



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2023 – 08:50 AM EDT

PDB ID : 3HK9  
Title : Crystal structure of uronate isomerase from *Bacillus halodurans* complexed with zinc and D-Glucuronate  
Authors : Fedorov, A.A.; Fedorov, E.V.; Nguyen, T.T.; Raushel, F.M.; Almo, S.C.  
Deposited on : 2009-05-22  
Resolution : 2.10 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 : 2.35  
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) : 2.35

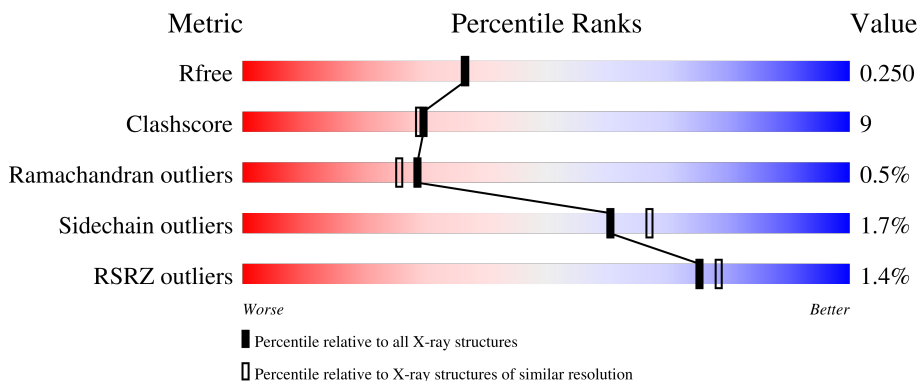
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

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




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	427	
1	B	427	
1	C	427	
1	D	427	
1	E	427	

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Mol	Chain	Length	Quality of chain
1	F	427	 2% 76% 19% ..
1	G	427	 % 74% 21% ..
1	H	427	 % 76% 19% ..
1	I	427	 % 78% 19% ..
1	J	427	 % 75% 20% ..
1	K	427	 2% 76% 20% ..
1	L	427	 % 78% 17% ..

## 2 Entry composition [i](#)

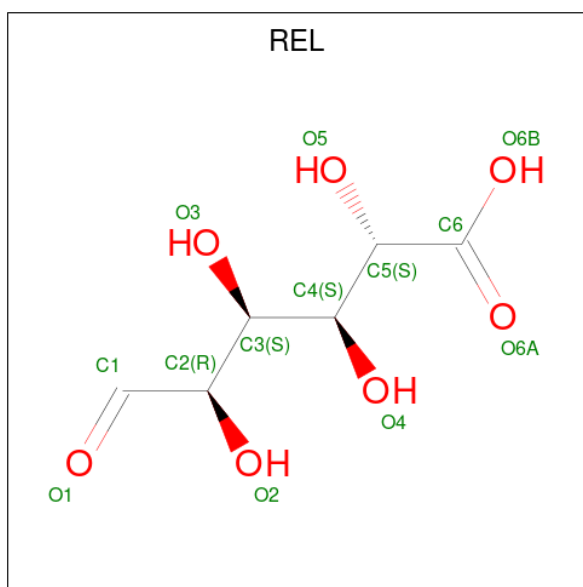
There are 6 unique types of molecules in this entry. The entry contains 42892 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Uronate isomerase.

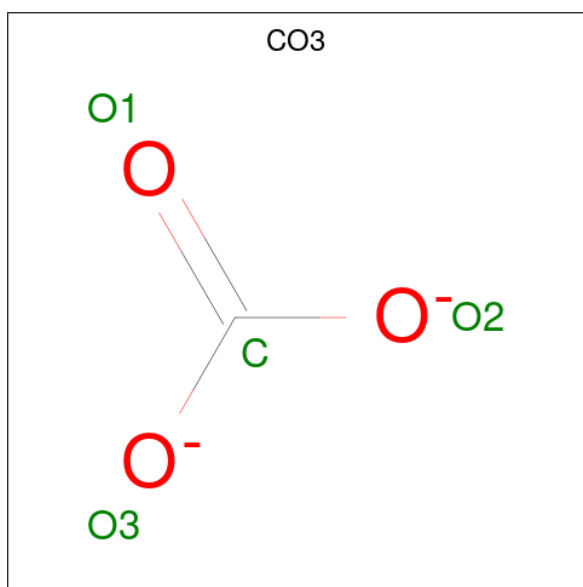
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	413	3404	2170	588	626	20	0	0	0
1	B	413	3404	2170	588	626	20	0	0	0
1	C	413	3404	2170	588	626	20	0	0	0
1	D	413	3404	2170	588	626	20	0	0	0
1	E	413	3404	2170	588	626	20	0	0	0
1	F	413	3404	2170	588	626	20	0	0	0
1	G	413	3404	2170	588	626	20	0	0	0
1	H	413	3404	2170	588	626	20	0	0	0
1	I	413	3404	2170	588	626	20	0	0	0
1	J	413	3404	2170	588	626	20	0	0	0
1	K	413	3404	2170	588	626	20	0	0	0
1	L	413	3404	2170	588	626	20	0	0	0

- Molecule 2 is D-glucuronic acid (three-letter code: REL) (formula: C<sub>6</sub>H<sub>10</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 6 7	0	0
2	B	1	Total C O 13 6 7	0	0
2	C	1	Total C O 13 6 7	0	0
2	D	1	Total C O 13 6 7	0	0
2	E	1	Total C O 13 6 7	0	0
2	F	1	Total C O 13 6 7	0	0
2	G	1	Total C O 13 6 7	0	0
2	H	1	Total C O 13 6 7	0	0
2	I	1	Total C O 13 6 7	0	0
2	J	1	Total C O 13 6 7	0	0
2	K	1	Total C O 13 6 7	0	0
2	L	1	Total C O 13 6 7	0	0

- Molecule 3 is CARBONATE ION (three-letter code: CO3) (formula: CO<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 1 3	0	0
3	A	1	Total C O 4 1 3	0	0
3	C	1	Total C O 4 1 3	0	0
3	D	1	Total C O 4 1 3	0	0
3	D	1	Total C O 4 1 3	0	0
3	F	1	Total C O 4 1 3	0	0
3	G	1	Total C O 4 1 3	0	0
3	H	1	Total C O 4 1 3	0	0
3	I	1	Total C O 4 1 3	0	0
3	J	1	Total C O 4 1 3	0	0
3	K	1	Total C O 4 1 3	0	0
3	L	1	Total C O 4 1 3	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0
4	B	1	Total Zn 1 1	0	0
4	C	1	Total Zn 1 1	0	0
4	D	1	Total Zn 1 1	0	0
4	E	1	Total Zn 1 1	0	0
4	F	1	Total Zn 1 1	0	0
4	G	1	Total Zn 1 1	0	0
4	H	1	Total Zn 1 1	0	0
4	I	1	Total Zn 1 1	0	0
4	J	1	Total Zn 1 1	0	0
4	K	1	Total Zn 1 1	0	0
4	L	1	Total Zn 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0
5	H	1	Total Cl 1 1	0	0
5	K	1	Total Cl 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	155	Total O 155 155	0	0
6	B	123	Total O 123 123	0	0

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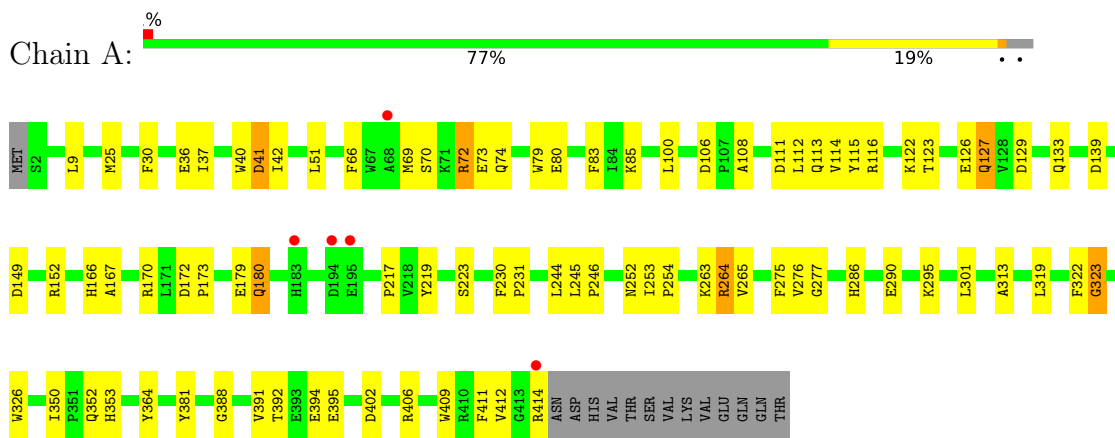
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	C	169	Total 169	O 169	0	0
6	D	189	Total 189	O 189	0	0
6	E	128	Total 128	O 128	0	0
6	F	163	Total 163	O 163	0	0
6	G	136	Total 136	O 136	0	0
6	H	143	Total 143	O 143	0	0
6	I	141	Total 141	O 141	0	0
6	J	160	Total 160	O 160	0	0
6	K	135	Total 135	O 135	0	0
6	L	182	Total 182	O 182	0	0



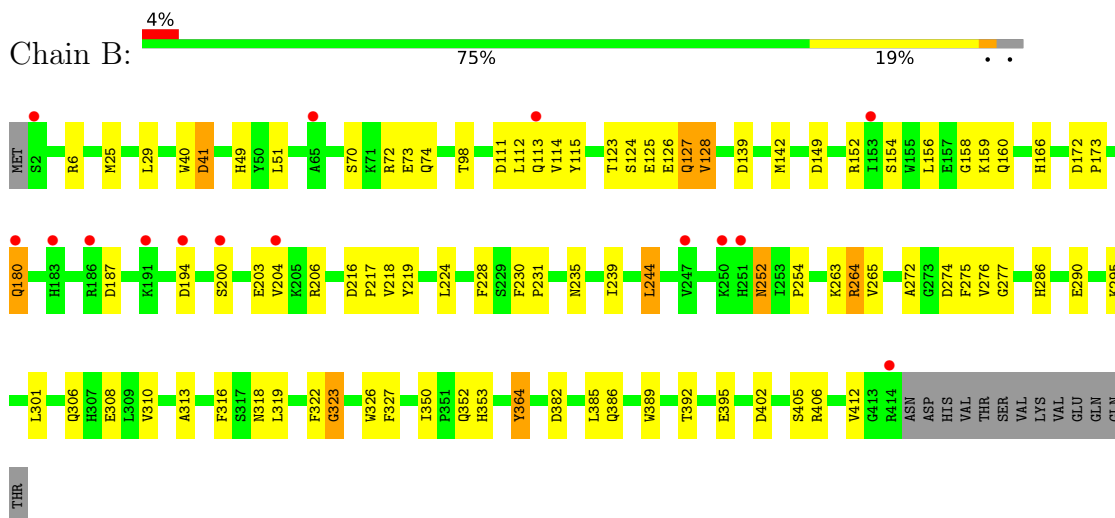
### 3 Residue-property plots

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.

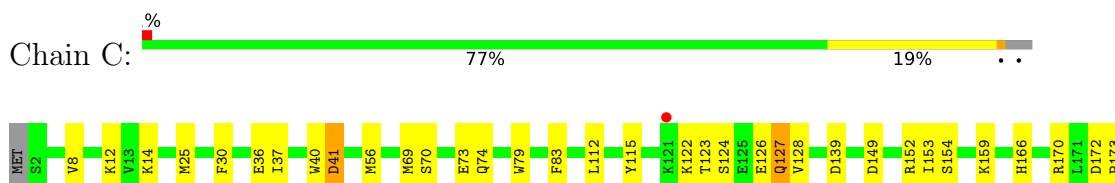
- Molecule 1: Uronate isomerase

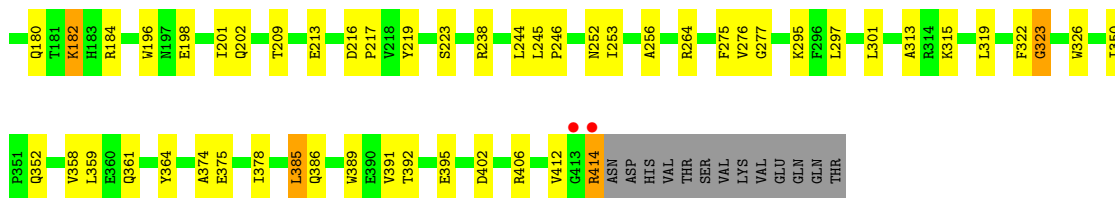


- Molecule 1: Uronate isomerase

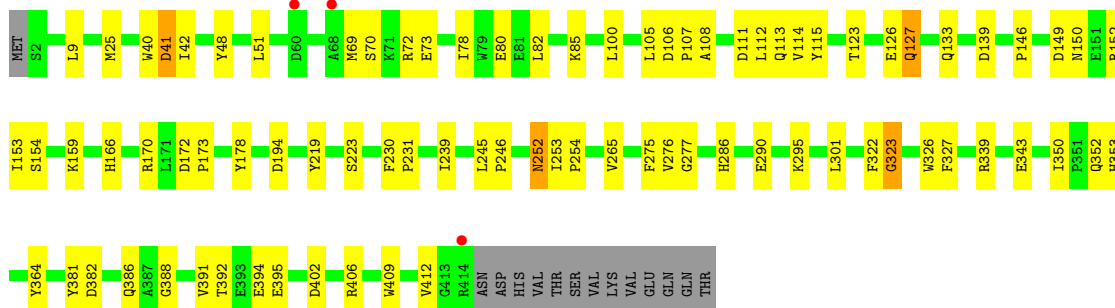
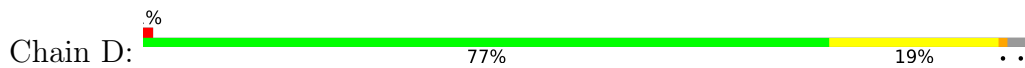


- Molecule 1: Uronate isomerase

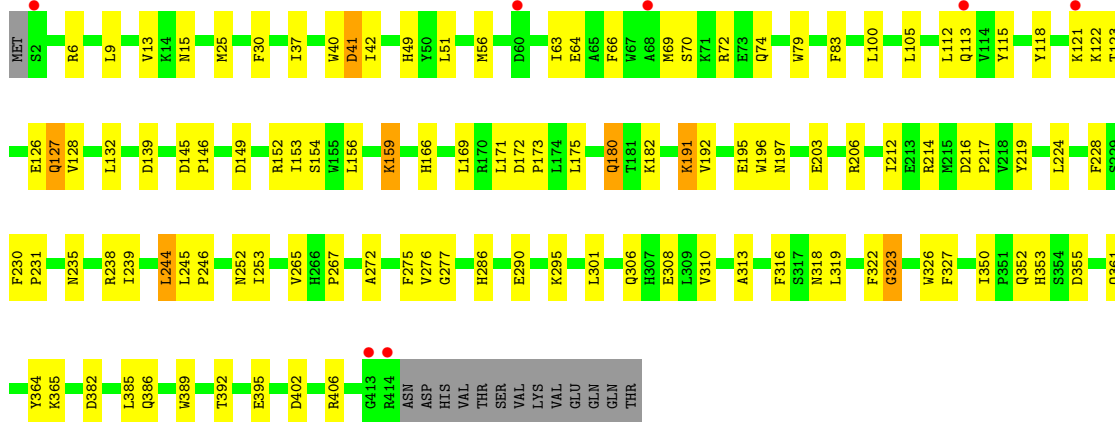




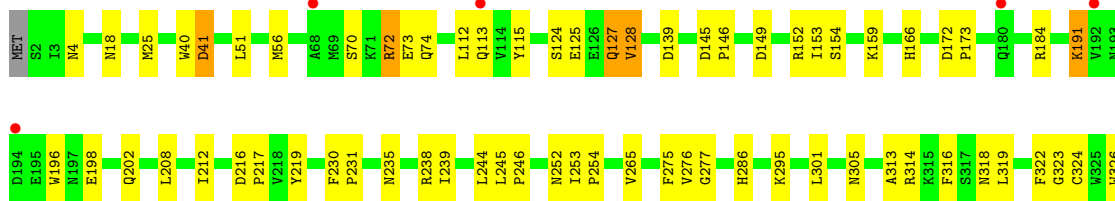
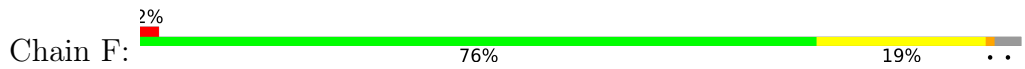
• Molecule 1: Uronate isomerase

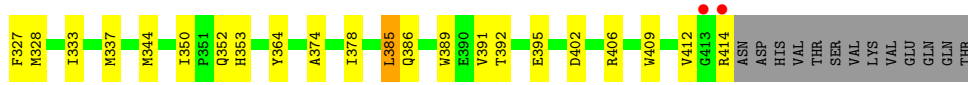


• Molecule 1: Uronate isomerase

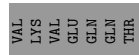
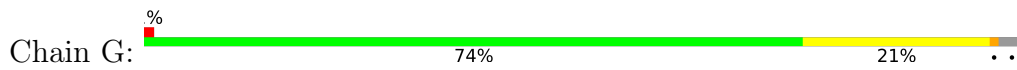


• Molecule 1: Uronate isomerase

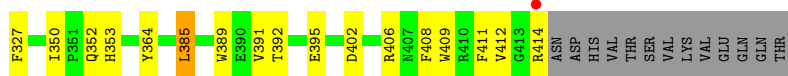
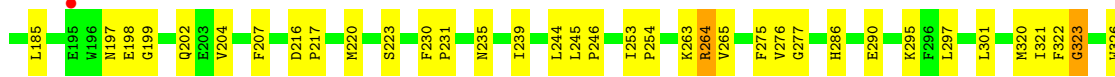
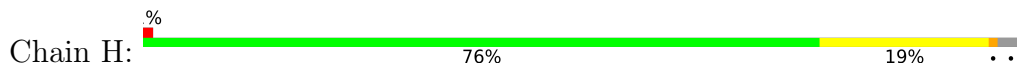




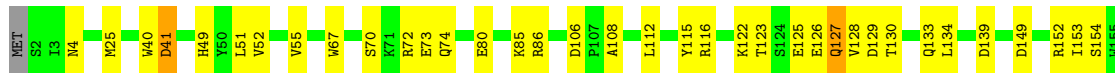
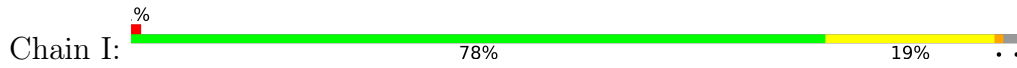
● Molecule 1: Uronate isomerase



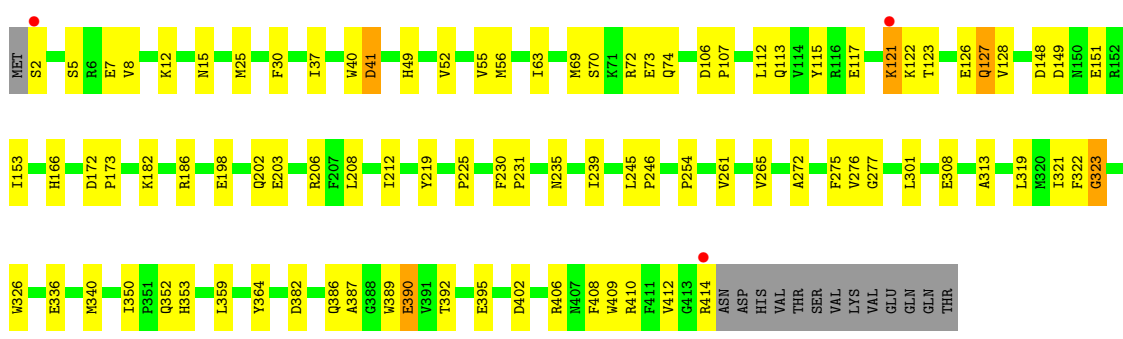
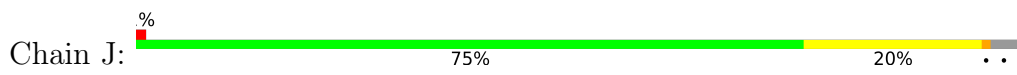
● Molecule 1: Uronate isomerase



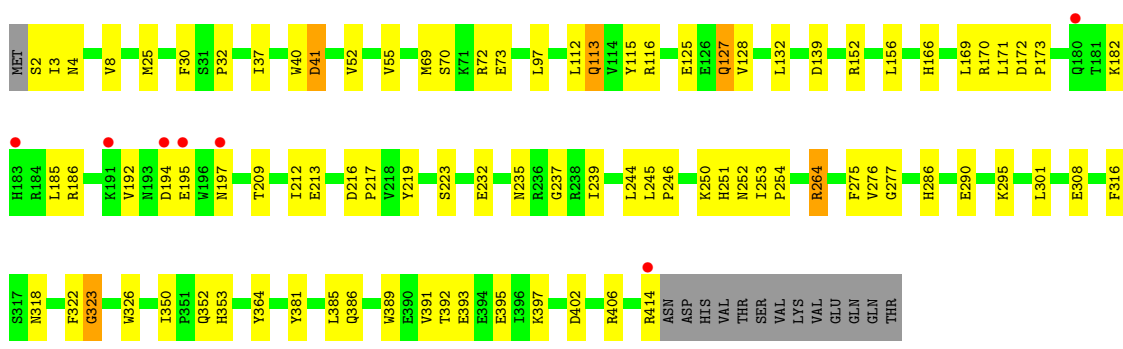
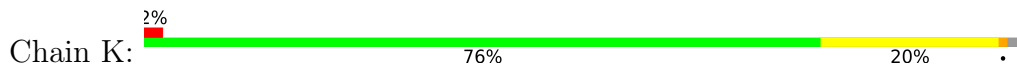
● Molecule 1: Uronate isomerase



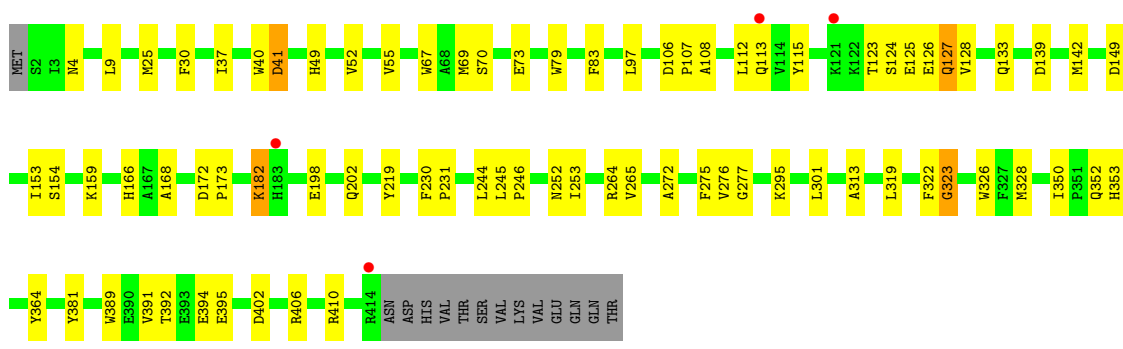
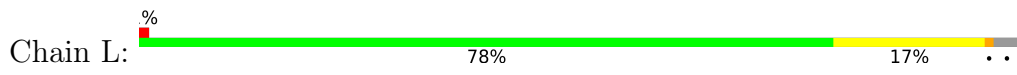
● Molecule 1: Uronate isomerase



• Molecule 1: Uronate isomerase



• Molecule 1: Uronate isomerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	274.09Å 156.88Å 185.21Å 90.00° 115.78° 90.00°	Depositor
Resolution (Å)	24.95 – 2.10 39.46 – 2.09	Depositor EDS
% Data completeness (in resolution range)	98.7 (24.95-2.10) 97.9 (39.46-2.09)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.08Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.227 , 0.258 0.221 , 0.250	Depositor DCC
$R_{free}$ test set	20501 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.5	Xtrriage
Anisotropy	0.207	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	42892	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2942e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: CL, ZN, CO3, REL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.34	0/3488	0.60	0/4726
1	B	0.33	0/3488	0.60	0/4726
1	C	0.34	0/3488	0.61	0/4726
1	D	0.35	0/3488	0.62	0/4726
1	E	0.34	0/3488	0.61	0/4726
1	F	0.34	0/3488	0.61	0/4726
1	G	0.33	0/3488	0.61	0/4726
1	H	0.34	0/3488	0.60	0/4726
1	I	0.33	0/3488	0.61	0/4726
1	J	0.34	0/3488	0.61	0/4726
1	K	0.33	0/3488	0.60	0/4726
1	L	0.34	0/3488	0.61	0/4726
All	All	0.34	0/41856	0.61	0/56712

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	3404	0	3328	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3404	0	3328	65	0
1	C	3404	0	3328	59	0
1	D	3404	0	3328	59	0
1	E	3404	0	3328	77	0
1	F	3404	0	3328	67	0
1	G	3404	0	3328	66	0
1	H	3404	0	3328	67	0
1	I	3404	0	3328	55	0
1	J	3404	0	3328	67	0
1	K	3404	0	3328	58	0
1	L	3404	0	3328	56	0
2	A	13	0	8	1	0
2	B	13	0	8	0	0
2	C	13	0	8	1	0
2	D	13	0	8	1	0
2	E	13	0	8	0	0
2	F	13	0	8	1	0
2	G	13	0	8	1	0
2	H	13	0	8	1	0
2	I	13	0	8	0	0
2	J	13	0	8	0	0
2	K	13	0	8	1	0
2	L	13	0	8	1	0
3	A	8	0	0	0	0
3	C	4	0	0	0	0
3	D	8	0	0	0	0
3	F	4	0	0	0	0
3	G	4	0	0	0	0
3	H	4	0	0	0	0
3	I	4	0	0	0	0
3	J	4	0	0	0	0
3	K	4	0	0	0	0
3	L	4	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
5	A	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
5	K	1	0	0	0	0
6	A	155	0	0	4	0
6	B	123	0	0	1	0
6	C	169	0	0	4	0
6	D	189	0	0	4	0
6	E	128	0	0	5	0
6	F	163	0	0	2	0
6	G	136	0	0	6	0
6	H	143	0	0	6	0
6	I	141	0	0	3	0
6	J	160	0	0	5	0
6	K	135	0	0	3	0
6	L	182	0	0	7	0
All	All	42892	0	40032	759	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 9.

All (759) 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:F:333:ILE:HG22	1:F:337:MET:HE2	1.21	1.10
1:F:72:ARG:HH11	1:F:72:ARG:HB2	1.20	1.05
1:G:127:GLN:HE21	1:G:127:GLN:HA	1.34	0.92
1:H:4:ASN:HB3	6:H:1604:HOH:O	1.72	0.90
1:J:127:GLN:HA	1:J:127:GLN:HE21	1.35	0.90
1:C:385:LEU:HD11	1:C:391:VAL:HG12	1.54	0.89
1:A:127:GLN:HE21	1:A:127:GLN:HA	1.37	0.88
1:B:72:ARG:HB2	1:B:72:ARG:HH11	1.40	0.86
1:D:127:GLN:HE21	1:D:127:GLN:HA	1.41	0.86
1:F:127:GLN:HE21	1:F:127:GLN:HA	1.40	0.86
1:K:32:PRO:HG3	1:K:128:VAL:HG11	1.58	0.86
1:I:127:GLN:HE21	1:I:127:GLN:HA	1.42	0.85
1:L:127:GLN:HE21	1:L:127:GLN:HA	1.42	0.84
1:C:127:GLN:HA	1:C:127:GLN:HE21	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:72:ARG:HH11	1:E:72:ARG:HB2	1.41	0.84
1:F:72:ARG:HB2	1:F:72:ARG:NH1	1.93	0.83
1:C:36:GLU:HG2	6:C:1956:HOH:O	1.79	0.82
1:B:111:ASP:O	1:B:114:VAL:HG12	1.79	0.81
1:H:127:GLN:HE21	1:H:127:GLN:HA	1.44	0.81
1:D:72:ARG:HH11	1:D:72:ARG:HB2	1.47	0.79
1:F:324:CYS:HB3	1:F:337:MET:HE1	1.65	0.79
1:H:40:TRP:O	1:H:41:ASP:HB3	1.81	0.78
1:D:113:GLN:HA	1:D:113:GLN:HE21	1.49	0.78
1:B:72:ARG:HB2	1:B:72:ARG:NH1	1.99	0.78
1:B:392:THR:OG1	1:B:395:GLU:HG3	1.85	0.77
1:E:72:ARG:HB2	1:E:72:ARG:NH1	1.98	0.77
1:J:2:SER:OG	1:J:390:GLU:HG3	1.85	0.77
1:K:127:GLN:HA	1:K:127:GLN:HE21	1.49	0.76
1:F:124:SER:O	1:F:128:VAL:HG12	1.86	0.76
1:E:195:GLU:HG2	6:E:453:HOH:O	1.85	0.75
1:J:72:ARG:HB2	1:J:72:ARG:HH11	1.52	0.74
1:B:127:GLN:HA	1:B:127:GLN:HE21	1.53	0.74
1:J:410:ARG:HD3	6:J:436:HOH:O	1.86	0.74
1:J:72:ARG:HB2	1:J:72:ARG:NH1	2.02	0.74
1:L:410:ARG:HD3	6:L:866:HOH:O	1.87	0.73
1:C:402:ASP:HA	1:C:406:ARG:HB2	1.71	0.73
1:A:394:GLU:HG2	6:A:553:HOH:O	1.90	0.72
1:E:127:GLN:HA	1:E:127:GLN:HE21	1.55	0.71
1:F:252:ASN:HD21	1:F:295:LYS:HE3	1.54	0.71
1:H:32:PRO:HG3	1:H:128:VAL:HG11	1.73	0.71
1:D:72:ARG:HB2	1:D:72:ARG:NH1	2.06	0.70
1:K:381:TYR:O	1:K:385:LEU:HD23	1.91	0.70
6:G:1153:HOH:O	1:H:321:ILE:HG12	1.91	0.69
1:B:323:GLY:HA2	1:B:352:GLN:HA	1.73	0.69
1:K:264:ARG:HH11	1:K:264:ARG:HB2	1.58	0.69
1:A:127:GLN:HA	1:A:127:GLN:NE2	2.08	0.69
1:C:392:THR:OG1	1:C:395:GLU:HG3	1.93	0.69
1:C:152:ARG:HH22	1:C:184:ARG:HH22	1.42	0.68
1:F:113:GLN:HE21	1:F:113:GLN:HA	1.58	0.68
1:L:113:GLN:HE21	1:L:113:GLN:HA	1.58	0.68
1:E:25:MET:HG3	6:E:450:HOH:O	1.92	0.68
1:E:182:LYS:HB2	1:E:192:VAL:HG21	1.75	0.68
1:B:124:SER:O	1:B:128:VAL:HG12	1.93	0.68
1:F:402:ASP:HA	1:F:406:ARG:HB2	1.76	0.68
1:I:72:ARG:NH2	1:I:116:ARG:HD3	2.09	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:GLN:H	1:B:180:GLN:NE2	1.92	0.68
1:B:402:ASP:HA	1:B:406:ARG:HB2	1.75	0.67
1:F:333:ILE:CG2	1:F:337:MET:HE2	2.13	0.67
1:K:301:LEU:HD11	1:K:326:TRP:HB3	1.76	0.67
1:H:149:ASP:O	1:H:153:ILE:HG12	1.93	0.66
1:G:392:THR:OG1	1:G:395:GLU:HG3	1.95	0.66
1:K:70:SER:OG	1:K:73:GLU:HG3	1.95	0.66
1:E:323:GLY:HA2	1:E:352:GLN:HA	1.76	0.66
1:H:385:LEU:HD11	1:H:391:VAL:HG22	1.76	0.66
1:L:127:GLN:HA	1:L:127:GLN:NE2	2.11	0.66
1:C:323:GLY:HA2	1:C:352:GLN:HA	1.78	0.66
1:D:254:PRO:HG3	1:D:295:LYS:HE3	1.77	0.66
1:F:392:THR:OG1	1:F:395:GLU:HG3	1.95	0.65
1:B:25:MET:HG3	6:B:434:HOH:O	1.95	0.65
1:A:80:GLU:HG3	1:A:85:LYS:NZ	2.11	0.65
1:A:263:LYS:HB3	1:A:264:ARG:HD2	1.78	0.65
1:J:392:THR:OG1	1:J:395:GLU:HG3	1.96	0.65
1:D:127:GLN:HA	1:D:127:GLN:NE2	2.12	0.65
1:G:80:GLU:O	1:G:85:LYS:HG2	1.97	0.65
1:E:70:SER:O	1:E:74:GLN:HG3	1.97	0.65
1:K:72:ARG:NH2	1:K:116:ARG:HD3	2.12	0.65
1:I:127:GLN:HA	1:I:127:GLN:NE2	2.12	0.64
1:F:323:GLY:HA2	1:F:352:GLN:HA	1.79	0.64
1:D:113:GLN:HA	1:D:113:GLN:NE2	2.12	0.64
1:D:339:ARG:O	1:D:343:GLU:HG3	1.98	0.64
1:K:323:GLY:HA2	1:K:352:GLN:HA	1.80	0.64
1:F:70:SER:O	1:F:74:GLN:HG3	1.96	0.64
1:E:180:GLN:H	1:E:180:GLN:NE2	1.96	0.63
1:G:198:GLU:O	1:G:202:GLN:HG2	1.99	0.63
1:A:323:GLY:HA2	1:A:352:GLN:HA	1.80	0.62
1:B:6:ARG:HH11	1:B:6:ARG:HG2	1.65	0.62
1:C:70:SER:OG	1:C:73:GLU:HG3	2.00	0.62
1:D:323:GLY:HA2	1:D:352:GLN:HA	1.81	0.62
1:H:323:GLY:HA2	1:H:352:GLN:HA	1.82	0.62
1:C:385:LEU:CD1	1:C:391:VAL:HG12	2.30	0.61
1:H:198:GLU:O	1:H:202:GLN:HG2	2.01	0.61
1:C:149:ASP:O	1:C:153:ILE:HG13	1.99	0.61
1:G:323:GLY:HA2	1:G:352:GLN:HA	1.81	0.61
1:A:72:ARG:HH11	1:A:72:ARG:HA	1.65	0.61
1:K:170:ARG:NH2	1:K:223:SER:HB3	2.15	0.61
1:F:127:GLN:HA	1:F:127:GLN:NE2	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:GLU:HG3	1:A:85:LYS:HZ1	1.65	0.60
1:J:323:GLY:HA2	1:J:352:GLN:HA	1.81	0.60
1:D:402:ASP:HA	1:D:406:ARG:HB2	1.82	0.60
1:C:412:VAL:HG23	1:C:414:ARG:HB2	1.84	0.60
1:K:125:GLU:O	1:K:128:VAL:HG22	2.01	0.60
1:J:70:SER:O	1:J:74:GLN:HG3	2.02	0.60
1:F:70:SER:OG	1:F:73:GLU:HG3	2.02	0.60
1:H:392:THR:OG1	1:H:395:GLU:HG3	2.02	0.60
1:L:124:SER:O	1:L:128:VAL:HG22	2.02	0.60
1:A:72:ARG:NH1	1:A:72:ARG:HB2	2.17	0.59
1:E:123:THR:OG1	1:E:126:GLU:HG3	2.02	0.59
1:I:123:THR:OG1	1:I:126:GLU:HG3	2.01	0.59
1:B:219:TYR:HB3	1:B:254:PRO:HG2	1.84	0.59
1:J:382:ASP:O	1:J:386:GLN:HG2	2.02	0.59
1:L:113:GLN:HA	1:L:113:GLN:NE2	2.17	0.59
1:H:139:ASP:OD1	1:H:166:HIS:HE1	1.86	0.59
1:J:219:TYR:HB3	1:J:254:PRO:HG2	1.83	0.59
1:C:127:GLN:HA	1:C:127:GLN:NE2	2.16	0.59
1:E:402:ASP:HA	1:E:406:ARG:HB2	1.83	0.59
1:K:127:GLN:HA	1:K:127:GLN:NE2	2.17	0.59
1:G:385:LEU:HD23	1:G:385:LEU:O	2.02	0.59
1:H:48:TYR:HB3	1:H:51:LEU:HD13	1.85	0.59
1:G:402:ASP:HA	1:G:406:ARG:HB2	1.84	0.59
1:A:252:ASN:ND2	1:A:295:LYS:HE2	2.17	0.59
1:F:333:ILE:HG22	1:F:337:MET:CE	2.14	0.59
1:G:219:TYR:HA	1:G:253:ILE:CG2	2.32	0.59
1:C:25:MET:HG3	6:C:432:HOH:O	2.02	0.58
1:G:371:SER:O	1:G:375:GLU:HG3	2.03	0.58
1:A:402:ASP:HA	1:A:406:ARG:HB2	1.84	0.58
6:H:432:HOH:O	1:I:308:GLU:HG2	2.03	0.58
1:G:382:ASP:O	1:G:386:GLN:HG2	2.03	0.58
1:H:385:LEU:HD12	1:H:389:TRP:O	2.03	0.58
1:C:70:SER:O	1:C:74:GLN:HG3	2.04	0.58
1:K:3:ILE:HG23	1:K:8:VAL:HG23	1.86	0.58
1:E:172:ASP:HB2	1:E:173:PRO:HD3	1.86	0.58
1:I:186:ARG:NH1	1:I:192:VAL:O	2.36	0.58
1:C:264:ARG:HG2	6:C:805:HOH:O	2.04	0.58
1:I:323:GLY:HA2	1:I:352:GLN:HA	1.86	0.58
1:D:25:MET:HG3	6:D:440:HOH:O	2.04	0.57
1:L:25:MET:HG3	6:L:453:HOH:O	2.03	0.57
1:L:323:GLY:HA2	1:L:352:GLN:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:112:LEU:HA	1:E:115:TYR:CD2	2.39	0.57
1:E:149:ASP:O	1:E:153:ILE:HG12	2.03	0.57
1:I:25:MET:HG3	6:I:453:HOH:O	2.04	0.57
1:J:166:HIS:HD2	6:J:1185:HOH:O	1.87	0.57
1:H:402:ASP:HA	1:H:406:ARG:HB2	1.85	0.57
1:B:111:ASP:HB3	1:B:114:VAL:HG12	1.87	0.57
1:F:198:GLU:O	1:F:202:GLN:HG2	2.05	0.57
1:A:152:ARG:HG2	1:A:152:ARG:HH11	1.69	0.57
1:B:123:THR:OG1	1:B:126:GLU:HG3	2.05	0.57
1:D:48:TYR:HB3	1:D:51:LEU:HD13	1.87	0.57
1:K:25:MET:HG3	6:K:609:HOH:O	2.04	0.57
1:B:382:ASP:O	1:B:386:GLN:HG2	2.06	0.56
1:H:146:PRO:O	1:H:152:ARG:HD3	2.05	0.56
1:L:123:THR:OG1	1:L:126:GLU:HG3	2.05	0.56
1:B:112:LEU:HA	1:B:115:TYR:CD2	2.41	0.56
1:L:276:VAL:HG22	1:L:277:GLY:N	2.20	0.56
1:B:152:ARG:NH1	1:B:152:ARG:HB3	2.20	0.56
1:E:252:ASN:ND2	1:E:295:LYS:HE2	2.21	0.56
1:B:6:ARG:HG3	1:B:382:ASP:OD1	2.06	0.56
1:H:70:SER:OG	1:H:73:GLU:HG3	2.06	0.56
1:G:56:MET:HE3	6:H:599:HOH:O	2.05	0.56
1:I:127:GLN:HE21	1:I:127:GLN:CA	2.14	0.56
1:K:402:ASP:HA	1:K:406:ARG:HB2	1.87	0.56
1:G:166:HIS:HD2	6:G:1241:HOH:O	1.87	0.56
1:I:125:GLU:O	1:I:128:VAL:HG22	2.06	0.56
1:F:219:TYR:HB3	1:F:254:PRO:HG2	1.88	0.55
1:J:121:LYS:NZ	1:J:121:LYS:HB3	2.21	0.55
1:C:219:TYR:HA	1:C:253:ILE:CG2	2.36	0.55
1:J:122:LYS:NZ	1:J:127:GLN:NE2	2.55	0.55
1:I:219:TYR:HB3	1:I:254:PRO:HG2	1.88	0.55
1:K:245:LEU:HB2	1:K:246:PRO:HD3	1.87	0.55
1:L:106:ASP:OD2	1:L:108:ALA:HB3	2.06	0.55
2:A:428:REL:O5	2:A:428:REL:H2	2.07	0.55
1:E:113:GLN:NE2	1:E:113:GLN:HA	2.22	0.55
1:G:6:ARG:HG2	1:G:6:ARG:HH11	1.72	0.55
1:H:127:GLN:HA	1:H:127:GLN:NE2	2.20	0.55
1:H:263:LYS:CB	1:H:264:ARG:HE	2.20	0.55
1:I:301:LEU:CD1	1:I:326:TRP:HB3	2.36	0.55
1:F:113:GLN:HA	1:F:113:GLN:NE2	2.21	0.55
1:A:25:MET:HG3	6:A:452:HOH:O	2.06	0.55
1:B:230:PHE:HA	1:B:231:PRO:C	2.26	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:402:ASP:HA	1:L:406:ARG:HB2	1.88	0.55
1:B:70:SER:O	1:B:74:GLN:HG3	2.06	0.55
1:E:301:LEU:HD11	1:E:326:TRP:HB3	1.89	0.55
1:G:254:PRO:HG3	1:G:295:LYS:HE3	1.88	0.55
1:F:25:MET:HG3	6:F:434:HOH:O	2.07	0.54
1:H:245:LEU:HB2	1:H:246:PRO:HD3	1.88	0.54
1:L:328:MET:HA	1:L:328:MET:HE2	1.89	0.54
1:G:149:ASP:O	1:G:153:ILE:HG13	2.07	0.54
1:J:149:ASP:O	1:J:153:ILE:HG13	2.08	0.54
1:A:301:LEU:HD11	1:A:326:TRP:HB3	1.89	0.54
6:D:1696:HOH:O	1:F:56:MET:HE3	2.06	0.54
1:K:172:ASP:HB2	1:K:173:PRO:HD3	1.89	0.54
1:J:128:VAL:CG2	6:J:1476:HOH:O	2.54	0.54
1:L:252:ASN:ND2	1:L:295:LYS:HE2	2.23	0.54
1:B:263:LYS:HB3	1:B:264:ARG:HD3	1.88	0.54
1:L:172:ASP:HB2	1:L:173:PRO:HD3	1.90	0.54
1:B:127:GLN:HA	1:B:127:GLN:NE2	2.22	0.54
1:G:343:GLU:HG2	6:G:432:HOH:O	2.08	0.54
1:B:139:ASP:OD1	1:B:166:HIS:HE1	1.91	0.54
1:D:152:ARG:HG2	1:D:152:ARG:HH11	1.73	0.54
1:E:66:PHE:O	1:E:69:MET:HG2	2.07	0.54
1:J:5:SER:OG	1:J:7:GLU:HG2	2.07	0.53
1:B:254:PRO:HG3	1:B:412:VAL:HG12	1.90	0.53
1:F:385:LEU:HD13	1:F:391:VAL:HG13	1.91	0.53
1:I:80:GLU:HG3	1:I:85:LYS:HE2	1.89	0.53
1:E:156:LEU:HD21	1:E:214:ARG:NH1	2.24	0.53
1:C:245:LEU:HB2	1:C:246:PRO:HD3	1.90	0.53
1:G:172:ASP:HB2	1:G:173:PRO:HD3	1.90	0.53
1:J:276:VAL:HG22	1:J:277:GLY:N	2.23	0.53
1:L:202:GLN:HE21	1:L:202:GLN:HA	1.72	0.53
1:C:128:VAL:CG2	6:C:1358:HOH:O	2.55	0.53
1:C:374:ALA:O	1:C:378:ILE:HG13	2.08	0.53
1:I:276:VAL:HG22	1:I:277:GLY:N	2.23	0.53
1:D:40:TRP:O	1:D:41:ASP:CG	2.47	0.53
1:G:127:GLN:HA	1:G:127:GLN:NE2	2.14	0.53
1:I:313:ALA:HA	1:I:319:LEU:HD23	1.91	0.53
1:L:392:THR:OG1	1:L:395:GLU:HG3	2.08	0.53
1:F:219:TYR:HA	1:F:253:ILE:CG2	2.38	0.53
1:K:30:PHE:CE2	1:K:37:ILE:HG12	2.44	0.53
1:K:216:ASP:OD1	1:K:414:ARG:NH2	2.42	0.53
2:K:428:REL:O5	2:K:428:REL:H2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:245:LEU:HB2	1:E:246:PRO:HD3	1.90	0.53
1:J:56:MET:HE2	1:J:63:ILE:HB	1.90	0.53
1:A:111:ASP:OD1	1:A:114:VAL:HG23	2.09	0.53
1:I:154:SER:O	1:I:159:LYS:HB2	2.09	0.53
1:A:172:ASP:HB2	1:A:173:PRO:HD3	1.91	0.52
1:B:49:HIS:HB2	1:B:272:ALA:HB2	1.90	0.52
2:F:428:REL:O5	2:F:428:REL:H2	2.09	0.52
1:G:219:TYR:HA	1:G:253:ILE:HG22	1.90	0.52
1:H:263:LYS:HB3	1:H:264:ARG:HE	1.75	0.52
1:D:70:SER:OG	1:D:73:GLU:HG3	2.09	0.52
1:D:78:ILE:HG23	1:D:82:LEU:HD12	1.91	0.52
1:F:385:LEU:HD12	1:F:389:TRP:O	2.09	0.52
1:I:172:ASP:HB2	1:I:173:PRO:HD3	1.91	0.52
1:B:172:ASP:HB2	1:B:173:PRO:HD3	1.91	0.52
1:D:301:LEU:HD11	1:D:326:TRP:HB3	1.92	0.52
1:E:118:TYR:HA	1:E:121:LYS:HE3	1.92	0.52
1:E:267:PRO:HG2	6:E:1783:HOH:O	2.08	0.52
1:J:198:GLU:O	1:J:202:GLN:HG2	2.10	0.52
1:K:301:LEU:CD1	1:K:326:TRP:HB3	2.39	0.52
1:A:40:TRP:O	1:A:41:ASP:CG	2.48	0.52
1:B:265:VAL:HG21	1:B:275:PHE:HB2	1.92	0.52
1:G:124:SER:O	1:G:128:VAL:HG13	2.10	0.52
1:A:391:VAL:HG23	1:A:391:VAL:O	2.10	0.52
1:E:265:VAL:HG21	1:E:275:PHE:HB2	1.92	0.52
1:H:352:GLN:HG3	1:H:353:HIS:N	2.24	0.52
1:L:202:GLN:HA	1:L:202:GLN:NE2	2.24	0.52
1:C:172:ASP:HB2	1:C:173:PRO:HD3	1.91	0.52
1:E:197:ASN:HB2	6:E:1840:HOH:O	2.09	0.52
1:E:392:THR:OG1	1:E:395:GLU:HG3	2.09	0.52
1:H:172:ASP:HB2	1:H:173:PRO:HD3	1.92	0.52
1:C:123:THR:OG1	1:C:126:GLU:HG3	2.10	0.52
1:E:219:TYR:HA	1:E:253:ILE:CG2	2.40	0.52
1:G:180:GLN:H	1:G:180:GLN:NE2	2.08	0.52
1:K:316:PHE:HB3	1:K:318:ASN:OD1	2.09	0.52
1:A:72:ARG:HH11	1:A:72:ARG:CA	2.23	0.52
1:B:70:SER:OG	1:B:73:GLU:HG3	2.10	0.52
1:F:276:VAL:HG22	1:F:277:GLY:N	2.25	0.52
1:G:352:GLN:HG3	1:G:353:HIS:N	2.24	0.52
1:D:139:ASP:OD1	1:D:166:HIS:HE1	1.93	0.51
2:D:428:REL:H2	2:D:428:REL:O5	2.10	0.51
1:E:382:ASP:O	1:E:386:GLN:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:172:ASP:HB2	1:J:173:PRO:HD3	1.92	0.51
1:A:72:ARG:HH11	1:A:72:ARG:CB	2.23	0.51
1:C:209:THR:O	1:C:213:GLU:HG3	2.10	0.51
1:E:49:HIS:HB2	1:E:272:ALA:HB2	1.91	0.51
1:C:152:ARG:HH22	1:C:184:ARG:NH2	2.06	0.51
1:H:125:GLU:O	1:H:128:VAL:HG22	2.10	0.51
1:J:127:GLN:HA	1:J:127:GLN:NE2	2.14	0.51
1:F:196:TRP:CD1	1:F:238:ARG:HD2	2.44	0.51
1:H:181:THR:HG22	1:H:185:LEU:CD2	2.40	0.51
1:F:219:TYR:HA	1:F:253:ILE:HG22	1.91	0.51
1:G:336:GLU:O	1:G:340:MET:HG3	2.11	0.51
1:D:252:ASN:ND2	1:D:295:LYS:HE2	2.26	0.51
1:E:212:ILE:HD13	1:E:253:ILE:HD12	1.91	0.51
1:C:276:VAL:HG22	1:C:277:GLY:N	2.25	0.51
1:G:276:VAL:HG22	1:G:277:GLY:N	2.25	0.51
1:H:25:MET:HG3	6:H:479:HOH:O	2.10	0.51
1:H:301:LEU:HD11	1:H:326:TRP:HB3	1.91	0.51
1:J:112:LEU:HA	1:J:115:TYR:CD2	2.46	0.51
1:E:6:ARG:HG2	1:E:6:ARG:HH11	1.76	0.51
1:A:388:GLY:HA2	1:K:4:ASN:OD1	2.11	0.51
1:I:218:VAL:HG23	1:I:219:TYR:CD2	2.46	0.51
1:J:128:VAL:HA	1:J:359:LEU:HD21	1.93	0.51
1:B:111:ASP:HB3	1:B:114:VAL:CG1	2.41	0.50
1:B:180:GLN:H	1:B:180:GLN:HE21	1.57	0.50
1:K:392:THR:OG1	1:K:395:GLU:HG3	2.11	0.50
1:I:130:THR:O	1:I:134:LEU:HG	2.12	0.50
1:I:149:ASP:O	1:I:153:ILE:HG13	2.11	0.50
1:G:245:LEU:HB2	1:G:246:PRO:HD3	1.93	0.50
1:H:235:ASN:O	1:H:239:ILE:HG13	2.11	0.50
1:I:106:ASP:OD2	1:I:108:ALA:HB3	2.11	0.50
1:D:286:HIS:CE1	1:D:290:GLU:HG3	2.46	0.50
1:E:127:GLN:HA	1:E:127:GLN:NE2	2.24	0.50
1:I:301:LEU:HD11	1:I:326:TRP:HB3	1.93	0.50
1:D:51:LEU:HD12	1:D:51:LEU:N	2.27	0.50
1:K:112:LEU:HA	1:K:115:TYR:CD2	2.45	0.50
1:A:113:GLN:NE2	1:A:116:ARG:HH11	2.09	0.50
1:B:252:ASN:ND2	1:B:295:LYS:HE2	2.26	0.50
1:B:301:LEU:HD11	1:B:326:TRP:HB3	1.93	0.50
1:H:276:VAL:HG22	1:H:277:GLY:N	2.26	0.50
1:F:409:TRP:HE3	1:F:414:ARG:HB2	1.77	0.50
1:H:385:LEU:HD13	1:H:391:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:70:SER:OG	1:I:73:GLU:HG3	2.12	0.50
1:A:69:MET:CE	1:A:73:GLU:HB3	2.42	0.49
1:D:146:PRO:O	1:D:152:ARG:HB2	2.12	0.49
1:E:276:VAL:HG22	1:E:277:GLY:N	2.27	0.49
1:H:286:HIS:CE1	1:H:290:GLU:HG3	2.47	0.49
1:A:179:GLU:HB2	1:A:180:GLN:OE1	2.11	0.49
1:E:286:HIS:CE1	1:E:290:GLU:HG3	2.47	0.49
1:G:235:ASN:O	1:G:239:ILE:HG13	2.11	0.49
1:H:244:LEU:HD13	1:H:244:LEU:C	2.33	0.49
1:J:245:LEU:HB2	1:J:246:PRO:HD3	1.93	0.49
1:J:352:GLN:HG3	1:J:353:HIS:N	2.26	0.49
1:J:402:ASP:HA	1:J:406:ARG:HB2	1.94	0.49
1:K:389:TRP:HD1	1:K:391:VAL:HG12	1.78	0.49
1:F:51:LEU:N	1:F:51:LEU:HD12	2.27	0.49
1:H:70:SER:O	1:H:74:GLN:HG3	2.12	0.49
1:J:409:TRP:HE3	1:J:414:ARG:HB2	1.77	0.49
1:K:352:GLN:HG3	1:K:353:HIS:N	2.26	0.49
1:A:79:TRP:O	1:A:83:PHE:HB2	2.12	0.49
1:E:180:GLN:NE2	1:E:180:GLN:N	2.60	0.49
1:L:70:SER:OG	1:L:73:GLU:HG3	2.11	0.49
1:A:122:LYS:NZ	1:A:127:GLN:NE2	2.60	0.49
1:A:170:ARG:NH2	1:A:223:SER:HB3	2.28	0.49
1:C:14:LYS:NZ	1:C:375:GLU:OE2	2.45	0.49
1:F:172:ASP:HB2	1:F:173:PRO:HD3	1.93	0.49
1:J:230:PHE:HA	1:J:231:PRO:C	2.33	0.49
1:G:230:PHE:HA	1:G:231:PRO:C	2.31	0.49
1:H:408:PHE:O	1:H:412:VAL:HG22	2.12	0.49
1:I:49:HIS:HB2	1:I:272:ALA:HB2	1.94	0.49
1:K:128:VAL:O	1:K:132:LEU:HG	2.13	0.49
1:C:79:TRP:O	1:C:83:PHE:HB2	2.12	0.49
1:D:392:THR:OG1	1:D:395:GLU:HG3	2.11	0.49
1:E:235:ASN:O	1:E:239:ILE:HG13	2.12	0.49
1:H:181:THR:O	1:H:185:LEU:HD23	2.12	0.49
1:B:113:GLN:HA	1:B:113:GLN:NE2	2.28	0.49
1:F:245:LEU:HB2	1:F:246:PRO:HD3	1.95	0.49
1:K:113:GLN:HE22	1:K:116:ARG:HH11	1.59	0.49
1:A:219:TYR:HB3	1:A:254:PRO:HG2	1.95	0.49
1:G:40:TRP:O	1:G:41:ASP:CG	2.51	0.49
1:L:301:LEU:CD1	1:L:326:TRP:HB3	2.42	0.49
1:A:245:LEU:HB2	1:A:246:PRO:HD3	1.95	0.48
1:E:128:VAL:O	1:E:132:LEU:HG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:244:LEU:C	1:E:244:LEU:HD13	2.34	0.48
1:H:72:ARG:HH12	1:H:116:ARG:HD3	1.78	0.48
1:L:391:VAL:O	1:L:391:VAL:HG23	2.12	0.48
1:B:158:GLY:O	1:B:160:GLN:HG2	2.13	0.48
1:B:40:TRP:O	1:B:41:ASP:CG	2.51	0.48
1:C:198:GLU:O	1:C:202:GLN:HG2	2.13	0.48
1:E:352:GLN:HG3	1:E:353:HIS:N	2.28	0.48
1:G:5:SER:OG	1:G:7:GLU:HG2	2.13	0.48
1:B:385:LEU:HA	1:B:389:TRP:O	2.13	0.48
1:F:231:PRO:HD3	1:F:286:HIS:CD2	2.48	0.48
1:H:295:LYS:HE3	1:H:411:PHE:O	2.13	0.48
1:E:51:LEU:N	1:E:51:LEU:HD12	2.28	0.48
1:H:40:TRP:O	1:H:41:ASP:CB	2.57	0.48
1:K:254:PRO:HG3	1:K:295:LYS:HE3	1.93	0.48
1:L:139:ASP:OD1	1:L:166:HIS:HE1	1.95	0.48
1:C:252:ASN:HD21	1:C:295:LYS:HE3	1.77	0.48
1:I:402:ASP:HA	1:I:406:ARG:HB2	1.95	0.48
1:J:122:LYS:NZ	1:J:127:GLN:HE22	2.11	0.48
1:K:69:MET:HB3	1:K:73:GLU:HB2	1.96	0.48
1:K:152:ARG:HD2	1:K:156:LEU:HD11	1.94	0.48
1:K:276:VAL:HG22	1:K:277:GLY:N	2.28	0.48
1:B:154:SER:O	1:B:159:LYS:HB2	2.14	0.48
1:C:154:SER:O	1:C:159:LYS:HB2	2.13	0.48
1:D:172:ASP:HB2	1:D:173:PRO:HD3	1.96	0.48
1:D:352:GLN:HG3	1:D:353:HIS:N	2.28	0.48
1:C:8:VAL:O	1:C:12:LYS:HG2	2.13	0.48
1:D:388:GLY:HA2	1:H:4:ASN:OD1	2.13	0.48
1:I:230:PHE:HA	1:I:231:PRO:C	2.34	0.48
1:J:49:HIS:HB2	1:J:272:ALA:HB2	1.94	0.48
1:J:301:LEU:CD1	1:J:326:TRP:HB3	2.44	0.48
1:L:113:GLN:HG2	6:L:1347:HOH:O	2.13	0.48
1:E:316:PHE:HB3	1:E:318:ASN:OD1	2.14	0.48
1:F:40:TRP:O	1:F:41:ASP:CG	2.52	0.48
1:J:30:PHE:CE2	1:J:37:ILE:HG13	2.49	0.48
1:A:313:ALA:HA	1:A:319:LEU:HD23	1.96	0.47
1:A:112:LEU:HA	1:A:115:TYR:CD2	2.49	0.47
1:D:69:MET:HB3	1:D:73:GLU:HB2	1.95	0.47
1:D:276:VAL:HG22	1:D:277:GLY:N	2.29	0.47
1:G:385:LEU:HA	1:G:389:TRP:O	2.14	0.47
1:K:209:THR:O	1:K:213:GLU:HG3	2.13	0.47
1:G:128:VAL:CG2	6:G:665:HOH:O	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:32:PRO:HG2	1:H:128:VAL:HG21	1.96	0.47
1:K:139:ASP:OD1	1:K:166:HIS:HE1	1.96	0.47
1:L:125:GLU:O	1:L:128:VAL:HG23	2.14	0.47
1:E:275:PHE:CG	1:E:276:VAL:N	2.82	0.47
1:I:219:TYR:HA	1:I:253:ILE:CG2	2.44	0.47
1:J:182:LYS:O	1:J:186:ARG:HG2	2.14	0.47
1:J:265:VAL:HG21	1:J:275:PHE:HB2	1.95	0.47
1:A:123:THR:OG1	1:A:126:GLU:HG3	2.13	0.47
6:A:445:HOH:O	1:B:308:GLU:HG2	2.14	0.47
1:B:203:GLU:OE1	1:B:206:ARG:NH1	2.47	0.47
1:G:139:ASP:OD1	1:G:166:HIS:HE1	1.97	0.47
1:I:174:LEU:HD13	1:I:175:LEU:HD12	1.96	0.47
1:B:316:PHE:HB3	1:B:318:ASN:OD1	2.14	0.47
1:K:286:HIS:CE1	1:K:290:GLU:HG3	2.49	0.47
1:F:385:LEU:HD11	1:F:391:VAL:HG22	1.95	0.47
1:G:65:ALA:O	1:G:69:MET:HG3	2.14	0.47
1:H:322:PHE:HA	1:H:350:ILE:O	2.14	0.47
1:A:286:HIS:CE1	1:A:290:GLU:HG3	2.49	0.47
1:C:122:LYS:HG3	1:C:126:GLU:HB2	1.97	0.47
1:F:301:LEU:CD1	1:F:326:TRP:HB3	2.45	0.47
2:L:428:REL:H2	2:L:428:REL:O5	2.14	0.47
6:A:1421:HOH:O	1:C:56:MET:HE3	2.14	0.47
1:C:385:LEU:HD12	1:C:389:TRP:O	2.15	0.47
1:F:244:LEU:HD13	1:F:244:LEU:C	2.35	0.47
1:F:314:ARG:HD2	1:F:344:MET:HB3	1.96	0.47
1:A:9:LEU:HD21	1:A:381:TYR:HB2	1.96	0.47
1:A:72:ARG:HH11	1:A:72:ARG:HB2	1.80	0.47
1:B:274:ASP:O	1:C:315:LYS:HD2	2.15	0.47
1:G:25:MET:HG3	6:G:445:HOH:O	2.13	0.47
1:G:198:GLU:HA	1:G:198:GLU:OE1	2.15	0.47
1:J:308:GLU:HG2	6:J:450:HOH:O	2.14	0.47
1:A:127:GLN:HE21	1:A:127:GLN:CA	2.11	0.46
1:I:41:ASP:OD2	1:I:41:ASP:C	2.54	0.46
1:B:216:ASP:N	1:B:217:PRO:CD	2.78	0.46
1:F:149:ASP:O	1:F:153:ILE:HG13	2.15	0.46
1:J:322:PHE:HA	1:J:350:ILE:O	2.15	0.46
1:K:195:GLU:HG3	1:K:197:ASN:HD22	1.81	0.46
1:A:66:PHE:CZ	1:A:74:GLN:HB3	2.50	0.46
1:A:352:GLN:HG3	1:A:353:HIS:N	2.30	0.46
1:C:30:PHE:CE2	1:C:37:ILE:HG13	2.50	0.46
1:L:9:LEU:HD21	1:L:381:TYR:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:HIS:CE1	1:B:290:GLU:HG3	2.50	0.46
1:D:394:GLU:HB2	6:D:1235:HOH:O	2.14	0.46
1:G:385:LEU:HD23	1:G:385:LEU:C	2.36	0.46
1:H:122:LYS:HD3	6:H:1304:HOH:O	2.16	0.46
1:L:219:TYR:HA	1:L:253:ILE:CG2	2.45	0.46
1:B:218:VAL:HG23	1:B:219:TYR:CD2	2.51	0.46
1:L:265:VAL:HG11	1:L:275:PHE:HB3	1.97	0.46
1:B:306:GLN:O	1:B:310:VAL:HG23	2.15	0.46
1:E:139:ASP:OD1	1:E:166:HIS:HE1	1.98	0.46
1:F:230:PHE:HA	1:F:231:PRO:C	2.35	0.46
1:G:70:SER:O	1:G:74:GLN:HG3	2.15	0.46
1:J:203:GLU:OE2	1:J:206:ARG:NH1	2.49	0.46
1:A:322:PHE:HA	1:A:350:ILE:O	2.16	0.46
1:B:125:GLU:O	1:B:128:VAL:HG13	2.15	0.46
1:B:276:VAL:HG22	1:B:277:GLY:N	2.31	0.46
1:F:191:LYS:HB3	1:F:191:LYS:NZ	2.31	0.46
1:L:154:SER:O	1:L:159:LYS:HB2	2.15	0.46
1:A:51:LEU:N	1:A:51:LEU:HD12	2.31	0.46
1:B:51:LEU:HD12	1:B:51:LEU:N	2.31	0.46
1:D:127:GLN:HE21	1:D:127:GLN:CA	2.15	0.46
1:G:180:GLN:NE2	1:G:180:GLN:N	2.63	0.46
1:J:113:GLN:HA	1:J:113:GLN:NE2	2.30	0.46
1:B:322:PHE:HA	1:B:350:ILE:O	2.16	0.46
1:B:352:GLN:HG3	1:B:353:HIS:N	2.30	0.46
1:H:264:ARG:HG2	1:H:264:ARG:HH11	1.80	0.46
1:J:198:GLU:HA	1:J:198:GLU:OE1	2.16	0.46
1:K:393:GLU:O	1:K:397:LYS:HG2	2.15	0.46
1:L:69:MET:HB3	1:L:73:GLU:HB2	1.98	0.46
1:L:198:GLU:O	1:L:202:GLN:HG2	2.16	0.46
1:A:230:PHE:HA	1:A:231:PRO:C	2.35	0.46
1:B:235:ASN:O	1:B:239:ILE:HG13	2.16	0.46
1:C:122:LYS:CG	1:C:126:GLU:HB2	2.46	0.46
1:H:216:ASP:N	1:H:217:PRO:CD	2.79	0.46
1:H:254:PRO:HG3	1:H:295:LYS:HE2	1.97	0.46
1:J:122:LYS:HZ1	1:J:127:GLN:NE2	2.13	0.46
1:J:254:PRO:HG3	1:J:412:VAL:HG12	1.97	0.46
1:C:40:TRP:O	1:C:41:ASP:CG	2.54	0.45
1:C:127:GLN:HG3	1:C:359:LEU:HD23	1.97	0.45
1:E:306:GLN:O	1:E:310:VAL:HG23	2.16	0.45
1:G:122:LYS:HZ1	1:G:127:GLN:HA	1.80	0.45
1:G:286:HIS:CE1	1:G:290:GLU:HG3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:107:PRO:HA	1:J:115:TYR:OH	2.15	0.45
1:E:230:PHE:HA	1:E:231:PRO:C	2.35	0.45
1:E:385:LEU:HA	1:E:389:TRP:O	2.16	0.45
1:F:328:MET:HB3	1:F:337:MET:HE1	1.98	0.45
1:I:152:ARG:O	1:I:156:LEU:HG	2.17	0.45
1:L:142:MET:O	1:L:168:ALA:HB3	2.16	0.45
1:L:322:PHE:HA	1:L:350:ILE:O	2.16	0.45
1:A:392:THR:OG1	1:A:395:GLU:HG3	2.16	0.45
1:G:409:TRP:HA	1:G:412:VAL:HG22	1.97	0.45
1:G:169:LEU:HG	1:G:171:LEU:HD21	1.98	0.45
1:H:128:VAL:O	1:H:132:LEU:HG	2.15	0.45
1:H:139:ASP:OD1	1:H:166:HIS:CE1	2.69	0.45
1:K:182:LYS:HA	1:K:185:LEU:HD12	1.98	0.45
1:A:219:TYR:HA	1:A:253:ILE:CG2	2.47	0.45
1:A:265:VAL:HG21	1:A:275:PHE:HB2	1.99	0.45
6:D:435:HOH:O	1:E:308:GLU:HG2	2.17	0.45
1:E:79:TRP:O	1:E:83:PHE:HB2	2.17	0.45
1:E:152:ARG:HH11	1:E:152:ARG:HG2	1.81	0.45
1:E:286:HIS:NE2	1:E:290:GLU:HG3	2.32	0.45
1:H:275:PHE:CG	1:H:276:VAL:N	2.82	0.45
1:I:264:ARG:HG2	6:I:1147:HOH:O	2.17	0.45
1:I:391:VAL:HG23	1:I:391:VAL:O	2.16	0.45
1:K:52:VAL:O	1:K:55:VAL:HG12	2.16	0.45
1:L:301:LEU:HD11	1:L:326:TRP:HB3	1.99	0.45
1:D:382:ASP:O	1:D:386:GLN:HG2	2.17	0.45
1:D:391:VAL:O	1:D:391:VAL:HG23	2.17	0.45
1:G:128:VAL:HA	1:G:359:LEU:HD21	1.97	0.45
1:J:113:GLN:O	1:J:117:GLU:HG3	2.16	0.45
1:A:30:PHE:CE2	1:A:37:ILE:HG12	2.52	0.45
1:A:106:ASP:OD2	1:A:108:ALA:HB3	2.16	0.45
1:F:125:GLU:O	1:F:128:VAL:HG13	2.17	0.45
1:L:149:ASP:O	1:L:153:ILE:HG13	2.16	0.45
1:L:230:PHE:HA	1:L:231:PRO:C	2.37	0.45
1:C:244:LEU:HD13	1:C:244:LEU:C	2.37	0.45
1:D:113:GLN:NE2	1:D:113:GLN:CA	2.78	0.45
1:E:122:LYS:NZ	1:E:127:GLN:NE2	2.64	0.45
1:I:70:SER:O	1:I:74:GLN:HG3	2.17	0.45
1:B:29:LEU:O	1:B:142:MET:HG2	2.17	0.45
1:C:124:SER:O	1:C:128:VAL:HG13	2.17	0.45
1:L:30:PHE:CE2	1:L:37:ILE:HG12	2.52	0.45
1:F:72:ARG:HH11	1:F:72:ARG:CB	2.09	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:352:GLN:HG3	1:F:353:HIS:N	2.32	0.45
1:I:122:LYS:NZ	1:I:127:GLN:NE2	2.64	0.45
1:L:40:TRP:CE3	1:L:127:GLN:HG2	2.52	0.45
1:A:113:GLN:HE22	1:A:116:ARG:HH11	1.64	0.44
1:D:9:LEU:HD21	1:D:381:TYR:HB2	1.98	0.44
1:D:245:LEU:HB2	1:D:246:PRO:HD3	1.98	0.44
1:D:409:TRP:HA	1:D:412:VAL:HG22	1.98	0.44
1:E:6:ARG:HG3	1:E:382:ASP:OD1	2.17	0.44
1:F:145:ASP:HA	1:F:146:PRO:HD2	1.91	0.44
1:F:301:LEU:HD11	1:F:326:TRP:HB3	1.99	0.44
1:J:276:VAL:CG2	1:J:277:GLY:N	2.80	0.44
1:D:106:ASP:OD2	1:D:108:ALA:HB3	2.17	0.44
1:E:40:TRP:O	1:E:41:ASP:CG	2.55	0.44
1:G:308:GLU:HG2	6:G:443:HOH:O	2.16	0.44
1:H:220:MET:CE	1:H:253:ILE:HD11	2.48	0.44
1:H:301:LEU:CD1	1:H:326:TRP:HB3	2.46	0.44
1:J:25:MET:HG3	6:J:439:HOH:O	2.17	0.44
1:K:40:TRP:O	1:K:41:ASP:CG	2.55	0.44
1:K:170:ARG:HH21	1:K:223:SER:HB3	1.82	0.44
1:D:170:ARG:NH2	1:D:223:SER:HB3	2.33	0.44
1:E:128:VAL:CG2	6:E:1666:HOH:O	2.65	0.44
1:E:313:ALA:HA	1:E:319:LEU:HD23	1.99	0.44
1:G:313:ALA:HA	1:G:319:LEU:HD23	1.98	0.44
1:I:414:ARG:HG3	1:I:414:ARG:HH11	1.82	0.44
1:K:2:SER:HA	6:K:1242:HOH:O	2.17	0.44
1:L:67:TRP:HA	1:L:67:TRP:CE3	2.52	0.44
1:A:276:VAL:HG22	1:A:277:GLY:N	2.32	0.44
1:B:113:GLN:HA	1:B:113:GLN:HE21	1.83	0.44
1:G:185:LEU:HB3	1:G:190:TYR:HB2	1.99	0.44
1:H:197:ASN:ND2	1:H:199:GLY:H	2.15	0.44
1:I:112:LEU:HA	1:I:115:TYR:CD2	2.53	0.44
1:J:203:GLU:CD	1:J:206:ARG:NH1	2.70	0.44
1:A:42:ILE:HD13	1:A:100:LEU:HD21	1.99	0.44
1:D:219:TYR:HA	1:D:253:ILE:CG2	2.47	0.44
1:D:231:PRO:HD3	1:D:286:HIS:CG	2.52	0.44
1:G:358:VAL:HB	1:G:361:GLN:HG3	1.99	0.44
1:L:40:TRP:O	1:L:41:ASP:CG	2.55	0.44
1:C:275:PHE:CG	1:C:276:VAL:N	2.86	0.44
1:D:112:LEU:HA	1:D:115:TYR:CD2	2.53	0.44
1:F:112:LEU:HA	1:F:115:TYR:CD2	2.52	0.44
1:I:67:TRP:HA	1:I:67:TRP:CE3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:250:LYS:HD3	1:K:251:HIS:CE1	2.53	0.44
1:L:182:LYS:HB2	1:L:182:LYS:NZ	2.33	0.44
1:C:69:MET:HB3	1:C:73:GLU:HB2	1.98	0.44
1:C:313:ALA:HA	1:C:319:LEU:HD23	1.99	0.44
1:D:326:TRP:HB3	1:D:327:PHE:H	1.52	0.44
1:J:208:LEU:O	1:J:212:ILE:HG13	2.18	0.44
1:J:225:PRO:HA	1:J:261:VAL:O	2.17	0.44
1:L:276:VAL:CG2	1:L:277:GLY:N	2.80	0.44
1:F:139:ASP:OD1	1:F:166:HIS:HE1	2.01	0.44
1:H:113:GLN:NE2	1:H:113:GLN:HA	2.33	0.44
1:F:322:PHE:HA	1:F:350:ILE:O	2.17	0.44
1:A:286:HIS:NE2	1:A:290:GLU:HG3	2.33	0.43
1:F:374:ALA:O	1:F:378:ILE:HG13	2.17	0.43
1:G:275:PHE:CG	1:G:276:VAL:N	2.86	0.43
1:G:322:PHE:HA	1:G:350:ILE:O	2.18	0.43
1:H:123:THR:OG1	1:H:126:GLU:HG3	2.18	0.43
1:H:385:LEU:HD12	1:H:385:LEU:HA	1.92	0.43
1:J:275:PHE:CG	1:J:276:VAL:N	2.86	0.43
1:L:313:ALA:HA	1:L:319:LEU:HD23	2.00	0.43
1:L:352:GLN:HG3	1:L:353:HIS:N	2.33	0.43
1:E:30:PHE:CE2	1:E:37:ILE:HG13	2.53	0.43
1:F:4:ASN:HB2	6:I:1261:HOH:O	2.18	0.43
1:F:235:ASN:O	1:F:239:ILE:HG13	2.19	0.43
1:H:40:TRP:CE3	1:H:127:GLN:HG2	2.53	0.43
1:I:275:PHE:CG	1:I:276:VAL:N	2.86	0.43
1:L:52:VAL:O	1:L:55:VAL:HG12	2.18	0.43
1:A:70:SER:O	1:A:74:GLN:HG3	2.18	0.43
1:C:182:LYS:HB2	1:C:182:LYS:NZ	2.33	0.43
1:D:80:GLU:O	1:D:85:LYS:HG3	2.18	0.43
1:I:139:ASP:OD1	1:I:166:HIS:HE1	2.01	0.43
1:I:276:VAL:CG2	1:I:277:GLY:N	2.81	0.43
1:J:235:ASN:O	1:J:239:ILE:HG13	2.18	0.43
1:C:196:TRP:CZ2	1:C:201:ILE:HG12	2.54	0.43
1:D:178:TYR:CD1	1:D:239:ILE:HD11	2.54	0.43
1:E:191:LYS:HB2	1:E:191:LYS:NZ	2.33	0.43
1:F:326:TRP:HB3	1:F:327:PHE:H	1.58	0.43
1:H:265:VAL:HG21	1:H:275:PHE:HB2	1.99	0.43
1:J:336:GLU:O	1:J:340:MET:HG3	2.19	0.43
1:K:186:ARG:NH2	1:K:192:VAL:O	2.44	0.43
1:A:139:ASP:OD1	1:A:166:HIS:HE1	2.00	0.43
1:B:231:PRO:HD3	1:B:286:HIS:CG	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:ASP:OD1	1:C:166:HIS:HE1	2.00	0.43
1:E:154:SER:O	1:E:159:LYS:HB2	2.18	0.43
1:F:152:ARG:HH22	1:F:184:ARG:HH22	1.67	0.43
1:G:112:LEU:HA	1:G:115:TYR:CD2	2.53	0.43
1:J:69:MET:HB2	1:J:73:GLU:HB2	2.00	0.43
1:J:122:LYS:HZ3	1:J:127:GLN:HE22	1.66	0.43
1:L:128:VAL:CG2	6:L:986:HOH:O	2.67	0.43
1:A:149:ASP:OD1	1:A:152:ARG:NH2	2.51	0.43
1:A:409:TRP:HA	1:A:412:VAL:HG22	1.99	0.43
1:I:128:VAL:HG23	1:I:129:ASP:N	2.33	0.43
2:H:428:REL:H2	2:H:428:REL:O5	2.18	0.43
1:I:40:TRP:O	1:I:41:ASP:CB	2.67	0.43
1:J:128:VAL:HG12	1:J:359:LEU:HD22	2.00	0.43
1:J:321:ILE:HG12	6:L:1830:HOH:O	2.17	0.43
1:L:264:ARG:HG2	6:L:610:HOH:O	2.18	0.43
1:D:150:ASN:O	1:D:153:ILE:HG22	2.19	0.43
1:E:224:LEU:HD13	1:E:228:PHE:CD1	2.53	0.43
1:F:275:PHE:CG	1:F:276:VAL:N	2.87	0.43
1:A:244:LEU:HD13	1:A:244:LEU:C	2.38	0.43
1:B:244:LEU:C	1:B:244:LEU:HD13	2.39	0.43
1:A:295:LYS:HB3	1:A:411:PHE:CZ	2.54	0.43
1:G:201:ILE:O	1:G:205:LYS:HG3	2.18	0.43
1:H:128:VAL:CG2	6:H:1281:HOH:O	2.67	0.43
1:J:389:TRP:HB2	1:L:97:LEU:HD13	2.01	0.43
1:L:112:LEU:HA	1:L:115:TYR:CD2	2.53	0.43
1:E:180:GLN:H	1:E:180:GLN:HE21	1.62	0.42
1:F:216:ASP:N	1:F:217:PRO:CD	2.82	0.42
1:G:409:TRP:HE3	1:G:414:ARG:HB2	1.83	0.42
1:C:256:ALA:HA	1:C:297:LEU:O	2.19	0.42
1:D:105:LEU:O	1:D:107:PRO:HD3	2.18	0.42
1:E:42:ILE:HD13	1:E:100:LEU:HD21	1.99	0.42
1:E:301:LEU:CD1	1:E:326:TRP:HB3	2.49	0.42
1:H:79:TRP:O	1:H:83:PHE:HB2	2.19	0.42
1:H:230:PHE:HA	1:H:231:PRO:C	2.40	0.42
1:D:286:HIS:NE2	1:D:290:GLU:HG3	2.33	0.42
1:L:245:LEU:HB2	1:L:246:PRO:HD3	2.01	0.42
1:C:128:VAL:HA	1:C:359:LEU:HD21	2.01	0.42
1:C:385:LEU:HD12	1:C:385:LEU:HA	1.86	0.42
1:D:123:THR:OG1	1:D:126:GLU:HG3	2.19	0.42
1:D:149:ASP:OD1	1:D:152:ARG:NH2	2.52	0.42
1:D:154:SER:HB3	1:D:159:LYS:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:316:PHE:HB3	1:I:318:ASN:OD1	2.18	0.42
1:K:244:LEU:HD13	1:K:244:LEU:C	2.40	0.42
1:B:6:ARG:HG2	1:B:6:ARG:NH1	2.32	0.42
1:H:170:ARG:NH2	1:H:223:SER:HB3	2.34	0.42
1:J:128:VAL:HG12	1:J:359:LEU:CD2	2.49	0.42
1:C:180:GLN:NE2	1:C:180:GLN:N	2.68	0.42
1:C:216:ASP:N	1:C:217:PRO:CD	2.83	0.42
1:E:69:MET:HG3	1:E:74:GLN:HG2	2.02	0.42
1:E:326:TRP:HB3	1:E:327:PHE:H	1.61	0.42
1:H:414:ARG:HG3	1:H:414:ARG:HH11	1.85	0.42
1:I:40:TRP:O	1:I:41:ASP:CG	2.58	0.42
1:J:387:ALA:O	1:L:107:PRO:HG2	2.20	0.42
1:E:56:MET:HE1	1:E:63:ILE:N	2.34	0.42
1:H:66:PHE:O	1:H:69:MET:HG2	2.19	0.42
1:H:69:MET:HB2	1:H:73:GLU:HB2	2.01	0.42
1:K:232:GLU:O	1:K:237:GLY:HA3	2.20	0.42
1:A:167:ALA:O	1:A:217:PRO:HA	2.19	0.42
1:A:252:ASN:HD21	1:A:295:LYS:HE2	1.83	0.42
1:B:152:ARG:HD2	1:B:156:LEU:HD11	2.01	0.42
1:C:358:VAL:HB	1:C:361:GLN:HG3	2.02	0.42
1:D:322:PHE:HA	1:D:350:ILE:O	2.20	0.42
1:E:361:GLN:O	1:E:365:LYS:HG2	2.20	0.42
1:G:180:GLN:H	1:G:180:GLN:HE21	1.66	0.42
1:K:216:ASP:N	1:K:217:PRO:CD	2.83	0.42
1:L:79:TRP:O	1:L:83:PHE:HB2	2.20	0.42
1:C:219:TYR:HA	1:C:253:ILE:HG22	2.01	0.42
1:H:181:THR:HG22	1:H:185:LEU:HD21	2.02	0.42
1:K:97:LEU:HD13	1:L:389:TRP:HB2	2.01	0.42
1:D:139:ASP:OD1	1:D:166:HIS:CE1	2.73	0.42
1:H:297:LEU:HD23	1:H:320:MET:HB3	2.02	0.42
1:J:8:VAL:O	1:J:12:LYS:HG2	2.19	0.42
1:A:301:LEU:CD1	1:A:326:TRP:HB3	2.49	0.41
1:D:42:ILE:HD13	1:D:100:LEU:HD21	2.01	0.41
1:E:9:LEU:O	1:E:13:VAL:HG23	2.20	0.41
1:F:389:TRP:HD1	1:F:391:VAL:HG12	1.84	0.41
1:G:152:ARG:HG2	1:G:156:LEU:HG	2.01	0.41
1:K:32:PRO:HG2	1:K:128:VAL:HG21	2.00	0.41
1:B:275:PHE:CG	1:B:276:VAL:N	2.84	0.41
2:C:428:REL:H2	2:C:428:REL:O5	2.20	0.41
1:D:230:PHE:HA	1:D:231:PRO:C	2.39	0.41
1:E:216:ASP:N	1:E:217:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:408:PHE:O	1:J:412:VAL:HG22	2.20	0.41
1:K:219:TYR:HA	1:K:253:ILE:CG2	2.50	0.41
1:A:409:TRP:HE3	1:A:414:ARG:HB2	1.84	0.41
1:B:98:THR:HB	1:B:364:TYR:HB2	2.02	0.41
1:E:196:TRP:CD1	1:E:238:ARG:HD2	2.54	0.41
1:E:244:LEU:C	1:E:244:LEU:CD1	2.88	0.41
1:G:196:TRP:CD1	1:G:238:ARG:HD2	2.55	0.41
1:J:40:TRP:O	1:J:41:ASP:CG	2.58	0.41
1:J:301:LEU:HD11	1:J:326:TRP:HB3	2.03	0.41
1:K:308:GLU:HG2	6:K:433:HOH:O	2.19	0.41
1:E:63:ILE:HG23	1:E:64:GLU:N	2.36	0.41
1:I:392:THR:OG1	1:I:395:GLU:HG3	2.20	0.41
1:K:275:PHE:CG	1:K:276:VAL:N	2.87	0.41
1:B:200:SER:O	1:B:204:VAL:HG23	2.21	0.41
1:D:40:TRP:CE3	1:D:127:GLN:HG2	2.56	0.41
1:F:18:ASN:ND2	6:F:1397:HOH:O	2.53	0.41
1:G:190:TYR:CD1	1:G:206:ARG:NH1	2.89	0.41
1:G:276:VAL:CG2	1:G:277:GLY:N	2.84	0.41
1:I:374:ALA:O	1:I:378:ILE:HG13	2.20	0.41
1:K:40:TRP:CE3	1:K:127:GLN:HG2	2.55	0.41
1:B:149:ASP:OD1	1:B:152:ARG:NH2	2.53	0.41
1:B:326:TRP:HB3	1:B:327:PHE:H	1.57	0.41
1:C:196:TRP:CD1	1:C:238:ARG:HD2	2.55	0.41
1:E:169:LEU:HG	1:E:171:LEU:HD21	2.03	0.41
1:I:231:PRO:HD3	1:I:286:HIS:CD2	2.55	0.41
1:I:322:PHE:HA	1:I:350:ILE:O	2.20	0.41
1:K:235:ASN:O	1:K:239:ILE:HG13	2.21	0.41
1:A:122:LYS:NZ	1:A:127:GLN:HE22	2.18	0.41
1:A:275:PHE:CG	1:A:276:VAL:N	2.88	0.41
1:C:112:LEU:HA	1:C:115:TYR:CD2	2.56	0.41
1:C:322:PHE:HA	1:C:350:ILE:O	2.20	0.41
1:E:100:LEU:O	1:E:105:LEU:HB2	2.20	0.41
1:F:386:GLN:NE2	1:I:4:ASN:OD1	2.54	0.41
1:G:49:HIS:HB2	1:G:272:ALA:HB2	2.02	0.41
1:G:152:ARG:NH2	1:G:184:ARG:HH22	2.19	0.41
1:I:192:VAL:O	1:I:192:VAL:HG23	2.21	0.41
1:L:159:LYS:HD3	1:L:159:LYS:HA	1.91	0.41
1:F:316:PHE:HB3	1:F:318:ASN:OD1	2.20	0.41
2:G:428:REL:H2	2:G:428:REL:O5	2.21	0.41
1:H:326:TRP:HB3	1:H:327:PHE:H	1.65	0.41
1:A:69:MET:HE1	1:A:73:GLU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:LEU:CD1	1:C:326:TRP:HB3	2.51	0.41
1:D:391:VAL:O	1:D:391:VAL:CG2	2.69	0.41
1:E:322:PHE:HA	1:E:350:ILE:O	2.20	0.41
1:F:254:PRO:HG3	1:F:412:VAL:HG12	2.02	0.41
1:F:265:VAL:HG21	1:F:275:PHE:HB2	2.03	0.41
1:F:313:ALA:HA	1:F:319:LEU:HD23	2.02	0.41
1:G:254:PRO:HG2	1:G:412:VAL:HA	2.03	0.41
1:I:51:LEU:HD12	1:I:51:LEU:N	2.36	0.41
1:I:186:ARG:HG2	1:I:186:ARG:HH11	1.85	0.41
1:I:235:ASN:O	1:I:239:ILE:HG13	2.20	0.41
1:K:139:ASP:OD1	1:K:166:HIS:CE1	2.73	0.41
1:B:224:LEU:HD13	1:B:228:PHE:CD1	2.55	0.41
1:B:244:LEU:C	1:B:244:LEU:CD1	2.90	0.41
1:D:301:LEU:CD1	1:D:326:TRP:HB3	2.50	0.41
1:J:106:ASP:HA	1:J:107:PRO:HD2	1.94	0.41
1:K:169:LEU:HG	1:K:171:LEU:HD21	2.02	0.41
1:K:212:ILE:HD13	1:K:253:ILE:HD12	2.02	0.41
1:B:313:ALA:HA	1:B:319:LEU:HD23	2.03	0.40
1:E:113:GLN:HA	1:E:113:GLN:HE21	1.84	0.40
1:G:30:PHE:CE2	1:G:37:ILE:HG13	2.56	0.40
1:J:52:VAL:O	1:J:55:VAL:HG12	2.21	0.40
1:K:322:PHE:HA	1:K:350:ILE:O	2.21	0.40
1:J:123:THR:OG1	1:J:126:GLU:HG3	2.21	0.40
1:K:385:LEU:HD21	1:K:391:VAL:HG22	2.04	0.40
1:D:111:ASP:OD1	1:D:114:VAL:HG23	2.21	0.40
1:D:265:VAL:HG21	1:D:275:PHE:HB2	2.02	0.40
1:G:265:VAL:HG21	1:G:275:PHE:HB2	2.04	0.40
1:G:288:LEU:CD2	1:G:319:LEU:HB2	2.51	0.40
1:I:245:LEU:HB2	1:I:246:PRO:HD3	2.04	0.40
1:J:313:ALA:HA	1:J:319:LEU:HD23	2.03	0.40
1:L:49:HIS:HB2	1:L:272:ALA:HB2	2.02	0.40
1:L:394:GLU:HB2	6:L:674:HOH:O	2.20	0.40
1:C:386:GLN:NE2	1:L:4:ASN:OD1	2.55	0.40
1:E:149:ASP:OD1	1:E:152:ARG:NH2	2.54	0.40
1:E:203:GLU:OE1	1:E:206:ARG:NH1	2.54	0.40
1:F:208:LEU:O	1:F:212:ILE:HG13	2.21	0.40
1:F:276:VAL:CG2	1:F:277:GLY:N	2.83	0.40
1:G:6:ARG:HG2	1:G:6:ARG:NH1	2.37	0.40
1:G:6:ARG:HG3	1:G:382:ASP:OD1	2.22	0.40
1:G:301:LEU:HD11	1:G:326:TRP:HB3	2.04	0.40
1:I:52:VAL:O	1:I:55:VAL:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:148:ASP:OD2	1:J:151:GLU:HG3	2.22	0.40
1:C:170:ARG:NH2	1:C:223:SER:HB3	2.36	0.40
1:E:145:ASP:HA	1:E:146:PRO:HD2	1.92	0.40
1:F:40:TRP:O	1:F:41:ASP:CB	2.70	0.40
1:F:154:SER:O	1:F:159:LYS:HB2	2.22	0.40
1:H:204:VAL:O	1:H:207:PHE:HB3	2.22	0.40
1:H:409:TRP:HA	1:H:412:VAL:HG22	2.03	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	411/427 (96%)	398 (97%)	10 (2%)	3 (1%)	22 18
1	B	411/427 (96%)	398 (97%)	10 (2%)	3 (1%)	22 18
1	C	411/427 (96%)	399 (97%)	10 (2%)	2 (0%)	29 26
1	D	411/427 (96%)	399 (97%)	10 (2%)	2 (0%)	29 26
1	E	411/427 (96%)	396 (96%)	12 (3%)	3 (1%)	22 18
1	F	411/427 (96%)	396 (96%)	14 (3%)	1 (0%)	47 49
1	G	411/427 (96%)	401 (98%)	8 (2%)	2 (0%)	29 26
1	H	411/427 (96%)	394 (96%)	15 (4%)	2 (0%)	29 26
1	I	411/427 (96%)	396 (96%)	13 (3%)	2 (0%)	29 26
1	J	411/427 (96%)	401 (98%)	8 (2%)	2 (0%)	29 26
1	K	411/427 (96%)	399 (97%)	10 (2%)	2 (0%)	29 26
1	L	411/427 (96%)	399 (97%)	10 (2%)	2 (0%)	29 26
All	All	4932/5124 (96%)	4776 (97%)	130 (3%)	26 (0%)	29 26

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	ASP
1	H	41	ASP
1	I	41	ASP
1	J	41	ASP
1	K	41	ASP
1	L	41	ASP
1	A	41	ASP
1	C	41	ASP
1	D	41	ASP
1	E	41	ASP
1	F	41	ASP
1	G	41	ASP
1	G	323	GLY
1	H	323	GLY
1	J	323	GLY
1	K	323	GLY
1	B	323	GLY
1	E	159	LYS
1	E	323	GLY
1	A	36	GLU
1	I	323	GLY
1	L	323	GLY
1	A	323	GLY
1	B	405	SER
1	C	323	GLY
1	D	323	GLY

### 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	373/387 (96%)	366 (98%)	7 (2%)	57 63
1	B	373/387 (96%)	364 (98%)	9 (2%)	49 53
1	C	373/387 (96%)	368 (99%)	5 (1%)	69 75
1	D	373/387 (96%)	368 (99%)	5 (1%)	69 75
1	E	373/387 (96%)	365 (98%)	8 (2%)	53 59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	373/387 (96%)	366 (98%)	7 (2%)	57	63
1	G	373/387 (96%)	366 (98%)	7 (2%)	57	63
1	H	373/387 (96%)	368 (99%)	5 (1%)	69	75
1	I	373/387 (96%)	368 (99%)	5 (1%)	69	75
1	J	373/387 (96%)	368 (99%)	5 (1%)	69	75
1	K	373/387 (96%)	366 (98%)	7 (2%)	57	63
1	L	373/387 (96%)	368 (99%)	5 (1%)	69	75
All	All	4476/4644 (96%)	4401 (98%)	75 (2%)	60	67

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ARG
1	A	127	GLN
1	A	129	ASP
1	A	133	GLN
1	A	180	GLN
1	A	264	ARG
1	A	364	TYR
1	B	127	GLN
1	B	128	VAL
1	B	180	GLN
1	B	187	ASP
1	B	194	ASP
1	B	244	LEU
1	B	252	ASN
1	B	264	ARG
1	B	364	TYR
1	C	127	GLN
1	C	182	LYS
1	C	364	TYR
1	C	385	LEU
1	C	414	ARG
1	D	127	GLN
1	D	133	GLN
1	D	194	ASP
1	D	252	ASN
1	D	364	TYR
1	E	15	ASN
1	E	127	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	175	LEU
1	E	180	GLN
1	E	191	LYS
1	E	244	LEU
1	E	355	ASP
1	E	364	TYR
1	F	72	ARG
1	F	127	GLN
1	F	128	VAL
1	F	191	LYS
1	F	305	ASN
1	F	364	TYR
1	F	385	LEU
1	G	15	ASN
1	G	72	ARG
1	G	127	GLN
1	G	180	GLN
1	G	187	ASP
1	G	194	ASP
1	G	364	TYR
1	H	41	ASP
1	H	127	GLN
1	H	264	ARG
1	H	364	TYR
1	H	385	LEU
1	I	86	ARG
1	I	127	GLN
1	I	133	GLN
1	I	355	ASP
1	I	364	TYR
1	J	15	ASN
1	J	121	LYS
1	J	127	GLN
1	J	364	TYR
1	J	390	GLU
1	K	113	GLN
1	K	127	GLN
1	K	194	ASP
1	K	252	ASN
1	K	264	ARG
1	K	364	TYR
1	K	386	GLN

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Mol	Chain	Res	Type
1	L	127	GLN
1	L	133	GLN
1	L	182	LYS
1	L	244	LEU
1	L	364	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	113	GLN
1	A	127	GLN
1	A	166	HIS
1	A	252	ASN
1	A	293	ASN
1	B	18	ASN
1	B	113	GLN
1	B	127	GLN
1	B	166	HIS
1	B	180	GLN
1	B	202	GLN
1	B	252	ASN
1	B	293	ASN
1	C	18	ASN
1	C	127	GLN
1	C	166	HIS
1	C	180	GLN
1	C	202	GLN
1	C	252	ASN
1	C	293	ASN
1	C	386	GLN
1	D	18	ASN
1	D	74	GLN
1	D	113	GLN
1	D	127	GLN
1	D	166	HIS
1	D	202	GLN
1	D	252	ASN
1	D	293	ASN
1	E	18	ASN
1	E	113	GLN
1	E	127	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	160	GLN
1	E	166	HIS
1	E	180	GLN
1	E	202	GLN
1	E	235	ASN
1	E	252	ASN
1	E	293	ASN
1	F	18	ASN
1	F	101	GLN
1	F	113	GLN
1	F	127	GLN
1	F	166	HIS
1	F	180	GLN
1	F	202	GLN
1	F	252	ASN
1	F	293	ASN
1	F	386	GLN
1	G	18	ASN
1	G	127	GLN
1	G	160	GLN
1	G	166	HIS
1	G	180	GLN
1	G	193	ASN
1	H	18	ASN
1	H	127	GLN
1	H	166	HIS
1	H	180	GLN
1	H	193	ASN
1	H	197	ASN
1	H	286	HIS
1	H	386	GLN
1	I	18	ASN
1	I	127	GLN
1	I	166	HIS
1	I	293	ASN
1	J	18	ASN
1	J	113	GLN
1	J	127	GLN
1	J	166	HIS
1	J	252	ASN
1	K	18	ASN
1	K	113	GLN

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Mol	Chain	Res	Type
1	K	127	GLN
1	K	160	GLN
1	K	166	HIS
1	K	252	ASN
1	K	286	HIS
1	K	386	GLN
1	L	18	ASN
1	L	113	GLN
1	L	127	GLN
1	L	166	HIS
1	L	202	GLN
1	L	252	ASN
1	L	293	ASN

### 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 monosaccharides in this entry.

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

Of 40 ligands modelled in this entry, 16 are monoatomic - leaving 24 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	REL	L	428	4	11,12,12	0.97	0	15,16,16	1.27	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	REL	C	428	4	11,12,12	1.03	0	15,16,16	1.29	2 (13%)
2	REL	I	428	4	11,12,12	0.97	0	15,16,16	1.24	2 (13%)
2	REL	A	428	4	11,12,12	1.12	0	15,16,16	1.35	2 (13%)
2	REL	F	428	4	11,12,12	0.96	0	15,16,16	1.34	2 (13%)
3	CO3	I	429	-	2,3,3	0.46	0	2,3,3	0.05	0
3	CO3	K	429	-	2,3,3	0.37	0	2,3,3	0.21	0
2	REL	B	428	4	11,12,12	1.05	0	15,16,16	1.37	3 (20%)
2	REL	J	428	4	11,12,12	1.01	0	15,16,16	1.28	3 (20%)
3	CO3	F	429	-	2,3,3	0.40	0	2,3,3	0.01	0
3	CO3	D	430	-	2,3,3	0.40	0	2,3,3	0.09	0
2	REL	D	428	4	11,12,12	0.97	0	15,16,16	1.23	1 (6%)
2	REL	K	428	4	11,12,12	0.93	0	15,16,16	1.31	3 (20%)
3	CO3	L	429	-	2,3,3	0.48	0	2,3,3	0.09	0
3	CO3	G	429	-	2,3,3	0.36	0	2,3,3	0.17	0
2	REL	G	428	4	11,12,12	0.96	0	15,16,16	1.31	2 (13%)
3	CO3	D	429	-	2,3,3	0.46	0	2,3,3	0.18	0
3	CO3	H	429	-	2,3,3	0.35	0	2,3,3	0.11	0
3	CO3	A	430	-	2,3,3	0.35	0	2,3,3	0.07	0
2	REL	H	428	4	11,12,12	0.95	0	15,16,16	1.25	3 (20%)
3	CO3	J	429	-	2,3,3	0.43	0	2,3,3	0.24	0
2	REL	E	428	4	11,12,12	1.11	0	15,16,16	1.41	3 (20%)
3	CO3	A	429	-	2,3,3	0.42	0	2,3,3	0.23	0
3	CO3	C	429	-	2,3,3	0.43	0	2,3,3	0.01	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	REL	F	428	4	-	9/16/18/18	-
2	REL	K	428	4	-	9/16/18/18	-
2	REL	L	428	4	-	9/16/18/18	-
2	REL	A	428	4	-	8/16/18/18	-
2	REL	E	428	4	-	8/16/18/18	-
2	REL	G	428	4	-	10/16/18/18	-
2	REL	C	428	4	-	10/16/18/18	-
2	REL	B	428	4	-	8/16/18/18	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	REL	J	428	4	-	9/16/18/18	-
2	REL	I	428	4	-	10/16/18/18	-
2	REL	H	428	4	-	9/16/18/18	-
2	REL	D	428	4	-	9/16/18/18	-

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	428	REL	C4-C5-C6	3.42	113.62	109.32
2	E	428	REL	C4-C5-C6	3.34	113.52	109.32
2	A	428	REL	C4-C5-C6	3.02	113.12	109.32
2	G	428	REL	C4-C5-C6	2.60	112.59	109.32
2	K	428	REL	C4-C5-C6	2.52	112.49	109.32
2	J	428	REL	C4-C5-C6	2.51	112.48	109.32
2	L	428	REL	C4-C5-C6	2.49	112.45	109.32
2	F	428	REL	O6A-C6-C5	-2.41	115.28	121.63
2	C	428	REL	C4-C5-C6	2.41	112.35	109.32
2	J	428	REL	O6A-C6-C5	-2.41	115.30	121.63
2	K	428	REL	O6A-C6-C5	-2.40	115.32	121.63
2	E	428	REL	O6A-C6-C5	-2.37	115.39	121.63
2	I	428	REL	C4-C5-C6	2.37	112.30	109.32
2	H	428	REL	O6A-C6-C5	-2.36	115.43	121.63
2	G	428	REL	O6A-C6-C5	-2.35	115.44	121.63
2	F	428	REL	C4-C5-C6	2.34	112.27	109.32
2	B	428	REL	O6A-C6-C5	-2.31	115.56	121.63
2	I	428	REL	O6A-C6-C5	-2.31	115.57	121.63
2	C	428	REL	O6A-C6-C5	-2.29	115.61	121.63
2	L	428	REL	O6A-C6-C5	-2.27	115.67	121.63
2	D	428	REL	O6A-C6-C5	-2.25	115.73	121.63
2	B	428	REL	O6B-C6-C5	2.24	119.33	113.27
2	H	428	REL	C4-C5-C6	2.22	112.11	109.32
2	K	428	REL	O6B-C6-C5	2.16	119.12	113.27
2	A	428	REL	O6A-C6-C5	-2.14	116.02	121.63
2	E	428	REL	O6B-C6-C5	2.13	119.03	113.27
2	H	428	REL	O6B-C6-C5	2.11	118.97	113.27
2	J	428	REL	O6B-C6-C5	2.10	118.95	113.27

There are no chirality outliers.

All (108) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	428	REL	O2-C2-C3-C4
2	A	428	REL	C1-C2-C3-C4
2	A	428	REL	O2-C2-C3-O3
2	A	428	REL	C1-C2-C3-O3
2	B	428	REL	O2-C2-C3-C4
2	B	428	REL	C1-C2-C3-C4
2	B	428	REL	O2-C2-C3-O3
2	B	428	REL	C1-C2-C3-O3
2	C	428	REL	O2-C2-C3-C4
2	C	428	REL	C1-C2-C3-C4
2	C	428	REL	O2-C2-C3-O3
2	C	428	REL	C1-C2-C3-O3
2	D	428	REL	O2-C2-C3-C4
2	D	428	REL	C1-C2-C3-C4
2	D	428	REL	O2-C2-C3-O3
2	D	428	REL	C1-C2-C3-O3
2	E	428	REL	O2-C2-C3-C4
2	E	428	REL	C1-C2-C3-C4
2	E	428	REL	O2-C2-C3-O3
2	E	428	REL	C1-C2-C3-O3
2	F	428	REL	O2-C2-C3-C4
2	F	428	REL	C1-C2-C3-C4
2	F	428	REL	O2-C2-C3-O3
2	G	428	REL	O2-C2-C3-C4
2	G	428	REL	C1-C2-C3-C4
2	G	428	REL	O2-C2-C3-O3
2	G	428	REL	C1-C2-C3-O3
2	H	428	REL	O2-C2-C3-C4
2	H	428	REL	C1-C2-C3-C4
2	H	428	REL	O2-C2-C3-O3
2	H	428	REL	C1-C2-C3-O3
2	I	428	REL	O2-C2-C3-C4
2	I	428	REL	C1-C2-C3-C4
2	I	428	REL	O2-C2-C3-O3
2	I	428	REL	C1-C2-C3-O3
2	J	428	REL	O2-C2-C3-C4
2	J	428	REL	C1-C2-C3-C4
2	J	428	REL	O2-C2-C3-O3
2	J	428	REL	C1-C2-C3-O3
2	K	428	REL	O2-C2-C3-C4
2	K	428	REL	C1-C2-C3-C4
2	K	428	REL	O2-C2-C3-O3
2	L	428	REL	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
2	L	428	REL	C1-C2-C3-C4
2	L	428	REL	O2-C2-C3-O3
2	L	428	REL	C1-C2-C3-O3
2	B	428	REL	O5-C5-C6-O6A
2	B	428	REL	O5-C5-C6-O6B
2	E	428	REL	O5-C5-C6-O6A
2	E	428	REL	O5-C5-C6-O6B
2	F	428	REL	C1-C2-C3-O3
2	K	428	REL	C1-C2-C3-O3
2	C	428	REL	O5-C5-C6-O6A
2	G	428	REL	O5-C5-C6-O6A
2	L	428	REL	O5-C5-C6-O6A
2	D	428	REL	O5-C5-C6-O6A
2	F	428	REL	O5-C5-C6-O6A
2	I	428	REL	O5-C5-C6-O6A
2	J	428	REL	O5-C5-C6-O6A
2	K	428	REL	O5-C5-C6-O6A
2	A	428	REL	O5-C5-C6-O6A
2	C	428	REL	O5-C5-C6-O6B
2	D	428	REL	O5-C5-C6-O6B
2	F	428	REL	O5-C5-C6-O6B
2	G	428	REL	O5-C5-C6-O6B
2	I	428	REL	O5-C5-C6-O6B
2	J	428	REL	O5-C5-C6-O6B
2	L	428	REL	O5-C5-C6-O6B
2	K	428	REL	O5-C5-C6-O6B
2	A	428	REL	O5-C5-C6-O6B
2	H	428	REL	O5-C5-C6-O6B
2	H	428	REL	O5-C5-C6-O6A
2	E	428	REL	C2-C3-C4-C5
2	G	428	REL	C2-C3-C4-C5
2	B	428	REL	C2-C3-C4-C5
2	A	428	REL	C4-C5-C6-O6A
2	H	428	REL	C4-C5-C6-O6B
2	H	428	REL	C4-C5-C6-O6A
2	K	428	REL	C4-C5-C6-O6A
2	C	428	REL	C2-C3-C4-C5
2	H	428	REL	C2-C3-C4-C5
2	I	428	REL	C2-C3-C4-C5
2	J	428	REL	C2-C3-C4-C5
2	A	428	REL	C4-C5-C6-O6B
2	D	428	REL	C4-C5-C6-O6A

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Mol	Chain	Res	Type	Atoms
2	I	428	REL	C4-C5-C6-O6A
2	E	428	REL	O3-C3-C4-C5
2	K	428	REL	C4-C5-C6-O6B
2	G	428	REL	O3-C3-C4-C5
2	D	428	REL	C4-C5-C6-O6B
2	J	428	REL	C4-C5-C6-O6B
2	I	428	REL	C4-C5-C6-O6B
2	B	428	REL	O3-C3-C4-C5
2	J	428	REL	C4-C5-C6-O6A
2	F	428	REL	C4-C5-C6-O6A
2	F	428	REL	C4-C5-C6-O6B
2	D	428	REL	C2-C3-C4-C5
2	F	428	REL	C2-C3-C4-C5
2	C	428	REL	C4-C5-C6-O6B
2	L	428	REL	C4-C5-C6-O6B
2	G	428	REL	C4-C5-C6-O6B
2	C	428	REL	C4-C5-C6-O6A
2	K	428	REL	C2-C3-C4-C5
2	L	428	REL	C2-C3-C4-C5
2	G	428	REL	C4-C5-C6-O6A
2	L	428	REL	C4-C5-C6-O6A
2	C	428	REL	O3-C3-C4-C5
2	I	428	REL	O3-C3-C4-C5

There are no ring outliers.

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	428	REL	1	0
2	C	428	REL	1	0
2	A	428	REL	1	0
2	F	428	REL	1	0
2	D	428	REL	1	0
2	K	428	REL	1	0
2	G	428	REL	1	0
2	H	428	REL	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	413/427 (96%)	-0.17	5 (1%) 79 82	18, 28, 47, 64	0
1	B	413/427 (96%)	0.05	15 (3%) 42 49	19, 30, 50, 65	0
1	C	413/427 (96%)	-0.20	3 (0%) 87 89	17, 27, 43, 63	0
1	D	413/427 (96%)	-0.31	3 (0%) 87 89	15, 25, 42, 62	0
1	E	413/427 (96%)	-0.10	7 (1%) 70 74	18, 29, 47, 65	0
1	F	413/427 (96%)	-0.10	7 (1%) 70 74	18, 28, 46, 65	0
1	G	413/427 (96%)	-0.10	6 (1%) 73 77	18, 28, 46, 64	0
1	H	413/427 (96%)	-0.17	3 (0%) 87 89	17, 28, 47, 65	0
1	I	413/427 (96%)	-0.17	5 (1%) 79 82	18, 28, 48, 64	0
1	J	413/427 (96%)	-0.22	3 (0%) 87 89	16, 27, 43, 64	0
1	K	413/427 (96%)	-0.19	7 (1%) 70 74	17, 27, 47, 62	0
1	L	413/427 (96%)	-0.30	4 (0%) 82 85	16, 25, 44, 62	0
All	All	4956/5124 (96%)	-0.17	68 (1%) 75 78	15, 28, 46, 65	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	414	ARG	5.7
1	B	414	ARG	4.5
1	H	414	ARG	4.5
1	D	414	ARG	4.4
1	L	414	ARG	4.3
1	K	414	ARG	3.9
1	J	414	ARG	3.6
1	E	414	ARG	3.6
1	I	414	ARG	3.5
1	E	121	LYS	3.5
1	G	414	ARG	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	414	ARG	3.3
1	B	113	GLN	3.2
1	I	183	HIS	3.1
1	A	414	ARG	2.9
1	B	153	ILE	2.9
1	B	204	VAL	2.8
1	E	68	ALA	2.8
1	A	194	ASP	2.8
1	G	199	GLY	2.7
1	D	68	ALA	2.7
1	E	413	GLY	2.7
1	B	191	LYS	2.6
1	A	68	ALA	2.6
1	C	121	LYS	2.6
1	B	247	VAL	2.6
1	K	183	HIS	2.6
1	B	186	ARG	2.5
1	G	250	LYS	2.5
1	G	194	ASP	2.5
1	F	413	GLY	2.5
1	D	60	ASP	2.5
1	A	195	GLU	2.4
1	B	194	ASP	2.4
1	F	194	ASP	2.4
1	I	194	ASP	2.4
1	A	183	HIS	2.4
1	K	197	ASN	2.4
1	J	2	SER	2.3
1	G	198	GLU	2.3
1	B	2	SER	2.3
1	H	195	GLU	2.3
1	K	194	ASP	2.3
1	C	413	GLY	2.3
1	E	2	SER	2.3
1	B	65	ALA	2.3
1	B	183	HIS	2.2
1	F	180	GLN	2.2
1	B	200	SER	2.2
1	I	186	ARG	2.2
1	K	180	GLN	2.1
1	B	250	LYS	2.1
1	G	195	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	251	HIS	2.1
1	B	180	GLN	2.1
1	H	128	VAL	2.1
1	L	121	LYS	2.1
1	I	264	ARG	2.1
1	L	183	HIS	2.1
1	K	191	LYS	2.1
1	E	60	ASP	2.1
1	E	113	GLN	2.1
1	F	68	ALA	2.1
1	F	113	GLN	2.0
1	L	113	GLN	2.0
1	F	192	VAL	2.0
1	J	121	LYS	2.0
1	K	195	GLU	2.0

## 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 monosaccharides 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	REL	L	428	13/13	0.91	0.13	24,27,29,29	0
2	REL	I	428	13/13	0.92	0.12	27,31,32,32	0
2	REL	A	428	13/13	0.93	0.12	28,31,32,32	0
2	REL	K	428	13/13	0.93	0.12	26,30,31,31	0
2	REL	B	428	13/13	0.93	0.15	29,31,34,34	0
2	REL	F	428	13/13	0.94	0.12	25,28,31,31	0
2	REL	H	428	13/13	0.94	0.10	25,31,33,33	0
2	REL	C	428	13/13	0.94	0.10	26,29,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	REL	D	428	13/13	0.94	0.12	25,27,28,29	0
2	REL	E	428	13/13	0.94	0.12	27,30,34,34	0
2	REL	G	428	13/13	0.95	0.14	25,27,29,29	0
3	CO3	A	429	4/4	0.95	0.11	23,24,25,27	0
3	CO3	F	429	4/4	0.95	0.14	24,25,26,29	0
3	CO3	C	429	4/4	0.96	0.14	22,22,23,24	0
2	REL	J	428	13/13	0.96	0.12	25,28,31,31	0
3	CO3	I	429	4/4	0.97	0.14	23,24,26,26	0
3	CO3	A	430	4/4	0.98	0.12	21,22,23,25	0
3	CO3	H	429	4/4	0.98	0.13	24,25,25,25	0
3	CO3	D	429	4/4	0.98	0.14	18,20,21,21	0
3	CO3	K	429	4/4	0.98	0.13	20,22,22,23	0
4	ZN	E	429	1/1	0.98	0.08	27,27,27,27	0
4	ZN	I	430	1/1	0.98	0.12	32,32,32,32	0
3	CO3	D	430	4/4	0.99	0.11	20,20,21,24	0
3	CO3	L	429	4/4	0.99	0.12	19,20,23,25	0
4	ZN	A	431	1/1	0.99	0.08	27,27,27,27	0
4	ZN	B	429	1/1	0.99	0.12	36,36,36,36	0
4	ZN	D	431	1/1	0.99	0.06	21,21,21,21	0
3	CO3	G	429	4/4	0.99	0.07	19,21,22,22	0
4	ZN	F	430	1/1	0.99	0.13	30,30,30,30	0
3	CO3	J	429	4/4	0.99	0.10	18,18,20,22	0
4	ZN	K	430	1/1	0.99	0.09	29,29,29,29	0
4	ZN	L	430	1/1	0.99	0.10	24,24,24,24	0
4	ZN	C	430	1/1	1.00	0.09	26,26,26,26	0
4	ZN	J	430	1/1	1.00	0.10	25,25,25,25	0
4	ZN	G	430	1/1	1.00	0.09	27,27,27,27	0
4	ZN	H	430	1/1	1.00	0.14	33,33,33,33	0
5	CL	A	432	1/1	1.00	0.13	23,23,23,23	0
5	CL	F	431	1/1	1.00	0.08	20,20,20,20	0
5	CL	H	431	1/1	1.00	0.14	21,21,21,21	0
5	CL	K	431	1/1	1.00	0.12	21,21,21,21	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.