



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 04:55 pm BST

PDB ID : 2QL3  
Title : Crystal structure of the C-terminal domain of a probable LysR family transcriptional regulator from *Rhodococcus* sp. RHA1  
Authors : Tan, K.; Skarina, T.; Kagen, O.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2007-07-12  
Resolution : 2.05 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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

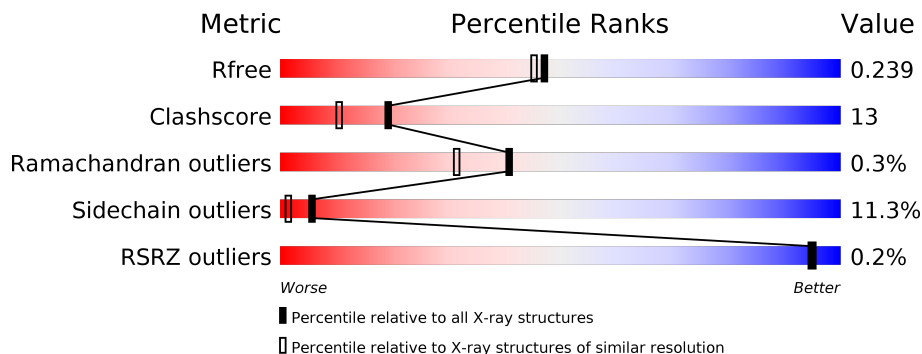
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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

Mol	Chain	Length	Quality of chain
1	A	209	 70% 23% . .
1	B	209	 73% 21% . . .
1	C	209	 65% 27% 5% . .
1	D	209	 66% 27% 5% .
1	E	209	 75% 20% . .
1	F	209	 73% 20% 6% .

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Mol	Chain	Length	Quality of chain
1	G	209	 66% 25% 6% ..
1	H	209	 72% 20% 6% .
1	I	209	 76% 20% ..
1	J	209	 75% 20% ..
1	K	209	 72% 20% 6% .
1	L	209	 72% 22% ..

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	PO4	B	1670	-	-	X	-
2	PO4	H	1631	-	-	X	-
2	PO4	K	1669	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 20701 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Probable transcriptional regulator, LysR family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	205	1574	1009	274	284	2	5	0	0	0
1	B	205	1578	1013	274	284	2	5	0	1	0
1	C	205	1588	1022	274	284	2	6	0	3	0
1	D	205	1583	1018	274	284	2	5	0	2	0
1	E	205	1599	1030	277	284	2	6	0	5	0
1	F	205	1584	1019	274	284	2	5	0	2	0
1	G	205	1574	1009	274	284	2	5	0	0	0
1	H	205	1579	1013	274	284	2	6	0	1	0
1	I	205	1574	1009	274	284	2	5	0	0	0
1	J	205	1578	1013	274	284	2	5	0	1	0
1	K	205	1579	1013	274	284	2	6	0	1	0
1	L	205	1582	1015	275	285	2	5	0	1	0

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
A	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
A	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
A	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
A	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
A	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
A	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
A	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
B	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
B	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
B	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
B	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
B	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
B	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
B	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
B	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
B	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
C	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
C	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
C	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
C	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
C	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
C	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
C	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
C	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
C	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
D	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
D	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
D	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
D	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
D	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
D	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
D	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
D	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
D	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
E	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
E	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
E	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
E	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
E	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
E	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
E	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
E	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
E	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
F	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
F	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8

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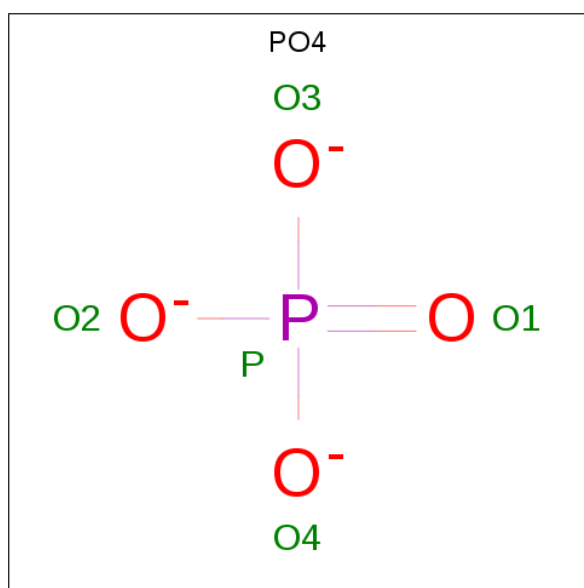
Chain	Residue	Modelled	Actual	Comment	Reference
F	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
F	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
F	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
F	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
F	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
F	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
F	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
G	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
G	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
G	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
G	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
G	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
G	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
G	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
G	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
G	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
H	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
H	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
H	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
H	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
H	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
H	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
H	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
H	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
H	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
I	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
I	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
I	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
I	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
I	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
I	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
I	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
I	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
I	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
J	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
J	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
J	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
J	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
J	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
J	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
J	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
J	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
K	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
K	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
K	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
K	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
K	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
K	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
K	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
K	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
K	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8
L	97	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
L	98	HIS	-	CLONING ARTIFACT	UNP Q0SFM8
L	119	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
L	171	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
L	176	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
L	202	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
L	215	MSE	MET	MODIFIED RESIDUE	UNP Q0SFM8
L	304	GLY	-	CLONING ARTIFACT	UNP Q0SFM8
L	305	SER	-	CLONING ARTIFACT	UNP Q0SFM8

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	E	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	E	1	5	4	1	0	0
2	E	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	G	1	5	4	1	0	0
2	G	1	5	4	1	0	0
2	G	1	5	4	1	0	0
2	H	1	5	4	1	0	0
2	H	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	H	1	5	4	1	0	0
2	H	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	I	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	K	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	K	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	116	Total	O	0	0
			116	116		
3	B	118	Total	O	0	0
			118	118		
3	C	67	Total	O	0	0
			67	67		
3	D	90	Total	O	0	0
			90	90		
3	E	122	Total	O	0	0
			122	122		
3	F	109	Total	O	0	0
			109	109		
3	G	81	Total	O	0	0
			81	81		
3	H	93	Total	O	0	0
			93	93		

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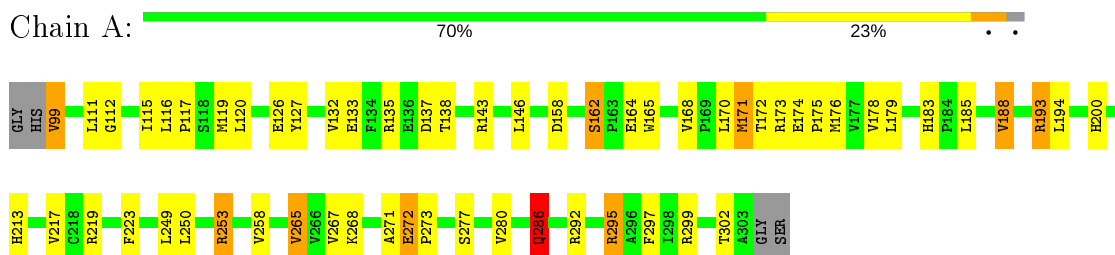
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	I	135	Total 135	O 135	0	0
3	J	130	Total 130	O 130	0	0
3	K	121	Total 121	O 121	0	0
3	L	167	Total 167	O 167	0	0

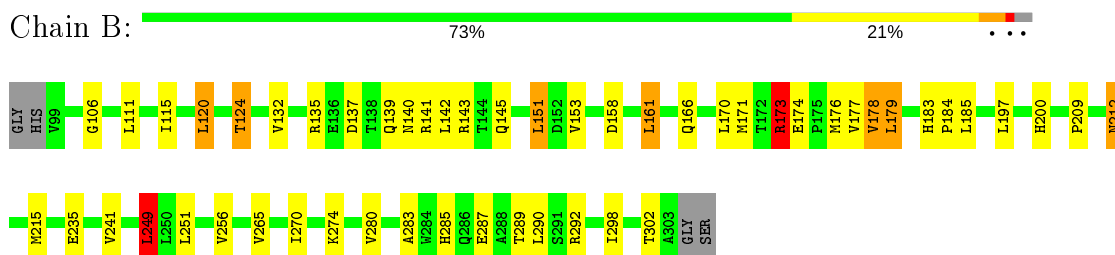
### 3 Residue-property plots

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

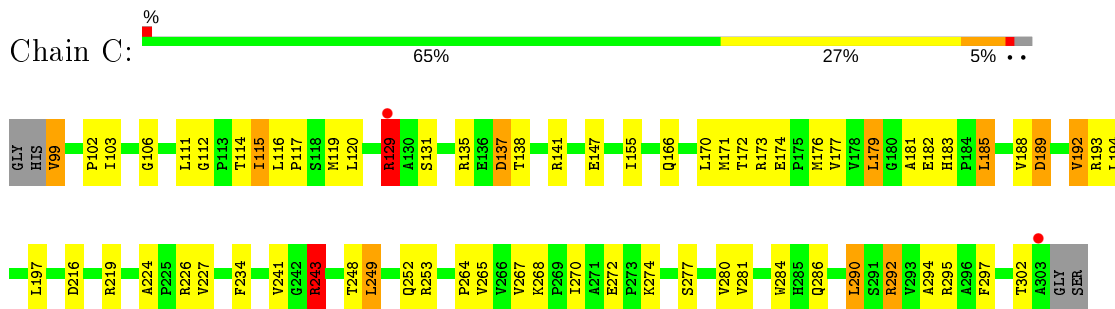
- Molecule 1: Probable transcriptional regulator, LysR family protein



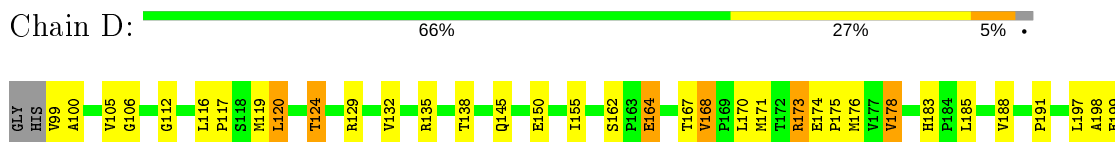
- Molecule 1: Probable transcriptional regulator, LysR family protein



- Molecule 1: Probable transcriptional regulator, LysR family protein



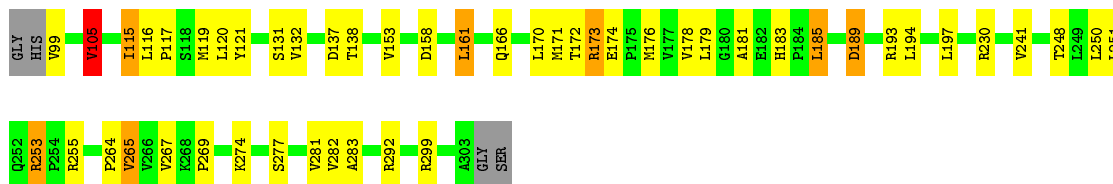
- Molecule 1: Probable transcriptional regulator, LysR family protein





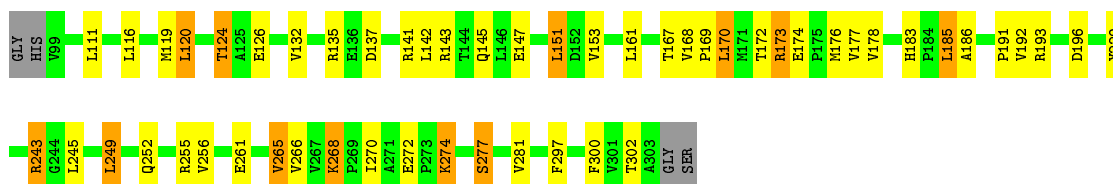
- Molecule 1: Probable transcriptional regulator, LysR family protein

Chain E: 75% 20%



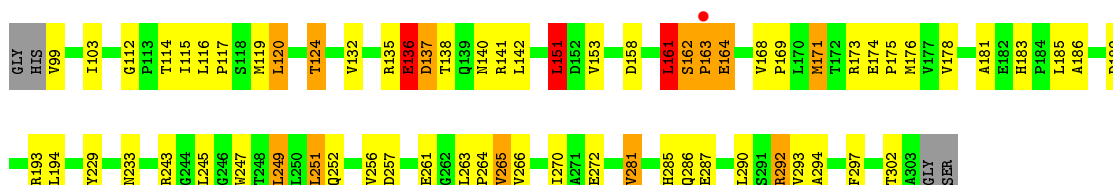
- Molecule 1: Probable transcriptional regulator, LysR family protein

Chain F: 73% 20% 6%



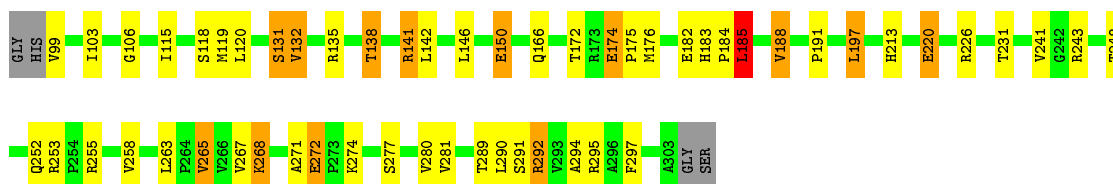
- Molecule 1: Probable transcriptional regulator, LysR family protein

Chain G: 66% 25% 6%



- Molecule 1: Probable transcriptional regulator, LysR family protein

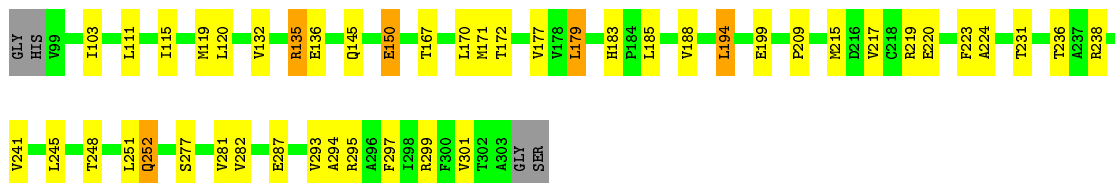
Chain H: 72% 20% 6%



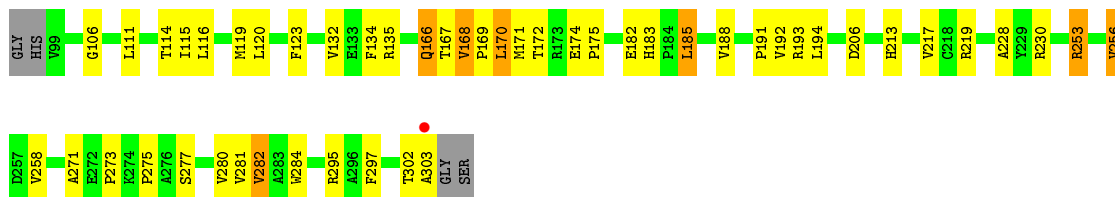
- Molecule 1: Probable transcriptional regulator, LysR family protein

Chain I: 76% 20%

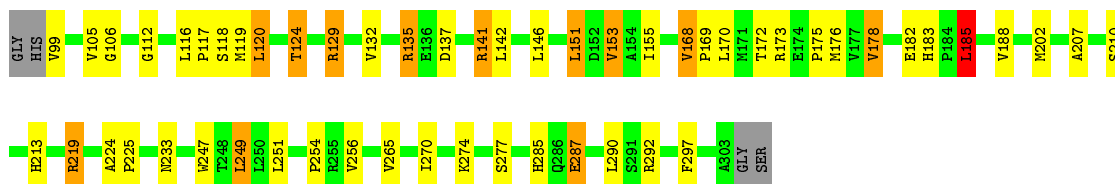




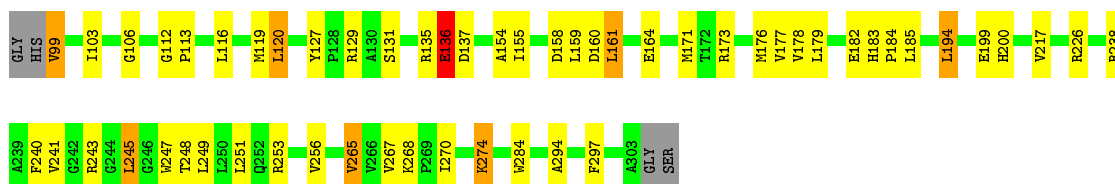
- Molecule 1: Probable transcriptional regulator, LysR family protein



- Molecule 1: Probable transcriptional regulator, LysR family protein



- Molecule 1: Probable transcriptional regulator, LysR family protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.28Å 114.28Å 175.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.60 – 2.05 36.58 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.3 (36.60-2.05) 99.3 (36.58-2.05)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.85 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.175 , 0.239 0.177 , 0.239	Depositor DCC
$R_{free}$ test set	7989 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.4	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 31.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l 0.036 for h,-h-k,-l 0.059 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	20701	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% 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

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.94	1/1610 (0.1%)	1.00	8/2199 (0.4%)
1	B	0.89	1/1617 (0.1%)	0.98	3/2209 (0.1%)
1	C	0.86	0/1633	0.91	3/2230 (0.1%)
1	D	0.89	0/1625	0.96	2/2220 (0.1%)
1	E	0.96	0/1650	1.02	4/2254 (0.2%)
1	F	0.95	1/1626 (0.1%)	1.01	4/2221 (0.2%)
1	G	0.86	1/1610 (0.1%)	0.93	4/2199 (0.2%)
1	H	0.93	1/1618 (0.1%)	0.94	5/2209 (0.2%)
1	I	1.06	2/1610 (0.1%)	1.04	4/2199 (0.2%)
1	J	0.96	1/1617 (0.1%)	0.96	2/2209 (0.1%)
1	K	0.97	1/1618 (0.1%)	1.03	4/2209 (0.2%)
1	L	1.02	0/1618	1.01	5/2210 (0.2%)
All	All	0.94	9/19452 (0.0%)	0.98	48/26568 (0.2%)

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	C	0	1
1	G	0	3
All	All	0	4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	136	GLU	CB-CG	-6.16	1.40	1.52
1	H	182	GLU	CB-CG	5.83	1.63	1.52
1	A	126	GLU	CB-CG	5.77	1.63	1.52
1	B	235	GLU	CG-CD	5.76	1.60	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	220	GLU	CD-OE2	5.55	1.31	1.25
1	K	173	ARG	CG-CD	5.53	1.65	1.51
1	F	229	TYR	CD2-CE2	5.36	1.47	1.39
1	G	247	TRP	CB-CG	5.23	1.59	1.50
1	J	228	ALA	CA-CB	5.22	1.63	1.52

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	253	ARG	NE-CZ-NH1	11.23	125.91	120.30
1	J	253	ARG	NE-CZ-NH2	-9.21	115.70	120.30
1	K	141	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	A	253	ARG	NE-CZ-NH2	8.02	124.31	120.30
1	F	196	ASP	CB-CG-OD1	-8.01	111.09	118.30
1	K	141	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	L	238	ARG	NE-CZ-NH1	7.35	123.98	120.30
1	A	292	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	K	219	ARG	NE-CZ-NH2	6.93	123.77	120.30
1	D	295	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	L	238	ARG	NE-CZ-NH2	-6.81	116.90	120.30
1	F	249[A]	LEU	CA-CB-CG	6.80	130.94	115.30
1	F	249[B]	LEU	CA-CB-CG	6.80	130.94	115.30
1	E	193	ARG	NE-CZ-NH2	-6.75	116.93	120.30
1	D	295	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	G	265	VAL	CG1-CB-CG2	6.61	121.48	110.90
1	G	257	ASP	CB-CG-OD2	6.44	124.09	118.30
1	H	265	VAL	CG1-CB-CG2	6.31	121.00	110.90
1	H	185	LEU	CA-CB-CG	6.16	129.46	115.30
1	H	243	ARG	NE-CZ-NH2	6.16	123.38	120.30
1	E	105	VAL	CG1-CB-CG2	6.14	120.72	110.90
1	E	265	VAL	CG1-CB-CG2	6.02	120.53	110.90
1	C	243	ARG	NE-CZ-NH1	-5.99	117.31	120.30
1	C	290	LEU	CA-CB-CG	5.95	128.97	115.30
1	A	292	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	A	265	VAL	CG1-CB-CG2	5.87	120.30	110.90
1	F	255	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	143	ARG	NE-CZ-NH2	-5.79	117.40	120.30
1	E	193	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	K	185	LEU	CA-CB-CG	5.62	128.24	115.30
1	L	120	LEU	CB-CG-CD1	5.56	120.46	111.00
1	H	243	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	A	158	ASP	CB-CG-OD1	5.47	123.22	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	249	LEU	CA-CB-CG	5.41	127.74	115.30
1	I	220	GLU	CA-CB-CG	5.34	125.14	113.40
1	L	265	VAL	CG1-CB-CG2	5.34	119.44	110.90
1	B	212	ASN	N-CA-CB	5.33	120.20	110.60
1	H	141	ARG	NE-CZ-NH2	5.33	122.97	120.30
1	B	249	LEU	CA-CB-CG	5.30	127.48	115.30
1	I	238	ARG	NE-CZ-NH2	5.28	122.94	120.30
1	L	136	GLU	CB-CA-C	5.24	120.88	110.40
1	G	151	LEU	CA-CB-CG	5.22	127.32	115.30
1	G	136	GLU	CB-CA-C	5.18	120.76	110.40
1	A	253	ARG	NE-CZ-NH1	-5.13	117.73	120.30
1	I	136	GLU	CB-CA-C	5.13	120.67	110.40
1	I	219	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	B	173	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	A	249	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	129	ARG	Peptide
1	G	161	LEU	Peptide
1	G	162	SER	Peptide
1	G	163	PRO	Peptide

## 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	1574	0	1580	48	0
1	B	1578	0	1589	41	0
1	C	1588	0	1609	47	0
1	D	1583	0	1600	57	0
1	E	1599	0	1629	37	0
1	F	1584	0	1602	38	0
1	G	1574	0	1580	52	0
1	H	1579	0	1589	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	1574	0	1580	31	0
1	J	1578	0	1589	39	0
1	K	1579	0	1589	50	0
1	L	1582	0	1590	35	0
2	A	30	0	0	2	0
2	B	25	0	0	4	0
2	C	30	0	0	3	0
2	D	25	0	0	2	0
2	E	15	0	0	2	0
2	F	70	0	0	3	0
2	G	15	0	0	1	0
2	H	20	0	0	4	0
2	I	35	0	0	0	0
2	J	35	0	0	1	0
2	K	50	0	0	5	0
2	L	30	0	0	1	0
3	A	116	0	0	7	0
3	B	118	0	0	0	0
3	C	67	0	0	1	0
3	D	90	0	0	0	0
3	E	122	0	0	1	0
3	F	109	0	0	3	0
3	G	81	0	0	3	0
3	H	93	0	0	2	0
3	I	135	0	0	7	0
3	J	130	0	0	0	0
3	K	121	0	0	2	0
3	L	167	0	0	2	0
All	All	20701	0	19126	495	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 13.

All (495) 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:K:202:MSE:HE2	1:K:247:TRP:CH2	1.75	1.20
1:H:119:MSE:HE3	1:H:297:PHE:HZ	1.18	1.06
1:E:170:LEU:HD11	1:E:282:VAL:CG2	1.87	1.05
1:D:219:ARG:HH11	1:D:219:ARG:HG2	0.88	1.04
1:C:119:MSE:HE3	1:C:297:PHE:HZ	1.21	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:173:ARG:NH1	2:D:1660:PO4:O3	1.94	1.01
1:H:119:MSE:HE3	1:H:297:PHE:CZ	1.95	1.01
1:D:119:MSE:HE1	1:D:155:ILE:HG13	1.39	1.00
1:G:162:SER:OG	1:G:164:GLU:HB3	1.59	1.00
1:K:202:MSE:HE3	1:K:225:PRO:HB3	1.42	0.99
1:E:170:LEU:HD11	1:E:282:VAL:HG23	1.42	0.99
1:K:183:HIS:HD2	1:K:185:LEU:H	1.10	0.97
1:K:202:MSE:HE3	1:K:225:PRO:CB	1.94	0.96
1:E:176[A]:MSE:SE	1:E:253[A]:ARG:HG3	2.17	0.95
1:J:167:THR:HB	1:J:281[A]:VAL:HG21	1.48	0.94
1:D:219:ARG:CG	1:D:219:ARG:HH11	1.80	0.93
1:A:193:ARG:HE	1:A:272:GLU:HG3	1.34	0.93
1:D:219:ARG:NH1	1:D:219:ARG:HG2	1.67	0.93
1:K:116:LEU:HD13	1:K:119:MSE:HE2	1.49	0.92
1:G:161:LEU:HD22	1:G:161:LEU:H	1.32	0.92
1:A:183:HIS:HD2	1:A:185:LEU:H	1.22	0.88
1:C:119:MSE:HE3	1:C:297:PHE:CZ	2.08	0.87
1:H:119:MSE:CE	1:H:297:PHE:HZ	1.88	0.86
1:E:170:LEU:CD1	1:E:282:VAL:HG23	2.05	0.86
1:D:119:MSE:HE1	1:D:155:ILE:CG1	2.04	0.86
1:K:202:MSE:CE	1:K:225:PRO:HB3	2.07	0.84
1:H:191:PRO:HB2	1:H:271:ALA:HB2	1.61	0.83
1:J:167:THR:HB	1:J:281[A]:VAL:CG2	2.09	0.82
1:A:119:MSE:HE3	1:A:297:PHE:HZ	1.45	0.82
1:E:183:HIS:HD2	1:E:185:LEU:H	1.25	0.82
1:B:178:VAL:HG23	1:B:265[A]:VAL:HG13	1.62	0.81
1:K:119:MSE:HE3	1:K:297:PHE:HZ	1.44	0.81
1:E:194:LEU:HD12	1:E:197:LEU:HD12	1.61	0.81
1:F:176:MSE:HG2	3:F:1719:HOH:O	1.81	0.80
1:K:202:MSE:HE2	1:K:247:TRP:HH2	1.41	0.80
1:K:183:HIS:CD2	1:K:185:LEU:H	1.98	0.80
1:H:183:HIS:CD2	1:H:185:LEU:HD22	2.17	0.80
1:K:202:MSE:CE	1:K:225:PRO:CB	2.60	0.79
1:F:268:LYS:NZ	2:F:1675:PO4:O1	2.16	0.78
1:J:183:HIS:HD2	1:J:185:LEU:H	1.32	0.78
1:E:178[A]:VAL:HG22	1:E:248:THR:HG22	1.66	0.77
1:I:183:HIS:HD2	1:I:185:LEU:H	1.30	0.77
1:C:189:ASP:N	1:C:189:ASP:OD2	2.16	0.77
1:B:183:HIS:HD2	1:B:185:LEU:H	1.30	0.77
1:G:158:ASP:HA	1:G:161:LEU:HD11	1.67	0.77
1:B:173:ARG:NH1	2:B:1670:PO4:P	2.58	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:119:MSE:HE1	1:K:155:ILE:HG13	1.67	0.76
1:D:119:MSE:HE3	1:D:297:PHE:CZ	2.21	0.76
1:F:173:ARG:HD2	1:F:176:MSE:HE2	1.68	0.75
1:B:173:ARG:HH12	2:B:1670:PO4:P	2.09	0.75
1:D:162:SER:OG	1:D:164:GLU:HG3	1.87	0.75
1:D:191:PRO:HB2	1:D:271:ALA:HB2	1.66	0.75
1:K:202:MSE:CE	1:K:247:TRP:CH2	2.65	0.75
1:B:302:THR:HG23	1:J:273:PRO:HB3	1.69	0.74
1:E:172:THR:HG22	1:E:277:SER:HB3	1.69	0.74
1:J:166:GLN:HG2	1:J:284:TRP:CZ2	2.23	0.74
1:D:198:ALA:O	1:D:199:GLU:HB2	1.86	0.74
1:F:126:GLU:HG3	1:F:300:PHE:CE1	2.23	0.74
1:B:173:ARG:NH1	2:B:1670:PO4:O1	2.21	0.74
1:H:183:HIS:HD2	1:H:185:LEU:HD22	1.52	0.73
1:G:119:MSE:HE3	1:G:297:PHE:CZ	2.23	0.73
1:F:120:LEU:O	1:F:124:THR:HB	1.88	0.73
1:C:174:GLU:OE2	1:C:274:LYS:HE2	1.88	0.72
1:B:111:LEU:HD22	1:B:115:ILE:HD12	1.69	0.72
1:B:183:HIS:CD2	1:B:185:LEU:H	2.07	0.72
1:F:183:HIS:HD2	1:F:185:LEU:H	1.38	0.72
1:L:183:HIS:HD2	1:L:185:LEU:H	1.35	0.72
1:D:119:MSE:HE1	1:D:155:ILE:CD1	2.19	0.72
1:H:99:VAL:HA	1:H:292:ARG:HD2	1.72	0.72
1:C:99:VAL:HA	1:C:292:ARG:HH11	1.55	0.71
1:A:119:MSE:HE3	1:A:297:PHE:CZ	2.25	0.71
1:B:111:LEU:HD22	1:B:115:ILE:CD1	2.20	0.71
1:J:119:MSE:HE3	1:J:297:PHE:CZ	2.25	0.71
1:E:115:ILE:HG13	1:E:119:MSE:HE3	1.71	0.71
1:I:119:MSE:HE1	1:I:297:PHE:HZ	1.54	0.71
1:H:295:ARG:NH1	2:H:1631:PO4:P	2.64	0.71
1:H:174:GLU:OE1	1:H:274:LYS:CE	2.39	0.71
1:K:292:ARG:N	2:K:1673:PO4:O3	2.20	0.71
1:L:119:MSE:HE3	1:L:297:PHE:CZ	2.26	0.70
1:G:233:ASN:HB2	3:G:1722:HOH:O	1.91	0.70
1:J:119:MSE:HE3	1:J:297:PHE:HZ	1.56	0.69
1:D:119:MSE:CE	1:D:155:ILE:HG13	2.20	0.69
1:H:99:VAL:HB	1:H:292:ARG:HD2	1.75	0.69
1:C:183:HIS:HD2	1:C:185:LEU:H	1.40	0.69
1:E:178[A]:VAL:HG23	1:E:241:VAL:HG11	1.74	0.69
1:I:183:HIS:HE1	3:I:1696:HOH:O	1.76	0.69
1:I:224:ALA:O	1:K:219:ARG:NH1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:PRO:HG3	1:A:213:HIS:HE1	1.58	0.68
1:D:183:HIS:HD2	1:D:185:LEU:H	1.40	0.68
1:K:120:LEU:O	1:K:124:THR:HB	1.92	0.68
1:L:99:VAL:HG13	1:L:127:TYR:CE2	2.28	0.68
1:I:119:MSE:CE	1:I:297:PHE:HZ	2.06	0.68
1:E:138:THR:OG1	2:E:1644:PO4:O3	2.12	0.68
1:C:174:GLU:O	1:C:176[A]:MSE:HE2	1.94	0.68
1:A:183:HIS:CD2	1:A:185:LEU:H	2.07	0.67
1:E:115:ILE:HG13	1:E:119:MSE:CE	2.24	0.67
1:K:112:GLY:O	1:K:117:PRO:HD3	1.94	0.67
1:H:103:ILE:HG22	1:H:131:SER:O	1.95	0.67
1:D:173:ARG:NH2	1:D:176:MSE:HE3	2.08	0.67
1:D:168:VAL:HG22	1:D:302:THR:HG21	1.77	0.67
1:H:138:THR:HG22	1:H:141:ARG:H	1.59	0.67
1:H:295:ARG:NH1	2:H:1631:PO4:O1	2.28	0.67
1:B:178:VAL:HG23	1:B:265[A]:VAL:CG1	2.25	0.67
1:E:170:LEU:HD11	1:E:282:VAL:HG22	1.77	0.67
1:G:261:GLU:O	1:H:255:ARG:HD2	1.95	0.66
1:D:100:ALA:O	1:D:293[A]:VAL:HG11	1.95	0.66
1:G:183:HIS:HD2	1:G:185:LEU:H	1.44	0.66
1:G:120:LEU:O	1:G:124:THR:HB	1.96	0.66
1:H:115:ILE:CD1	1:H:280:VAL:HG11	2.26	0.66
1:F:193:ARG:HG2	1:F:272:GLU:OE1	1.96	0.66
1:B:115:ILE:HD13	1:B:280:VAL:HG11	1.78	0.65
1:D:173:ARG:HH21	1:D:176:MSE:CE	2.09	0.65
1:C:99:VAL:HA	1:C:292:ARG:NH1	2.11	0.65
1:H:174:GLU:OE1	1:H:274:LYS:HE2	1.97	0.65
1:L:119:MSE:CE	1:L:297:PHE:HZ	2.09	0.65
1:L:119:MSE:HE3	1:L:297:PHE:HZ	1.60	0.65
1:J:183:HIS:CD2	1:J:185:LEU:H	2.15	0.64
1:B:298:ILE:O	1:B:302:THR:HG22	1.98	0.64
1:H:295:ARG:HH11	2:H:1631:PO4:P	2.21	0.64
1:D:120:LEU:O	1:D:124:THR:HB	1.98	0.63
1:F:170:LEU:CD1	1:F:302:THR:HG22	2.27	0.63
1:G:119:MSE:HE3	1:G:297:PHE:HZ	1.63	0.63
1:G:161:LEU:H	1:G:161:LEU:CD2	2.04	0.63
1:D:173:ARG:NH2	1:D:176:MSE:CE	2.61	0.62
1:C:138:THR:OG1	2:C:1607:PO4:O3	2.13	0.62
1:H:185:LEU:HD21	1:H:197:LEU:HD11	1.80	0.62
1:A:188:VAL:O	1:A:268:LYS:HE2	1.99	0.62
1:C:176[A]:MSE:SE	1:C:253:ARG:HB2	2.50	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:PRO:HG3	1:A:213:HIS:CE1	2.35	0.62
1:C:177:VAL:HG12	1:C:179:LEU:HD13	1.82	0.62
1:J:119:MSE:CE	1:J:297:PHE:HZ	2.11	0.62
1:G:115:ILE:HD12	1:G:252:GLN:HE22	1.65	0.61
1:K:202:MSE:HE3	1:K:225:PRO:HB2	1.79	0.61
1:K:119:MSE:HE3	1:K:297:PHE:CZ	2.31	0.61
1:A:119:MSE:CE	1:A:297:PHE:HZ	2.13	0.61
1:B:120:LEU:O	1:B:124:THR:HB	2.00	0.61
1:E:170:LEU:CD1	1:E:282:VAL:CG2	2.70	0.61
1:H:174:GLU:OE1	1:H:274:LYS:HE3	1.99	0.61
1:G:175:PRO:HB3	1:G:251:LEU:HD12	1.82	0.61
1:D:173:ARG:HH21	1:D:176:MSE:HE3	1.66	0.61
1:E:178[A]:VAL:HG22	1:E:248:THR:CG2	2.29	0.60
1:L:284:TRP:NE1	2:L:1656:PO4:O1	2.32	0.60
1:D:119:MSE:HE3	1:D:297:PHE:HZ	1.65	0.60
1:H:103:ILE:HD12	1:H:294:ALA:HA	1.82	0.60
1:L:116:LEU:HD13	1:L:119:MSE:HE2	1.84	0.60
1:G:186:ALA:HB1	1:G:266:VAL:HG21	1.84	0.60
1:C:102:PRO:HA	1:C:131:SER:HB3	1.83	0.60
1:I:295:ARG:NH2	1:I:299:ARG:HE	1.99	0.60
1:D:297:PHE:O	1:D:301:VAL:HB	2.01	0.60
1:K:249:LEU:HD21	1:K:270:ILE:HD11	1.84	0.60
1:L:194:LEU:HD13	1:L:270:ILE:HG23	1.84	0.60
1:E:183:HIS:CD2	1:E:185:LEU:H	2.14	0.59
1:J:302:THR:O	1:J:303:ALA:CB	2.50	0.59
1:K:129:ARG:HD2	1:K:129:ARG:N	2.17	0.59
1:K:105:VAL:HB	1:K:153:VAL:HG12	1.83	0.59
1:K:175:PRO:HG3	1:K:213:HIS:HE1	1.68	0.59
1:I:119:MSE:CE	1:I:297:PHE:CZ	2.85	0.59
1:L:177:VAL:HG22	1:L:249[B]:LEU:HD12	1.83	0.59
1:B:177:VAL:HG12	1:B:179:LEU:HD13	1.85	0.59
1:C:115:ILE:HD12	1:C:280:VAL:HG11	1.83	0.59
1:G:229:TYR:HE1	1:H:132:VAL:HG22	1.68	0.59
1:H:176[A]:MSE:SE	1:H:253:ARG:HB2	2.52	0.59
1:B:158:ASP:HA	1:B:161:LEU:HD12	1.84	0.59
1:A:219:ARG:NH2	1:C:226:ARG:HD3	2.19	0.58
1:F:119:MSE:HE3	1:F:297:PHE:CZ	2.38	0.58
1:G:119:MSE:CE	1:G:297:PHE:HZ	2.16	0.58
1:A:183:HIS:HE1	3:A:1729:HOH:O	1.85	0.58
1:I:231:THR:HG21	1:I:236:THR:HG22	1.86	0.58
1:C:177:VAL:HG23	1:C:270:ILE:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:170:LEU:HD12	1:F:302:THR:HG22	1.83	0.57
1:H:188:VAL:O	1:H:268:LYS:NZ	2.36	0.57
1:I:183:HIS:CD2	1:I:185:LEU:H	2.18	0.57
1:H:106:GLY:HA2	1:H:135:ARG:O	2.04	0.57
1:I:231:THR:HG22	1:J:134:PHE:HE1	1.68	0.57
1:K:116:LEU:HD13	1:K:119:MSE:CE	2.31	0.57
1:F:119:MSE:CE	1:F:297:PHE:HZ	2.17	0.57
1:G:103:ILE:HD12	1:G:294:ALA:HA	1.86	0.57
1:I:103:ILE:HD12	1:I:294:ALA:HA	1.85	0.57
1:G:114:THR:HG21	1:G:252:GLN:HG2	1.87	0.57
1:B:140:ASN:OD1	1:B:143:ARG:NH2	2.38	0.57
1:G:302:THR:HG22	1:G:302:THR:O	2.04	0.57
1:L:171:MSE:HE1	3:L:1754:HOH:O	2.05	0.56
1:A:172:THR:CG2	1:A:277:SER:HB3	2.35	0.56
1:I:135:ARG:HG3	3:I:1790:HOH:O	2.04	0.56
1:A:168:VAL:HG11	1:A:302:THR:HG21	1.87	0.56
1:I:119:MSE:HE3	1:I:297:PHE:CZ	2.40	0.56
1:J:168:VAL:HG13	1:J:282:VAL:HG13	1.87	0.56
1:L:99:VAL:HG13	1:L:127:TYR:CD2	2.40	0.56
1:A:115:ILE:HD11	1:A:171:MSE:SE	2.55	0.56
1:A:172:THR:HG22	1:A:277:SER:HB3	1.87	0.56
1:G:164:GLU:HG3	1:G:285:HIS:HE1	1.69	0.56
1:B:197:LEU:HA	1:B:200:HIS:HD2	1.70	0.56
1:C:193:ARG:HD3	1:C:272:GLU:OE2	2.04	0.56
1:K:146:LEU:HD12	1:K:151:LEU:HB3	1.88	0.56
1:L:199:GLU:O	1:L:226:ARG:NH1	2.39	0.56
1:H:99:VAL:HA	1:H:292:ARG:CD	2.35	0.56
1:A:173:ARG:NH2	1:A:253:ARG:H	2.04	0.55
1:G:164:GLU:CG	1:G:285:HIS:CE1	2.90	0.55
1:B:141:ARG:NH2	2:B:1651:PO4:O1	2.40	0.55
1:K:142:LEU:HD23	1:K:142:LEU:C	2.27	0.55
1:F:126:GLU:HG3	1:F:300:PHE:HE1	1.71	0.55
1:E:178[A]:VAL:CG2	1:E:248:THR:HG22	2.34	0.55
1:G:249:LEU:HD21	1:G:270:ILE:HD11	1.89	0.55
1:A:213:HIS:O	1:A:217:VAL:HG13	2.06	0.55
1:J:114:THR:OG1	1:J:115:ILE:HD12	2.07	0.55
1:J:302:THR:O	1:J:303:ALA:HB2	2.07	0.55
1:K:142:LEU:HD23	1:K:142:LEU:O	2.06	0.55
1:F:183:HIS:CD2	1:F:185:LEU:H	2.21	0.55
1:E:176[B]:MSE:HG2	1:E:269:PRO:HA	1.89	0.54
1:L:183:HIS:CD2	1:L:185:LEU:H	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:141:ARG:NH2	2:K:1669:PO4:O3	2.40	0.54
1:K:202:MSE:HE1	1:K:225:PRO:HG3	1.89	0.54
1:D:178:VAL:HG22	1:D:241:VAL:HG11	1.88	0.54
1:E:153[A]:VAL:CG1	1:E:282:VAL:HG12	2.38	0.54
1:F:119:MSE:HE3	1:F:297:PHE:HZ	1.73	0.54
1:F:176:MSE:SE	3:F:1719:HOH:O	2.75	0.54
1:L:158:ASP:HA	1:L:161:LEU:HD22	1.89	0.54
1:B:178:VAL:HG22	1:B:241:VAL:HG11	1.89	0.54
1:F:256:VAL:HG22	1:G:256:VAL:HG22	1.90	0.54
1:J:167:THR:CB	1:J:281[A]:VAL:HG21	2.31	0.54
1:G:194:LEU:HD13	1:G:270:ILE:HG23	1.89	0.53
1:F:274:LYS:HG2	2:K:1608:PO4:O2	2.07	0.53
1:H:252:GLN:NE2	2:H:1617:PO4:O2	2.39	0.53
1:E:172:THR:CG2	1:E:277:SER:HB3	2.38	0.53
1:G:164:GLU:HG2	1:G:285:HIS:CE1	2.43	0.53
1:I:295:ARG:CZ	1:I:299:ARG:HE	2.22	0.53
1:A:99:VAL:HG12	1:A:127:TYR:CD1	2.44	0.53
1:A:138:THR:OG1	2:A:1626:PO4:O2	2.15	0.53
1:C:137:ASP:OD1	1:C:141:ARG:HD3	2.09	0.53
1:F:174:GLU:HG2	2:F:1650:PO4:O4	2.09	0.53
1:C:103:ILE:HD12	1:C:294:ALA:HA	1.90	0.52
1:C:114:THR:HG21	1:C:252:GLN:HG2	1.91	0.52
1:E:116:LEU:N	1:E:117:PRO:HD3	2.24	0.52
1:C:216:ASP:OD1	1:C:219:ARG:NH2	2.30	0.52
1:C:119:MSE:HE1	1:C:155:ILE:HG13	1.92	0.52
1:H:115:ILE:HD13	1:H:280:VAL:HG11	1.90	0.52
1:A:193:ARG:NE	1:A:272:GLU:HG3	2.16	0.52
1:K:188:VAL:HG23	3:K:1711:HOH:O	2.09	0.52
1:D:197:LEU:HA	1:D:200:HIS:HD2	1.75	0.52
1:L:176:MSE:HG3	1:L:267:VAL:HG13	1.92	0.52
1:B:249:LEU:HD21	1:B:270:ILE:CD1	2.40	0.51
1:G:193:ARG:HD2	1:J:166:GLN:NE2	2.24	0.51
1:A:164:GLU:O	1:A:286:GLN:HB2	2.10	0.51
1:K:172:THR:OG1	1:K:277:SER:HB2	2.08	0.51
1:K:207:ALA:O	1:K:210:SER:HB2	2.10	0.51
1:B:111:LEU:CD2	1:B:115:ILE:HD12	2.40	0.51
1:B:249:LEU:CD2	1:B:270:ILE:HD11	2.41	0.51
1:G:171:MSE:CE	1:G:173:ARG:HG3	2.40	0.51
1:J:169:PRO:HA	1:J:281[B]:VAL:HG12	1.93	0.51
1:A:219:ARG:NE	1:C:226:ARG:HG2	2.25	0.51
1:F:193:ARG:CG	1:F:272:GLU:OE1	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:176[A]:MSE:HG3	1:H:267:VAL:HG13	1.92	0.51
1:E:189:ASP:HB2	2:E:1624:PO4:O4	2.11	0.51
1:D:198:ALA:O	1:D:199:GLU:CB	2.54	0.51
1:K:116:LEU:CD1	1:K:119:MSE:HE2	2.34	0.51
1:J:256:VAL:HG22	1:J:258:VAL:HG12	1.92	0.50
1:B:178:VAL:CG2	1:B:265[A]:VAL:CG1	2.89	0.50
1:H:183:HIS:HD2	1:H:185:LEU:H	1.59	0.50
1:G:256:VAL:HG21	1:H:258:VAL:HG11	1.94	0.50
1:L:106:GLY:HA2	1:L:135:ARG:O	2.11	0.50
1:I:145:GLN:HA	1:I:150:GLU:HG3	1.94	0.50
1:E:116:LEU:N	1:E:117:PRO:CD	2.75	0.50
1:K:118:SER:OG	1:L:243:ARG:NH1	2.45	0.50
1:C:182:GLU:N	2:C:1619:PO4:O3	2.36	0.50
1:C:181:ALA:HB2	1:C:264:PRO:HG2	1.94	0.49
1:C:194:LEU:HD12	1:C:197:LEU:HD12	1.94	0.49
1:A:135:ARG:NH2	3:A:1786:HOH:O	2.45	0.49
1:J:172:THR:HB	1:J:277:SER:HB3	1.94	0.49
1:F:111:LEU:HD23	1:F:252:GLN:HE22	1.77	0.49
1:F:143:ARG:O	1:F:147:GLU:HG2	2.13	0.49
1:F:176:MSE:CG	3:F:1719:HOH:O	2.51	0.49
1:D:174:GLU:OE1	1:D:274:LYS:HE2	2.13	0.49
1:L:194:LEU:CD2	1:L:217:VAL:HG12	2.42	0.49
1:C:234:PHE:CZ	1:C:252:GLN:HB3	2.47	0.49
1:H:241:VAL:HG21	1:H:248:THR:HG22	1.94	0.49
1:A:162:SER:HB2	1:A:164:GLU:H	1.78	0.48
1:K:249:LEU:HD21	1:K:270:ILE:CD1	2.42	0.48
1:K:185:LEU:O	1:K:188:VAL:HG22	2.14	0.48
1:L:194:LEU:HD21	1:L:217:VAL:HG12	1.95	0.48
1:E:171:MSE:HE2	1:E:173:ARG:HD3	1.94	0.48
1:A:299:ARG:NH2	3:A:1775:HOH:O	2.46	0.48
1:D:99:VAL:HG13	1:D:129:ARG:HH22	1.77	0.48
1:A:173:ARG:NH1	3:A:1764:HOH:O	2.45	0.48
1:F:116:LEU:HD13	1:F:119:MSE:HE2	1.95	0.48
1:G:138:THR:OG1	1:G:141:ARG:HG3	2.14	0.48
1:I:293:VAL:HG12	3:I:1738:HOH:O	2.12	0.48
1:J:166:GLN:HG3	1:J:167:THR:N	2.28	0.48
1:D:241:VAL:HG21	1:D:248:THR:HG22	1.96	0.48
1:K:106:GLY:HA2	1:K:135:ARG:O	2.13	0.48
1:K:141:ARG:HH22	2:K:1669:PO4:P	2.37	0.48
1:K:175:PRO:HG3	1:K:213:HIS:CE1	2.47	0.48
1:K:256:VAL:HG12	3:K:1777:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:99:VAL:CA	1:H:292:ARG:HD2	2.42	0.48
1:A:146:LEU:HD23	1:A:165:TRP:CE2	2.49	0.48
1:G:136:GLU:OE1	1:H:231:THR:OG1	2.19	0.47
1:A:223:PHE:O	1:C:224:ALA:HB2	2.13	0.47
1:F:177:VAL:HG23	1:F:270:ILE:CG1	2.44	0.47
1:C:183:HIS:CD2	1:C:185:LEU:H	2.25	0.47
1:D:164:GLU:HG3	1:D:164:GLU:H	1.59	0.47
1:G:164:GLU:HG3	1:G:285:HIS:CE1	2.47	0.47
1:L:241:VAL:HG21	1:L:248:THR:HG22	1.95	0.47
1:A:116:LEU:HD13	1:A:119:MSE:HE2	1.97	0.47
1:D:145:GLN:HG2	1:D:150:GLU:OE2	2.14	0.47
1:D:285:HIS:HD2	1:D:287:GLU:HB2	1.78	0.47
1:H:99:VAL:CB	1:H:292:ARG:HD2	2.42	0.47
1:I:177:VAL:CG1	1:I:179:LEU:HD13	2.44	0.47
1:J:166:GLN:HG2	1:J:284:TRP:CE2	2.48	0.47
1:A:115:ILE:HD13	1:A:280:VAL:HG11	1.96	0.47
1:J:175:PRO:HG2	1:J:275:PRO:HB2	1.96	0.47
1:E:173:ARG:HH11	1:E:253[A]:ARG:H	1.60	0.47
1:L:183:HIS:CE1	1:L:200:HIS:HD2	2.31	0.47
1:D:162:SER:HG	1:D:164:GLU:HG3	1.78	0.47
1:E:255:ARG:HD3	1:F:261:GLU:O	2.15	0.47
1:K:137:ASP:OD2	1:K:141:ARG:NH1	2.47	0.47
1:B:174:GLU:OE1	1:B:274:LYS:HD2	2.15	0.46
1:I:177:VAL:HG12	1:I:179:LEU:HD13	1.98	0.46
1:B:183:HIS:CD2	1:B:184:PRO:HD2	2.50	0.46
1:F:111:LEU:HD23	1:F:252:GLN:NE2	2.30	0.46
1:G:164:GLU:CG	1:G:285:HIS:HE1	2.28	0.46
1:B:158:ASP:HA	1:B:161:LEU:CD1	2.45	0.46
1:D:138:THR:OG1	2:D:1657:PO4:O2	2.20	0.46
1:A:258:VAL:HG11	1:B:256:VAL:HG21	1.98	0.46
1:D:173:ARG:HH21	1:D:176:MSE:HE1	1.81	0.46
1:E:158:ASP:HA	1:E:161:LEU:HD22	1.96	0.46
1:C:103:ILE:HG22	1:C:131:SER:O	2.16	0.46
1:K:182:GLU:N	2:K:1620:PO4:O1	2.41	0.46
1:B:285:HIS:HD2	1:B:287:GLU:H	1.64	0.46
1:D:256:VAL:HG13	1:D:256:VAL:O	2.16	0.46
1:D:119:MSE:CE	1:D:297:PHE:HZ	2.29	0.46
1:J:194:LEU:HD21	1:J:217:VAL:HG23	1.98	0.46
1:F:161:LEU:HD12	1:F:167:THR:HG21	1.98	0.46
1:C:112:GLY:O	1:C:117:PRO:HD3	2.16	0.46
1:C:192:VAL:HG12	1:C:268:LYS:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:VAL:HG21	1:C:248:THR:HG22	1.97	0.46
1:E:173:ARG:HH11	1:E:253[B]:ARG:H	1.62	0.46
1:F:169:PRO:HA	1:F:281:VAL:HG12	1.97	0.46
1:L:240:PHE:O	1:L:245:LEU:HB2	2.15	0.46
1:E:178[B]:VAL:HG21	1:E:250:LEU:HD12	1.98	0.46
1:F:137:ASP:OD1	1:F:141:ARG:HD3	2.16	0.46
1:B:139:GLN:NE2	1:B:209:PRO:HB3	2.31	0.45
1:G:135:ARG:HD2	1:G:151:LEU:HD13	1.98	0.45
1:D:119:MSE:HE1	1:D:155:ILE:HD11	1.96	0.45
1:B:173:ARG:HD2	1:B:176:MSE:HE2	1.98	0.45
1:D:119:MSE:HG3	1:D:301:VAL:HG22	1.97	0.45
1:D:219:ARG:CG	1:D:219:ARG:NH1	2.52	0.45
1:C:116:LEU:HD13	1:C:119:MSE:HE2	1.98	0.45
1:I:241:VAL:HG21	1:I:248:THR:HG22	1.97	0.45
1:A:219:ARG:HG3	1:C:224:ALA:HB3	1.98	0.45
1:B:178:VAL:CG2	1:B:265[A]:VAL:HG11	2.46	0.45
1:A:223:PHE:C	1:C:224:ALA:HB2	2.36	0.45
1:C:302:THR:HG22	1:C:302:THR:O	2.17	0.45
1:E:174:GLU:OE1	1:E:274:LYS:HE3	2.17	0.45
1:G:183:HIS:CD2	1:G:185:LEU:H	2.28	0.45
1:A:213:HIS:O	1:A:217:VAL:CG1	2.65	0.45
1:C:129:ARG:HB3	1:C:129:ARG:NH2	2.32	0.45
1:I:150:GLU:H	1:I:150:GLU:HG2	1.53	0.45
1:L:177:VAL:HG22	1:L:249[B]:LEU:CD1	2.47	0.45
1:C:106:GLY:HA2	1:C:135:ARG:O	2.17	0.45
1:G:173:ARG:HB2	3:G:1723:HOH:O	2.17	0.45
1:G:99:VAL:HG22	1:G:292:ARG:HD3	1.98	0.45
1:A:200:HIS:HB3	3:A:1729:HOH:O	2.17	0.44
1:I:209:PRO:HG3	3:I:1705:HOH:O	2.17	0.44
1:F:173:ARG:HD2	1:F:176:MSE:CE	2.43	0.44
1:I:172:THR:HG23	3:I:1759:HOH:O	2.17	0.44
1:J:111:LEU:CD2	1:J:115:ILE:HD13	2.47	0.44
1:F:142:LEU:HA	1:F:145:GLN:HE21	1.82	0.44
1:H:175:PRO:HG3	1:H:213:HIS:HE1	1.83	0.44
1:H:183:HIS:CD2	1:H:184:PRO:HD2	2.52	0.44
1:I:194:LEU:HD11	1:I:217:VAL:HG12	1.98	0.44
1:I:111:LEU:HD23	1:I:252:GLN:OE1	2.17	0.44
1:J:123:PHE:CE1	1:J:297:PHE:HA	2.52	0.44
1:A:295:ARG:NH2	1:A:299:ARG:NH2	2.66	0.44
1:F:145:GLN:HB2	1:F:151:LEU:HD22	2.00	0.44
1:G:171:MSE:HE3	1:G:173:ARG:CG	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:169:PRO:HA	1:G:281:VAL:HA	1.99	0.44
1:B:177:VAL:HG23	1:B:270:ILE:HD11	1.98	0.44
1:K:285:HIS:CE1	1:K:287:GLU:HB2	2.53	0.44
1:L:247:TRP:HZ3	1:L:249[B]:LEU:HD13	1.83	0.44
1:L:274:LYS:HE2	3:L:1780:HOH:O	2.18	0.44
1:A:272:GLU:HA	1:A:273:PRO:HA	1.78	0.44
1:G:162:SER:OG	1:G:164:GLU:OE1	2.30	0.44
1:G:243:ARG:HD3	1:G:263:LEU:CD1	2.46	0.44
1:I:183:HIS:CE1	3:I:1696:HOH:O	2.60	0.44
1:J:206:ASP:HB3	2:J:1668:PO4:O1	2.17	0.44
1:C:114:THR:HG21	1:C:252:GLN:CG	2.47	0.44
1:D:105:VAL:HG13	1:D:132:VAL:HG13	2.00	0.44
1:K:168:VAL:HA	1:K:169:PRO:HD3	1.88	0.44
1:F:186:ALA:HB1	1:F:266:VAL:HG21	2.00	0.43
1:K:183:HIS:HD2	1:K:185:LEU:N	1.94	0.43
1:D:213:HIS:CE1	1:D:251[A]:LEU:HD21	2.52	0.43
1:L:183:HIS:CD2	1:L:184:PRO:HD2	2.53	0.43
1:C:295:ARG:NH1	2:C:1663:PO4:O1	2.50	0.43
1:C:176[B]:MSE:HE2	1:C:267:VAL:HG12	1.98	0.43
1:I:167:THR:HA	1:I:282:VAL:O	2.18	0.43
1:I:223:PHE:C	1:K:224:ALA:HB2	2.38	0.43
1:D:285:HIS:CD2	1:D:287:GLU:H	2.36	0.43
1:E:253[B]:ARG:HD2	1:E:267:VAL:HG11	2.00	0.43
1:G:140:ASN:HB2	2:G:1678:PO4:O3	2.18	0.43
1:J:116:LEU:HD13	1:J:119:MSE:HE2	2.00	0.43
1:F:172:THR:OG1	1:F:277:SER:HB3	2.18	0.43
1:J:191:PRO:HB2	1:J:271:ALA:N	2.33	0.43
1:H:183:HIS:HE1	3:H:1679:HOH:O	2.01	0.43
1:I:231:THR:HG21	1:I:236:THR:CG2	2.48	0.43
1:D:290:LEU:HD13	1:D:298:ILE:CD1	2.48	0.43
1:F:192:VAL:HG23	1:F:268:LYS:HG2	2.01	0.43
1:G:243:ARG:HD3	1:G:263:LEU:HD11	2.00	0.43
1:B:106:GLY:HA2	1:B:135:ARG:O	2.18	0.43
3:A:1713:HOH:O	1:B:124:THR:HG21	2.17	0.43
1:D:173:ARG:NH2	1:D:176:MSE:HE1	2.32	0.43
1:E:105:VAL:HG13	1:E:132[B]:VAL:HG13	2.01	0.43
1:F:178:VAL:HG13	1:F:265:VAL:HG13	1.99	0.43
1:E:121:TYR:HB2	1:F:243:ARG:HG3	2.01	0.43
1:H:220:GLU:HG2	3:H:1686:HOH:O	2.18	0.43
1:C:166:GLN:HB2	1:C:284:TRP:CE2	2.53	0.42
1:B:166:GLN:O	1:B:283:ALA:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:177:VAL:HG23	1:C:270:ILE:CG1	2.49	0.42
1:G:116:LEU:HD13	1:G:119:MSE:HE2	2.01	0.42
1:J:167:THR:HB	1:J:281[A]:VAL:HG22	1.97	0.42
1:L:116:LEU:HD13	1:L:119:MSE:CE	2.48	0.42
1:A:183:HIS:HD2	1:A:185:LEU:N	2.03	0.42
1:A:299:ARG:NE	3:A:1768:HOH:O	2.52	0.42
1:G:112:GLY:O	1:G:117:PRO:HD3	2.20	0.42
1:J:174:GLU:HA	1:J:175:PRO:HD3	1.92	0.42
1:J:185:LEU:O	1:J:188:VAL:HG12	2.19	0.42
1:J:213:HIS:O	1:J:217:VAL:HG13	2.19	0.42
1:G:164:GLU:HG2	1:G:285:HIS:ND1	2.35	0.42
1:I:115:ILE:HG12	1:I:171:MSE:HE1	1.99	0.42
1:L:176:MSE:SE	1:L:253:ARG:HB2	2.70	0.42
1:A:112:GLY:O	1:A:117:PRO:HD3	2.19	0.42
1:B:249:LEU:HD21	1:B:270:ILE:HD11	2.00	0.42
1:K:249:LEU:CD2	1:K:270:ILE:HD11	2.50	0.42
1:A:176:MSE:SE	1:A:253:ARG:HB2	2.70	0.42
1:H:150:GLU:H	1:H:150:GLU:HG2	1.62	0.42
1:D:116:LEU:N	1:D:117:PRO:CD	2.82	0.42
1:J:168:VAL:C	1:J:281[A]:VAL:HG23	2.39	0.42
1:E:181:ALA:HB2	1:E:264:PRO:HG2	2.01	0.42
1:D:253:ARG:HG3	1:D:267:VAL:HG11	2.02	0.42
1:A:253:ARG:HD3	1:A:267:VAL:HG11	2.02	0.42
1:C:243:ARG:HD3	1:C:243:ARG:O	2.19	0.41
1:D:112:GLY:O	1:D:117:PRO:HD3	2.20	0.41
1:L:106:GLY:O	1:L:154:ALA:HA	2.20	0.41
1:K:233:ASN:HD22	1:L:136:GLU:CD	2.23	0.41
1:C:174:GLU:OE1	1:H:289:THR:OG1	2.35	0.41
1:D:167:THR:HA	1:D:282:VAL:O	2.21	0.41
1:G:229:TYR:HE1	1:H:132:VAL:CG2	2.32	0.41
1:L:159:LEU:O	1:L:160:ASP:HB2	2.20	0.41
1:A:173:ARG:HH22	1:A:253:ARG:H	1.68	0.41
1:G:137:ASP:HB3	1:G:142:LEU:HD13	2.01	0.41
1:H:291:SER:O	1:H:295:ARG:HG3	2.19	0.41
1:I:215:MSE:HE1	3:I:1681:HOH:O	2.19	0.41
1:A:172:THR:N	2:A:1674:PO4:O3	2.37	0.41
1:D:119:MSE:HE3	1:D:297:PHE:CE2	2.55	0.41
1:D:219:ARG:O	1:D:222:GLY:N	2.43	0.41
1:G:163:PRO:O	1:G:164:GLU:CB	2.68	0.41
1:L:112:GLY:N	1:L:113:PRO:CD	2.84	0.41
1:D:175:PRO:HG3	1:D:213:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:181:ALA:HB2	1:G:264:PRO:HG2	2.02	0.41
1:G:243:ARG:NH1	1:H:118:SER:HB3	2.35	0.41
1:A:219:ARG:HD3	3:C:1716:HOH:O	2.20	0.41
1:B:302:THR:HG23	1:J:273:PRO:CB	2.45	0.41
1:D:272:GLU:HA	1:D:273:PRO:HA	1.97	0.41
1:C:302:THR:O	1:C:302:THR:CG2	2.68	0.41
1:E:166:GLN:O	1:E:283:ALA:HA	2.21	0.41
1:H:272:GLU:HG3	1:H:272:GLU:O	2.21	0.41
1:I:103:ILE:HB	1:I:293:VAL:HG22	2.01	0.41
1:L:119:MSE:HE1	1:L:297:PHE:HZ	1.85	0.41
1:A:271:ALA:C	1:A:272:GLU:HG2	2.41	0.41
1:B:145:GLN:HB3	1:B:151:LEU:HD22	2.03	0.41
1:D:191:PRO:CB	1:D:271:ALA:HB2	2.43	0.41
1:E:153[A]:VAL:HG11	1:E:282:VAL:HG12	2.03	0.41
1:K:178:VAL:HG23	1:K:265:VAL:HB	2.03	0.41
1:L:103:ILE:HD12	1:L:294:ALA:HA	2.03	0.41
1:D:243:ARG:HD3	1:D:243:ARG:HA	1.90	0.41
1:F:173:ARG:HH12	2:F:1628:PO4:P	2.43	0.41
1:J:170:LEU:HD13	1:J:282:VAL:HG12	2.02	0.41
1:K:202:MSE:HE1	1:K:225:PRO:CB	2.49	0.41
1:D:100:ALA:O	1:D:293[A]:VAL:CG1	2.64	0.41
1:G:135:ARG:HD2	1:G:151:LEU:CD1	2.51	0.41
1:J:106:GLY:HA2	1:J:135:ARG:O	2.21	0.41
1:K:202:MSE:HE1	1:K:225:PRO:CG	2.51	0.41
1:A:178:VAL:HG21	1:A:250:LEU:HD12	2.02	0.40
1:B:289:THR:O	1:C:147:GLU:OE2	2.39	0.40
1:D:106:GLY:HA2	1:D:135:ARG:O	2.21	0.40
1:E:299:ARG:HD2	3:E:1711:HOH:O	2.21	0.40
1:G:171:MSE:CE	1:G:173:ARG:CG	2.99	0.40
1:H:142:LEU:HD23	1:H:142:LEU:C	2.41	0.40
1:D:100:ALA:O	1:D:293[B]:VAL:CG2	2.70	0.40
1:A:295:ARG:NH2	1:A:299:ARG:HH21	2.20	0.40
1:B:178:VAL:HG21	1:B:265[A]:VAL:HG11	2.03	0.40
1:B:274:LYS:HB3	1:B:274:LYS:HE3	1.91	0.40
1:G:272:GLU:OE1	1:J:295:ARG:NH1	2.49	0.40
1:H:263:LEU:HA	1:H:263:LEU:HD23	1.89	0.40
1:J:171:MSE:HG2	1:J:280:VAL:HB	2.03	0.40
3:G:1717:HOH:O	1:J:295:ARG:HD3	2.21	0.40
1:L:249[A]:LEU:CD2	1:L:270:ILE:HD11	2.52	0.40

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	203/209 (97%)	198 (98%)	3 (2%)	2 (1%)	15	6
1	B	204/209 (98%)	203 (100%)	1 (0%)	0	100	100
1	C	206/209 (99%)	203 (98%)	2 (1%)	1 (0%)	29	18
1	D	205/209 (98%)	198 (97%)	6 (3%)	1 (0%)	29	18
1	E	208/209 (100%)	206 (99%)	2 (1%)	0	100	100
1	F	205/209 (98%)	203 (99%)	2 (1%)	0	100	100
1	G	203/209 (97%)	199 (98%)	3 (2%)	1 (0%)	29	18
1	H	204/209 (98%)	201 (98%)	2 (1%)	1 (0%)	29	18
1	I	203/209 (97%)	199 (98%)	3 (2%)	1 (0%)	29	18
1	J	204/209 (98%)	202 (99%)	2 (1%)	0	100	100
1	K	204/209 (98%)	202 (99%)	2 (1%)	0	100	100
1	L	204/209 (98%)	197 (97%)	6 (3%)	1 (0%)	29	18
All	All	2453/2508 (98%)	2411 (98%)	34 (1%)	8 (0%)	41	31

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	256	VAL
1	A	188	VAL
1	G	164	GLU
1	I	188	VAL
1	A	286	GLN
1	H	272	GLU
1	C	171	MSE
1	L	256	VAL

### 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	165/162 (102%)	148 (90%)	17 (10%)	7	2
1	B	166/162 (102%)	147 (89%)	19 (11%)	5	1
1	C	168/162 (104%)	145 (86%)	23 (14%)	3	1
1	D	167/162 (103%)	148 (89%)	19 (11%)	5	1
1	E	170/162 (105%)	152 (89%)	18 (11%)	6	2
1	F	167/162 (103%)	148 (89%)	19 (11%)	5	1
1	G	165/162 (102%)	141 (86%)	24 (14%)	3	1
1	H	166/162 (102%)	146 (88%)	20 (12%)	5	1
1	I	165/162 (102%)	150 (91%)	15 (9%)	9	3
1	J	166/162 (102%)	152 (92%)	14 (8%)	11	4
1	K	166/162 (102%)	146 (88%)	20 (12%)	5	1
1	L	166/162 (102%)	147 (89%)	19 (11%)	5	1
All	All	1997/1944 (103%)	1770 (89%)	227 (11%)	6	1

All (227) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	VAL
1	A	111	LEU
1	A	120	LEU
1	A	132	VAL
1	A	133	GLU
1	A	137	ASP
1	A	162	SER
1	A	170	LEU
1	A	171	MSE
1	A	174	GLU
1	A	179	LEU
1	A	193	ARG
1	A	194	LEU
1	A	265	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	272	GLU
1	A	286	GLN
1	A	295	ARG
1	B	120	LEU
1	B	124	THR
1	B	132	VAL
1	B	137	ASP
1	B	142	LEU
1	B	151	LEU
1	B	153	VAL
1	B	161	LEU
1	B	170	LEU
1	B	171	MSE
1	B	173	ARG
1	B	178	VAL
1	B	179	LEU
1	B	212	ASN
1	B	215	MSE
1	B	249	LEU
1	B	251	LEU
1	B	290	LEU
1	B	292	ARG
1	C	99	VAL
1	C	111	LEU
1	C	115	ILE
1	C	120	LEU
1	C	129	ARG
1	C	137	ASP
1	C	170	LEU
1	C	172	THR
1	C	173	ARG
1	C	179	LEU
1	C	185	LEU
1	C	188	VAL
1	C	189	ASP
1	C	192	VAL
1	C	227	VAL
1	C	243	ARG
1	C	249	LEU
1	C	265	VAL
1	C	277	SER
1	C	281	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	286	GLN
1	C	290	LEU
1	C	292	ARG
1	D	120	LEU
1	D	124	THR
1	D	164	GLU
1	D	168	VAL
1	D	170	LEU
1	D	171	MSE
1	D	173	ARG
1	D	178	VAL
1	D	188	VAL
1	D	204	LEU
1	D	211	THR
1	D	219	ARG
1	D	227	VAL
1	D	230	ARG
1	D	265	VAL
1	D	281	VAL
1	D	282	VAL
1	D	289	THR
1	D	301	VAL
1	E	99	VAL
1	E	105	VAL
1	E	115	ILE
1	E	120	LEU
1	E	131	SER
1	E	137	ASP
1	E	161	LEU
1	E	173	ARG
1	E	179	LEU
1	E	185	LEU
1	E	189	ASP
1	E	230	ARG
1	E	251	LEU
1	E	253[A]	ARG
1	E	253[B]	ARG
1	E	265	VAL
1	E	281	VAL
1	E	292	ARG
1	F	120	LEU
1	F	124	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	F	132	VAL
1	F	135	ARG
1	F	151	LEU
1	F	153	VAL
1	F	168	VAL
1	F	170	LEU
1	F	173	ARG
1	F	185	LEU
1	F	191	PRO
1	F	243	ARG
1	F	245	LEU
1	F	249[A]	LEU
1	F	249[B]	LEU
1	F	265	VAL
1	F	268	LYS
1	F	274	LYS
1	F	277	SER
1	G	120	LEU
1	G	124	THR
1	G	132	VAL
1	G	136	GLU
1	G	137	ASP
1	G	151	LEU
1	G	153	VAL
1	G	161	LEU
1	G	168	VAL
1	G	171	MSE
1	G	174	GLU
1	G	176	MSE
1	G	178	VAL
1	G	189	ASP
1	G	245	LEU
1	G	249	LEU
1	G	251	LEU
1	G	265	VAL
1	G	281	VAL
1	G	286	GLN
1	G	287	GLU
1	G	290	LEU
1	G	292	ARG
1	G	293	VAL
1	H	120	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	H	131	SER
1	H	132	VAL
1	H	138	THR
1	H	146	LEU
1	H	150	GLU
1	H	166	GLN
1	H	172	THR
1	H	174	GLU
1	H	185	LEU
1	H	188	VAL
1	H	197	LEU
1	H	220	GLU
1	H	226	ARG
1	H	265	VAL
1	H	268	LYS
1	H	277	SER
1	H	281	VAL
1	H	290	LEU
1	H	292	ARG
1	I	120	LEU
1	I	132	VAL
1	I	135	ARG
1	I	150	GLU
1	I	170	LEU
1	I	179	LEU
1	I	194	LEU
1	I	199	GLU
1	I	245	LEU
1	I	251	LEU
1	I	252	GLN
1	I	277	SER
1	I	281	VAL
1	I	287	GLU
1	I	301	VAL
1	J	120	LEU
1	J	132	VAL
1	J	166	GLN
1	J	168	VAL
1	J	170	LEU
1	J	182	GLU
1	J	185	LEU
1	J	192	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	193	ARG
1	J	219	ARG
1	J	230	ARG
1	J	253	ARG
1	J	256	VAL
1	J	282	VAL
1	K	99	VAL
1	K	120	LEU
1	K	124	THR
1	K	129	ARG
1	K	132	VAL
1	K	135	ARG
1	K	151	LEU
1	K	153	VAL
1	K	168	VAL
1	K	170	LEU
1	K	176[A]	MSE
1	K	176[B]	MSE
1	K	178	VAL
1	K	185	LEU
1	K	249	LEU
1	K	251	LEU
1	K	254	PRO
1	K	274	LYS
1	K	287	GLU
1	K	290	LEU
1	L	99	VAL
1	L	120	LEU
1	L	129	ARG
1	L	131	SER
1	L	136	GLU
1	L	137	ASP
1	L	155	ILE
1	L	161	LEU
1	L	164	GLU
1	L	173	ARG
1	L	178	VAL
1	L	179	LEU
1	L	182	GLU
1	L	194	LEU
1	L	245	LEU
1	L	251	LEU

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Mol	Chain	Res	Type
1	L	265	VAL
1	L	268	LYS
1	L	274	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	183	HIS
1	A	213	HIS
1	A	252	GLN
1	B	139	GLN
1	B	183	HIS
1	B	200	HIS
1	B	212	ASN
1	B	252	GLN
1	B	285	HIS
1	C	183	HIS
1	C	286	GLN
1	D	183	HIS
1	D	200	HIS
1	D	285	HIS
1	E	183	HIS
1	E	252	GLN
1	E	286	GLN
1	F	183	HIS
1	F	212	ASN
1	F	252	GLN
1	F	286	GLN
1	G	183	HIS
1	G	212	ASN
1	G	252	GLN
1	G	286	GLN
1	H	183	HIS
1	I	145	GLN
1	I	183	HIS
1	J	183	HIS
1	J	252	GLN
1	K	183	HIS
1	K	213	HIS
1	K	233	ASN
1	K	286	GLN

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Mol	Chain	Res	Type
1	L	183	HIS
1	L	200	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 carbohydrates in this entry.

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

76 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	PO4	D	1660	-	4,4,4	0.93	0	6,6,6	0.63	0
2	PO4	K	1608	-	4,4,4	0.94	0	6,6,6	0.49	0
2	PO4	D	1659	-	4,4,4	0.74	0	6,6,6	0.73	0
2	PO4	J	1668	-	4,4,4	0.69	0	6,6,6	0.71	0
2	PO4	A	1641	-	4,4,4	0.86	0	6,6,6	1.08	1 (16%)
2	PO4	C	1648	-	4,4,4	0.82	0	6,6,6	0.62	0
2	PO4	I	1621	-	4,4,4	0.81	0	6,6,6	1.34	1 (16%)
2	PO4	B	1651	-	4,4,4	0.92	0	6,6,6	0.72	0
2	PO4	I	1645	-	4,4,4	0.65	0	6,6,6	0.79	0
2	PO4	H	1604	-	4,4,4	0.95	0	6,6,6	1.15	1 (16%)
2	PO4	F	1650	-	4,4,4	0.84	0	6,6,6	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	F	1605	-	4,4,4	0.90	0	6,6,6	0.84	0
2	PO4	L	1622	-	4,4,4	1.07	0	6,6,6	1.04	0
2	PO4	J	1653	-	4,4,4	0.60	0	6,6,6	0.54	0
2	PO4	L	1602	-	4,4,4	1.24	0	6,6,6	1.46	1 (16%)
2	PO4	D	1657	-	4,4,4	0.80	0	6,6,6	0.67	0
2	PO4	H	1676	-	4,4,4	0.64	0	6,6,6	0.85	0
2	PO4	F	1611	-	4,4,4	0.55	0	6,6,6	1.10	0
2	PO4	K	1669	-	4,4,4	0.78	0	6,6,6	0.68	0
2	PO4	F	1652	-	4,4,4	0.84	0	6,6,6	0.57	0
2	PO4	I	1665	-	4,4,4	0.91	0	6,6,6	0.31	0
2	PO4	C	1619	-	4,4,4	0.79	0	6,6,6	1.53	1 (16%)
2	PO4	K	1634	-	4,4,4	0.86	0	6,6,6	0.59	0
2	PO4	K	1672	-	4,4,4	0.68	0	6,6,6	0.90	0
2	PO4	K	1673	-	4,4,4	0.99	0	6,6,6	1.03	0
2	PO4	J	1633	-	4,4,4	0.66	0	6,6,6	0.83	0
2	PO4	A	1664	-	4,4,4	0.67	0	6,6,6	0.43	0
2	PO4	F	1639	-	4,4,4	0.88	0	6,6,6	0.60	0
2	PO4	I	1655	-	4,4,4	0.52	0	6,6,6	1.29	1 (16%)
2	PO4	A	1626	-	4,4,4	0.92	0	6,6,6	0.90	0
2	PO4	A	1674	-	4,4,4	0.89	0	6,6,6	0.68	0
2	PO4	B	1638	-	4,4,4	0.97	0	6,6,6	0.56	0
2	PO4	K	1610	-	4,4,4	0.83	0	6,6,6	0.62	0
2	PO4	F	1647	-	4,4,4	0.79	0	6,6,6	0.66	0
2	PO4	H	1631	-	4,4,4	0.85	0	6,6,6	0.53	0
2	PO4	A	1615	-	4,4,4	0.85	0	6,6,6	0.58	0
2	PO4	F	1675	-	4,4,4	0.47	0	6,6,6	0.77	0
2	PO4	B	1677	-	4,4,4	0.65	0	6,6,6	0.84	0
2	PO4	L	1656	-	4,4,4	0.41	0	6,6,6	1.35	1 (16%)
2	PO4	L	1609	-	4,4,4	0.85	0	6,6,6	0.62	0
2	PO4	A	1616	-	4,4,4	0.83	0	6,6,6	0.52	0
2	PO4	J	1667	-	4,4,4	0.83	0	6,6,6	0.69	0
2	PO4	K	1661	-	4,4,4	0.78	0	6,6,6	0.72	0
2	PO4	I	1662	-	4,4,4	0.74	0	6,6,6	0.75	0
2	PO4	I	1632	-	4,4,4	0.80	0	6,6,6	1.00	0
2	PO4	F	1627	-	4,4,4	0.68	0	6,6,6	0.72	0
2	PO4	J	1603	-	4,4,4	0.59	0	6,6,6	0.83	0
2	PO4	C	1607	-	4,4,4	0.61	0	6,6,6	1.13	1 (16%)
2	PO4	J	1614	-	4,4,4	0.67	0	6,6,6	0.49	0
2	PO4	G	1678	-	4,4,4	1.05	0	6,6,6	0.71	0
2	PO4	E	1644	-	4,4,4	0.89	0	6,6,6	0.67	0
2	PO4	E	1642	-	4,4,4	0.85	0	6,6,6	0.45	0
2	PO4	J	1613	-	4,4,4	0.91	0	6,6,6	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	K	1625	-	4,4,4	0.78	0	6,6,6	0.40	0
2	PO4	F	1628	-	4,4,4	1.01	0	6,6,6	1.06	0
2	PO4	F	1640	-	4,4,4	0.77	0	6,6,6	0.49	0
2	PO4	K	1620	-	4,4,4	0.33	0	6,6,6	1.22	0
2	PO4	F	1635	-	4,4,4	0.42	0	6,6,6	0.58	0
2	PO4	D	1629	-	4,4,4	0.83	0	6,6,6	0.74	0
2	PO4	C	1623	-	4,4,4	0.95	0	6,6,6	0.58	0
2	PO4	G	1654	-	4,4,4	0.87	0	6,6,6	0.41	0
2	PO4	E	1624	-	4,4,4	0.92	0	6,6,6	0.29	0
2	PO4	C	1612	-	4,4,4	0.97	0	6,6,6	0.30	0
2	PO4	G	1637	-	4,4,4	0.50	0	6,6,6	1.09	1 (16%)
2	PO4	D	1658	-	4,4,4	0.93	0	6,6,6	0.77	0
2	PO4	I	1606	-	4,4,4	0.99	0	6,6,6	1.34	1 (16%)
2	PO4	B	1630	-	4,4,4	0.95	0	6,6,6	0.83	0
2	PO4	F	1646	-	4,4,4	0.61	0	6,6,6	0.70	0
2	PO4	F	1636	-	4,4,4	0.80	0	6,6,6	0.68	0
2	PO4	H	1617	-	4,4,4	0.85	0	6,6,6	0.78	0
2	PO4	L	1643	-	4,4,4	0.79	0	6,6,6	0.62	0
2	PO4	C	1663	-	4,4,4	0.68	0	6,6,6	0.55	0
2	PO4	L	1666	-	4,4,4	0.82	0	6,6,6	0.56	0
2	PO4	K	1601	-	4,4,4	0.82	0	6,6,6	1.53	1 (16%)
2	PO4	F	1618	-	4,4,4	0.83	0	6,6,6	0.68	0
2	PO4	B	1670	-	4,4,4	0.84	0	6,6,6	0.68	0

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1619	PO4	O4-P-O2	2.95	117.44	107.97
2	L	1602	PO4	O3-P-O2	2.68	116.57	107.97
2	H	1604	PO4	O4-P-O3	2.53	116.10	107.97
2	I	1621	PO4	O2-P-O1	-2.53	101.64	110.89
2	L	1656	PO4	O2-P-O1	-2.52	101.66	110.89
2	G	1637	PO4	O3-P-O2	2.32	115.42	107.97
2	K	1601	PO4	O3-P-O2	2.22	115.09	107.97
2	C	1607	PO4	O4-P-O3	-2.18	100.96	107.97
2	A	1641	PO4	O4-P-O3	2.15	114.87	107.97
2	I	1655	PO4	O4-P-O3	2.11	114.74	107.97
2	I	1606	PO4	O3-P-O2	2.04	114.52	107.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

23 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1660	PO4	1	0
2	K	1608	PO4	1	0
2	J	1668	PO4	1	0
2	B	1651	PO4	1	0
2	F	1650	PO4	1	0
2	D	1657	PO4	1	0
2	K	1669	PO4	2	0
2	C	1619	PO4	1	0
2	K	1673	PO4	1	0
2	A	1626	PO4	1	0
2	A	1674	PO4	1	0
2	H	1631	PO4	3	0
2	F	1675	PO4	1	0
2	L	1656	PO4	1	0
2	C	1607	PO4	1	0
2	G	1678	PO4	1	0
2	E	1644	PO4	1	0
2	F	1628	PO4	1	0
2	K	1620	PO4	1	0
2	E	1624	PO4	1	0
2	H	1617	PO4	1	0
2	C	1663	PO4	1	0
2	B	1670	PO4	3	0

## 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	200/209 (95%)	-0.42	0 <a href="#">100</a>   <a href="#">100</a>	23, 30, 39, 44	0
1	B	200/209 (95%)	-0.30	0 <a href="#">100</a>   <a href="#">100</a>	23, 32, 46, 49	0
1	C	200/209 (95%)	-0.10	2 (1%) <a href="#">82</a>   <a href="#">84</a>	26, 36, 47, 53	0
1	D	200/209 (95%)	-0.27	0 <a href="#">100</a>   <a href="#">100</a>	26, 33, 44, 52	0
1	E	200/209 (95%)	-0.42	0 <a href="#">100</a>   <a href="#">100</a>	22, 29, 41, 49	0
1	F	200/209 (95%)	-0.40	0 <a href="#">100</a>   <a href="#">100</a>	21, 30, 40, 45	0
1	G	200/209 (95%)	-0.08	1 (0%) <a href="#">91</a>   <a href="#">92</a>	25, 37, 53, 59	0
1	H	200/209 (95%)	-0.29	0 <a href="#">100</a>   <a href="#">100</a>	22, 32, 45, 51	0
1	I	200/209 (95%)	-0.44	0 <a href="#">100</a>   <a href="#">100</a>	20, 26, 38, 46	0
1	J	200/209 (95%)	-0.35	1 (0%) <a href="#">91</a>   <a href="#">92</a>	21, 29, 40, 48	0
1	K	200/209 (95%)	-0.34	0 <a href="#">100</a>   <a href="#">100</a>	21, 29, 42, 47	0
1	L	200/209 (95%)	-0.41	0 <a href="#">100</a>   <a href="#">100</a>	20, 27, 38, 50	0
All	All	2400/2508 (95%)	-0.32	4 (0%) <a href="#">95</a>   <a href="#">95</a>	20, 31, 45, 59	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	163	PRO	3.3
1	C	303	ALA	3.2
1	C	129	ARG	2.6
1	J	303	ALA	2.1

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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(Å <sup>2</sup> )	Q<0.9
2	PO4	B	1677	5/5	0.52	0.36	88,89,90,91	0
2	PO4	A	1641	5/5	0.67	0.33	67,67,70,74	0
2	PO4	L	1622	5/5	0.69	0.28	77,79,81,81	0
2	PO4	L	1643	5/5	0.70	0.20	113,113,114,114	0
2	PO4	L	1656	5/5	0.75	0.30	71,75,77,77	0
2	PO4	F	1652	5/5	0.75	0.33	128,128,128,128	0
2	PO4	F	1640	5/5	0.78	0.25	92,92,93,94	0
2	PO4	J	1653	5/5	0.79	0.26	112,112,113,113	0
2	PO4	G	1654	5/5	0.80	0.19	134,135,135,135	0
2	PO4	B	1651	5/5	0.80	0.22	91,92,93,94	0
2	PO4	J	1633	5/5	0.80	0.20	90,91,91,92	0
2	PO4	H	1676	5/5	0.80	0.22	81,81,83,83	0
2	PO4	I	1655	5/5	0.81	0.32	66,68,70,73	0
2	PO4	E	1642	5/5	0.82	0.17	104,104,105,106	0
2	PO4	F	1618	5/5	0.82	0.27	86,87,88,88	0
2	PO4	F	1639	5/5	0.83	0.21	91,91,92,92	0
2	PO4	F	1650	5/5	0.83	0.39	96,96,97,97	0
2	PO4	D	1660	5/5	0.85	0.21	66,67,70,70	0
2	PO4	F	1611	5/5	0.85	0.14	64,65,67,68	0
2	PO4	D	1629	5/5	0.86	0.17	67,68,72,72	0
2	PO4	E	1624	5/5	0.86	0.16	92,93,93,94	0
2	PO4	F	1675	5/5	0.87	0.21	75,76,78,78	0
2	PO4	D	1657	5/5	0.88	0.20	93,94,94,94	0
2	PO4	A	1664	5/5	0.89	0.18	91,91,92,92	0
2	PO4	C	1663	5/5	0.89	0.36	93,93,94,94	0
2	PO4	A	1674	5/5	0.89	0.25	78,78,79,79	0
2	PO4	I	1662	5/5	0.89	0.20	66,69,69,70	0
2	PO4	G	1637	5/5	0.90	0.18	65,66,69,69	0
2	PO4	A	1616	5/5	0.90	0.24	72,72,74,74	0
2	PO4	F	1646	5/5	0.90	0.15	75,76,78,78	0
2	PO4	J	1667	5/5	0.90	0.24	92,92,93,93	0
2	PO4	C	1623	5/5	0.90	0.16	77,78,79,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	K	1673	5/5	0.90	0.20	68,68,71,71	0
2	PO4	B	1638	5/5	0.90	0.18	76,78,78,80	0
2	PO4	E	1644	5/5	0.91	0.17	68,68,70,70	0
2	PO4	A	1615	5/5	0.91	0.20	71,71,72,73	0
2	PO4	D	1659	5/5	0.92	0.14	76,76,77,77	0
2	PO4	K	1672	5/5	0.92	0.21	59,61,62,64	0
2	PO4	K	1625	5/5	0.92	0.19	88,88,89,89	0
2	PO4	K	1608	5/5	0.92	0.12	83,83,83,84	0
2	PO4	K	1620	5/5	0.92	0.18	55,58,58,60	0
2	PO4	C	1648	5/5	0.92	0.17	85,85,86,87	0
2	PO4	K	1669	5/5	0.92	0.17	81,82,82,83	0
2	PO4	I	1632	5/5	0.92	0.27	77,78,79,80	0
2	PO4	J	1613	5/5	0.93	0.12	69,70,71,73	0
2	PO4	I	1621	5/5	0.93	0.12	60,60,61,64	0
2	PO4	I	1606	5/5	0.93	0.11	46,49,53,56	0
2	PO4	G	1678	5/5	0.93	0.32	45,46,47,51	0
2	PO4	K	1610	5/5	0.93	0.11	61,63,64,65	0
2	PO4	H	1631	5/5	0.93	0.15	61,64,66,66	0
2	PO4	K	1634	5/5	0.94	0.18	91,92,92,93	0
2	PO4	I	1665	5/5	0.94	0.09	90,90,90,90	0
2	PO4	F	1647	5/5	0.94	0.20	77,77,78,78	0
2	PO4	I	1645	5/5	0.95	0.14	64,66,67,67	0
2	PO4	F	1636	5/5	0.95	0.23	54,55,57,58	0
2	PO4	J	1614	5/5	0.95	0.11	59,60,61,62	0
2	PO4	J	1668	5/5	0.95	0.27	78,78,79,80	0
2	PO4	K	1661	5/5	0.95	0.29	90,90,90,90	0
2	PO4	L	1666	5/5	0.95	0.24	86,86,86,87	0
2	PO4	L	1609	5/5	0.95	0.17	54,56,59,59	0
2	PO4	D	1658	5/5	0.95	0.40	45,46,47,48	0
2	PO4	F	1635	5/5	0.96	0.13	46,47,51,53	0
2	PO4	C	1619	5/5	0.96	0.17	49,49,51,53	0
2	PO4	H	1604	5/5	0.96	0.12	53,54,56,56	0
2	PO4	A	1626	5/5	0.96	0.12	27,34,41,42	0
2	PO4	H	1617	5/5	0.96	0.17	55,56,57,58	0
2	PO4	B	1670	5/5	0.96	0.22	71,73,74,74	0
2	PO4	F	1628	5/5	0.97	0.11	54,54,57,58	0
2	PO4	C	1607	5/5	0.98	0.12	34,42,45,45	0
2	PO4	B	1630	5/5	0.98	0.25	58,58,59,60	0
2	PO4	K	1601	5/5	0.98	0.07	29,29,32,33	0
2	PO4	C	1612	5/5	0.98	0.08	62,62,63,63	0
2	PO4	F	1605	5/5	0.98	0.12	47,49,51,52	0
2	PO4	J	1603	5/5	0.98	0.14	36,38,39,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	L	1602	5/5	0.99	0.07	44,45,46,48	0
2	PO4	F	1627	5/5	0.99	0.05	46,47,49,50	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.