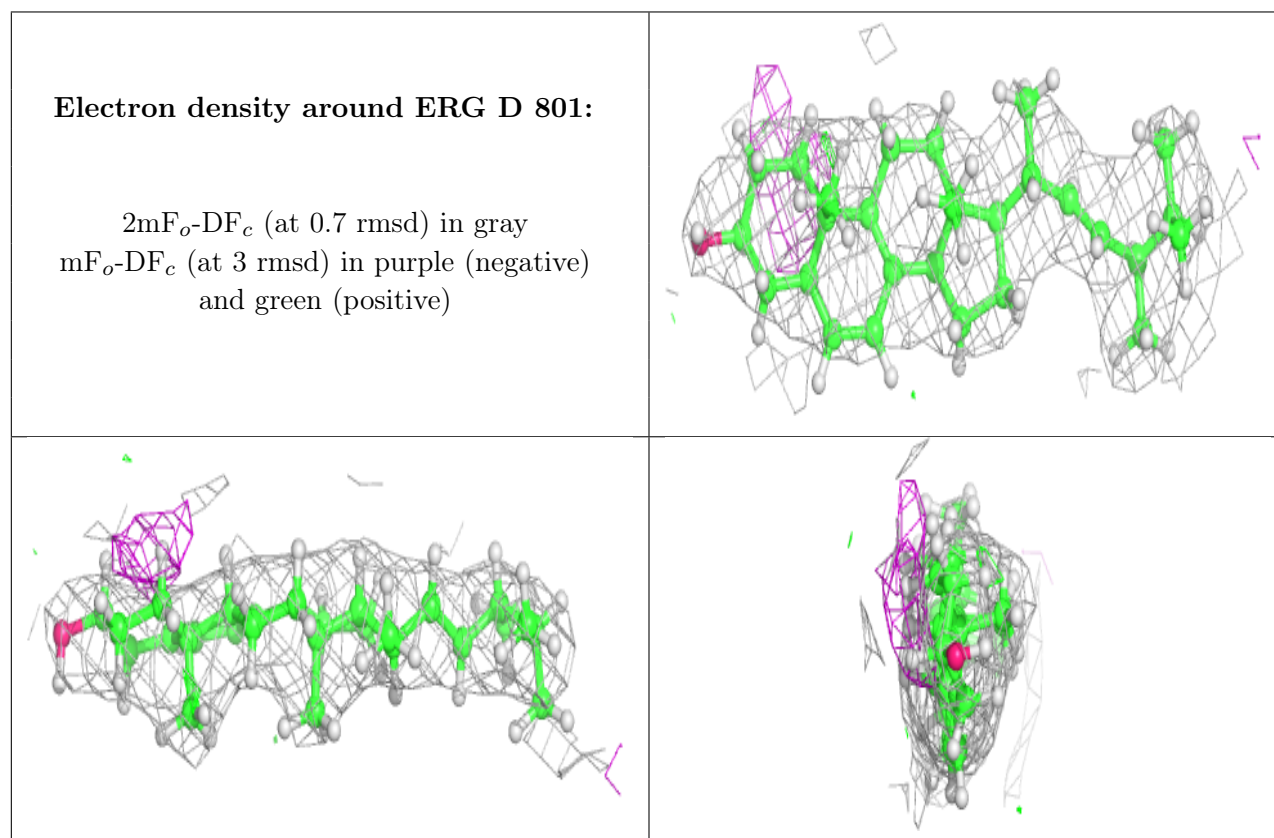
There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

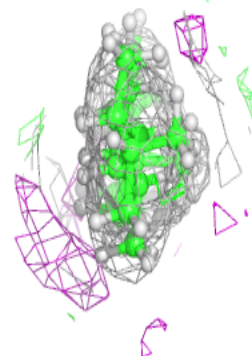
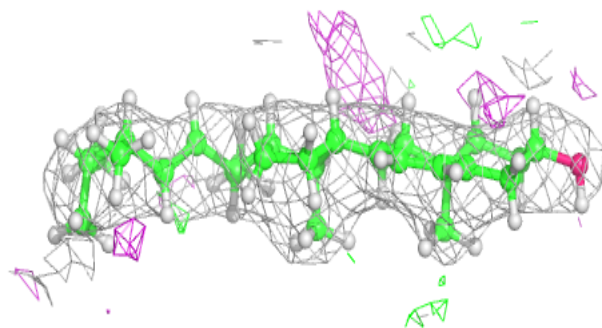
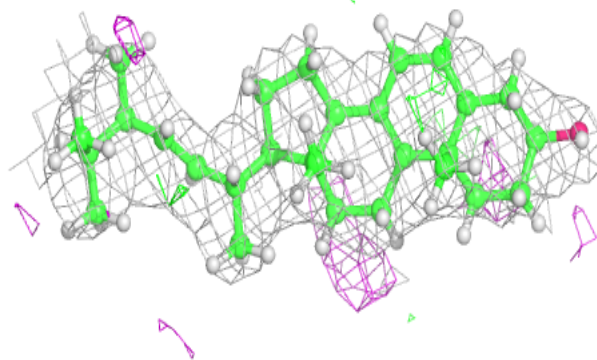
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ERG	D	801	29/29	0.92	0.19	45,67,85,101	0
2	ERG	C	801	29/29	0.94	0.22	40,60,80,89	0
2	ERG	B	801	29/29	0.94	0.20	46,63,80,85	0
2	ERG	A	801	29/29	0.96	0.19	39,63,89,94	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

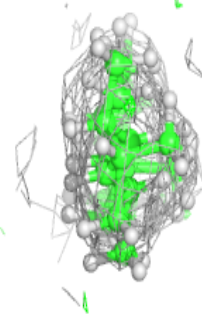
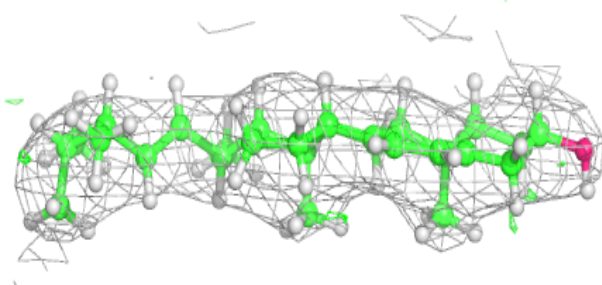
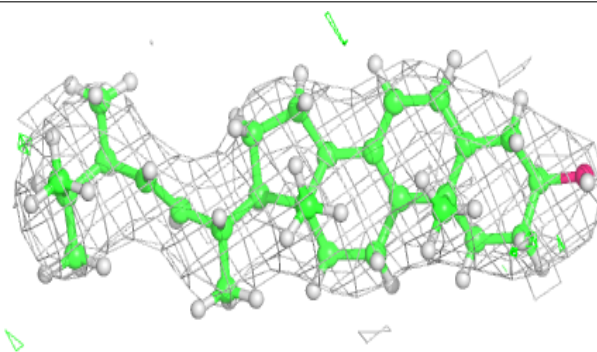


**Electron density around ERG C 801:**

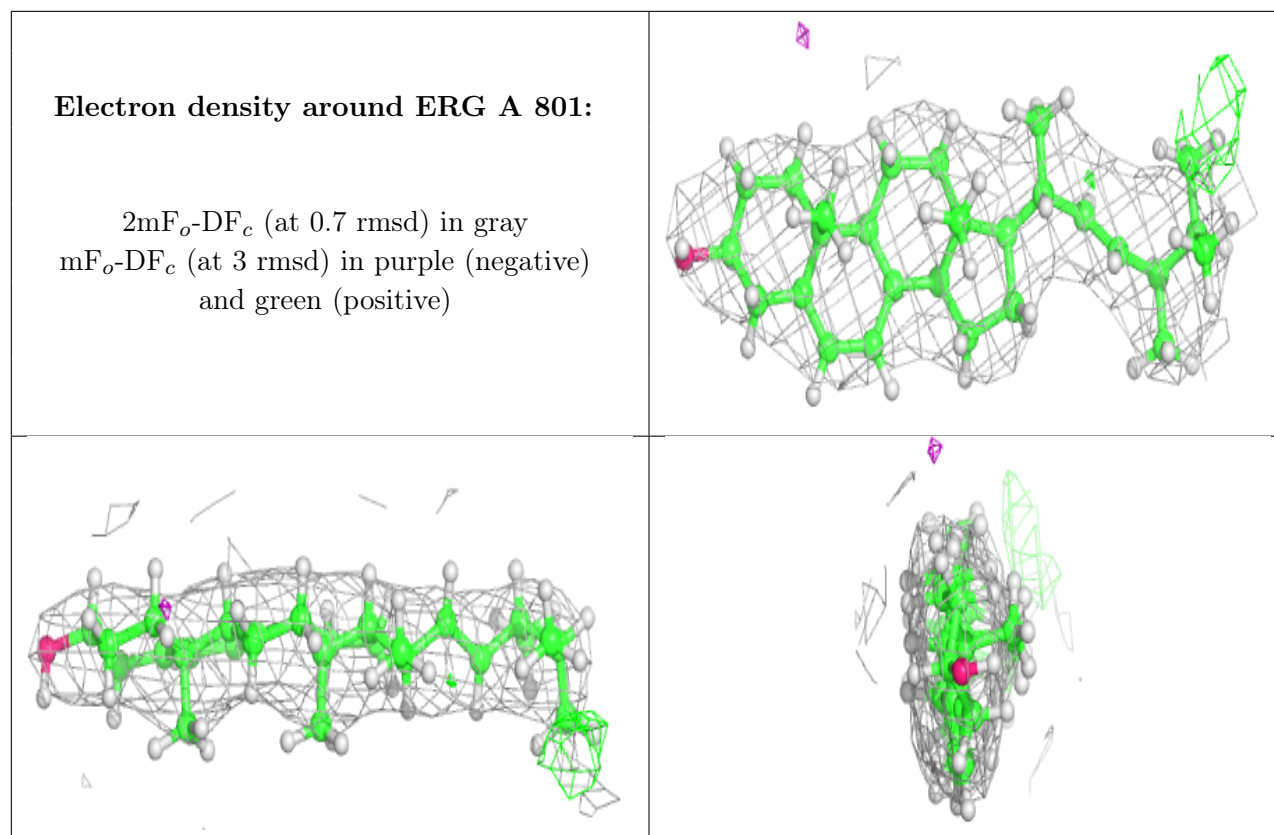
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ERG B 801:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)







## 6.5 Other polymers [i](#)

There are no such residues in this entry.