



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:14 AM GMT

PDB ID : 2C4R  
Title : CATALYTIC DOMAIN OF E. COLI RNASE E  
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Deposited on : 2005-10-21  
Resolution : 3.60 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

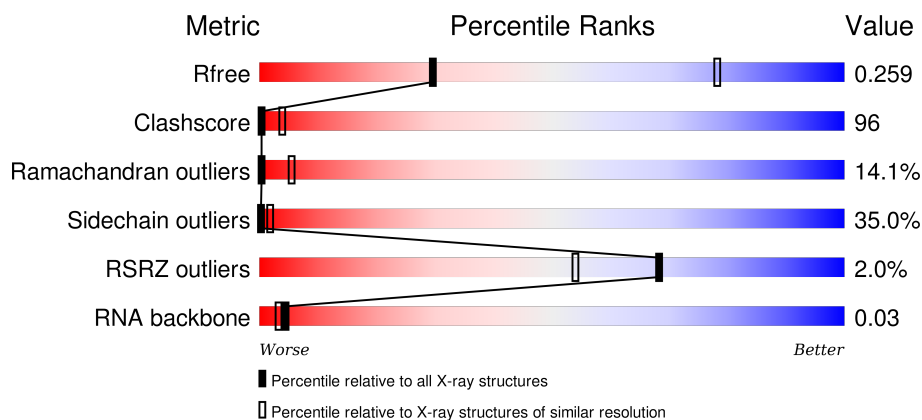
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.60 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))
$R_{free}$	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)
RNA backbone	2183	1058 (4.40-2.80)

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. 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	L	517	
2	R	10	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3778 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 RIBONUCLEASE E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	491	Total	C	N	O	S	0	0	0
			3557	2223	649	674	11			

- Molecule 2 is a RNA chain called SSRNA MOLECULE: 5'-R(\*AP\*CP\*AP\*GP\*UP\*AP\*UP\*UP\*GP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	10	Total	C	N	O	P	0	0	0
			212	95	36	71	10			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	2	Total	Mg	0	0
			2	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	1	Total	Zn	0	0
			1	1		

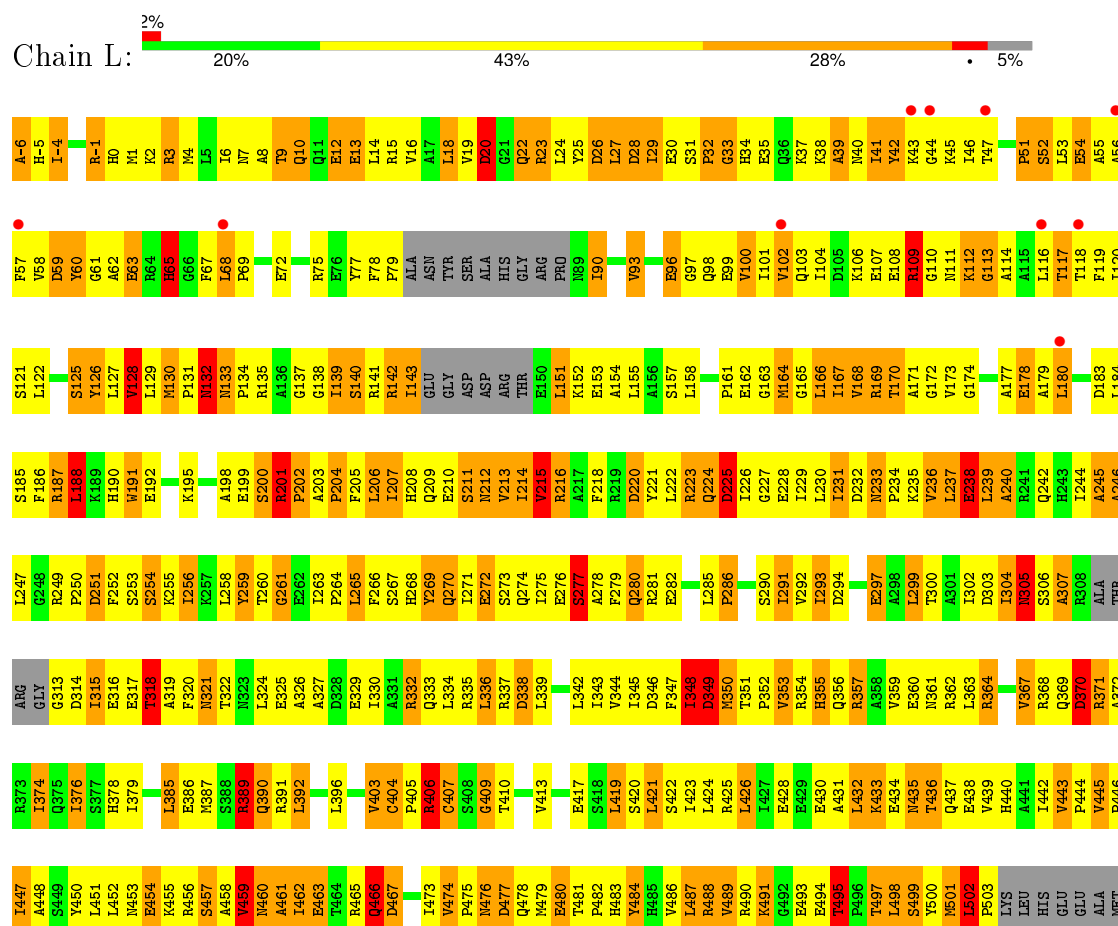
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	5	Total	O	0	0
			5	5		
5	R	1	Total	O	0	0
			1	1		

### 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 errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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: RIBONUCLEASE E



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	196.59 Å   196.59 Å   140.77 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	25.00 – 3.60 49.15 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (25.00-3.60) 99.7 (49.15-3.60)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 3.57 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.319   ,   0.347 0.233   ,   0.259	Depositor DCC
$R_{free}$ test set	973 reflections (5.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	122.6	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 94.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 18978 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3778	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	L	0.77	2/3610 (0.1%)	0.90	15/4917 (0.3%)
2	R	1.58	2/236 (0.8%)	3.16	36/363 (9.9%)
All	All	0.84	4/3846 (0.1%)	1.20	51/5280 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	21

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	407	CYS	CB-SG	-23.96	1.41	1.82
2	R	1	A	OP3-P	-10.74	1.48	1.61
1	L	407	CYS	C-N	-7.04	1.17	1.34
2	R	4	G	C3'-O3'	6.39	1.51	1.42

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	6	A	O4'-C1'-N9	12.97	118.58	108.20
1	L	406	ARG	O-C-N	-12.54	102.63	122.70
2	R	6	A	O4'-C4'-C3'	-12.54	91.47	104.00
2	R	1	A	O4'-C1'-N9	12.43	118.14	108.20
2	R	4	G	C1'-O4'-C4'	-12.09	100.23	109.90
2	R	4	G	P-O3'-C3'	11.99	134.09	119.70
2	R	10	G	O4'-C1'-N9	11.17	117.14	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	4	G	N9-C1'-C2'	11.05	128.37	114.00
2	R	5	U	O4'-C1'-C2'	-11.02	94.78	105.80
2	R	1	A	C1'-O4'-C4'	-10.35	101.62	109.90
2	R	10	G	C8-N9-C4	-9.81	102.48	106.40
2	R	4	G	C3'-C2'-C1'	-9.72	93.72	101.50
2	R	5	U	O4'-C1'-N1	-9.71	100.43	108.20
1	L	421	LEU	CA-CB-CG	-9.62	93.18	115.30
2	R	10	G	C4'-C3'-C2'	-9.58	93.02	102.60
1	L	406	ARG	CA-C-N	7.89	134.56	117.20
2	R	2	C	O5'-C5'-C4'	-7.79	96.90	111.70
1	L	502	LEU	CA-CB-CG	-7.71	97.57	115.30
2	R	9	U	P-O3'-C3'	-7.64	110.54	119.70
1	L	406	ARG	C-N-CA	7.44	140.29	121.70
1	L	336	LEU	CB-CG-CD2	-7.03	99.05	111.00
2	R	10	G	N7-C8-N9	6.86	116.53	113.10
2	R	1	A	O4'-C1'-C2'	-6.82	98.98	105.80
2	R	6	A	C1'-O4'-C4'	-6.79	104.46	109.90
2	R	10	G	N3-C4-C5	-6.66	125.27	128.60
2	R	10	G	C1'-O4'-C4'	-6.28	104.87	109.90
2	R	6	A	N9-C1'-C2'	-6.25	105.13	112.00
2	R	10	G	C4-N9-C1'	6.23	134.59	126.50
2	R	1	A	C8-N9-C4	-6.12	103.35	105.80
2	R	1	A	N7-C8-N9	6.00	116.80	113.80
1	L	407	CYS	N-CA-C	-5.98	94.84	111.00
2	R	1	A	N9-C1'-C2'	5.94	121.73	114.00
2	R	10	G	C6-C5-N7	-5.75	126.95	130.40
2	R	4	G	C5'-C4'-C3'	5.45	124.71	116.00
2	R	10	G	C3'-C2'-C1'	5.43	105.84	101.50
2	R	2	C	O3'-P-O5'	-5.39	93.76	104.00
2	R	4	G	OP2-P-O3'	5.32	116.90	105.20
2	R	10	G	C4-C5-C6	5.32	121.99	118.80
1	L	28	ASP	CB-CG-OD2	5.28	123.05	118.30
2	R	5	U	C5'-C4'-O4'	5.24	115.39	109.10
1	L	225	ASP	CB-CG-OD2	5.24	123.02	118.30
2	R	4	G	P-O5'-C5'	5.24	129.28	120.90
1	L	294	ASP	CB-CG-OD2	5.23	123.01	118.30
1	L	421	LEU	CB-CG-CD2	-5.23	102.11	111.00
1	L	220	ASP	CB-CG-OD2	5.21	122.98	118.30
1	L	370	ASP	CB-CG-OD2	5.20	122.98	118.30
1	L	20	ASP	CB-CG-OD2	5.19	122.97	118.30
1	L	349	ASP	CB-CG-OD2	5.17	122.95	118.30
2	R	2	C	C1'-O4'-C4'	-5.16	105.77	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	4	G	O4'-C1'-C2'	-5.14	100.66	105.80
2	R	2	C	P-O3'-C3'	5.06	125.77	119.70

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	-6	ALA	Peptide
1	L	109	ARG	Peptide
1	L	113	GLY	Peptide
1	L	130	MET	Peptide
1	L	132	ASN	Peptide
1	L	151	LEU	Peptide
1	L	161	PRO	Peptide
1	L	174	GLY	Peptide
1	L	201	ARG	Peptide
1	L	249	ARG	Peptide
1	L	254	SER	Peptide
1	L	305	ASN	Peptide
1	L	313	GLY	Peptide
1	L	389	ARG	Peptide
1	L	406	ARG	Mainchain
1	L	409	GLY	Peptide
1	L	460	ASN	Peptide
1	L	480	GLU	Peptide
1	L	495	THR	Peptide
1	L	56	ALA	Peptide
1	L	61	GLY	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	3557	0	3325	649	0
2	R	212	0	107	67	0
3	L	2	0	0	0	0
4	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	5	0	0	4	0
5	R	1	0	0	1	0
All	All	3778	0	3432	690	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 96.

All (690) 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:L:222:LEU:HD23	1:L:226:ILE:CD1	1.28	1.58
1:L:222:LEU:CD2	1:L:226:ILE:CD1	1.98	1.41
1:L:206:LEU:HD12	1:L:207:ILE:N	1.24	1.41
1:L:222:LEU:CD2	1:L:226:ILE:HD12	1.49	1.41
1:L:128:VAL:CG1	1:L:167:ILE:CD1	2.02	1.35
1:L:276:GLU:O	1:L:278:ALA:N	1.61	1.34
2:R:2:C:O2	2:R:2:C:H3'	1.16	1.33
1:L:206:LEU:CD1	1:L:207:ILE:H	1.42	1.31
1:L:128:VAL:HG11	1:L:167:ILE:CD1	1.58	1.30
1:L:458:ALA:O	1:L:461:ALA:HB3	1.26	1.28
1:L:-4:ILE:HD13	1:L:-1:ARG:NH1	1.52	1.25
1:L:259:TYR:CD2	1:L:265:LEU:HG	1.72	1.24
1:L:128:VAL:CG1	1:L:167:ILE:HD13	1.62	1.21
1:L:222:LEU:HD23	1:L:226:ILE:HD13	1.21	1.19
1:L:436:THR:HG23	1:L:488:ARG:HE	1.11	1.15
1:L:102:VAL:HG11	1:L:116:LEU:HD13	1.21	1.15
1:L:143:ILE:HD13	1:L:173:VAL:HG23	1.28	1.14
1:L:128:VAL:CG1	1:L:167:ILE:HD12	1.71	1.13
1:L:222:LEU:HD22	1:L:226:ILE:HD12	1.29	1.13
1:L:10:GLN:HA	1:L:10:GLN:OE1	1.41	1.12
1:L:239:LEU:HD23	1:L:239:LEU:H	1.14	1.12
2:R:2:C:C3'	2:R:2:C:O2	1.97	1.11
1:L:169:ARG:CG	1:L:169:ARG:HH11	1.65	1.10
1:L:184:LEU:O	1:L:188:LEU:HD12	1.51	1.09
1:L:332:ARG:HH11	1:L:332:ARG:HG2	1.15	1.09
1:L:43:LYS:CB	1:L:203:ALA:HB1	1.82	1.08
1:L:473:ILE:O	1:L:473:ILE:HG22	1.47	1.08
1:L:169:ARG:NH1	1:L:169:ARG:HG2	1.57	1.07
1:L:106:LYS:O	1:L:114:ALA:HB1	1.53	1.07
2:R:7:U:H5'	2:R:7:U:H6	1.06	1.06
1:L:169:ARG:NH1	2:R:1:A:OP3	1.88	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:259:TYR:HD2	1:L:265:LEU:HG	0.96	1.06
1:L:239:LEU:N	1:L:239:LEU:HD23	1.65	1.05
1:L:436:THR:HG23	1:L:488:ARG:NE	1.71	1.03
1:L:96:GLU:HG2	1:L:97:GLY:H	1.22	1.03
1:L:67:PHE:CD1	2:R:10:G:C4	2.47	1.03
1:L:348:ILE:CG2	1:L:349:ASP:H	1.71	1.03
2:R:4:G:OP2	2:R:5:U:N3	1.91	1.03
1:L:367:VAL:HG21	1:L:374:ILE:HD12	1.03	1.03
2:R:7:U:C5'	2:R:7:U:H6	1.71	1.02
1:L:140:SER:OG	1:L:170:THR:N	1.91	1.01
1:L:55:ALA:HB2	1:L:69:PRO:HA	1.41	1.01
1:L:130:MET:HB2	1:L:165:GLY:O	1.58	1.01
1:L:293:ILE:HG23	1:L:302:ILE:HG12	1.40	1.01
1:L:137:GLY:O	2:R:2:C:H1'	1.61	1.01
2:R:5:U:C6	2:R:5:U:H5'	1.95	1.01
1:L:501:MET:HA	1:L:501:MET:CE	1.88	1.01
1:L:237:LEU:O	1:L:237:LEU:HD23	1.59	1.00
1:L:367:VAL:CG2	1:L:374:ILE:HD12	1.91	1.00
1:L:143:ILE:HD13	1:L:173:VAL:CG2	1.90	1.00
1:L:235:LYS:O	1:L:238:GLU:HB2	1.60	1.00
1:L:130:MET:O	1:L:164:MET:HB2	1.62	1.00
1:L:169:ARG:HG2	1:L:169:ARG:HH11	0.83	1.00
1:L:7:ASN:HB2	1:L:266:PHE:HE1	1.26	1.00
1:L:259:TYR:HE2	1:L:265:LEU:HA	1.27	0.99
1:L:57:PHE:HZ	2:R:10:G:HO2'	1.04	0.98
1:L:406:ARG:HE	1:L:481:THR:HG22	1.25	0.98
1:L:233:ASN:ND2	1:L:236:VAL:HG23	1.75	0.98
1:L:348:ILE:HG22	1:L:349:ASP:N	1.77	0.97
1:L:143:ILE:CD1	1:L:173:VAL:HG23	1.94	0.96
1:L:481:THR:CG2	1:L:482:PRO:HD3	1.95	0.96
1:L:129:LEU:HD11	1:L:164:MET:HG3	1.47	0.96
1:L:58:VAL:O	1:L:65:HIS:HB3	1.65	0.96
1:L:259:TYR:HD1	1:L:260:THR:N	1.62	0.96
2:R:7:U:H5'	2:R:7:U:C6	1.99	0.96
1:L:222:LEU:CD2	1:L:226:ILE:HD13	1.78	0.95
1:L:18:LEU:O	1:L:25:TYR:CD2	2.20	0.95
2:R:9:U:C5	2:R:10:G:N2	2.35	0.95
1:L:167:ILE:HG12	2:R:2:C:H6	1.31	0.94
1:L:299:LEU:O	1:L:299:LEU:HD12	1.66	0.94
1:L:347:PHE:O	1:L:348:ILE:O	1.85	0.94
2:R:9:U:C6	2:R:10:G:N2	2.36	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:230:LEU:HD23	1:L:230:LEU:N	1.84	0.93
2:R:5:U:H3'	2:R:5:U:H6	1.32	0.92
1:L:180:LEU:HD23	1:L:180:LEU:N	1.83	0.92
1:L:259:TYR:CE2	1:L:265:LEU:HA	2.04	0.92
1:L:-4:ILE:CD1	1:L:-1:ARG:NH1	2.33	0.92
1:L:348:ILE:CG2	1:L:349:ASP:N	2.30	0.92
1:L:129:LEU:HD12	1:L:130:MET:H	1.32	0.92
2:R:7:U:C5'	2:R:7:U:C6	2.53	0.91
1:L:233:ASN:HD21	1:L:236:VAL:HG23	1.32	0.91
1:L:102:VAL:HG11	1:L:116:LEU:CD1	2.01	0.91
1:L:447:ILE:HD13	1:L:447:ILE:N	1.85	0.90
1:L:130:MET:O	1:L:132:ASN:N	2.04	0.90
1:L:501:MET:HA	1:L:501:MET:HE3	1.51	0.89
1:L:-4:ILE:HD13	1:L:-1:ARG:HH12	1.36	0.89
1:L:96:GLU:HG2	1:L:97:GLY:N	1.87	0.89
1:L:131:PRO:HA	1:L:164:MET:CG	2.02	0.89
1:L:67:PHE:HE1	2:R:10:G:H1'	1.38	0.89
1:L:10:GLN:OE1	1:L:10:GLN:CA	2.21	0.89
1:L:203:ALA:N	1:L:204:PRO:CD	2.36	0.88
1:L:128:VAL:HG12	1:L:167:ILE:HD12	1.53	0.88
1:L:403:VAL:O	1:L:404:CYS:C	2.12	0.88
1:L:481:THR:HG23	1:L:482:PRO:HD3	1.54	0.87
1:L:476:ASN:OD1	1:L:477:ASP:N	2.06	0.87
1:L:7:ASN:HB2	1:L:266:PHE:CE1	2.10	0.87
1:L:442:ILE:HD13	1:L:474:VAL:HG13	1.56	0.87
1:L:1:MET:HE2	1:L:228:GLU:HG3	1.57	0.87
1:L:222:LEU:HA	1:L:226:ILE:CD1	2.05	0.87
1:L:-4:ILE:N	1:L:-4:ILE:HD12	1.88	0.87
1:L:1:MET:CE	1:L:228:GLU:HG3	2.06	0.86
1:L:332:ARG:CG	1:L:332:ARG:HH11	1.89	0.86
1:L:334:LEU:HD23	1:L:339:LEU:HD12	1.56	0.86
1:L:129:LEU:HD12	1:L:130:MET:N	1.90	0.86
2:R:2:C:C2	2:R:2:C:H3'	2.11	0.85
1:L:473:ILE:O	1:L:473:ILE:CG2	2.23	0.85
1:L:205:PHE:CD1	1:L:206:LEU:O	2.29	0.85
1:L:364:ARG:NH2	1:L:364:ARG:HG3	1.90	0.85
1:L:203:ALA:N	1:L:204:PRO:HD3	1.92	0.85
1:L:291:ILE:O	1:L:291:ILE:HG22	1.77	0.84
1:L:334:LEU:CD2	1:L:339:LEU:HD12	2.07	0.84
1:L:55:ALA:CB	1:L:69:PRO:HA	2.07	0.84
1:L:406:ARG:HE	1:L:481:THR:CG2	1.91	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:256:ILE:O	1:L:256:ILE:HG22	1.77	0.84
1:L:239:LEU:N	1:L:239:LEU:CD2	2.40	0.84
1:L:332:ARG:NH1	1:L:332:ARG:HG2	1.88	0.84
1:L:259:TYR:HE1	1:L:261:GLY:CA	1.91	0.83
1:L:265:LEU:HD23	1:L:265:LEU:C	1.95	0.83
2:R:5:U:C5'	2:R:5:U:C6	2.61	0.83
1:L:436:THR:CG2	1:L:488:ARG:HE	1.91	0.83
1:L:259:TYR:HD2	1:L:265:LEU:CG	1.86	0.83
1:L:236:VAL:O	1:L:238:GLU:N	2.12	0.83
1:L:299:LEU:O	1:L:299:LEU:CD1	2.25	0.83
1:L:-4:ILE:CD1	1:L:-1:ARG:HH12	1.90	0.83
1:L:44:GLY:O	1:L:100:VAL:N	2.12	0.83
1:L:274:GLN:O	1:L:277:SER:HB3	1.79	0.82
1:L:67:PHE:CE1	2:R:10:G:H1'	2.12	0.82
1:L:483:HIS:O	1:L:484:TYR:HB3	1.79	0.82
2:R:5:U:C3'	2:R:5:U:C6	2.63	0.82
1:L:41:ILE:HG13	1:L:208:HIS:HB3	1.62	0.82
1:L:406:ARG:NE	1:L:481:THR:HG22	1.93	0.81
1:L:211:SER:HB2	1:L:215:VAL:HG21	1.60	0.81
2:R:5:U:H3'	2:R:5:U:C6	2.15	0.81
1:L:276:GLU:O	1:L:277:SER:C	2.18	0.81
1:L:42:TYR:N	1:L:42:TYR:CD1	2.45	0.81
1:L:404:CYS:SG	1:L:407:CYS:HB2	2.21	0.80
1:L:140:SER:C	1:L:142:ARG:H	1.82	0.80
1:L:206:LEU:CD1	1:L:207:ILE:N	2.17	0.80
1:L:42:TYR:N	1:L:42:TYR:HD1	1.79	0.80
1:L:128:VAL:HG13	1:L:167:ILE:CD1	2.11	0.80
1:L:498:LEU:HD12	1:L:500:TYR:CZ	2.17	0.80
1:L:237:LEU:O	1:L:237:LEU:CD2	2.30	0.80
1:L:259:TYR:HE1	1:L:261:GLY:HA3	1.45	0.80
1:L:102:VAL:CG1	1:L:116:LEU:HD13	2.08	0.79
1:L:442:ILE:HD13	1:L:474:VAL:CG1	2.12	0.79
1:L:453:ASN:O	1:L:455:LYS:N	2.15	0.79
1:L:222:LEU:HA	1:L:226:ILE:HD11	1.65	0.79
1:L:495:THR:OG1	1:L:497:THR:HB	1.82	0.79
1:L:117:THR:OG1	1:L:119:PHE:HB2	1.82	0.79
1:L:238:GLU:HA	1:L:238:GLU:OE2	1.81	0.79
1:L:184:LEU:O	1:L:188:LEU:CD1	2.31	0.79
1:L:29:ILE:O	1:L:29:ILE:CG2	2.30	0.79
1:L:72:GLU:O	1:L:119:PHE:CD2	2.35	0.79
1:L:458:ALA:O	1:L:461:ALA:CB	2.22	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:453:ASN:O	1:L:454:GLU:C	2.21	0.79
1:L:364:ARG:HH21	1:L:364:ARG:HG3	1.47	0.79
2:R:4:G:H1'	2:R:5:U:OP2	1.82	0.78
1:L:131:PRO:HA	1:L:164:MET:HG3	1.65	0.78
1:L:346:ASP:OD2	5:L:2003:HOH:O	2.02	0.78
1:L:259:TYR:CD1	1:L:260:THR:N	2.51	0.78
1:L:29:ILE:O	1:L:29:ILE:HG22	1.81	0.78
1:L:7:ASN:ND2	1:L:232:ASP:OD1	2.16	0.78
1:L:137:GLY:O	2:R:2:C:C1'	2.32	0.78
1:L:348:ILE:HG23	1:L:349:ASP:H	1.48	0.78
1:L:169:ARG:NH2	1:L:220:ASP:OD1	2.18	0.77
1:L:428:GLU:O	1:L:432:LEU:HD22	1.84	0.77
1:L:27:LEU:HG	1:L:28:ASP:N	1.97	0.77
1:L:222:LEU:HD23	1:L:226:ILE:HD12	1.15	0.77
1:L:128:VAL:HG11	1:L:167:ILE:HD13	0.80	0.76
1:L:293:ILE:HG23	1:L:302:ILE:CG1	2.13	0.76
1:L:134:PRO:HD3	1:L:163:GLY:O	1.85	0.76
1:L:367:VAL:O	1:L:367:VAL:CG2	2.33	0.76
1:L:222:LEU:HD23	1:L:226:ILE:HD11	1.62	0.76
1:L:67:PHE:CD1	2:R:10:G:N9	2.54	0.76
1:L:40:ASN:ND2	1:L:209:GLN:HA	2.00	0.76
1:L:265:LEU:CD2	1:L:265:LEU:C	2.55	0.75
2:R:2:C:C3'	2:R:2:C:C2	2.69	0.75
1:L:367:VAL:HG21	1:L:374:ILE:CD1	2.00	0.75
1:L:201:ARG:HG3	1:L:202:PRO:O	1.86	0.75
1:L:55:ALA:HB1	1:L:68:LEU:O	1.87	0.75
1:L:237:LEU:HA	1:L:240:ALA:CB	2.17	0.74
1:L:304:ILE:HD11	1:L:330:ILE:HD11	1.67	0.74
1:L:450:TYR:CE1	1:L:454:GLU:HG2	2.22	0.74
1:L:233:ASN:ND2	1:L:236:VAL:CG2	2.49	0.74
1:L:372:ALA:HB2	1:L:392:LEU:HG	1.68	0.74
1:L:128:VAL:O	1:L:128:VAL:CG1	2.36	0.74
1:L:22:GLN:HG2	1:L:269:TYR:O	1.86	0.74
1:L:-5:HIS:C	1:L:-4:ILE:HD12	2.09	0.73
1:L:103:GLN:HG3	1:L:104:ILE:H	1.54	0.73
1:L:41:ILE:HG23	1:L:103:GLN:HB2	1.69	0.73
1:L:212:ASN:OD1	1:L:214:ILE:N	2.21	0.73
2:R:9:U:OP1	5:R:2001:HOH:O	2.05	0.72
1:L:291:ILE:HD13	1:L:330:ILE:HG13	1.71	0.72
1:L:131:PRO:HA	1:L:164:MET:CB	2.19	0.72
1:L:346:ASP:OD2	5:L:2004:HOH:O	2.06	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:38:LYS:O	1:L:39:ALA:HB3	1.90	0.72
2:R:4:G:H4'	2:R:5:U:C5'	2.20	0.71
1:L:370:ASP:OD1	1:L:389:ARG:NH2	2.22	0.71
1:L:481:THR:HG23	1:L:482:PRO:CD	2.20	0.71
1:L:481:THR:HG22	1:L:482:PRO:HD3	1.71	0.71
1:L:423:ILE:HD11	1:L:484:TYR:CD2	2.25	0.71
1:L:237:LEU:O	1:L:240:ALA:HB3	1.90	0.71
1:L:31:SER:O	1:L:32:PRO:O	2.09	0.71
1:L:203:ALA:O	1:L:205:PHE:N	2.22	0.71
1:L:476:ASN:OD1	1:L:476:ASN:C	2.28	0.71
1:L:259:TYR:HE1	1:L:261:GLY:N	1.88	0.71
1:L:122:LEU:O	1:L:128:VAL:HA	1.90	0.70
1:L:465:ARG:O	1:L:467:ASP:N	2.23	0.70
1:L:305:ASN:C	1:L:305:ASN:HD22	1.93	0.70
2:R:5:U:H2'	2:R:6:A:O5'	1.91	0.70
1:L:130:MET:CB	1:L:165:GLY:O	2.37	0.70
1:L:41:ILE:O	1:L:207:ILE:HB	1.91	0.70
1:L:297:GLU:O	1:L:297:GLU:HG3	1.91	0.70
1:L:67:PHE:CD2	1:L:69:PRO:HD3	2.27	0.70
1:L:2:LYS:HA	1:L:20:ASP:HA	1.74	0.70
1:L:140:SER:C	1:L:142:ARG:N	2.45	0.70
1:L:443:VAL:HG23	1:L:447:ILE:HB	1.74	0.70
1:L:447:ILE:H	1:L:447:ILE:HD13	1.56	0.69
1:L:317:GLU:OE1	1:L:321:ASN:HB2	1.92	0.69
1:L:75:ARG:O	1:L:78:PHE:CB	2.40	0.69
1:L:445:VAL:HG12	1:L:446:PRO:CD	2.22	0.69
1:L:348:ILE:HG22	1:L:349:ASP:H	1.37	0.69
1:L:72:GLU:O	1:L:119:PHE:HD2	1.74	0.69
1:L:138:GLY:HA3	2:R:2:C:O2'	1.92	0.69
1:L:276:GLU:C	1:L:278:ALA:N	2.45	0.69
1:L:372:ALA:HB1	1:L:390:GLN:HG2	1.75	0.69
1:L:350:MET:SD	1:L:355:HIS:HB3	2.32	0.69
1:L:58:VAL:O	1:L:65:HIS:CB	2.41	0.69
1:L:244:ILE:O	1:L:245:ALA:C	2.31	0.69
1:L:167:ILE:HG12	2:R:2:C:C6	2.23	0.68
1:L:266:PHE:CD2	1:L:271:ILE:HD11	2.28	0.68
2:R:5:U:C2'	2:R:6:A:O5'	2.41	0.68
1:L:460:ASN:O	1:L:462:ILE:N	2.27	0.68
1:L:128:VAL:HG12	1:L:167:ILE:CD1	2.11	0.68
2:R:9:U:H6	2:R:10:G:H21	1.39	0.68
1:L:259:TYR:CE1	1:L:261:GLY:N	2.61	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:476:ASN:OD1	1:L:478:GLN:N	2.24	0.68
1:L:390:GLN:NE2	2:R:6:A:H5'	2.09	0.68
1:L:447:ILE:CD1	1:L:447:ILE:N	2.57	0.68
1:L:203:ALA:O	1:L:205:PHE:CD2	2.46	0.68
1:L:40:ASN:C	1:L:41:ILE:HG12	2.14	0.68
1:L:-6:ALA:O	1:L:-4:ILE:CD1	2.42	0.68
1:L:448:ALA:HB3	1:L:475:PRO:HB3	1.75	0.67
1:L:2:LYS:HG2	1:L:20:ASP:HB2	1.75	0.67
1:L:125:SER:O	1:L:169:ARG:HD3	1.95	0.67
1:L:481:THR:N	1:L:482:PRO:CD	2.58	0.67
1:L:25:TYR:O	1:L:26:ASP:HB2	1.94	0.67
1:L:445:VAL:HG12	1:L:446:PRO:N	2.08	0.67
1:L:128:VAL:HG13	1:L:167:ILE:HD12	1.69	0.67
1:L:67:PHE:HD1	2:R:10:G:C8	2.13	0.67
1:L:103:GLN:HG3	1:L:104:ILE:N	2.10	0.66
1:L:205:PHE:CE1	1:L:206:LEU:O	2.48	0.66
1:L:238:GLU:CA	1:L:238:GLU:OE2	2.43	0.66
1:L:303:ASP:OD2	5:L:2001:HOH:O	2.12	0.66
1:L:131:PRO:C	1:L:164:MET:HB3	2.16	0.66
1:L:486:VAL:HG12	1:L:486:VAL:O	1.94	0.66
1:L:417:GLU:N	1:L:417:GLU:OE2	2.26	0.66
1:L:126:TYR:HD1	1:L:172:GLY:HA2	1.61	0.66
1:L:466:GLN:NE2	1:L:466:GLN:HA	2.11	0.65
1:L:212:ASN:OD1	1:L:213:VAL:N	2.28	0.65
1:L:151:LEU:O	1:L:155:LEU:N	2.26	0.65
1:L:367:VAL:O	1:L:367:VAL:HG22	1.96	0.65
1:L:45:LYS:HA	1:L:98:GLN:O	1.95	0.65
1:L:120:ILE:N	1:L:120:ILE:HD12	2.11	0.65
1:L:132:ASN:CG	1:L:132:ASN:O	2.35	0.65
1:L:403:VAL:O	1:L:405:PRO:N	2.29	0.65
1:L:134:PRO:HA	1:L:165:GLY:N	2.10	0.65
2:R:2:C:O2'	2:R:3:A:P	2.55	0.65
2:R:9:U:H5	2:R:10:G:H22	1.41	0.65
1:L:137:GLY:O	2:R:2:C:C2'	2.45	0.65
1:L:494:GLU:O	1:L:494:GLU:HG2	1.96	0.65
1:L:177:ALA:O	1:L:178:GLU:C	2.34	0.64
1:L:404:CYS:SG	1:L:404:CYS:O	2.55	0.64
1:L:223:ARG:HB2	1:L:225:ASP:OD2	1.98	0.64
1:L:67:PHE:CE1	2:R:10:G:C4	2.85	0.64
1:L:12:GLU:O	1:L:13:GLU:HB2	1.97	0.64
1:L:443:VAL:HG21	1:L:447:ILE:HG22	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:180:LEU:N	1:L:180:LEU:CD2	2.57	0.64
1:L:436:THR:CG2	1:L:488:ARG:NE	2.55	0.63
1:L:286:PRO:HB2	1:L:325:GLU:OE1	1.98	0.63
1:L:291:ILE:O	1:L:291:ILE:CG2	2.46	0.63
1:L:319:ALA:HB1	1:L:348:ILE:HG21	1.80	0.63
1:L:203:ALA:H	1:L:204:PRO:HD3	1.63	0.63
1:L:259:TYR:CE2	1:L:265:LEU:HG	2.30	0.63
1:L:369:GLN:O	1:L:370:ASP:C	2.34	0.63
2:R:4:G:H4'	2:R:5:U:H5'	1.79	0.63
1:L:335:ARG:HH11	1:L:335:ARG:HG3	1.63	0.63
1:L:256:ILE:O	1:L:256:ILE:CG2	2.47	0.63
1:L:62:ALA:O	1:L:63:GLU:C	2.36	0.63
1:L:259:TYR:CD2	1:L:265:LEU:CG	2.65	0.63
2:R:5:U:C5	2:R:5:U:H5'	2.34	0.63
1:L:347:PHE:C	1:L:348:ILE:O	2.35	0.63
1:L:259:TYR:HD1	1:L:260:THR:H	1.45	0.62
1:L:484:TYR:CD1	1:L:484:TYR:C	2.73	0.62
1:L:224:GLN:HA	1:L:224:GLN:NE2	2.09	0.62
1:L:-4:ILE:N	1:L:-4:ILE:CD1	2.55	0.62
1:L:237:LEU:C	1:L:240:ALA:HB3	2.19	0.62
1:L:234:PRO:HG3	1:L:258:LEU:HD11	1.82	0.62
1:L:108:GLU:HA	1:L:113:GLY:O	2.00	0.62
1:L:436:THR:CG2	1:L:488:ARG:HG3	2.30	0.62
1:L:270:GLN:OE1	1:L:270:GLN:HA	2.00	0.62
2:R:4:G:OP2	2:R:5:U:C2	2.53	0.61
1:L:353:VAL:HA	1:L:356:GLN:NE2	2.15	0.61
1:L:62:ALA:O	1:L:63:GLU:O	2.18	0.61
1:L:67:PHE:CE1	2:R:10:G:C1'	2.83	0.61
1:L:130:MET:C	1:L:164:MET:HB2	2.20	0.61
1:L:170:THR:O	1:L:170:THR:CG2	2.48	0.61
1:L:60:TYR:HD2	1:L:60:TYR:H	1.49	0.61
1:L:452:LEU:O	1:L:456:ARG:HB2	2.00	0.60
1:L:-1:ARG:HG2	1:L:0:HIS:CE1	2.36	0.60
1:L:477:ASP:N	1:L:477:ASP:OD2	2.34	0.60
1:L:259:TYR:CE1	1:L:261:GLY:CA	2.81	0.60
1:L:30:GLU:OE2	1:L:213:VAL:N	2.35	0.60
1:L:188:LEU:HA	1:L:191:TRP:HB3	1.83	0.60
1:L:202:PRO:C	1:L:204:PRO:HD2	2.22	0.60
1:L:304:ILE:HD11	1:L:330:ILE:CD1	2.31	0.60
1:L:236:VAL:C	1:L:238:GLU:N	2.54	0.60
1:L:306:SER:OG	1:L:307:ALA:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:2:C:O2	2:R:2:C:C2'	2.49	0.60
1:L:101:ILE:O	1:L:120:ILE:HD11	2.02	0.60
1:L:103:GLN:CG	1:L:104:ILE:N	2.65	0.60
1:L:127:LEU:HD21	1:L:168:VAL:HG13	1.83	0.60
2:R:6:A:H2'	2:R:7:U:H5''	1.82	0.60
1:L:502:LEU:O	1:L:503:PRO:C	2.40	0.60
1:L:457:SER:O	1:L:461:ALA:HB2	2.00	0.60
1:L:212:ASN:OD1	1:L:212:ASN:C	2.39	0.60
1:L:131:PRO:CA	1:L:164:MET:CB	2.80	0.59
1:L:53:LEU:O	1:L:54:GLU:CB	2.50	0.59
2:R:4:G:P	2:R:5:U:H3	2.23	0.59
1:L:137:GLY:HA2	1:L:166:LEU:O	2.03	0.59
1:L:55:ALA:HB1	1:L:68:LEU:C	2.23	0.59
1:L:237:LEU:HA	1:L:240:ALA:HB2	1.83	0.59
1:L:132:ASN:N	1:L:164:MET:HB3	2.18	0.59
1:L:431:ALA:O	1:L:466:GLN:HG3	2.02	0.59
1:L:170:THR:O	1:L:170:THR:HG22	2.01	0.59
1:L:60:TYR:HE1	1:L:104:ILE:HD11	1.67	0.58
1:L:454:GLU:N	1:L:454:GLU:OE1	2.33	0.58
1:L:180:LEU:HD23	1:L:180:LEU:H	1.63	0.58
1:L:154:ALA:HB1	1:L:177:ALA:HB2	1.85	0.58
1:L:291:ILE:CD1	1:L:330:ILE:HG13	2.32	0.58
1:L:77:TYR:O	1:L:79:PRO:HD3	2.04	0.58
1:L:43:LYS:CB	1:L:203:ALA:CB	2.72	0.58
1:L:44:GLY:N	1:L:100:VAL:O	2.35	0.58
1:L:448:ALA:CB	1:L:475:PRO:HB3	2.32	0.58
2:R:5:U:C6	2:R:5:U:C4'	2.85	0.58
1:L:122:LEU:O	1:L:129:LEU:N	2.34	0.58
1:L:133:ASN:O	1:L:133:ASN:ND2	2.37	0.58
1:L:41:ILE:C	1:L:42:TYR:CD1	2.76	0.58
1:L:279:PHE:CZ	1:L:396:LEU:HD21	2.39	0.58
1:L:259:TYR:CD1	1:L:259:TYR:C	2.73	0.57
1:L:67:PHE:CD1	2:R:10:G:C5	2.91	0.57
1:L:260:THR:O	1:L:261:GLY:C	2.42	0.57
1:L:1:MET:HE1	1:L:228:GLU:HG3	1.85	0.57
1:L:109:ARG:O	1:L:111:ASN:N	2.37	0.57
1:L:140:SER:O	1:L:142:ARG:N	2.37	0.57
1:L:8:ALA:CB	1:L:236:VAL:HG21	2.34	0.57
1:L:55:ALA:CB	1:L:69:PRO:CA	2.80	0.57
1:L:128:VAL:O	1:L:128:VAL:HG13	2.05	0.57
1:L:259:TYR:CE1	1:L:261:GLY:HA3	2.32	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:131:PRO:HB2	1:L:191:TRP:CE2	2.39	0.57
1:L:67:PHE:HE1	2:R:10:G:C1'	2.14	0.57
1:L:166:LEU:O	1:L:166:LEU:HD23	2.03	0.57
1:L:-4:ILE:HD13	1:L:-1:ARG:CZ	2.28	0.57
1:L:1:MET:HE2	1:L:228:GLU:N	2.20	0.57
1:L:102:VAL:HG13	1:L:116:LEU:HB3	1.87	0.56
1:L:40:ASN:HB3	1:L:42:TYR:HE1	1.71	0.56
1:L:6:ILE:HB	1:L:231:ILE:HG13	1.86	0.56
2:R:6:A:C6	2:R:7:U:N3	2.74	0.56
1:L:18:LEU:O	1:L:25:TYR:CE2	2.57	0.56
1:L:1:MET:CE	1:L:227:GLY:HA3	2.36	0.56
1:L:38:LYS:O	1:L:39:ALA:CB	2.53	0.56
1:L:360:GLU:OE2	1:L:379:ILE:N	2.36	0.56
1:L:498:LEU:HB2	1:L:501:MET:HB2	1.88	0.56
1:L:391:ARG:NH2	2:R:8:U:OP1	2.38	0.56
1:L:498:LEU:HD12	1:L:500:TYR:OH	2.06	0.56
1:L:188:LEU:O	1:L:191:TRP:N	2.38	0.56
1:L:40:ASN:HB3	1:L:42:TYR:CE1	2.41	0.56
1:L:303:ASP:OD2	5:L:2004:HOH:O	2.17	0.56
1:L:3:ARG:N	1:L:19:VAL:O	2.36	0.56
1:L:265:LEU:O	1:L:265:LEU:HD23	2.06	0.56
1:L:445:VAL:CG1	1:L:446:PRO:N	2.67	0.56
1:L:314:ASP:OD1	1:L:315:ILE:N	2.39	0.56
1:L:132:ASN:N	1:L:164:MET:CB	2.69	0.56
1:L:187:ARG:O	1:L:188:LEU:C	2.45	0.56
1:L:236:VAL:O	1:L:237:LEU:C	2.44	0.56
1:L:357:ARG:NH1	1:L:360:GLU:OE2	2.39	0.56
1:L:445:VAL:N	1:L:446:PRO:CD	2.69	0.56
1:L:51:PRO:C	1:L:53:LEU:H	2.09	0.56
1:L:120:ILE:CD1	1:L:120:ILE:N	2.68	0.56
1:L:167:ILE:HG22	1:L:168:VAL:H	1.70	0.55
1:L:58:VAL:HG21	1:L:116:LEU:HD12	1.87	0.55
1:L:140:SER:HB2	1:L:143:ILE:HG13	1.89	0.55
1:L:127:LEU:CD2	1:L:168:VAL:HG13	2.36	0.55
1:L:30:GLU:HB2	1:L:213:VAL:HB	1.88	0.55
1:L:59:ASP:OD1	1:L:65:HIS:CD2	2.60	0.55
1:L:166:LEU:C	1:L:166:LEU:HD23	2.27	0.55
1:L:276:GLU:O	1:L:279:PHE:N	2.38	0.55
1:L:259:TYR:HD1	1:L:259:TYR:C	2.08	0.55
1:L:317:GLU:O	1:L:318:THR:C	2.45	0.55
1:L:237:LEU:C	1:L:237:LEU:CD2	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:320:PHE:HB2	1:L:355:HIS:CD2	2.41	0.55
1:L:19:VAL:HG13	1:L:23:ARG:O	2.07	0.55
1:L:450:TYR:CD1	1:L:454:GLU:HG2	2.42	0.55
1:L:391:ARG:HH21	2:R:8:U:P	2.30	0.55
1:L:67:PHE:CD1	2:R:10:G:C8	2.95	0.55
1:L:27:LEU:CG	1:L:28:ASP:N	2.70	0.55
1:L:252:PHE:HA	1:L:255:LYS:HB2	1.87	0.55
1:L:22:GLN:O	1:L:274:GLN:NE2	2.38	0.54
1:L:265:LEU:HD21	1:L:269:TYR:HD1	1.72	0.54
1:L:351:THR:N	1:L:352:PRO:HD2	2.23	0.54
1:L:140:SER:OG	1:L:170:THR:CA	2.54	0.54
1:L:347:PHE:HE2	1:L:385:LEU:HD22	1.72	0.54
1:L:466:GLN:O	1:L:467:ASP:C	2.45	0.54
1:L:239:LEU:O	1:L:240:ALA:C	2.44	0.54
1:L:413:VAL:HG11	1:L:481:THR:HG21	1.89	0.54
1:L:169:ARG:C	1:L:171:ALA:H	2.10	0.54
1:L:190:HIS:O	1:L:192:GLU:N	2.40	0.54
1:L:263:ILE:HG23	1:L:264:PRO:HD2	1.89	0.54
1:L:119:PHE:HA	1:L:132:ASN:ND2	2.22	0.54
1:L:246:ALA:O	1:L:247:LEU:C	2.45	0.54
1:L:490:ARG:O	1:L:491:LYS:O	2.26	0.54
2:R:2:C:O2'	2:R:3:A:OP1	2.26	0.54
1:L:96:GLU:CG	1:L:97:GLY:N	2.66	0.54
1:L:251:ASP:O	1:L:252:PHE:CD1	2.61	0.54
1:L:127:LEU:HD12	1:L:183:ASP:HB3	1.89	0.53
1:L:187:ARG:O	1:L:190:HIS:N	2.42	0.53
1:L:213:VAL:HG13	1:L:214:ILE:N	2.23	0.53
1:L:237:LEU:HA	1:L:240:ALA:HB3	1.90	0.53
1:L:112:LYS:CB	2:R:10:G:C5	2.91	0.53
1:L:229:ILE:HB	1:L:256:ILE:HG12	1.91	0.53
1:L:128:VAL:O	1:L:128:VAL:HG12	2.08	0.53
1:L:213:VAL:CG1	1:L:214:ILE:N	2.70	0.53
1:L:33:GLY:O	1:L:35:GLU:N	2.37	0.53
1:L:30:GLU:CB	1:L:213:VAL:HB	2.38	0.53
1:L:155:LEU:O	1:L:158:LEU:CB	2.57	0.53
1:L:368:ARG:NH1	1:L:368:ARG:CG	2.72	0.53
1:L:177:ALA:O	1:L:179:ALA:N	2.41	0.53
1:L:479:MET:SD	1:L:484:TYR:HA	2.50	0.52
1:L:434:GLU:O	1:L:435:ASN:CB	2.57	0.52
1:L:8:ALA:HB3	1:L:233:ASN:HD22	1.74	0.52
1:L:490:ARG:O	1:L:493:GLU:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:167:ILE:H	1:L:167:ILE:HD12	1.74	0.52
1:L:329:GLU:OE1	1:L:332:ARG:NH1	2.42	0.52
1:L:271:ILE:O	1:L:271:ILE:HG13	2.10	0.52
1:L:233:ASN:HD22	1:L:236:VAL:CG2	2.21	0.52
1:L:367:VAL:O	1:L:367:VAL:HG23	2.09	0.52
1:L:41:ILE:C	1:L:42:TYR:HD1	2.11	0.52
1:L:55:ALA:HB2	1:L:69:PRO:CA	2.28	0.52
1:L:58:VAL:C	1:L:65:HIS:HB3	2.28	0.52
1:L:370:ASP:CG	1:L:389:ARG:HH21	2.11	0.52
1:L:498:LEU:HD12	1:L:500:TYR:CE2	2.44	0.52
1:L:359:VAL:O	1:L:362:ARG:HB3	2.09	0.52
1:L:362:ARG:HD2	1:L:362:ARG:O	2.10	0.52
1:L:237:LEU:CD1	1:L:258:LEU:HB2	2.39	0.52
1:L:8:ALA:HB1	1:L:236:VAL:HG21	1.92	0.52
2:R:4:G:H4'	2:R:5:U:H5''	1.91	0.52
1:L:4:MET:CE	1:L:18:LEU:HD21	2.40	0.52
1:L:222:LEU:HA	1:L:226:ILE:HD12	1.79	0.52
1:L:40:ASN:CB	1:L:42:TYR:HE1	2.22	0.52
1:L:291:ILE:HG12	1:L:304:ILE:HG13	1.91	0.52
1:L:356:GLN:O	1:L:360:GLU:HG3	2.10	0.52
1:L:214:ILE:HG22	1:L:215:VAL:N	2.24	0.52
1:L:58:VAL:CG2	1:L:116:LEU:HD12	2.40	0.51
1:L:242:GLN:O	1:L:245:ALA:HB3	2.10	0.51
1:L:237:LEU:HD12	1:L:258:LEU:HB2	1.92	0.51
1:L:237:LEU:CA	1:L:240:ALA:CB	2.88	0.51
1:L:299:LEU:HD13	1:L:299:LEU:O	2.10	0.51
1:L:436:THR:HG22	1:L:488:ARG:HG3	1.92	0.51
1:L:126:TYR:N	1:L:126:TYR:CD2	2.79	0.51
1:L:498:LEU:O	1:L:499:SER:C	2.48	0.51
1:L:272:GLU:O	1:L:275:ILE:N	2.44	0.51
1:L:424:LEU:HB2	1:L:451:LEU:CD2	2.40	0.51
1:L:113:GLY:N	2:R:10:G:N7	2.41	0.51
2:R:8:U:H5''	2:R:9:U:OP2	2.10	0.51
1:L:198:ALA:C	1:L:200:SER:N	2.64	0.51
1:L:279:PHE:CE2	1:L:396:LEU:HD21	2.46	0.51
1:L:299:LEU:C	1:L:299:LEU:CD1	2.78	0.51
1:L:134:PRO:HG3	1:L:162:GLU:O	2.11	0.51
1:L:237:LEU:CA	1:L:240:ALA:HB3	2.41	0.51
1:L:-6:ALA:O	1:L:-4:ILE:HD11	2.11	0.50
1:L:481:THR:CG2	1:L:482:PRO:CD	2.78	0.50
1:L:8:ALA:CB	1:L:233:ASN:HD22	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:67:PHE:HB2	2:R:10:G:C5	2.47	0.50
1:L:119:PHE:CD1	1:L:133:ASN:OD1	2.64	0.50
1:L:202:PRO:C	1:L:204:PRO:CD	2.79	0.50
1:L:16:VAL:O	1:L:16:VAL:HG12	2.11	0.50
1:L:223:ARG:H	1:L:226:ILE:CD1	2.25	0.50
2:R:5:U:C5	2:R:6:A:C2	2.99	0.50
1:L:456:ARG:HG2	1:L:460:ASN:ND2	2.26	0.50
1:L:107:GLU:O	1:L:108:GLU:C	2.50	0.50
1:L:369:GLN:O	1:L:370:ASP:O	2.30	0.50
1:L:481:THR:OG1	1:L:481:THR:O	2.25	0.50
1:L:458:ALA:C	1:L:461:ALA:HB3	2.20	0.50
1:L:465:ARG:C	1:L:467:ASP:H	2.13	0.50
1:L:44:GLY:O	1:L:99:GLU:HA	2.11	0.50
1:L:137:GLY:CA	1:L:166:LEU:O	2.60	0.50
1:L:272:GLU:O	1:L:275:ILE:HB	2.12	0.50
1:L:132:ASN:H	1:L:164:MET:HB2	1.77	0.49
1:L:167:ILE:HD12	1:L:167:ILE:N	2.27	0.49
1:L:265:LEU:O	1:L:268:HIS:N	2.38	0.49
1:L:465:ARG:C	1:L:467:ASP:N	2.64	0.49
1:L:423:ILE:HD11	1:L:484:TYR:CG	2.47	0.49
1:L:327:ALA:CB	1:L:362:ARG:HG3	2.43	0.49
1:L:222:LEU:HD21	1:L:226:ILE:HD13	1.81	0.49
1:L:67:PHE:CE1	2:R:10:G:N9	2.80	0.49
1:L:462:ILE:HG22	1:L:463:GLU:N	2.28	0.49
1:L:-6:ALA:O	1:L:-4:ILE:HD12	2.12	0.49
1:L:58:VAL:O	1:L:65:HIS:CA	2.61	0.49
1:L:20:ASP:O	1:L:20:ASP:OD1	2.30	0.49
2:R:5:U:N1	2:R:5:U:H5'	2.25	0.49
1:L:143:ILE:CD1	1:L:173:VAL:CG2	2.71	0.49
1:L:490:ARG:O	1:L:491:LYS:C	2.50	0.48
1:L:119:PHE:CE1	1:L:133:ASN:OD1	2.67	0.48
1:L:426:LEU:HD12	1:L:426:LEU:O	2.14	0.48
1:L:130:MET:C	1:L:132:ASN:N	2.64	0.48
1:L:260:THR:O	1:L:261:GLY:O	2.30	0.48
1:L:305:ASN:C	1:L:305:ASN:ND2	2.64	0.48
1:L:443:VAL:HG21	1:L:447:ILE:CG2	2.42	0.48
1:L:192:GLU:O	1:L:195:LYS:N	2.41	0.48
1:L:1:MET:HE3	1:L:227:GLY:HA3	1.94	0.48
1:L:154:ALA:O	1:L:157:SER:OG	2.25	0.48
1:L:139:ILE:HG23	1:L:168:VAL:HG23	1.95	0.48
2:R:4:G:H1'	2:R:5:U:P	2.52	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:203:ALA:C	1:L:205:PHE:CD2	2.87	0.48
1:L:460:ASN:O	1:L:461:ALA:C	2.52	0.48
1:L:337:ARG:O	1:L:338:ASP:C	2.49	0.48
1:L:128:VAL:HG12	1:L:167:ILE:H	1.79	0.48
1:L:224:GLN:CA	1:L:224:GLN:NE2	2.77	0.48
1:L:376:ILE:HG22	1:L:376:ILE:O	2.13	0.48
1:L:333:GLN:O	1:L:334:LEU:C	2.50	0.48
1:L:320:PHE:HB2	1:L:355:HIS:HD2	1.79	0.47
1:L:474:VAL:HG22	1:L:474:VAL:O	2.12	0.47
1:L:363:LEU:HA	1:L:363:LEU:HD12	1.54	0.47
1:L:134:PRO:HA	1:L:165:GLY:CA	2.44	0.47
1:L:140:SER:OG	1:L:169:ARG:C	2.52	0.47
1:L:445:VAL:N	1:L:446:PRO:HD3	2.30	0.47
1:L:493:GLU:O	1:L:493:GLU:HG3	2.14	0.47
1:L:72:GLU:O	1:L:119:PHE:CE2	2.68	0.47
1:L:203:ALA:C	1:L:205:PHE:HD2	2.18	0.47
1:L:225:ASP:OD2	1:L:225:ASP:N	2.47	0.47
1:L:131:PRO:C	1:L:164:MET:CB	2.83	0.47
1:L:46:ILE:HD12	1:L:98:GLN:H	1.79	0.47
1:L:103:GLN:O	1:L:116:LEU:HA	2.15	0.47
1:L:432:LEU:O	1:L:434:GLU:N	2.47	0.47
2:R:7:U:H5"	2:R:7:U:C6	2.44	0.47
1:L:134:PRO:HA	1:L:164:MET:C	2.35	0.46
1:L:443:VAL:CG2	1:L:447:ILE:HB	2.42	0.46
1:L:120:ILE:O	1:L:131:PRO:HD2	2.16	0.46
1:L:231:ILE:HG22	1:L:233:ASN:H	1.80	0.46
1:L:132:ASN:O	1:L:133:ASN:HB3	2.16	0.46
1:L:-4:ILE:HD11	1:L:-1:ARG:HH12	1.75	0.46
1:L:285:LEU:O	1:L:286:PRO:C	2.53	0.46
1:L:364:ARG:CG	1:L:364:ARG:HH21	2.15	0.46
1:L:319:ALA:CB	1:L:348:ILE:HG21	2.45	0.46
1:L:272:GLU:O	1:L:273:SER:C	2.54	0.46
1:L:426:LEU:C	1:L:426:LEU:HD12	2.35	0.46
1:L:203:ALA:HA	1:L:205:PHE:CE2	2.51	0.46
1:L:456:ARG:O	1:L:459:VAL:HG23	2.16	0.46
1:L:423:ILE:HD11	1:L:484:TYR:CE2	2.50	0.46
1:L:154:ALA:CB	1:L:177:ALA:HB2	2.45	0.46
1:L:305:ASN:HA	1:L:348:ILE:HD11	1.96	0.46
1:L:440:HIS:ND1	1:L:502:LEU:HD13	2.30	0.46
1:L:58:VAL:HB	1:L:116:LEU:HD11	1.96	0.46
1:L:345:ILE:HG21	1:L:347:PHE:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:15:ARG:HG2	1:L:29:ILE:CG1	2.45	0.46
1:L:151:LEU:O	1:L:152:LYS:C	2.53	0.46
1:L:198:ALA:O	1:L:200:SER:N	2.49	0.46
1:L:198:ALA:C	1:L:200:SER:H	2.19	0.46
1:L:417:GLU:O	1:L:420:SER:N	2.49	0.45
1:L:117:THR:C	1:L:119:PHE:H	2.18	0.45
1:L:428:GLU:O	1:L:428:GLU:HG3	2.15	0.45
1:L:126:TYR:CD1	1:L:172:GLY:HA2	2.45	0.45
1:L:302:ILE:HD13	1:L:330:ILE:HG12	1.97	0.45
1:L:324:LEU:O	1:L:327:ALA:HB3	2.17	0.45
1:L:336:LEU:HA	1:L:336:LEU:HD23	1.59	0.45
1:L:120:ILE:HG22	1:L:122:LEU:HD12	1.98	0.45
1:L:451:LEU:HD13	1:L:473:ILE:HD13	1.98	0.45
1:L:315:ILE:O	1:L:316:GLU:C	2.55	0.45
1:L:210:GLU:OE1	1:L:211:SER:N	2.45	0.45
1:L:75:ARG:O	1:L:78:PHE:N	2.48	0.45
1:L:462:ILE:O	1:L:465:ARG:N	2.45	0.45
1:L:498:LEU:O	1:L:500:TYR:N	2.49	0.45
1:L:129:LEU:CD1	1:L:164:MET:HG3	2.34	0.45
1:L:222:LEU:HA	1:L:222:LEU:HD23	1.60	0.45
1:L:422:SER:O	1:L:423:ILE:C	2.55	0.45
1:L:487:LEU:HD23	1:L:487:LEU:N	2.32	0.45
1:L:127:LEU:HD23	1:L:168:VAL:HA	1.99	0.44
1:L:501:MET:CA	1:L:501:MET:CE	2.77	0.44
1:L:430:GLU:OE1	1:L:488:ARG:HD2	2.17	0.44
1:L:390:GLN:HB2	2:R:6:A:O3'	2.16	0.44
1:L:206:LEU:HD11	1:L:208:HIS:N	2.32	0.44
1:L:501:MET:HA	1:L:501:MET:HE2	1.90	0.44
1:L:481:THR:N	1:L:482:PRO:HD2	2.33	0.44
1:L:26:ASP:OD1	1:L:27:LEU:N	2.49	0.44
1:L:222:LEU:HD21	1:L:226:ILE:HG21	1.99	0.44
1:L:299:LEU:N	1:L:299:LEU:HD12	2.32	0.44
1:L:423:ILE:CD1	1:L:484:TYR:CG	3.01	0.44
1:L:502:LEU:HA	1:L:502:LEU:HD23	1.00	0.44
1:L:251:ASP:O	1:L:251:ASP:CG	2.55	0.44
1:L:221:TYR:CE2	1:L:371:ARG:HG3	2.52	0.44
1:L:179:ALA:O	1:L:183:ASP:N	2.49	0.44
1:L:40:ASN:HD21	1:L:209:GLN:NE2	2.15	0.44
1:L:367:VAL:HG23	1:L:370:ASP:HB2	2.00	0.44
1:L:419:LEU:HD12	1:L:423:ILE:HG12	1.99	0.44
1:L:265:LEU:HD21	1:L:269:TYR:CD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:498:LEU:O	1:L:501:MET:N	2.48	0.44
1:L:421:LEU:HA	1:L:421:LEU:HD23	1.49	0.43
1:L:222:LEU:CA	1:L:226:ILE:HD12	2.45	0.43
1:L:213:VAL:HG23	1:L:216:ARG:NH2	2.33	0.43
1:L:445:VAL:HG12	1:L:446:PRO:HD3	1.96	0.43
1:L:250:PRO:CD	1:L:251:ASP:H	2.31	0.43
1:L:190:HIS:O	1:L:191:TRP:C	2.55	0.43
1:L:24:LEU:HD21	1:L:336:LEU:HD21	2.00	0.43
1:L:352:PRO:HG2	1:L:355:HIS:CG	2.53	0.43
1:L:8:ALA:HB3	1:L:233:ASN:HB3	2.01	0.43
1:L:361:ASN:O	1:L:364:ARG:N	2.52	0.43
1:L:117:THR:HG1	1:L:119:PHE:HB2	1.79	0.43
1:L:205:PHE:CD1	1:L:205:PHE:C	2.92	0.43
1:L:237:LEU:C	1:L:237:LEU:HD23	2.23	0.43
1:L:304:ILE:O	1:L:305:ASN:HB3	2.19	0.43
1:L:280:GLN:HB2	1:L:280:GLN:HE21	1.69	0.43
1:L:304:ILE:HG12	1:L:326:ALA:CB	2.48	0.43
1:L:434:GLU:O	1:L:435:ASN:HB2	2.18	0.42
1:L:252:PHE:C	1:L:255:LYS:H	2.22	0.42
1:L:120:ILE:HG22	1:L:122:LEU:CD1	2.49	0.42
1:L:433:LYS:O	1:L:436:THR:OG1	2.34	0.42
1:L:167:ILE:HG22	1:L:168:VAL:N	2.34	0.42
2:R:1:A:H8	2:R:2:C:H5	1.67	0.42
1:L:55:ALA:HB1	1:L:69:PRO:N	2.34	0.42
1:L:205:PHE:HD1	1:L:206:LEU:O	1.94	0.42
1:L:37:LYS:O	1:L:40:ASN:OD1	2.38	0.42
1:L:4:MET:HG3	1:L:18:LEU:HD23	2.01	0.42
1:L:120:ILE:CD1	1:L:120:ILE:H	2.32	0.42
1:L:304:ILE:CD1	1:L:326:ALA:HB1	2.49	0.42
1:L:357:ARG:HA	1:L:357:ARG:HD3	1.57	0.42
1:L:361:ASN:O	1:L:362:ARG:C	2.58	0.42
1:L:58:VAL:HB	1:L:116:LEU:CD1	2.49	0.42
1:L:453:ASN:C	1:L:455:LYS:N	2.73	0.42
1:L:285:LEU:HD11	1:L:326:ALA:HB2	2.01	0.42
1:L:4:MET:HE2	1:L:18:LEU:HD21	2.01	0.42
1:L:497:THR:HG22	1:L:502:LEU:HD21	2.01	0.42
1:L:102:VAL:CG1	1:L:116:LEU:HB3	2.50	0.41
1:L:363:LEU:O	1:L:364:ARG:C	2.59	0.41
1:L:502:LEU:CB	1:L:503:PRO:HD2	2.50	0.41
1:L:452:LEU:HA	1:L:452:LEU:HD23	1.75	0.41
1:L:432:LEU:CD1	1:L:466:GLN:CD	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:280:GLN:NE2	1:L:282:GLU:O	2.53	0.41
1:L:342:LEU:O	1:L:343:ILE:HG13	2.19	0.41
1:L:438:GLU:C	1:L:489:VAL:HG23	2.40	0.41
1:L:139:ILE:HG22	1:L:140:SER:N	2.35	0.41
1:L:250:PRO:C	1:L:252:PHE:H	2.24	0.41
1:L:90:ILE:O	1:L:93:VAL:N	2.52	0.41
1:L:215:VAL:O	1:L:216:ARG:C	2.58	0.41
1:L:453:ASN:O	1:L:456:ARG:N	2.49	0.41
1:L:222:LEU:C	1:L:223:ARG:HG2	2.41	0.41
1:L:132:ASN:N	1:L:164:MET:HB2	2.35	0.41
1:L:169:ARG:C	1:L:171:ALA:N	2.71	0.41
1:L:498:LEU:N	1:L:498:LEU:HD23	2.35	0.41
1:L:300:THR:O	1:L:343:ILE:HA	2.21	0.41
1:L:183:ASP:O	1:L:186:PHE:N	2.54	0.41
1:L:443:VAL:HB	1:L:444:PRO:HD2	2.02	0.41
1:L:211:SER:O	1:L:216:ARG:HG3	2.20	0.41
1:L:206:LEU:CD1	1:L:208:HIS:N	2.83	0.41
1:L:7:ASN:HD21	1:L:9:THR:CG2	2.33	0.41
1:L:233:ASN:HA	1:L:234:PRO:HD3	1.80	0.41
1:L:19:VAL:HG13	1:L:23:ARG:C	2.41	0.41
1:L:14:LEU:O	1:L:14:LEU:HG	2.19	0.41
1:L:154:ALA:HB1	1:L:177:ALA:CB	2.48	0.41
1:L:460:ASN:C	1:L:462:ILE:N	2.74	0.41
1:L:320:PHE:CD1	1:L:355:HIS:CD2	3.09	0.41
1:L:281:ARG:NH1	1:L:292:VAL:HG11	2.36	0.41
1:L:236:VAL:C	1:L:238:GLU:H	2.24	0.40
1:L:372:ALA:CB	1:L:390:GLN:HG2	2.48	0.40
1:L:15:ARG:HG2	1:L:29:ILE:HG13	2.02	0.40
1:L:480:GLU:C	1:L:482:PRO:HD2	2.41	0.40
1:L:131:PRO:CA	1:L:164:MET:HB2	2.52	0.40
1:L:462:ILE:O	1:L:463:GLU:C	2.60	0.40
1:L:424:LEU:HB2	1:L:451:LEU:HD21	2.04	0.40
2:R:5:U:H5	2:R:6:A:C2	2.40	0.40
1:L:103:GLN:O	1:L:117:THR:N	2.51	0.40
1:L:143:ILE:HG23	1:L:173:VAL:HG21	2.04	0.40
1:L:169:ARG:CG	1:L:169:ARG:NH1	2.38	0.40
1:L:206:LEU:CG	1:L:207:ILE:N	2.82	0.40
1:L:437:GLN:NE2	1:L:437:GLN:HA	2.37	0.40
1:L:265:LEU:O	1:L:266:PHE:C	2.60	0.40
1:L:498:LEU:CD1	1:L:500:TYR:CE2	3.04	0.40
1:L:299:LEU:HD22	1:L:344:VAL:HG23	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:359:VAL:O	1:L:360:GLU:C	2.59	0.40
1:L:214:ILE:HG23	1:L:218:PHE:CE1	2.55	0.40
1:L:109:ARG:HG2	1:L:109:ARG:HH21	1.86	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	L	483/517 (93%)	324 (67%)	91 (19%)	68 (14%)	<b>0</b> <b>5</b>

All (68) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	13	GLU
1	L	26	ASP
1	L	32	PRO
1	L	34	HIS
1	L	63	GLU
1	L	132	ASN
1	L	135	ARG
1	L	141	ARG
1	L	170	THR
1	L	188	LEU
1	L	200	SER
1	L	212	ASN
1	L	237	LEU
1	L	251	ASP
1	L	277	SER
1	L	348	ILE
1	L	433	LYS
1	L	454	GLU

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Mol	Chain	Res	Type
1	L	457	SER
1	L	461	ALA
1	L	466	GLN
1	L	499	SER
1	L	54	GLU
1	L	110	GLY
1	L	140	SER
1	L	187	ARG
1	L	216	ARG
1	L	238	GLU
1	L	261	GLY
1	L	265	LEU
1	L	269	TYR
1	L	307	ALA
1	L	370	ASP
1	L	378	HIS
1	L	459	VAL
1	L	484	TYR
1	L	491	LYS
1	L	-1	ARG
1	L	33	GLY
1	L	178	GLU
1	L	199	GLU
1	L	204	PRO
1	L	245	ALA
1	L	246	ALA
1	L	435	ASN
1	L	39	ALA
1	L	52	SER
1	L	65	HIS
1	L	185	SER
1	L	191	TRP
1	L	286	PRO
1	L	409	GLY
1	L	467	ASP
1	L	93	VAL
1	L	112	LYS
1	L	153	GLU
1	L	202	PRO
1	L	318	THR
1	L	387	MET
1	L	90	ILE

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Mol	Chain	Res	Type
1	L	240	ALA
1	L	404	CYS
1	L	51	PRO
1	L	207	ILE
1	L	236	VAL
1	L	215	VAL
1	L	462	ILE
1	L	128	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	L	337/439 (77%)	219 (65%)	118 (35%)	<b>0</b> <b>2</b>

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	-4	ILE
1	L	3	ARG
1	L	9	THR
1	L	10	GLN
1	L	12	GLU
1	L	18	LEU
1	L	20	ASP
1	L	22	GLN
1	L	23	ARG
1	L	27	LEU
1	L	29	ILE
1	L	41	ILE
1	L	42	TYR
1	L	47	THR
1	L	52	SER
1	L	59	ASP
1	L	60	TYR
1	L	65	HIS

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Mol	Chain	Res	Type
1	L	68	LEU
1	L	96	GLU
1	L	100	VAL
1	L	102	VAL
1	L	109	ARG
1	L	117	THR
1	L	118	THR
1	L	121	SER
1	L	125	SER
1	L	126	TYR
1	L	128	VAL
1	L	133	ASN
1	L	139	ILE
1	L	142	ARG
1	L	143	ILE
1	L	164	MET
1	L	166	LEU
1	L	167	ILE
1	L	168	VAL
1	L	169	ARG
1	L	180	LEU
1	L	188	LEU
1	L	201	ARG
1	L	206	LEU
1	L	211	SER
1	L	213	VAL
1	L	214	ILE
1	L	215	VAL
1	L	223	ARG
1	L	224	GLN
1	L	225	ASP
1	L	231	ILE
1	L	233	ASN
1	L	238	GLU
1	L	239	LEU
1	L	253	SER
1	L	254	SER
1	L	256	ILE
1	L	259	TYR
1	L	267	SER
1	L	270	GLN
1	L	272	GLU

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Mol	Chain	Res	Type
1	L	277	SER
1	L	280	GLN
1	L	290	SER
1	L	291	ILE
1	L	293	ILE
1	L	297	GLU
1	L	299	LEU
1	L	304	ILE
1	L	305	ASN
1	L	315	ILE
1	L	318	THR
1	L	321	ASN
1	L	322	THR
1	L	332	ARG
1	L	338	ASP
1	L	348	ILE
1	L	349	ASP
1	L	350	MET
1	L	353	VAL
1	L	354	ARG
1	L	355	HIS
1	L	357	ARG
1	L	364	ARG
1	L	367	VAL
1	L	371	ARG
1	L	374	ILE
1	L	376	ILE
1	L	385	LEU
1	L	386	GLU
1	L	389	ARG
1	L	390	GLN
1	L	392	LEU
1	L	403	VAL
1	L	406	ARG
1	L	410	THR
1	L	419	LEU
1	L	425	ARG
1	L	426	LEU
1	L	432	LEU
1	L	436	THR
1	L	439	VAL
1	L	443	VAL

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Mol	Chain	Res	Type
1	L	445	VAL
1	L	447	ILE
1	L	459	VAL
1	L	463	GLU
1	L	466	GLN
1	L	474	VAL
1	L	476	ASN
1	L	477	ASP
1	L	487	LEU
1	L	488	ARG
1	L	489	VAL
1	L	495	THR
1	L	497	THR
1	L	498	LEU
1	L	501	MET
1	L	502	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	22	GLN
1	L	40	ASN
1	L	65	HIS
1	L	132	ASN
1	L	133	ASN
1	L	209	GLN
1	L	224	GLN
1	L	233	ASN
1	L	305	ASN
1	L	355	HIS
1	L	356	GLN
1	L	416	ASN
1	L	437	GLN
1	L	460	ASN
1	L	466	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	10/10 (100%)	8 (80%)	7 (70%)

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	2	C
2	R	3	A
2	R	4	G
2	R	5	U
2	R	6	A
2	R	7	U
2	R	8	U
2	R	10	G

All (7) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	R	1	A
2	R	2	C
2	R	3	A
2	R	4	G
2	R	5	U
2	R	6	A
2	R	7	U

## 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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [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	L	491/517 (94%)	-0.26	10 (2%) 68 54	21, 66, 85, 85	0
2	R	10/10 (100%)	-0.04	0 100 100	59, 79, 85, 85	0
All	All	501/527 (95%)	-0.25	10 (1%) 68 54	21, 67, 85, 85	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	56	ALA	4.2
1	L	44	GLY	2.7
1	L	57	PHE	2.7
1	L	47	THR	2.5
1	L	43	LYS	2.2
1	L	118	THR	2.2
1	L	180	LEU	2.2
1	L	68	LEU	2.1
1	L	102	VAL	2.1
1	L	116	LEU	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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	L	1511	1/1	0.97	0.10	-2.13	52,52,52,52	0
4	ZN	L	1512	1/1	0.96	0.32	-	85,85,85,85	1
3	MG	L	1510	1/1	0.83	1.07	-	48,48,48,48	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.