



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 03:15 AM BST

PDB ID : 1FLC  
Title : X-RAY STRUCTURE OF THE HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN OF INFLUENZA C VIRUS  
Authors : Rosenthal, P.B.; Zhang, X.; Formanowski, F.; Fitz, W.; Wong, C.H.; Meier-Ewert, H.; Skehel, J.J.; Wiley, D.C.  
Deposited on : 1999-02-22  
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

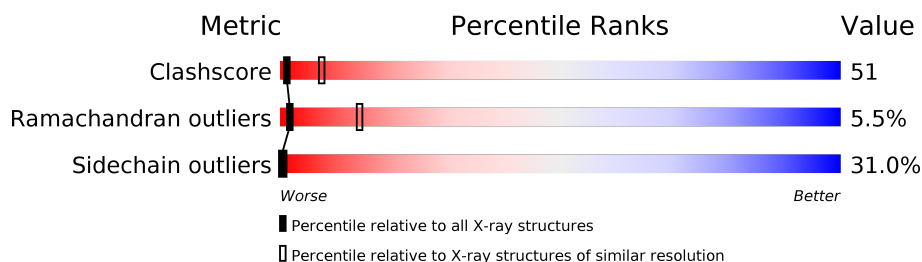
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	432	
1	C	432	
1	E	432	
2	B	175	
2	D	175	
2	F	175	
3	G	3	
3	H	3	

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Mol	Chain	Length	Quality of chain
3	I	3	 100%
3	J	3	 33% 67%
3	L	3	 33% 67%
3	M	3	 33% 67%
3	O	3	 100%
3	Q	3	 33% 33% 33%
3	R	3	 33% 33% 33%
3	S	3	 33% 33% 33%
3	T	3	 67% 33%
4	K	3	 67% 33%
4	P	3	 33% 67%
4	U	3	 100%
5	N	3	 33% 67%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	G	1	X	-	-	-
3	NAG	L	1	X	-	-	-
3	NAG	Q	1	X	-	-	-
4	NDG	K	2	-	-	X	-
4	MAN	K	3	-	-	X	-
4	NDG	U	2	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 14285 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 HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3339	2113	565	636	25			
1	C	427	Total	C	N	O	S	0	0	0
			3338	2112	565	636	25			
1	E	427	Total	C	N	O	S	0	0	0
			3339	2113	565	636	25			

- Molecule 2 is a protein called HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	162	Total	C	N	O	S	0	0	0
			1228	773	206	246	3			
2	D	162	Total	C	N	O	S	0	0	0
			1228	773	206	246	3			
2	F	162	Total	C	N	O	S	0	0	0
			1228	773	206	246	3			

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	L	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	M	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	O	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	Q	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	R	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	S	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	T	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	K	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	P	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	U	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



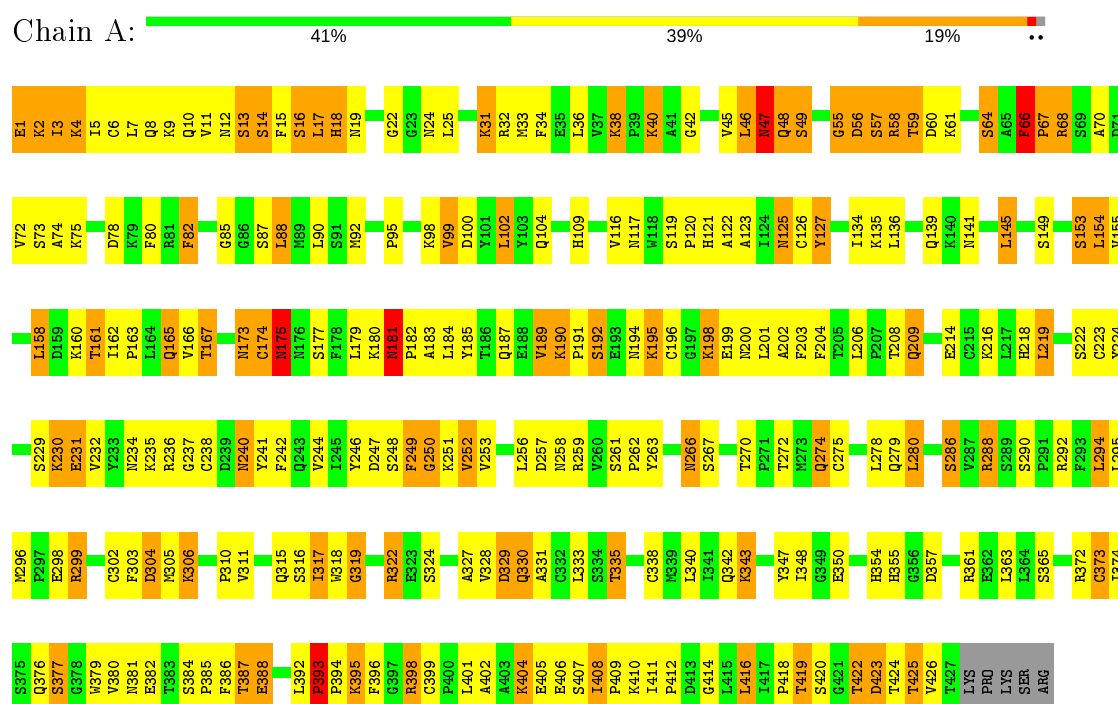
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	N	3	Total	C	N	O	0	0	0
			39	22	2	15			

### 3 Residue-property plots

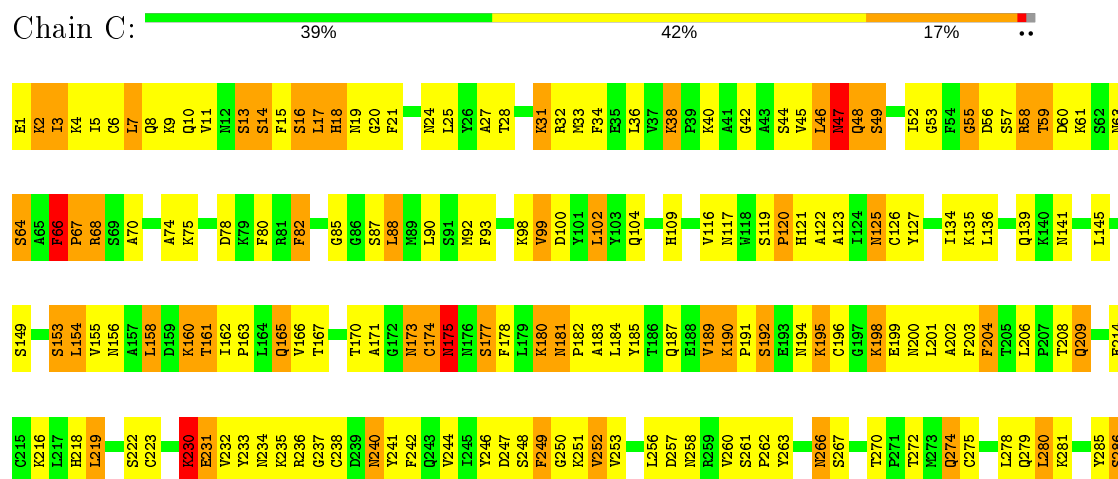
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

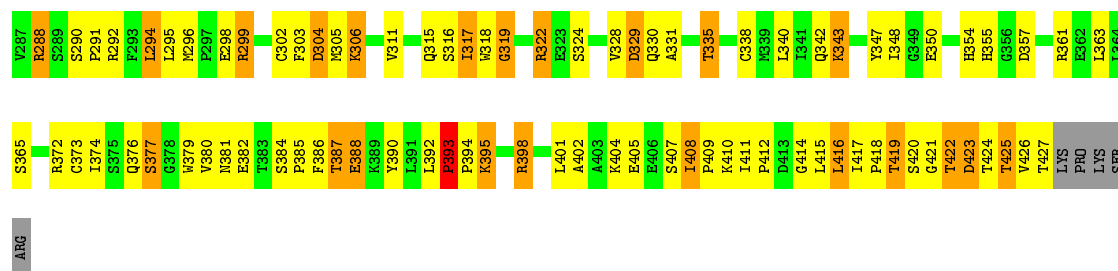
Note EDS was not executed.

#### • Molecule 1: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN



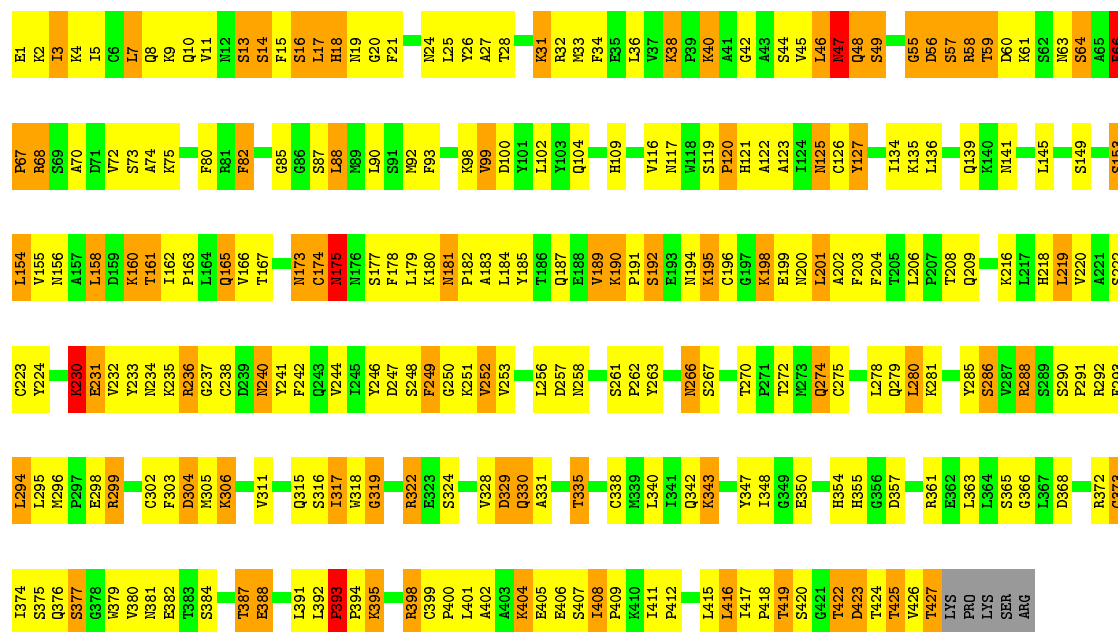
#### • Molecule 1: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN





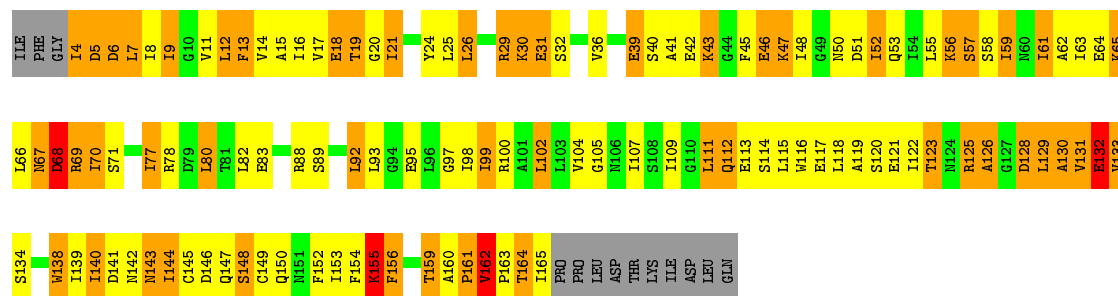
• Molecule 1: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN

Chain E: 39% 41% 18% ..



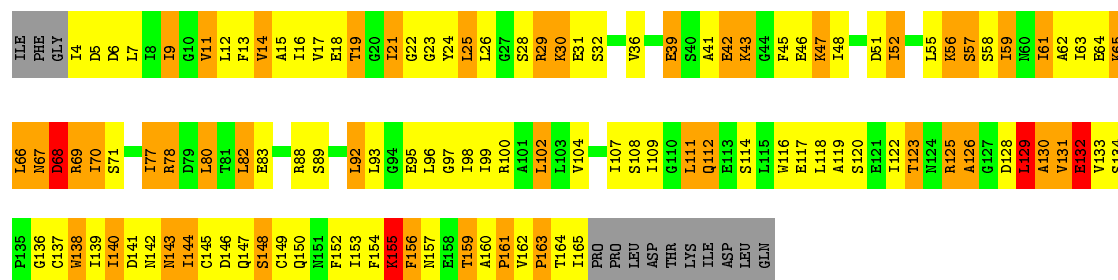
• Molecule 2: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN

Chain B: 24% 37% 29% 7%

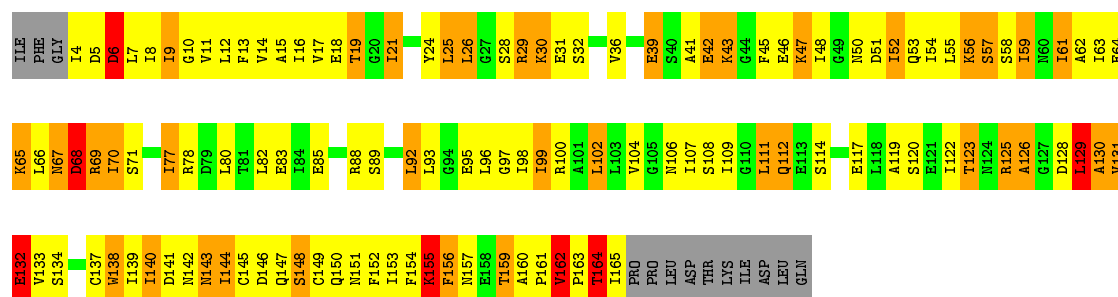
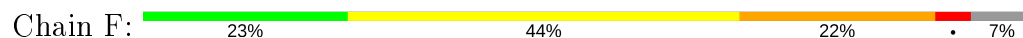


• Molecule 2: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN

Chain D: 25% 41% 25% 7%



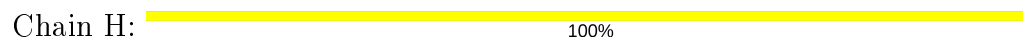
• Molecule 2: HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  67% 33%

MA01  
MA02  
MA03

- Molecule 4: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  67% 33%

MA01  
MA02  
MA03

- Molecule 4: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  33% 67%

MA01  
MA02  
MA03

- Molecule 4: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  100%

MA01  
MA02  
MA03

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  33% 67%

MA01  
MA02  
MA03

## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.40 Å   155.40 Å   414.40 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	10.00 – 3.20	Depositor
% Data completeness (in resolution range)	99.0 (10.00-3.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
Refinement program	X-PLOR 3.54	Depositor
R, $R_{free}$	0.223 , 0.267	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14285	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

## 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: BMA, NAG, NDG, MAN

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	0.68	0/3420	0.87	7/4622 (0.2%)
1	C	0.67	0/3418	0.87	6/4618 (0.1%)
1	E	0.68	0/3420	0.86	6/4622 (0.1%)
2	B	0.61	1/1241 (0.1%)	0.75	1/1678 (0.1%)
2	D	0.61	1/1241 (0.1%)	0.77	2/1678 (0.1%)
2	F	0.63	1/1241 (0.1%)	0.80	3/1678 (0.2%)
All	All	0.66	3/13981 (0.0%)	0.84	25/18896 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	E	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	39	GLU	CD-OE2	7.87	1.34	1.25
2	F	39	GLU	CD-OE2	7.71	1.34	1.25
2	B	39	GLU	CD-OE2	7.51	1.33	1.25

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	55	GLY	N-CA-C	6.17	128.54	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	175	ASN	C-N-CA	-6.11	106.43	121.70
1	A	304	ASP	N-CA-C	-6.03	94.71	111.00
1	E	304	ASP	N-CA-C	-5.91	95.04	111.00
1	C	304	ASP	N-CA-C	-5.87	95.15	111.00
1	A	175	ASN	C-N-CA	-5.71	107.42	121.70
2	B	69	ARG	N-CA-C	-5.70	95.61	111.00
1	A	55	GLY	N-CA-C	5.67	127.28	113.10
1	E	393	PRO	C-N-CD	5.64	140.24	128.40
1	A	319	GLY	N-CA-C	-5.63	99.02	113.10
1	C	175	ASN	C-N-CA	-5.63	107.63	121.70
1	E	55	GLY	N-CA-C	5.58	127.04	113.10
2	D	69	ARG	N-CA-C	-5.50	96.14	111.00
1	E	319	GLY	N-CA-C	-5.50	99.36	113.10
1	C	319	GLY	N-CA-C	-5.44	99.49	113.10
1	A	393	PRO	C-N-CD	5.43	139.80	128.40
2	F	162	VAL	N-CA-C	5.35	125.45	111.00
2	F	69	ARG	N-CA-C	-5.31	96.67	111.00
1	C	393	PRO	C-N-CD	5.30	139.52	128.40
1	C	66	PHE	N-CA-C	5.22	125.11	111.00
2	F	129	LEU	CA-CB-CG	5.17	127.19	115.30
1	A	66	PHE	N-CA-C	5.17	124.95	111.00
1	A	181	ASN	C-N-CD	5.12	139.15	128.40
2	D	129	LEU	CA-CB-CG	5.10	127.03	115.30
1	E	66	PHE	N-CA-C	5.06	124.65	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	249	PHE	Sidechain
1	C	249	PHE	Sidechain
1	E	249	PHE	Sidechain

## 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	3339	0	3251	331	0
1	C	3338	0	3245	349	0
1	E	3339	0	3250	336	0
2	B	1228	0	1232	199	0
2	D	1228	0	1232	234	0
2	F	1228	0	1232	188	0
3	G	39	0	34	2	0
3	H	39	0	34	0	0
3	I	39	0	34	0	0
3	J	39	0	34	0	0
3	L	39	0	34	3	0
3	M	39	0	34	0	0
3	O	39	0	34	0	0
3	Q	39	0	34	6	0
3	R	39	0	34	1	0
3	S	39	0	34	1	0
3	T	39	0	34	2	0
4	K	39	0	33	11	0
4	P	39	0	33	5	0
4	U	39	0	33	8	0
5	N	39	0	33	0	0
All	All	14285	0	13948	1441	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 51.

All (1441) 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:A:55:GLY:HA3	1:A:82:PHE:HB3	1.26	1.17
1:E:55:GLY:HA3	1:E:82:PHE:HB3	1.23	1.17
1:C:55:GLY:HA3	1:C:82:PHE:HB3	1.19	1.16
2:F:126:ALA:HB3	2:F:129:LEU:HG	1.25	1.15
2:B:126:ALA:HB3	2:B:129:LEU:HG	1.21	1.14
2:B:5:ASP:H	2:B:9:ILE:HG23	1.07	1.10
1:C:418:PRO:HD3	2:D:111:LEU:HD13	1.11	1.10
2:D:126:ALA:HB3	2:D:129:LEU:HG	1.28	1.10
1:A:249:PHE:HE2	1:C:252:VAL:HG11	1.07	1.10
1:A:257:ASP:HB2	1:E:249:PHE:CE1	1.88	1.09
2:D:30:LYS:HD2	2:D:32:SER:H	1.19	1.07
2:B:30:LYS:HD2	2:B:32:SER:H	1.21	1.05
1:A:249:PHE:CD2	1:C:252:VAL:HG21	1.91	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:418:PRO:HD3	2:F:111:LEU:HD13	1.31	1.04
4:K:2:NDG:O3	4:K:3:MAN:H5	1.57	1.03
2:B:129:LEU:O	2:B:131:VAL:HG12	1.56	1.03
1:A:2:LYS:HB3	2:B:31:GLU:HB2	1.37	1.03
1:E:377:SER:HB2	1:E:392:LEU:H	1.24	1.02
1:A:377:SER:HB2	1:A:392:LEU:H	1.20	1.02
2:F:129:LEU:O	2:F:131:VAL:HG12	1.58	1.01
2:F:30:LYS:HD2	2:F:32:SER:H	1.23	1.01
1:C:294:LEU:HD11	1:C:296:MET:HE3	1.42	1.01
1:C:377:SER:HB2	1:C:392:LEU:H	1.21	1.01
1:C:55:GLY:CA	1:C:82:PHE:HB3	1.88	1.01
1:C:10:GLN:NE2	2:D:25:LEU:HD21	1.75	1.01
1:E:166:VAL:HG21	1:E:185:TYR:HB3	1.42	1.01
1:E:1:GLU:N	2:F:142:ASN:H	1.59	1.01
1:E:55:GLY:CA	1:E:82:PHE:HB3	1.90	1.01
1:A:249:PHE:CE2	1:C:252:VAL:HG11	1.95	1.00
1:A:3:ILE:HA	2:B:30:LYS:HA	1.41	1.00
1:C:249:PHE:HE2	1:E:252:VAL:HG11	1.27	1.00
1:E:294:LEU:HD11	1:E:296:MET:HE3	1.38	1.00
1:A:55:GLY:CA	1:A:82:PHE:HB3	1.93	0.99
2:D:129:LEU:O	2:D:131:VAL:HG12	1.62	0.98
1:A:249:PHE:HD2	1:C:252:VAL:HG21	1.23	0.97
1:C:5:ILE:HG21	2:D:154:PHE:CD1	1.98	0.97
1:C:418:PRO:HD3	2:D:111:LEU:CD1	1.96	0.96
1:E:166:VAL:CG2	1:E:185:TYR:HB3	1.94	0.96
1:A:8:GLN:HE22	2:B:8:ILE:HA	1.28	0.95
1:A:216:LYS:HD3	1:A:305:MET:H	1.30	0.94
1:C:166:VAL:HG21	1:C:185:TYR:HB3	1.46	0.94
1:C:216:LYS:HD3	1:C:305:MET:H	1.32	0.94
1:C:3:ILE:HD11	2:D:140:ILE:HG22	1.48	0.93
1:C:418:PRO:HG3	2:D:111:LEU:HB3	1.51	0.93
1:E:1:GLU:H2	2:F:142:ASN:H	1.04	0.93
1:C:3:ILE:CD1	2:D:140:ILE:HG22	1.98	0.92
1:A:294:LEU:HD11	1:A:296:MET:HE3	1.51	0.92
1:A:257:ASP:HB2	1:E:249:PHE:CD1	2.05	0.92
1:A:166:VAL:HG21	1:A:185:TYR:HB3	1.49	0.92
1:C:166:VAL:CG2	1:C:185:TYR:HB3	2.00	0.92
1:C:10:GLN:HE21	2:D:25:LEU:HD21	1.34	0.91
1:A:8:GLN:HE22	2:B:8:ILE:CA	1.83	0.91
1:C:3:ILE:CG1	2:D:140:ILE:HG22	2.00	0.91
2:F:129:LEU:HA	2:F:140:ILE:HG12	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:LYS:HD3	1:E:305:MET:H	1.33	0.90
1:A:166:VAL:CG2	1:A:185:TYR:HB3	2.02	0.90
2:D:141:ASP:OD1	2:D:143:ASN:HB2	1.71	0.90
2:B:129:LEU:HA	2:B:140:ILE:HG12	1.54	0.89
1:C:9:LYS:HE2	2:D:112:GLN:HE22	1.36	0.89
1:E:8:GLN:HB3	2:F:25:LEU:HD12	1.55	0.88
2:B:4:ILE:HG22	2:B:9:ILE:HG21	1.55	0.88
1:C:31:LYS:NZ	1:C:411:ILE:HB	1.88	0.88
2:D:129:LEU:HA	2:D:140:ILE:HG12	1.56	0.88
1:A:31:LYS:NZ	1:A:411:ILE:HB	1.88	0.88
2:D:160:ALA:N	2:D:161:PRO:HD3	1.89	0.88
1:E:184:LEU:HD12	1:E:185:TYR:H	1.38	0.88
2:F:4:ILE:HG22	2:F:13:PHE:CD2	2.09	0.87
1:C:426:VAL:CG2	2:D:4:ILE:HG23	2.04	0.87
1:A:422:THR:HG21	2:F:51:ASP:HB3	1.55	0.87
1:A:184:LEU:HD12	1:A:185:TYR:H	1.40	0.87
1:A:230:LYS:HD2	1:A:234:ASN:HD21	1.41	0.86
1:E:31:LYS:NZ	1:E:411:ILE:HB	1.90	0.86
1:C:249:PHE:HD2	1:E:252:VAL:HG21	1.39	0.86
1:C:5:ILE:HG12	2:D:154:PHE:CE2	2.09	0.86
1:E:126:CYS:O	1:E:127:TYR:HB2	1.76	0.86
2:B:126:ALA:HB3	2:B:129:LEU:CG	2.03	0.85
1:E:3:ILE:HD11	2:F:140:ILE:HG22	1.58	0.85
1:A:80:PHE:HB3	1:A:82:PHE:CD2	2.11	0.85
1:A:231:GLU:CD	1:A:231:GLU:N	2.28	0.85
1:E:231:GLU:CD	1:E:231:GLU:N	2.30	0.85
1:C:249:PHE:CE2	1:E:252:VAL:HG11	2.12	0.84
1:C:426:VAL:HG21	2:D:4:ILE:HG23	1.59	0.84
2:B:5:ASP:HB2	2:B:9:ILE:HA	1.59	0.84
2:B:5:ASP:N	2:B:9:ILE:HG23	1.90	0.84
1:C:8:GLN:HB3	2:D:25:LEU:HD12	1.58	0.84
1:A:59:THR:HB	1:A:82:PHE:CD2	2.13	0.83
1:C:80:PHE:HB3	1:C:82:PHE:CD2	2.13	0.83
1:E:59:THR:HB	1:E:82:PHE:CD2	2.14	0.83
1:A:134:ILE:HD13	1:A:275:CYS:HB2	1.60	0.83
2:B:126:ALA:CB	2:B:129:LEU:HG	2.07	0.83
1:E:249:PHE:CG	1:E:250:GLY:N	2.43	0.83
2:F:126:ALA:HB3	2:F:129:LEU:CG	2.06	0.82
1:C:184:LEU:HD12	1:C:185:TYR:H	1.44	0.82
2:D:126:ALA:HB3	2:D:129:LEU:CG	2.09	0.82
1:E:4:LYS:O	2:F:28:SER:HA	1.79	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:80:PHE:HB3	1:E:82:PHE:CD2	2.14	0.82
2:F:126:ALA:CB	2:F:129:LEU:HG	2.09	0.82
1:C:249:PHE:CD2	1:E:252:VAL:HG21	2.15	0.82
1:E:181:ASN:HB3	1:E:182:PRO:HD3	1.60	0.82
1:C:249:PHE:CG	1:C:250:GLY:N	2.47	0.81
1:C:231:GLU:CD	1:C:231:GLU:N	2.34	0.81
1:A:249:PHE:CG	1:A:250:GLY:N	2.48	0.81
1:C:393:PRO:HB2	1:C:394:PRO:HD3	1.61	0.81
2:D:4:ILE:HG22	2:D:13:PHE:CB	2.10	0.81
1:C:181:ASN:HB3	1:C:182:PRO:HD3	1.62	0.80
2:B:68:ASP:C	2:B:70:ILE:H	1.83	0.80
1:C:25:LEU:HD11	2:D:107:ILE:CG2	2.11	0.80
1:A:126:CYS:O	1:A:127:TYR:HB2	1.80	0.80
2:F:65:LYS:HB2	2:F:65:LYS:HZ2	1.46	0.80
4:U:2:NDG:O3	4:U:3:MAN:H2	1.82	0.80
1:C:59:THR:HB	1:C:82:PHE:CD2	2.17	0.80
2:D:5:ASP:OD1	2:D:9:ILE:HA	1.80	0.80
1:A:181:ASN:HB3	1:A:182:PRO:HD3	1.62	0.80
1:A:288:ARG:NH1	1:A:288:ARG:HG3	1.97	0.79
1:C:230:LYS:HD2	1:C:234:ASN:HD21	1.45	0.79
1:C:3:ILE:HG13	2:D:140:ILE:O	1.82	0.79
1:C:38:LYS:H	1:C:38:LYS:HD3	1.48	0.79
1:C:420:SER:HB3	1:C:424:THR:OG1	1.83	0.79
1:C:25:LEU:HD11	2:D:107:ILE:HG21	1.62	0.79
1:E:134:ILE:HD13	1:E:275:CYS:HB2	1.65	0.79
1:A:19:ASN:ND2	4:U:2:NDG:H8C2	1.97	0.79
1:E:1:GLU:HG2	1:E:2:LYS:N	1.98	0.79
2:D:4:ILE:HG22	2:D:9:ILE:HG21	1.63	0.78
1:E:230:LYS:HD2	1:E:234:ASN:HD21	1.48	0.78
1:E:405:GLU:O	1:E:408:ILE:HG23	1.84	0.78
1:E:28:THR:HG21	3:Q:2:NAG:H82	1.64	0.78
1:C:3:ILE:HG12	2:D:140:ILE:HG22	1.66	0.78
1:C:405:GLU:O	1:C:408:ILE:HG23	1.83	0.78
2:B:131:VAL:HG21	2:B:139:ILE:HB	1.64	0.78
1:C:3:ILE:HD11	2:D:140:ILE:CG2	2.13	0.78
1:E:45:VAL:C	1:E:46:LEU:HD23	2.04	0.78
2:F:68:ASP:C	2:F:70:ILE:H	1.85	0.78
2:B:125:ARG:O	2:B:129:LEU:HD21	1.82	0.78
1:A:45:VAL:C	1:A:46:LEU:HD23	2.03	0.78
1:E:240:ASN:ND2	1:E:263:TYR:OH	2.15	0.78
2:D:9:ILE:HD13	2:D:9:ILE:N	1.99	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:46:LEU:O	1:E:48:GLN:N	2.17	0.77
1:A:257:ASP:HB2	1:E:249:PHE:HE1	1.46	0.77
1:A:240:ASN:ND2	1:A:263:TYR:OH	2.18	0.77
1:A:288:ARG:HH11	1:A:288:ARG:HG3	1.49	0.77
2:B:126:ALA:N	2:B:129:LEU:HD11	2.00	0.77
2:D:146:ASP:OD2	2:D:148:SER:HB2	1.85	0.77
1:A:22:GLY:N	2:F:106:ASN:OD1	2.18	0.77
1:A:154:LEU:HD22	1:A:155:VAL:N	2.00	0.76
2:B:141:ASP:OD1	2:B:143:ASN:HB2	1.84	0.76
1:C:46:LEU:O	1:C:48:GLN:N	2.18	0.76
2:B:21:ILE:HD12	2:B:21:ILE:H	1.50	0.76
1:C:338:CYS:O	2:D:78:ARG:NH2	2.18	0.76
1:A:319:GLY:H	1:A:354:HIS:CD2	2.04	0.76
1:E:294:LEU:HD11	1:E:296:MET:CE	2.13	0.76
1:E:418:PRO:HD3	2:F:111:LEU:CD1	2.15	0.76
1:C:126:CYS:O	1:C:127:TYR:HB2	1.84	0.76
2:F:7:LEU:HD23	2:F:29:ARG:HH12	1.49	0.76
2:B:5:ASP:O	2:B:9:ILE:HD13	1.84	0.76
1:C:294:LEU:HD11	1:C:296:MET:CE	2.15	0.76
1:A:158:LEU:HD21	1:A:298:GLU:HA	1.67	0.75
2:D:126:ALA:CB	2:D:129:LEU:HG	2.12	0.75
1:E:38:LYS:H	1:E:38:LYS:HD3	1.50	0.75
1:E:420:SER:HB3	1:E:424:THR:OG1	1.86	0.75
2:B:131:VAL:HG11	2:B:139:ILE:C	2.07	0.75
1:C:134:ILE:HD13	1:C:275:CYS:HB2	1.68	0.75
1:A:393:PRO:HB2	1:A:394:PRO:HD3	1.67	0.75
2:B:162:VAL:HG22	2:B:162:VAL:O	1.87	0.75
2:B:129:LEU:O	2:B:131:VAL:N	2.19	0.74
1:C:203:PHE:HD1	1:C:286:SER:HB3	1.51	0.74
1:E:158:LEU:HD21	1:E:298:GLU:HA	1.67	0.74
1:E:154:LEU:HD22	1:E:155:VAL:N	2.03	0.74
2:F:129:LEU:O	2:F:131:VAL:N	2.21	0.74
1:C:5:ILE:O	2:D:138:TRP:CD1	2.40	0.74
1:C:3:ILE:O	2:D:139:ILE:HG23	1.86	0.74
1:C:45:VAL:C	1:C:46:LEU:HD23	2.07	0.74
1:E:379:TRP:HZ3	1:E:381:ASN:HB3	1.52	0.74
1:C:340:LEU:H	1:C:376:GLN:HE22	1.33	0.74
2:D:68:ASP:C	2:D:70:ILE:H	1.86	0.74
2:B:125:ARG:C	2:B:129:LEU:HD21	2.08	0.74
2:B:138:TRP:N	2:B:138:TRP:CD1	2.56	0.74
2:B:131:VAL:CG2	2:B:139:ILE:H	2.01	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:ILE:HG22	2:B:9:ILE:CG2	2.18	0.74
1:C:59:THR:O	1:C:82:PHE:CE2	2.41	0.74
2:B:65:LYS:HB2	2:B:65:LYS:HZ2	1.52	0.74
1:C:163:PRO:HB2	1:C:165:GLN:OE1	1.88	0.74
1:C:158:LEU:HD21	1:C:298:GLU:HA	1.70	0.74
4:K:2:NDG:H4	4:K:3:MAN:H3	1.68	0.74
1:A:163:PRO:HB2	1:A:165:GLN:OE1	1.87	0.73
1:C:388:GLU:CD	1:C:388:GLU:H	1.90	0.73
2:D:65:LYS:HB2	2:D:65:LYS:NZ	2.03	0.73
2:F:55:LEU:HB3	2:F:107:ILE:HD12	1.70	0.73
1:C:60:ASP:HA	1:C:82:PHE:CD1	2.22	0.73
2:B:55:LEU:HB3	2:B:107:ILE:HD12	1.70	0.73
1:C:240:ASN:ND2	1:C:263:TYR:OH	2.20	0.73
1:E:66:PHE:HB3	1:E:67:PRO:HD3	1.70	0.73
1:A:216:LYS:HD3	1:A:305:MET:N	2.02	0.73
1:C:3:ILE:CD1	2:D:140:ILE:H	2.01	0.73
1:A:46:LEU:O	1:A:48:GLN:N	2.22	0.73
2:B:62:ALA:O	2:B:66:LEU:HD13	1.89	0.73
1:E:392:LEU:HD22	1:E:393:PRO:HD2	1.68	0.73
2:F:141:ASP:OD1	2:F:143:ASN:HB2	1.87	0.73
1:C:319:GLY:H	1:C:354:HIS:CD2	2.06	0.73
1:E:31:LYS:HZ1	1:E:411:ILE:HB	1.52	0.73
1:C:379:TRP:HZ3	1:C:381:ASN:HB3	1.54	0.73
2:D:152:PHE:HD2	2:D:153:ILE:HD13	1.54	0.73
2:F:146:ASP:OD2	2:F:148:SER:HB2	1.88	0.72
2:F:9:ILE:HG22	2:F:10:GLY:H	1.53	0.72
1:A:420:SER:HB3	1:A:424:THR:OG1	1.88	0.72
2:D:112:GLN:HA	2:D:112:GLN:HE21	1.53	0.72
2:F:126:ALA:N	2:F:129:LEU:HD11	2.05	0.72
1:A:231:GLU:OE1	1:A:232:VAL:N	2.21	0.72
1:C:154:LEU:HD22	1:C:155:VAL:N	2.03	0.72
1:A:230:LYS:HD2	1:A:234:ASN:ND2	2.04	0.72
2:D:160:ALA:H	2:D:161:PRO:HD3	1.54	0.72
2:F:112:GLN:HA	2:F:112:GLN:HE21	1.53	0.72
1:A:249:PHE:HE2	1:C:252:VAL:CG1	1.94	0.72
1:A:104:GLN:HB2	1:A:153:SER:HB2	1.71	0.71
1:C:288:ARG:HG3	1:C:288:ARG:NH1	2.04	0.71
1:C:58:ARG:NH1	1:C:354:HIS:O	2.22	0.71
1:C:5:ILE:O	2:D:138:TRP:HD1	1.73	0.71
1:E:60:ASP:HA	1:E:82:PHE:CD1	2.25	0.71
1:A:231:GLU:H	1:A:231:GLU:CD	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:LYS:HD3	1:E:305:MET:N	2.05	0.71
1:E:388:GLU:CD	1:E:388:GLU:H	1.91	0.71
1:A:66:PHE:HB3	1:A:67:PRO:HD3	1.73	0.71
2:B:146:ASP:OD2	2:B:148:SER:HB2	1.91	0.71
1:C:318:TRP:HB3	1:C:322:ARG:HG3	1.72	0.71
2:D:129:LEU:O	2:D:131:VAL:N	2.23	0.71
1:E:28:THR:HB	3:Q:2:NAG:H81	1.73	0.71
1:A:392:LEU:HD22	1:A:393:PRO:HD2	1.70	0.71
1:E:393:PRO:HB2	1:E:394:PRO:HD3	1.71	0.71
1:C:315:GLN:NE2	1:C:343:LYS:H	1.89	0.71
1:E:288:ARG:NH1	1:E:288:ARG:HG3	2.04	0.71
1:E:373:CYS:HG	1:E:399:CYS:HG	1.36	0.71
1:A:405:GLU:O	1:A:408:ILE:HG23	1.91	0.71
1:E:1:GLU:O	2:F:141:ASP:HA	1.91	0.70
1:A:59:THR:O	1:A:82:PHE:CE2	2.44	0.70
1:C:249:PHE:CE1	1:E:257:ASP:HB2	2.26	0.70
1:E:288:ARG:HG3	1:E:288:ARG:HH11	1.56	0.70
1:E:426:VAL:HG11	2:F:4:ILE:HG21	1.72	0.70
4:P:2:NDG:O3	4:P:3:MAN:H2	1.91	0.70
1:A:2:LYS:O	2:B:31:GLU:N	2.23	0.70
1:C:319:GLY:HA2	1:C:347:TYR:HB3	1.74	0.70
2:D:131:VAL:CG2	2:D:139:ILE:H	2.05	0.70
1:E:319:GLY:H	1:E:354:HIS:CD2	2.09	0.70
2:F:65:LYS:HB2	2:F:65:LYS:NZ	2.04	0.70
2:B:140:ILE:HD12	2:B:141:ASP:H	1.56	0.70
2:D:131:VAL:HG21	2:D:139:ILE:HB	1.74	0.70
2:F:131:VAL:CG2	2:F:139:ILE:H	2.05	0.70
4:K:2:NDG:O7	4:K:2:NDG:C3	2.39	0.70
2:D:131:VAL:HG11	2:D:139:ILE:C	2.12	0.70
1:E:376:GLN:HB2	1:E:394:PRO:HD2	1.73	0.70
1:E:418:PRO:HG3	2:F:111:LEU:HB3	1.73	0.70
1:C:288:ARG:HH11	1:C:288:ARG:HG3	1.57	0.69
2:D:21:ILE:HD12	2:D:21:ILE:H	1.57	0.69
2:F:152:PHE:HD2	2:F:153:ILE:HD13	1.57	0.69
2:F:4:ILE:HB	2:F:9:ILE:CD1	2.22	0.69
2:B:140:ILE:CD1	2:B:141:ASP:H	2.06	0.69
1:A:8:GLN:NE2	2:B:8:ILE:HA	2.07	0.69
1:C:420:SER:H	1:C:424:THR:HG21	1.57	0.69
1:E:392:LEU:CD2	1:E:393:PRO:HD2	2.21	0.69
2:F:131:VAL:HG11	2:F:139:ILE:C	2.12	0.69
2:F:45:PHE:HA	2:F:48:ILE:HD12	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:LYS:HD3	1:A:38:LYS:H	1.56	0.69
2:B:112:GLN:HA	2:B:112:GLN:HE21	1.56	0.69
1:C:3:ILE:HD13	1:C:5:ILE:CD1	2.23	0.69
1:A:80:PHE:HB3	1:A:82:PHE:CE2	2.26	0.69
2:D:55:LEU:HB3	2:D:107:ILE:HD12	1.73	0.69
2:F:125:ARG:O	2:F:129:LEU:HD21	1.93	0.69
1:E:1:GLU:HA	2:F:141:ASP:HA	1.72	0.69
1:C:38:LYS:N	1:C:38:LYS:HD3	2.07	0.69
1:A:60:ASP:HA	1:A:82:PHE:CD1	2.28	0.69
1:C:216:LYS:HD3	1:C:305:MET:N	2.05	0.69
1:E:230:LYS:HD2	1:E:234:ASN:ND2	2.08	0.69
1:A:340:LEU:H	1:A:376:GLN:HE22	1.38	0.69
1:E:315:GLN:NE2	1:E:343:LYS:H	1.91	0.69
1:E:231:GLU:H	1:E:231:GLU:CD	1.96	0.69
1:A:9:LYS:O	2:B:15:ALA:N	2.25	0.68
2:F:62:ALA:O	2:F:66:LEU:HD13	1.94	0.68
1:A:379:TRP:HZ3	1:A:381:ASN:HB3	1.58	0.68
1:A:33:MET:HE2	2:B:100:ARG:HB2	1.73	0.68
2:B:45:PHE:HA	2:B:48:ILE:HD12	1.76	0.68
1:C:426:VAL:HB	2:D:4:ILE:HD13	1.74	0.68
1:E:340:LEU:H	1:E:376:GLN:HE22	1.40	0.68
1:E:25:LEU:HD11	2:F:107:ILE:HG21	1.75	0.68
1:A:31:LYS:HB2	1:A:31:LYS:HZ3	1.58	0.68
1:A:319:GLY:HA2	1:A:347:TYR:HB3	1.75	0.68
2:B:65:LYS:NZ	2:B:65:LYS:HB2	2.08	0.68
1:C:1:GLU:OE1	1:C:2:LYS:HB2	1.94	0.68
1:C:230:LYS:HD2	1:C:234:ASN:ND2	2.08	0.68
1:C:60:ASP:HA	1:C:82:PHE:CE1	2.29	0.68
1:E:9:LYS:HE2	2:F:112:GLN:HE22	1.57	0.68
1:E:247:ASP:O	1:E:249:PHE:O	2.10	0.68
1:A:315:GLN:NE2	1:A:343:LYS:H	1.90	0.68
1:A:58:ARG:NH1	1:A:354:HIS:O	2.26	0.68
1:E:1:GLU:N	2:F:142:ASN:N	2.39	0.68
1:A:425:THR:HB	2:B:16:ILE:HD11	1.73	0.68
1:E:25:LEU:HD11	2:F:107:ILE:CG2	2.24	0.68
2:B:129:LEU:CD2	2:B:153:ILE:HD12	2.24	0.68
1:C:249:PHE:CD1	1:C:250:GLY:N	2.59	0.68
1:C:392:LEU:HD22	1:C:393:PRO:HD2	1.75	0.68
1:A:294:LEU:HD11	1:A:296:MET:CE	2.24	0.68
1:A:376:GLN:HB2	1:A:394:PRO:HD2	1.76	0.68
1:E:59:THR:O	1:E:82:PHE:CE2	2.47	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:GLU:CD	1:A:388:GLU:H	1.97	0.67
2:B:19:THR:O	3:G:1:NAG:H82	1.94	0.67
2:D:125:ARG:O	2:D:129:LEU:HD21	1.95	0.67
1:E:163:PRO:HB2	1:E:165:GLN:OE1	1.93	0.67
1:A:252:VAL:HG11	1:E:249:PHE:HE2	1.59	0.67
1:A:119:SER:HB3	1:A:120:PRO:HD2	1.76	0.67
1:A:426:VAL:HG11	2:B:4:ILE:HG12	1.77	0.67
1:C:66:PHE:HB3	1:C:67:PRO:HD3	1.76	0.67
2:D:154:PHE:O	2:D:156:PHE:N	2.28	0.67
2:B:122:ILE:HB	2:B:138:TRP:CH2	2.30	0.67
2:D:138:TRP:CD1	2:D:138:TRP:N	2.60	0.67
1:C:3:ILE:HD11	2:D:140:ILE:CB	2.24	0.67
2:F:138:TRP:N	2:F:138:TRP:CD1	2.61	0.67
2:B:152:PHE:HD2	2:B:153:ILE:HD13	1.60	0.67
1:E:60:ASP:HA	1:E:82:PHE:CE1	2.30	0.67
1:A:203:PHE:HD1	1:A:286:SER:HB3	1.60	0.67
2:B:4:ILE:HG23	2:B:13:PHE:CD2	2.30	0.67
1:E:231:GLU:OE1	1:E:232:VAL:N	2.25	0.67
1:E:1:GLU:HA	2:F:141:ASP:CA	2.24	0.67
2:B:5:ASP:H	2:B:9:ILE:CG2	1.97	0.67
1:E:1:GLU:CA	2:F:142:ASN:H	2.08	0.67
2:F:140:ILE:CD1	2:F:141:ASP:H	2.08	0.66
1:A:249:PHE:CE2	1:C:252:VAL:CG1	2.75	0.66
2:F:122:ILE:HB	2:F:138:TRP:CH2	2.30	0.66
1:A:420:SER:H	1:A:424:THR:HG21	1.59	0.66
1:E:294:LEU:C	1:E:294:LEU:HD22	2.15	0.66
2:F:125:ARG:C	2:F:129:LEU:HD21	2.15	0.66
1:A:392:LEU:CD2	1:A:393:PRO:HD2	2.26	0.66
1:A:66:PHE:O	1:A:67:PRO:C	2.34	0.66
2:D:45:PHE:HA	2:D:48:ILE:HD12	1.78	0.66
2:D:125:ARG:NH1	2:D:152:PHE:O	2.28	0.66
2:D:65:LYS:HB2	2:D:65:LYS:HZ2	1.58	0.66
1:E:58:ARG:NH2	1:E:317:ILE:O	2.29	0.66
2:F:140:ILE:HD12	2:F:141:ASP:H	1.61	0.66
2:F:131:VAL:HG21	2:F:139:ILE:HB	1.76	0.66
1:E:184:LEU:HD12	1:E:185:TYR:N	2.10	0.65
1:E:420:SER:H	1:E:424:THR:HG21	1.60	0.65
1:A:59:THR:HB	1:A:82:PHE:HD2	1.61	0.65
2:D:125:ARG:HB3	2:D:129:LEU:HD21	1.77	0.65
2:D:140:ILE:HD12	2:D:141:ASP:H	1.60	0.65
2:D:62:ALA:O	2:D:66:LEU:HD13	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:181:ASN:HB3	1:E:182:PRO:CD	2.26	0.65
1:E:249:PHE:CD1	1:E:250:GLY:N	2.59	0.65
1:E:59:THR:HB	1:E:82:PHE:HD2	1.61	0.65
1:A:33:MET:CE	2:B:100:ARG:HB2	2.26	0.65
2:D:126:ALA:N	2:D:129:LEU:HD11	2.11	0.65
2:D:140:ILE:CD1	2:D:141:ASP:H	2.08	0.65
1:E:203:PHE:HD1	1:E:286:SER:HB3	1.62	0.65
1:A:257:ASP:CB	1:E:249:PHE:CE1	2.76	0.65
1:A:318:TRP:HB3	1:A:322:ARG:HG3	1.77	0.65
2:D:122:ILE:HB	2:D:138:TRP:CH2	2.32	0.65
1:C:163:PRO:HG2	1:C:166:VAL:CG1	2.27	0.65
1:C:394:PRO:HG3	2:D:78:ARG:HG3	1.79	0.65
1:E:319:GLY:HA2	1:E:347:TYR:HB3	1.77	0.65
2:F:4:ILE:HB	2:F:9:ILE:HD13	1.79	0.65
2:D:9:ILE:HG21	2:D:13:PHE:HB2	1.79	0.65
1:A:1:GLU:OE1	1:A:1:GLU:N	2.27	0.65
1:C:85:GLY:O	1:C:99:VAL:HG13	1.97	0.65
2:D:30:LYS:HD2	2:D:32:SER:N	2.03	0.65
1:E:1:GLU:CA	2:F:141:ASP:HA	2.26	0.65
1:C:418:PRO:CG	2:D:111:LEU:HB3	2.27	0.65
1:E:10:GLN:HG3	2:F:15:ALA:HB3	1.79	0.65
1:E:1:GLU:H2	2:F:142:ASN:N	1.87	0.65
1:E:31:LYS:HB2	1:E:31:LYS:HZ3	1.61	0.65
2:F:21:ILE:H	2:F:21:ILE:HD12	1.62	0.65
2:B:116:TRP:HZ3	2:D:116:TRP:HH2	1.45	0.64
1:C:66:PHE:O	1:C:67:PRO:C	2.31	0.64
2:D:102:LEU:CD1	2:F:102:LEU:HD21	2.27	0.64
1:E:80:PHE:HB3	1:E:82:PHE:CE2	2.33	0.64
1:A:80:PHE:CB	1:A:82:PHE:CE2	2.80	0.64
2:D:125:ARG:C	2:D:129:LEU:HD21	2.18	0.64
2:D:152:PHE:CD2	2:D:153:ILE:HD13	2.33	0.64
2:D:30:LYS:CD	2:D:32:SER:H	2.04	0.64
1:E:126:CYS:HA	1:E:173:ASN:HD22	1.63	0.64
1:A:425:THR:CG2	2:B:16:ILE:HD11	2.28	0.64
1:A:126:CYS:HA	1:A:173:ASN:HD22	1.63	0.64
1:A:47:ASN:O	1:A:49:SER:N	2.30	0.64
1:C:416:LEU:HB2	2:D:52:ILE:HD13	1.79	0.64
1:C:416:LEU:HD22	2:D:56:LYS:HD2	1.78	0.64
1:E:38:LYS:HD3	1:E:38:LYS:N	2.10	0.64
1:A:424:THR:HG23	2:B:13:PHE:HA	1.80	0.64
2:F:125:ARG:HB3	2:F:129:LEU:HD21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:ASN:O	1:C:49:SER:N	2.31	0.64
1:E:104:GLN:HB2	1:E:153:SER:HB2	1.78	0.64
2:F:129:LEU:CD2	2:F:153:ILE:HD12	2.28	0.64
1:C:31:LYS:HB2	1:C:31:LYS:HZ3	1.63	0.64
2:F:5:ASP:OD2	2:F:9:ILE:HA	1.97	0.64
1:C:5:ILE:HG12	2:D:154:PHE:CD2	2.32	0.63
2:D:4:ILE:HG22	2:D:13:PHE:CG	2.32	0.63
1:C:58:ARG:NH2	1:C:317:ILE:O	2.28	0.63
1:E:58:ARG:NH1	1:E:354:HIS:O	2.30	0.63
1:E:416:LEU:HD22	2:F:56:LYS:HD2	1.80	0.63
1:A:163:PRO:HG2	1:A:166:VAL:CG1	2.28	0.63
1:A:181:ASN:HB3	1:A:182:PRO:CD	2.27	0.63
1:A:249:PHE:CD2	1:C:252:VAL:CG2	2.75	0.63
1:E:249:PHE:CD2	1:E:250:GLY:N	2.65	0.63
2:B:116:TRP:CZ3	2:D:116:TRP:HH2	2.16	0.63
1:A:249:PHE:CD1	1:A:250:GLY:N	2.62	0.63
1:A:288:ARG:NH2	1:C:260:VAL:HG12	2.14	0.63
1:A:34:PHE:HZ	2:B:66:LEU:HD23	1.63	0.63
1:C:231:GLU:H	1:C:231:GLU:CD	2.01	0.63
1:A:162:ILE:HG23	1:A:163:PRO:HD2	1.81	0.63
1:C:376:GLN:HB2	1:C:394:PRO:HD2	1.80	0.63
2:F:17:VAL:O	2:F:19:THR:N	2.32	0.63
1:E:294:LEU:HD21	1:E:296:MET:HE2	1.80	0.63
1:E:59:THR:HG21	1:E:80:PHE:CE2	2.34	0.63
1:C:34:PHE:HE2	2:D:96:LEU:HD13	1.64	0.62
1:C:7:LEU:HD21	2:D:118:LEU:HD13	1.82	0.62
2:D:5:ASP:H	2:D:9:ILE:HD12	1.63	0.62
1:A:288:ARG:HH22	1:C:260:VAL:HG12	1.63	0.62
1:C:181:ASN:HB3	1:C:182:PRO:CD	2.28	0.62
1:E:1:GLU:H1	2:F:142:ASN:CG	2.00	0.62
1:E:66:PHE:O	1:E:67:PRO:C	2.32	0.62
1:C:425:THR:HB	2:D:16:ILE:HD11	1.81	0.62
1:E:66:PHE:HB3	1:E:67:PRO:CD	2.28	0.62
4:K:2:NDG:O7	4:K:2:NDG:H3	1.99	0.62
2:B:125:ARG:HB3	2:B:129:LEU:HD21	1.79	0.62
1:C:80:PHE:HB3	1:C:82:PHE:CE2	2.34	0.62
2:F:164:THR:HG23	2:F:165:ILE:H	1.64	0.62
2:B:17:VAL:O	2:B:17:VAL:HG23	2.00	0.62
1:A:3:ILE:HD13	1:A:5:ILE:CD1	2.29	0.62
1:E:3:ILE:HD11	2:F:140:ILE:H	1.63	0.62
1:A:190:LYS:HD3	1:A:191:PRO:HD2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLY:H	1:A:354:HIS:HD2	1.47	0.62
1:A:249:PHE:CE2	1:C:252:VAL:HG21	2.34	0.62
2:B:17:VAL:O	2:B:19:THR:N	2.32	0.62
1:C:80:PHE:CB	1:C:82:PHE:CE2	2.82	0.62
2:D:41:ALA:O	2:D:43:LYS:N	2.33	0.62
4:U:1:NAG:O3	4:U:2:NDG:N2	2.33	0.62
1:C:104:GLN:HB2	1:C:153:SER:HB2	1.81	0.62
1:A:60:ASP:HA	1:A:82:PHE:CE1	2.35	0.61
1:C:126:CYS:HA	1:C:173:ASN:HD22	1.63	0.61
1:C:414:GLY:H	2:D:56:LYS:HE3	1.65	0.61
1:E:80:PHE:CB	1:E:82:PHE:CE2	2.83	0.61
1:A:184:LEU:HD12	1:A:185:TYR:N	2.12	0.61
2:B:4:ILE:CG2	2:B:9:ILE:HG21	2.29	0.61
1:C:31:LYS:HZ1	1:C:411:ILE:HB	1.60	0.61
2:F:152:PHE:CD2	2:F:153:ILE:HD13	2.35	0.61
2:F:17:VAL:HG23	2:F:17:VAL:O	2.00	0.61
2:B:125:ARG:NH1	2:B:152:PHE:O	2.34	0.61
1:E:163:PRO:HG2	1:E:166:VAL:CG1	2.30	0.61
2:B:68:ASP:C	2:B:70:ILE:N	2.52	0.61
1:E:46:LEU:N	1:E:46:LEU:HD23	2.16	0.61
1:A:249:PHE:CD2	1:A:250:GLY:N	2.69	0.61
1:A:426:VAL:HG21	2:B:4:ILE:HG21	1.81	0.61
1:A:425:THR:CB	2:B:16:ILE:HD11	2.31	0.61
1:C:203:PHE:CD1	1:C:286:SER:HB3	2.36	0.61
1:C:392:LEU:CD2	1:C:393:PRO:HD2	2.30	0.61
1:C:59:THR:HB	1:C:82:PHE:HD2	1.63	0.61
2:F:8:ILE:HG13	2:F:8:ILE:O	2.01	0.61
1:E:3:ILE:O	2:F:139:ILE:HG23	2.01	0.61
1:E:8:GLN:HB3	2:F:25:LEU:CD1	2.29	0.61
1:E:19:ASN:CB	4:P:2:NDG:H8C1	2.30	0.61
1:E:190:LYS:HD3	1:E:191:PRO:HD2	1.82	0.61
1:E:294:LEU:HD22	1:E:295:LEU:N	2.15	0.61
1:E:3:ILE:HD13	1:E:5:ILE:CD1	2.31	0.61
1:A:357:ASP:O	1:A:361:ARG:HG3	2.01	0.60
1:A:31:LYS:HZ2	1:A:411:ILE:HB	1.66	0.60
1:E:318:TRP:HB3	1:E:322:ARG:HG3	1.82	0.60
2:B:129:LEU:HD23	2:B:153:ILE:HD12	1.82	0.60
2:B:160:ALA:N	2:B:161:PRO:HD3	2.15	0.60
1:C:315:GLN:HE21	1:C:343:LYS:H	1.49	0.60
1:E:1:GLU:CG	1:E:2:LYS:N	2.64	0.60
1:E:24:ASN:H	1:E:419:THR:HG22	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:125:ARG:NH1	2:F:152:PHE:O	2.34	0.60
1:A:31:LYS:HZ1	1:A:411:ILE:HB	1.61	0.60
2:B:123:THR:HG1	2:B:138:TRP:HZ3	1.48	0.60
2:D:4:ILE:HG22	2:D:13:PHE:HB2	1.82	0.60
1:C:3:ILE:HD11	2:D:140:ILE:H	1.64	0.60
1:E:92:MET:O	1:E:181:ASN:HB2	2.02	0.60
1:A:241:TYR:O	1:A:258:ASN:HB2	2.01	0.60
1:E:376:GLN:CB	1:E:394:PRO:HD2	2.32	0.60
1:A:5:ILE:HD12	1:A:5:ILE:N	2.16	0.60
4:U:2:NDG:C3	4:U:2:NDG:O7	2.49	0.60
2:B:131:VAL:HG11	2:B:139:ILE:O	2.01	0.60
2:B:102:LEU:CD1	2:D:102:LEU:HD21	2.31	0.60
2:D:142:ASN:HA	2:D:145:CYS:O	2.01	0.60
1:A:261:SER:OG	1:A:262:PRO:HD2	2.03	0.59
1:A:66:PHE:HB3	1:A:67:PRO:CD	2.31	0.59
1:C:294:LEU:HD22	1:C:294:LEU:C	2.22	0.59
1:A:85:GLY:O	1:A:99:VAL:HG13	2.02	0.59
2:B:129:LEU:HD23	2:B:153:ILE:CD1	2.32	0.59
1:C:231:GLU:OE2	1:C:232:VAL:N	2.28	0.59
1:E:59:THR:HG21	1:E:80:PHE:CD2	2.37	0.59
2:D:161:PRO:HG2	2:D:162:VAL:H	1.67	0.59
2:D:68:ASP:C	2:D:70:ILE:N	2.56	0.59
1:E:85:GLY:O	1:E:99:VAL:HG13	2.02	0.59
1:C:10:GLN:O	2:D:23:GLY:N	2.30	0.59
1:C:241:TYR:O	1:C:258:ASN:HB2	2.02	0.59
1:C:59:THR:HG21	1:C:80:PHE:CE2	2.38	0.59
2:D:17:VAL:O	2:D:17:VAL:HG23	2.02	0.59
1:C:19:ASN:CG	4:K:2:NDG:H8C2	2.23	0.59
1:A:331:ALA:O	1:A:335:THR:HG23	2.02	0.59
2:B:159:THR:O	2:B:160:ALA:HB3	2.02	0.59
1:A:125:ASN:C	1:A:125:ASN:OD1	2.41	0.59
1:A:416:LEU:O	2:B:24:TYR:OH	2.09	0.59
2:B:152:PHE:CD2	2:B:153:ILE:HD13	2.37	0.59
2:D:17:VAL:O	2:D:19:THR:N	2.35	0.59
4:K:2:NDG:C4	4:K:3:MAN:H3	2.32	0.59
1:A:426:VAL:HG21	2:B:4:ILE:HG12	1.85	0.59
1:C:119:SER:HB3	1:C:120:PRO:HD2	1.84	0.59
1:C:31:LYS:HZ2	1:C:411:ILE:HB	1.67	0.59
1:C:249:PHE:CD2	1:C:250:GLY:N	2.71	0.58
4:U:1:NAG:O3	4:U:2:NDG:C7	2.51	0.58
1:C:18:HIS:CD2	1:C:412:PRO:HB3	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:HG21	2:D:154:PHE:CE1	2.38	0.58
2:F:154:PHE:O	2:F:156:PHE:N	2.36	0.58
1:A:315:GLN:HE21	1:A:343:LYS:H	1.49	0.58
1:C:319:GLY:H	1:C:354:HIS:HD2	1.51	0.58
1:C:46:LEU:HD23	1:C:46:LEU:N	2.18	0.58
1:C:3:ILE:HD12	2:D:140:ILE:H	1.68	0.58
2:D:29:ARG:HB2	2:D:36:VAL:HG13	1.84	0.58
1:C:66:PHE:HB3	1:C:67:PRO:CD	2.33	0.58
2:D:9:ILE:HD13	2:D:9:ILE:H	1.68	0.58
1:C:125:ASN:C	1:C:125:ASN:OD1	2.40	0.58
1:E:331:ALA:O	1:E:335:THR:HG23	2.03	0.58
1:E:66:PHE:O	1:E:68:ARG:N	2.37	0.58
1:E:3:ILE:CD1	2:F:140:ILE:HG22	2.32	0.58
1:C:184:LEU:HD12	1:C:185:TYR:N	2.17	0.58
1:C:187:GLN:O	1:C:189:VAL:HG12	2.02	0.58
1:C:87:SER:HB3	1:C:90:LEU:HD12	1.86	0.58
1:E:125:ASN:C	1:E:125:ASN:OD1	2.42	0.58
1:C:230:LYS:O	1:C:234:ASN:N	2.28	0.58
1:C:417:ILE:HA	2:D:24:TYR:OH	2.04	0.58
1:E:17:LEU:HD22	1:E:17:LEU:C	2.23	0.58
1:C:163:PRO:HG2	1:C:166:VAL:HG12	1.85	0.58
2:D:61:ILE:N	2:D:61:ILE:HD12	2.19	0.58
1:A:414:GLY:H	2:B:56:LYS:HE3	1.68	0.58
2:B:154:PHE:O	2:B:156:PHE:N	2.37	0.58
2:D:126:ALA:O	2:D:129:LEU:HD12	2.04	0.58
1:A:10:GLN:HG3	2:B:15:ALA:HB3	1.84	0.57
1:A:187:GLN:O	1:A:189:VAL:HG12	2.04	0.57
2:B:30:LYS:HD2	2:B:32:SER:N	2.05	0.57
1:A:163:PRO:HG2	1:A:166:VAL:HG12	1.86	0.57
2:B:131:VAL:O	2:B:132:GLU:C	2.42	0.57
2:B:126:ALA:O	2:B:129:LEU:HD12	2.04	0.57
1:E:315:GLN:HE21	1:E:343:LYS:H	1.50	0.57
1:E:311:VAL:O	1:E:338:CYS:HA	2.04	0.57
2:F:29:ARG:HB2	2:F:36:VAL:HG13	1.85	0.57
2:B:30:LYS:CD	2:B:32:SER:H	2.07	0.57
2:F:125:ARG:O	2:F:126:ALA:HB2	2.04	0.57
1:E:19:ASN:CG	4:P:2:NDG:H8C1	2.25	0.57
2:B:131:VAL:HG21	2:B:139:ILE:CB	2.34	0.57
1:C:92:MET:O	1:C:181:ASN:HB2	2.04	0.57
2:F:131:VAL:HG11	2:F:139:ILE:O	2.05	0.57
1:A:244:VAL:CG2	1:E:249:PHE:CE1	2.88	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:162:VAL:HG13	2:F:164:THR:H	1.69	0.57
2:B:41:ALA:O	2:B:43:LYS:N	2.38	0.57
1:C:162:ILE:HG23	1:C:163:PRO:HD2	1.86	0.57
1:C:393:PRO:O	1:C:395:LYS:HG2	2.05	0.57
2:D:129:LEU:CD2	2:D:153:ILE:HD12	2.34	0.57
1:E:18:HIS:CD2	1:E:412:PRO:HB3	2.39	0.57
1:E:416:LEU:HB2	2:F:52:ILE:HD13	1.86	0.57
1:A:149:SER:OG	1:A:303:PHE:HB3	2.05	0.57
1:A:104:GLN:CB	1:A:153:SER:HB2	2.35	0.57
2:B:125:ARG:O	2:B:126:ALA:HB2	2.05	0.57
2:B:29:ARG:HB2	2:B:36:VAL:HG13	1.87	0.57
2:D:163:PRO:O	2:D:165:ILE:N	2.37	0.57
2:B:141:ASP:HB3	2:B:144:ILE:HG12	1.87	0.56
2:D:161:PRO:O	2:D:162:VAL:HG13	2.05	0.56
2:D:21:ILE:CD1	2:D:21:ILE:H	2.15	0.56
1:E:1:GLU:HA	2:F:142:ASN:N	2.20	0.56
2:F:41:ALA:O	2:F:43:LYS:N	2.38	0.56
2:F:7:LEU:N	2:F:7:LEU:HD22	2.19	0.56
1:C:331:ALA:O	1:C:335:THR:HG23	2.06	0.56
2:D:102:LEU:HD13	2:F:102:LEU:HD21	1.86	0.56
2:F:131:VAL:HG21	2:F:139:ILE:H	1.71	0.56
1:A:59:THR:HG21	1:A:80:PHE:CD2	2.40	0.56
1:E:47:ASN:O	1:E:49:SER:N	2.38	0.56
2:F:9:ILE:HG22	2:F:10:GLY:N	2.18	0.56
1:A:322:ARG:HD2	1:A:354:HIS:CE1	2.39	0.56
1:A:18:HIS:CD2	1:A:412:PRO:HB3	2.41	0.56
2:D:125:ARG:O	2:D:126:ALA:HB2	2.05	0.56
2:F:7:LEU:HD23	2:F:29:ARG:NH1	2.20	0.56
1:E:379:TRP:CZ3	1:E:381:ASN:HB3	2.39	0.56
1:E:119:SER:HB3	1:E:120:PRO:HD2	1.87	0.56
4:U:1:NAG:O3	4:U:2:NDG:C8	2.53	0.56
1:C:66:PHE:O	1:C:68:ARG:N	2.38	0.56
1:C:66:PHE:CE1	1:C:70:ALA:HB2	2.41	0.56
2:F:97:GLY:O	2:F:100:ARG:HB3	2.04	0.56
1:A:46:LEU:N	1:A:46:LEU:HD23	2.18	0.56
1:A:59:THR:HG21	1:A:80:PHE:CE2	2.40	0.56
2:B:13:PHE:CD1	2:B:13:PHE:N	2.74	0.56
1:C:278:LEU:HD22	1:C:280:LEU:CD1	2.36	0.56
2:F:129:LEU:HD23	2:F:153:ILE:HD12	1.86	0.56
1:A:154:LEU:HD22	1:A:155:VAL:H	1.68	0.56
1:C:294:LEU:HD22	1:C:295:LEU:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:319:GLY:H	1:E:354:HIS:HD2	1.51	0.56
2:F:83:GLU:CD	2:F:83:GLU:H	2.08	0.56
1:C:393:PRO:HB2	1:C:394:PRO:CD	2.34	0.56
1:C:416:LEU:O	2:D:52:ILE:HD11	2.06	0.56
2:B:102:LEU:HD13	2:D:102:LEU:HD21	1.87	0.56
2:F:129:LEU:HD23	2:F:153:ILE:CD1	2.36	0.56
1:A:249:PHE:HD2	1:C:252:VAL:CG2	2.09	0.56
1:C:278:LEU:HD22	1:C:280:LEU:HD11	1.87	0.56
2:D:122:ILE:O	2:D:125:ARG:HB2	2.06	0.56
1:E:357:ASP:O	1:E:361:ARG:HG3	2.06	0.56
1:C:17:LEU:C	1:C:17:LEU:HD22	2.25	0.55
1:C:311:VAL:O	1:C:338:CYS:HA	2.05	0.55
1:E:187:GLN:O	1:E:189:VAL:HG12	2.06	0.55
2:D:30:LYS:HE3	2:D:32:SER:HB3	1.88	0.55
1:A:231:GLU:OE1	1:A:231:GLU:N	2.39	0.55
2:D:43:LYS:HB3	2:D:155:LYS:O	2.07	0.55
1:E:278:LEU:HD22	1:E:280:LEU:HD11	1.88	0.55
2:F:131:VAL:O	2:F:132:GLU:C	2.44	0.55
4:K:2:NDG:HB	4:K:3:MAN:H5	1.67	0.55
1:A:58:ARG:NH2	1:A:317:ILE:O	2.35	0.55
1:A:311:VAL:O	1:A:338:CYS:HA	2.06	0.55
2:B:122:ILE:O	2:B:125:ARG:HB2	2.06	0.55
2:D:4:ILE:CG2	2:D:9:ILE:HG13	2.36	0.55
1:A:66:PHE:O	1:A:68:ARG:N	2.39	0.55
1:E:422:THR:OG1	1:E:423:ASP:N	2.39	0.55
2:F:123:THR:HG1	2:F:138:TRP:HZ3	1.52	0.55
1:C:247:ASP:O	1:C:249:PHE:O	2.24	0.55
1:C:80:PHE:HB2	1:C:82:PHE:CE2	2.41	0.55
2:D:22:GLY:O	3:L:1:NAG:H61	2.07	0.55
1:E:163:PRO:HG2	1:E:166:VAL:HG12	1.88	0.55
1:E:266:ASN:CG	1:E:266:ASN:O	2.44	0.55
2:F:126:ALA:O	2:F:129:LEU:HD12	2.07	0.55
1:A:190:LYS:CD	1:A:191:PRO:HD2	2.37	0.55
1:A:92:MET:O	1:A:181:ASN:HB2	2.06	0.55
1:A:203:PHE:CE2	1:C:262:PRO:HB3	2.42	0.55
1:A:376:GLN:CB	1:A:394:PRO:HD2	2.37	0.55
2:B:47:LYS:NZ	1:C:423:ASP:OD2	2.35	0.55
1:E:162:ILE:HG23	1:E:163:PRO:HD2	1.89	0.55
2:F:43:LYS:HB3	2:F:155:LYS:O	2.07	0.55
1:A:244:VAL:HG21	1:E:249:PHE:CE1	2.42	0.54
1:C:59:THR:HG21	1:C:80:PHE:CD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:424:THR:O	2:D:13:PHE:HB3	2.07	0.54
2:B:7:LEU:HD13	2:B:36:VAL:HG21	1.89	0.54
1:C:5:ILE:HG21	2:D:154:PHE:CG	2.40	0.54
1:E:294:LEU:CD1	1:E:296:MET:HE3	2.26	0.54
1:A:10:GLN:HG3	2:B:15:ALA:CB	2.36	0.54
2:D:123:THR:HG1	2:D:138:TRP:HZ3	1.55	0.54
1:A:17:LEU:HD22	1:A:17:LEU:C	2.28	0.54
1:A:1:GLU:O	1:A:3:ILE:HG13	2.08	0.54
2:D:148:SER:OG	2:D:160:ALA:HB3	2.08	0.54
1:A:333:LEU:HA	2:B:78:ARG:NH2	2.22	0.54
1:A:249:PHE:CE1	1:C:244:VAL:CG2	2.90	0.54
1:C:249:PHE:HE1	1:E:257:ASP:HB2	1.70	0.54
4:U:2:NDG:H3	4:U:2:NDG:O7	2.06	0.54
2:B:160:ALA:H	2:B:161:PRO:HD3	1.72	0.54
1:C:190:LYS:HD3	1:C:191:PRO:HD2	1.89	0.54
1:E:393:PRO:O	1:E:395:LYS:HG2	2.08	0.54
1:E:87:SER:HB3	1:E:90:LEU:HD12	1.90	0.54
1:C:24:ASN:H	1:C:419:THR:HG22	1.73	0.54
2:F:164:THR:O	2:F:165:ILE:CB	2.56	0.54
2:B:131:VAL:HG21	2:B:139:ILE:H	1.71	0.54
2:B:30:LYS:HE3	2:B:32:SER:HB3	1.90	0.54
1:C:422:THR:OG1	1:C:423:ASP:N	2.41	0.54
4:K:2:NDG:H4	4:K:3:MAN:C3	2.30	0.54
1:A:247:ASP:O	1:A:249:PHE:O	2.26	0.53
1:A:294:LEU:HD22	1:A:294:LEU:C	2.28	0.53
1:A:319:GLY:N	1:A:354:HIS:CD2	2.76	0.53
1:A:38:LYS:HD3	1:A:38:LYS:N	2.16	0.53
2:D:131:VAL:O	2:D:132:GLU:C	2.46	0.53
2:D:13:PHE:CD1	2:D:13:PHE:N	2.75	0.53
1:E:1:GLU:CA	2:F:142:ASN:N	2.70	0.53
1:A:319:GLY:N	1:A:354:HIS:HD2	2.07	0.53
2:B:148:SER:OG	2:B:160:ALA:HB3	2.08	0.53
1:C:33:MET:HE2	2:D:100:ARG:HB2	1.90	0.53
1:E:116:VAL:HG13	1:E:117:ASN:N	2.23	0.53
1:A:294:LEU:HD22	1:A:295:LEU:N	2.23	0.53
1:C:1:GLU:CA	2:D:142:ASN:OD1	2.57	0.53
1:C:393:PRO:O	1:C:395:LYS:N	2.40	0.53
2:B:47:LYS:HZ1	1:C:423:ASP:CG	2.12	0.53
2:D:119:ALA:HA	2:D:138:TRP:HH2	1.73	0.53
1:E:154:LEU:HD22	1:E:155:VAL:H	1.72	0.53
2:F:64:GLU:OE1	2:F:65:LYS:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:N	1:C:5:ILE:HD12	2.23	0.53
2:D:131:VAL:HG21	2:D:139:ILE:H	1.72	0.53
2:D:64:GLU:OE1	2:D:65:LYS:N	2.41	0.53
1:E:20:GLY:HA3	2:F:104:VAL:HG12	1.89	0.53
1:E:241:TYR:O	1:E:258:ASN:HB2	2.09	0.53
1:E:241:TYR:O	1:E:242:PHE:HB3	2.08	0.53
1:A:266:ASN:CG	1:A:266:ASN:O	2.44	0.53
1:A:3:ILE:HD13	1:A:5:ILE:HD13	1.90	0.53
1:C:154:LEU:HD22	1:C:155:VAL:H	1.71	0.53
2:F:7:LEU:H	2:F:7:LEU:HD22	1.74	0.53
1:A:294:LEU:HD21	1:A:296:MET:HE2	1.91	0.53
1:A:249:PHE:CZ	1:C:244:VAL:HG11	2.43	0.53
2:D:129:LEU:HD12	2:D:130:ALA:H	1.73	0.53
1:A:393:PRO:O	1:A:395:LYS:HG2	2.08	0.53
1:A:68:ARG:CZ	1:A:68:ARG:HB3	2.39	0.53
2:D:129:LEU:HD23	2:D:153:ILE:CD1	2.39	0.53
1:E:5:ILE:HD12	1:E:5:ILE:N	2.23	0.53
2:F:61:ILE:N	2:F:61:ILE:HD12	2.24	0.53
1:A:203:PHE:CD1	1:A:286:SER:HB3	2.43	0.53
2:B:97:GLY:O	2:B:100:ARG:HB3	2.07	0.53
2:B:129:LEU:HD12	2:B:130:ALA:H	1.71	0.53
1:C:232:VAL:O	1:C:235:LYS:HB2	2.09	0.53
1:A:162:ILE:N	1:A:162:ILE:HD12	2.24	0.53
2:B:57:SER:O	2:B:61:ILE:HD13	2.09	0.53
1:C:261:SER:OG	1:C:262:PRO:HD2	2.08	0.53
1:C:288:ARG:CG	1:C:288:ARG:HH11	2.22	0.53
1:C:318:TRP:CB	1:C:322:ARG:HG3	2.37	0.53
1:A:425:THR:HB	2:B:16:ILE:CD1	2.37	0.53
1:C:4:LYS:HA	2:D:138:TRP:O	2.09	0.53
1:C:155:VAL:O	1:C:299:ARG:HG2	2.09	0.52
2:D:131:VAL:HG11	2:D:139:ILE:O	2.09	0.52
1:A:13:SER:C	1:A:15:PHE:H	2.11	0.52
1:A:278:LEU:HD22	1:A:280:LEU:HD11	1.91	0.52
2:D:125:ARG:O	2:D:126:ALA:CB	2.58	0.52
1:E:294:LEU:HD21	1:E:296:MET:CE	2.39	0.52
1:E:31:LYS:NZ	1:E:31:LYS:HB2	2.24	0.52
1:E:1:GLU:C	2:F:141:ASP:HA	2.28	0.52
1:A:288:ARG:HH11	1:A:288:ARG:CG	2.15	0.52
2:B:61:ILE:N	2:B:61:ILE:HD12	2.25	0.52
1:C:13:SER:C	1:C:15:PHE:H	2.12	0.52
1:C:357:ASP:O	1:C:361:ARG:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:SER:C	1:E:15:PHE:H	2.11	0.52
2:F:62:ALA:O	2:F:65:LYS:HB3	2.09	0.52
1:A:12:ASN:HB3	2:B:20:GLY:O	2.09	0.52
1:C:411:ILE:HG13	2:D:63:ILE:HD11	1.92	0.52
1:E:190:LYS:HD2	1:E:192:SER:OG	2.09	0.52
2:B:59:ILE:HG22	2:B:63:ILE:HD11	1.90	0.52
1:E:278:LEU:HD22	1:E:280:LEU:CD1	2.39	0.52
1:E:294:LEU:C	1:E:294:LEU:CD2	2.77	0.52
1:E:149:SER:OG	1:E:303:PHE:HB3	2.09	0.52
2:D:83:GLU:H	2:D:83:GLU:CD	2.13	0.52
1:E:80:PHE:HB2	1:E:82:PHE:CE2	2.44	0.52
1:C:424:THR:HG23	2:D:13:PHE:HA	1.90	0.52
2:D:141:ASP:HB3	2:D:144:ILE:HG12	1.91	0.52
1:E:66:PHE:CB	1:E:67:PRO:CD	2.87	0.52
2:F:163:PRO:C	2:F:164:THR:HG22	2.29	0.52
1:A:80:PHE:HB2	1:A:82:PHE:CE2	2.45	0.52
2:F:149:CYS:O	2:F:153:ILE:HG12	2.09	0.52
1:A:125:ASN:O	1:A:173:ASN:HB2	2.10	0.52
1:A:190:LYS:HD2	1:A:192:SER:OG	2.09	0.52
2:B:83:GLU:H	2:B:83:GLU:CD	2.14	0.52
1:C:163:PRO:HG2	1:C:166:VAL:HG11	1.91	0.52
1:E:206:LEU:HB3	1:E:218:HIS:CD2	2.45	0.52
1:A:252:VAL:HG21	1:E:249:PHE:HD2	1.74	0.52
2:D:92:LEU:HA	2:D:95:GLU:HG3	1.92	0.51
1:E:256:LEU:HD12	1:E:257:ASP:N	2.24	0.51
2:F:159:THR:O	2:F:160:ALA:HB3	2.11	0.51
1:A:425:THR:HG22	2:B:16:ILE:HD11	1.93	0.51
1:E:317:ILE:HG22	1:E:324:SER:HB3	1.91	0.51
2:F:13:PHE:N	2:F:13:PHE:CD1	2.77	0.51
1:C:149:SER:OG	1:C:303:PHE:HB3	2.10	0.51
1:E:230:LYS:O	1:E:234:ASN:N	2.30	0.51
1:E:232:VAL:O	1:E:235:LYS:HB2	2.10	0.51
1:A:181:ASN:O	1:A:183:ALA:N	2.44	0.51
2:B:8:ILE:O	2:B:8:ILE:HG13	2.10	0.51
1:A:8:GLN:NE2	2:B:9:ILE:H	2.08	0.51
1:C:294:LEU:HD21	1:C:296:MET:HE2	1.93	0.51
2:D:160:ALA:N	2:D:161:PRO:CD	2.68	0.51
1:C:414:GLY:N	2:D:56:LYS:HE3	2.26	0.51
1:A:174:CYS:O	1:A:175:ASN:C	2.49	0.51
1:A:256:LEU:HD12	1:A:257:ASP:N	2.26	0.51
1:A:87:SER:HB3	1:A:90:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:190:LYS:CD	1:E:191:PRO:HD2	2.39	0.51
1:E:68:ARG:CZ	1:E:68:ARG:HB3	2.40	0.51
1:A:116:VAL:HG13	1:A:117:ASN:N	2.26	0.51
1:E:241:TYR:CG	1:E:242:PHE:N	2.79	0.51
2:F:142:ASN:HA	2:F:145:CYS:O	2.11	0.51
2:F:5:ASP:OD1	2:F:6:ASP:N	2.43	0.51
1:A:422:THR:OG1	1:A:423:ASP:N	2.43	0.51
1:E:11:VAL:HG22	1:E:15:PHE:HB3	1.92	0.51
1:A:162:ILE:N	1:A:162:ILE:CD1	2.74	0.51
1:C:93:PHE:CD1	1:C:93:PHE:N	2.78	0.51
2:D:59:ILE:HG22	2:D:63:ILE:HD11	1.92	0.51
1:A:247:ASP:OD1	1:A:249:PHE:O	2.29	0.51
1:C:390:TYR:CE2	2:D:82:LEU:HG	2.45	0.51
1:C:3:ILE:HD13	1:C:5:ILE:HD13	1.93	0.51
1:E:141:ASN:HD22	1:E:279:GLN:HE21	1.58	0.51
1:A:163:PRO:HG2	1:A:166:VAL:HG11	1.93	0.51
1:A:266:ASN:ND2	1:A:266:ASN:O	2.44	0.51
2:B:125:ARG:O	2:B:126:ALA:CB	2.58	0.51
1:C:376:GLN:CB	1:C:394:PRO:HD2	2.41	0.51
1:C:66:PHE:CD2	1:C:67:PRO:HD3	2.46	0.51
2:F:125:ARG:O	2:F:126:ALA:CB	2.59	0.51
2:F:119:ALA:HA	2:F:138:TRP:HH2	1.76	0.51
1:A:8:GLN:NE2	2:B:9:ILE:N	2.58	0.50
1:C:304:ASP:C	1:C:304:ASP:OD1	2.49	0.50
1:C:322:ARG:HD2	1:C:354:HIS:CE1	2.46	0.50
2:D:159:THR:O	2:D:160:ALA:HB3	2.11	0.50
1:E:3:ILE:CD1	2:F:140:ILE:H	2.25	0.50
1:A:158:LEU:HD21	1:A:298:GLU:CA	2.39	0.50
1:A:206:LEU:HB3	1:A:218:HIS:CD2	2.46	0.50
1:A:58:ARG:HD2	1:A:347:TYR:OH	2.11	0.50
1:E:15:PHE:CD2	1:E:16:SER:N	2.80	0.50
1:A:241:TYR:CG	1:A:242:PHE:N	2.80	0.50
2:B:43:LYS:HB3	2:B:155:LYS:O	2.11	0.50
2:B:99:ILE:O	2:B:99:ILE:HG12	2.11	0.50
1:E:125:ASN:O	1:E:173:ASN:HB2	2.11	0.50
1:E:393:PRO:O	1:E:395:LYS:N	2.44	0.50
4:K:2:NDG:O7	4:K:2:NDG:O3	2.27	0.50
1:A:135:LYS:O	1:A:139:GLN:HG2	2.12	0.50
1:A:249:PHE:CE2	1:C:252:VAL:CB	2.95	0.50
1:A:24:ASN:H	1:A:419:THR:HG22	1.77	0.50
1:A:66:PHE:CB	1:A:67:PRO:CD	2.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:ILE:N	2:B:21:ILE:HD12	2.23	0.50
1:E:3:ILE:HD13	1:E:5:ILE:HD13	1.94	0.50
1:E:66:PHE:CB	1:E:67:PRO:HD3	2.39	0.50
1:A:393:PRO:O	1:A:395:LYS:N	2.44	0.50
1:C:222:SER:HB2	1:C:278:LEU:HD12	1.94	0.50
1:C:398:ARG:NH1	2:D:70:ILE:O	2.44	0.50
2:D:4:ILE:HG21	2:D:9:ILE:HG13	1.93	0.50
2:F:122:ILE:O	2:F:125:ARG:HB2	2.11	0.50
1:A:11:VAL:HG22	1:A:15:PHE:HB3	1.94	0.50
1:A:45:VAL:O	1:A:46:LEU:HD23	2.12	0.50
2:D:62:ALA:O	2:D:65:LYS:HB3	2.12	0.50
2:F:59:ILE:HG22	2:F:63:ILE:HD11	1.94	0.50
1:E:28:THR:CG2	3:Q:2:NAG:H82	2.37	0.50
2:B:43:LYS:HD3	2:B:156:PHE:HB2	1.94	0.50
1:E:10:GLN:HE21	2:F:25:LEU:HD21	1.76	0.50
1:A:1:GLU:C	1:A:3:ILE:H	2.14	0.50
1:A:3:ILE:HD12	1:A:3:ILE:C	2.32	0.50
1:C:6:CYS:HA	2:D:136:GLY:O	2.12	0.50
2:D:129:LEU:HD23	2:D:153:ILE:HD12	1.93	0.50
1:E:174:CYS:O	1:E:175:ASN:C	2.50	0.50
1:C:11:VAL:HG22	1:C:15:PHE:HB3	1.94	0.50
2:D:161:PRO:CG	2:D:162:VAL:H	2.22	0.50
2:B:162:VAL:CG2	2:B:162:VAL:O	2.60	0.49
1:C:266:ASN:O	1:C:266:ASN:CG	2.49	0.49
1:C:317:ILE:HG22	1:C:324:SER:HB3	1.94	0.49
1:C:319:GLY:N	1:C:354:HIS:CD2	2.78	0.49
1:C:398:ARG:NH1	1:C:398:ARG:HG2	2.27	0.49
1:C:55:GLY:C	1:C:82:PHE:HB3	2.32	0.49
1:E:3:ILE:HG13	2:F:140:ILE:O	2.10	0.49
1:A:232:VAL:O	1:A:235:LYS:HB2	2.11	0.49
2:F:148:SER:HB3	2:F:160:ALA:O	2.11	0.49
1:C:38:LYS:NZ	1:C:38:LYS:O	2.44	0.49
2:D:43:LYS:HD3	2:D:156:PHE:HB2	1.93	0.49
1:A:10:GLN:HA	2:B:15:ALA:HB3	1.95	0.49
1:A:418:PRO:HD3	2:B:111:LEU:HD13	1.94	0.49
2:B:163:PRO:C	2:B:165:ILE:H	2.15	0.49
1:C:247:ASP:OD1	1:C:249:PHE:O	2.31	0.49
1:C:377:SER:HB2	1:C:392:LEU:N	2.07	0.49
2:D:21:ILE:HA	3:L:1:NAG:O7	2.13	0.49
2:D:4:ILE:HA	2:D:13:PHE:CD2	2.47	0.49
1:E:121:HIS:C	1:E:123:ALA:N	2.66	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:VAL:HG23	1:A:196:CYS:HA	1.94	0.49
1:A:253:VAL:O	1:A:278:LEU:HD21	2.13	0.49
1:E:135:LYS:O	1:E:139:GLN:HG2	2.13	0.49
1:E:231:GLU:N	1:E:231:GLU:OE1	2.45	0.49
2:F:148:SER:OG	2:F:160:ALA:HB3	2.11	0.49
3:T:1:NAG:H61	3:T:2:NAG:C7	2.41	0.49
1:C:1:GLU:CA	2:D:142:ASN:N	2.75	0.49
1:C:34:PHE:CE2	2:D:96:LEU:HD13	2.46	0.49
1:E:10:GLN:NE2	2:F:25:LEU:HD21	2.27	0.49
1:A:266:ASN:ND2	1:A:266:ASN:C	2.66	0.49
1:A:55:GLY:C	1:A:82:PHE:HB3	2.33	0.49
2:B:119:ALA:HA	2:B:138:TRP:HH2	1.76	0.49
1:C:8:GLN:O	2:D:24:TYR:HA	2.13	0.49
1:E:162:ILE:N	1:E:162:ILE:HD12	2.27	0.49
2:B:39:GLU:OE1	2:B:155:LYS:HE3	2.13	0.49
2:B:161:PRO:C	2:B:162:VAL:HG12	2.33	0.49
2:D:5:ASP:OD2	2:D:9:ILE:HG23	2.12	0.49
1:A:181:ASN:O	1:A:182:PRO:C	2.46	0.49
1:A:333:LEU:HD11	1:A:340:LEU:HD23	1.93	0.49
1:A:377:SER:HB2	1:A:392:LEU:N	2.06	0.49
2:B:147:GLN:O	2:B:148:SER:C	2.51	0.49
1:C:181:ASN:O	1:C:183:ALA:N	2.46	0.49
2:D:57:SER:O	2:D:61:ILE:HD13	2.13	0.49
1:E:155:VAL:O	1:E:299:ARG:HG2	2.12	0.49
1:E:288:ARG:HH11	1:E:288:ARG:CG	2.24	0.49
1:A:252:VAL:HG11	1:E:249:PHE:CE2	2.44	0.49
1:A:426:VAL:HG11	2:B:4:ILE:CG1	2.42	0.49
1:C:319:GLY:N	1:C:354:HIS:HD2	2.10	0.49
1:E:189:VAL:HG23	1:E:196:CYS:HA	1.95	0.49
1:E:393:PRO:HB2	1:E:394:PRO:CD	2.42	0.49
2:F:43:LYS:HD3	2:F:156:PHE:HB2	1.95	0.49
2:F:4:ILE:CG1	2:F:5:ASP:N	2.74	0.49
1:C:231:GLU:HA	1:C:234:ASN:HB2	1.94	0.48
1:C:66:PHE:CB	1:C:67:PRO:CD	2.91	0.48
2:D:4:ILE:HA	2:D:13:PHE:CE2	2.48	0.48
1:E:401:LEU:N	1:E:401:LEU:HD12	2.28	0.48
1:C:125:ASN:O	1:C:173:ASN:HB2	2.13	0.48
2:D:4:ILE:HB	2:D:9:ILE:CG1	2.43	0.48
2:D:4:ILE:HB	2:D:9:ILE:HG13	1.93	0.48
2:F:147:GLN:O	2:F:148:SER:C	2.52	0.48
1:A:68:ARG:HA	1:A:350:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:PHE:CB	1:A:67:PRO:HD3	2.41	0.48
1:C:20:GLY:HA3	2:D:104:VAL:HG12	1.93	0.48
1:C:385:PRO:HG2	1:C:386:PHE:CD2	2.49	0.48
1:E:247:ASP:OD1	1:E:249:PHE:O	2.31	0.48
2:F:30:LYS:CD	2:F:32:SER:H	2.10	0.48
1:A:246:TYR:HA	1:A:251:LYS:O	2.13	0.48
1:A:5:ILE:CD1	1:A:5:ILE:N	2.76	0.48
1:C:249:PHE:CD1	1:E:257:ASP:HB2	2.48	0.48
1:A:257:ASP:CB	1:E:249:PHE:CD1	2.88	0.48
1:E:319:GLY:N	1:E:354:HIS:HD2	2.11	0.48
2:F:8:ILE:HG23	2:F:36:VAL:CG1	2.44	0.48
1:A:318:TRP:CB	1:A:322:ARG:HG3	2.44	0.48
1:C:10:GLN:HG3	2:D:15:ALA:HB3	1.95	0.48
1:C:85:GLY:O	1:C:99:VAL:CG1	2.61	0.48
1:E:329:ASP:HA	1:E:340:LEU:CD2	2.44	0.48
2:F:92:LEU:HA	2:F:95:GLU:HG3	1.95	0.48
1:A:3:ILE:HD12	1:A:4:LYS:N	2.29	0.48
2:D:4:ILE:HB	2:D:9:ILE:HD12	1.96	0.48
2:D:61:ILE:H	2:D:61:ILE:CD1	2.26	0.48
2:D:4:ILE:CG2	2:D:9:ILE:HG21	2.38	0.48
1:E:304:ASP:C	1:E:304:ASP:OD1	2.52	0.48
2:F:30:LYS:HE3	2:F:32:SER:HB3	1.95	0.48
1:A:278:LEU:HD22	1:A:280:LEU:CD1	2.43	0.48
2:B:64:GLU:OE1	2:B:65:LYS:N	2.47	0.48
1:C:135:LYS:O	1:C:139:GLN:HG2	2.12	0.48
1:A:203:PHE:CD1	1:C:262:PRO:HD3	2.49	0.48
1:C:379:TRP:CZ3	1:C:381:ASN:HB3	2.42	0.48
2:F:21:ILE:H	2:F:21:ILE:CD1	2.20	0.48
1:A:234:ASN:HA	1:A:237:GLY:O	2.14	0.48
1:C:66:PHE:CB	1:C:67:PRO:HD3	2.44	0.48
2:D:154:PHE:O	2:D:155:LYS:C	2.52	0.48
1:A:304:ASP:C	1:A:304:ASP:OD1	2.52	0.48
1:C:174:CYS:O	1:C:175:ASN:C	2.52	0.48
1:E:121:HIS:O	1:E:123:ALA:N	2.46	0.48
1:C:374:ILE:O	1:C:374:ILE:HG13	2.14	0.47
1:E:331:ALA:O	1:E:335:THR:CG2	2.62	0.47
1:A:385:PRO:HG2	1:A:386:PHE:CD2	2.48	0.47
1:A:66:PHE:CD2	1:A:67:PRO:HD3	2.49	0.47
2:B:125:ARG:HB3	2:B:129:LEU:CD2	2.45	0.47
2:F:131:VAL:HG21	2:F:139:ILE:CB	2.44	0.47
1:A:202:ALA:HB3	1:A:296:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:THR:HG22	2:B:164:THR:O	2.14	0.47
1:A:401:LEU:HD11	2:B:70:ILE:HD11	1.95	0.47
1:E:203:PHE:CD1	1:E:286:SER:HB3	2.45	0.47
1:E:424:THR:HG23	2:F:13:PHE:HA	1.97	0.47
2:B:43:LYS:O	2:B:46:GLU:HB2	2.14	0.47
1:C:68:ARG:CZ	1:C:68:ARG:HB3	2.45	0.47
1:A:244:VAL:HG22	1:E:249:PHE:CE1	2.49	0.47
1:E:33:MET:HE3	1:E:409:PRO:HB2	1.97	0.47
1:E:28:THR:HB	3:Q:2:NAG:C8	2.43	0.47
1:E:374:ILE:O	1:E:374:ILE:HG13	2.13	0.47
2:F:129:LEU:HD12	2:F:130:ALA:H	1.78	0.47
1:E:1:GLU:HA	2:F:141:ASP:CG	2.35	0.47
1:A:47:ASN:C	1:A:49:SER:H	2.18	0.47
1:A:66:PHE:CE1	1:A:70:ALA:HB2	2.49	0.47
2:B:5:ASP:CB	2:B:9:ILE:HA	2.38	0.47
1:E:163:PRO:HG2	1:E:166:VAL:HG11	1.95	0.47
1:E:26:TYR:OH	1:E:425:THR:HG21	2.14	0.47
1:E:68:ARG:HA	1:E:350:GLU:OE2	2.15	0.47
2:F:162:VAL:HA	2:F:163:PRO:HD3	1.47	0.47
2:F:54:ILE:O	2:F:57:SER:HB3	2.14	0.47
1:C:294:LEU:CD2	1:C:294:LEU:C	2.83	0.47
1:C:80:PHE:HB2	1:C:82:PHE:HE2	1.79	0.47
2:F:154:PHE:O	2:F:156:PHE:CD2	2.67	0.47
1:A:31:LYS:HB2	1:A:31:LYS:NZ	2.28	0.47
1:A:329:ASP:HA	1:A:340:LEU:CD2	2.45	0.47
1:C:121:HIS:O	1:C:123:ALA:N	2.48	0.47
2:D:67:ASN:OD1	2:D:67:ASN:N	2.48	0.47
1:E:127:TYR:N	1:E:173:ASN:ND2	2.62	0.47
1:A:304:ASP:OD1	1:A:306:LYS:HB2	2.14	0.47
1:A:329:ASP:HA	1:A:340:LEU:HD22	1.96	0.47
1:A:34:PHE:HZ	2:B:66:LEU:CD2	2.28	0.47
2:B:6:ASP:HB2	2:B:7:LEU:H	1.43	0.47
1:C:100:ASP:OD1	1:C:100:ASP:C	2.53	0.47
1:C:5:ILE:CG1	2:D:154:PHE:CE2	2.91	0.47
1:E:231:GLU:HA	1:E:234:ASN:HB2	1.97	0.47
1:E:55:GLY:C	1:E:82:PHE:HB3	2.33	0.47
1:A:19:ASN:CG	4:U:2:NDG:H8C2	2.35	0.46
1:A:1:GLU:HA	2:B:141:ASP:HA	1.98	0.46
1:A:1:GLU:O	1:A:3:ILE:N	2.41	0.46
1:C:160:LYS:HG3	1:C:162:ILE:CD1	2.45	0.46
1:C:387:THR:O	1:C:402:ALA:HA	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:ARG:HH11	1:C:398:ARG:HG2	1.80	0.46
1:C:47:ASN:C	1:C:49:SER:H	2.18	0.46
1:C:10:GLN:HE22	2:D:25:LEU:HD21	1.74	0.46
2:D:77:ILE:HD12	2:D:77:ILE:H	1.80	0.46
1:A:149:SER:HB3	1:A:304:ASP:O	2.15	0.46
1:A:377:SER:CB	1:A:392:LEU:H	2.09	0.46
1:A:25:LEU:HD23	1:A:418:PRO:HA	1.97	0.46
2:B:21:ILE:CD1	2:B:21:ILE:H	2.12	0.46
1:C:127:TYR:N	1:C:173:ASN:ND2	2.63	0.46
1:C:241:TYR:O	1:C:242:PHE:HB3	2.15	0.46
1:E:387:THR:HG22	1:E:400:PRO:HB2	1.96	0.46
2:F:164:THR:OG1	2:F:165:ILE:N	2.46	0.46
1:A:222:SER:HB2	1:A:278:LEU:HD12	1.96	0.46
1:A:354:HIS:C	1:A:355:HIS:ND1	2.69	0.46
1:A:374:ILE:O	1:A:374:ILE:HG13	2.14	0.46
1:A:406:GLU:CD	1:A:406:GLU:H	2.19	0.46
2:B:131:VAL:HG22	2:B:139:ILE:H	1.78	0.46
2:B:93:LEU:HA	2:B:93:LEU:HD23	1.74	0.46
1:C:190:LYS:CD	1:C:191:PRO:HD2	2.46	0.46
1:C:398:ARG:HH11	1:C:398:ARG:CG	2.29	0.46
1:E:178:PHE:CD2	1:E:179:LEU:N	2.83	0.46
1:E:38:LYS:NZ	1:E:38:LYS:O	2.47	0.46
1:A:331:ALA:O	1:A:335:THR:CG2	2.63	0.46
1:C:223:CYS:HA	1:C:274:GLN:O	2.16	0.46
1:E:329:ASP:HA	1:E:340:LEU:HD22	1.97	0.46
1:C:156:ASN:HA	1:C:299:ARG:HG2	1.98	0.46
2:D:41:ALA:C	2:D:43:LYS:H	2.19	0.46
1:A:379:TRP:CZ3	1:A:381:ASN:HB3	2.46	0.46
2:B:149:CYS:O	2:B:153:ILE:HG12	2.15	0.46
2:B:4:ILE:HG22	2:B:9:ILE:HD12	1.97	0.46
2:B:102:LEU:HD11	2:D:102:LEU:HD21	1.98	0.46
1:E:198:LYS:O	1:E:199:GLU:C	2.54	0.46
1:E:80:PHE:HB2	1:E:82:PHE:HE2	1.81	0.46
2:F:163:PRO:O	2:F:164:THR:HG22	2.16	0.46
1:A:15:PHE:CD2	1:A:16:SER:N	2.84	0.46
1:A:8:GLN:HE22	2:B:8:ILE:CB	2.28	0.46
1:C:246:TYR:HA	1:C:251:LYS:O	2.16	0.46
1:E:401:LEU:HD11	2:F:70:ILE:HD11	1.97	0.46
1:A:230:LYS:O	1:A:234:ASN:N	2.33	0.46
1:A:141:ASN:HD22	1:A:279:GLN:HE21	1.64	0.46
1:A:42:GLY:HA2	1:A:363:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:PHE:CE1	1:C:244:VAL:HG22	2.51	0.46
1:E:247:ASP:OD1	1:E:247:ASP:C	2.54	0.46
2:F:68:ASP:C	2:F:70:ILE:N	2.56	0.46
1:A:223:CYS:HA	1:A:274:GLN:O	2.15	0.46
2:B:142:ASN:HA	2:B:145:CYS:O	2.16	0.46
1:C:163:PRO:HD3	1:C:202:ALA:HB2	1.96	0.46
2:D:61:ILE:N	2:D:61:ILE:CD1	2.79	0.46
1:E:66:PHE:CD2	1:E:67:PRO:HD3	2.50	0.46
2:B:154:PHE:O	2:B:155:LYS:C	2.54	0.46
2:B:92:LEU:HA	2:B:95:GLU:HG3	1.97	0.46
1:C:1:GLU:CA	2:D:142:ASN:H	2.28	0.46
2:D:107:ILE:O	2:D:108:SER:C	2.54	0.46
1:E:398:ARG:HG2	1:E:398:ARG:NH1	2.30	0.46
1:A:198:LYS:O	1:A:199:GLU:C	2.54	0.45
1:A:393:PRO:HB2	1:A:394:PRO:CD	2.40	0.45
1:A:426:VAL:CG2	2:B:4:ILE:HG21	2.44	0.45
1:C:162:ILE:HD12	1:C:162:ILE:N	2.31	0.45
1:C:414:GLY:O	2:D:56:LYS:NZ	2.41	0.45
1:C:4:LYS:O	2:D:28:SER:HA	2.16	0.45
1:C:7:LEU:HA	1:C:7:LEU:HD13	1.73	0.45
2:D:149:CYS:O	2:D:153:ILE:N	2.36	0.45
1:E:222:SER:HB2	1:E:278:LEU:HD12	1.98	0.45
1:E:7:LEU:HA	1:E:7:LEU:HD13	1.74	0.45
1:A:249:PHE:CE1	1:C:257:ASP:HB2	2.51	0.45
1:C:68:ARG:HA	1:C:350:GLU:OE2	2.16	0.45
2:D:9:ILE:H	2:D:9:ILE:CD1	2.24	0.45
1:E:88:LEU:HD23	1:E:88:LEU:N	2.31	0.45
2:F:77:ILE:H	2:F:77:ILE:HD12	1.81	0.45
1:A:398:ARG:HG2	1:A:398:ARG:NH1	2.31	0.45
1:C:189:VAL:HG23	1:C:196:CYS:HA	1.98	0.45
1:C:5:ILE:HB	2:D:154:PHE:CZ	2.52	0.45
2:D:5:ASP:CG	2:D:9:ILE:HA	2.37	0.45
1:A:158:LEU:CD2	1:A:158:LEU:N	2.79	0.45
1:C:315:GLN:HG3	1:C:317:ILE:HD13	1.99	0.45
2:B:56:LYS:O	2:B:59:ILE:HG12	2.16	0.45
1:C:3:ILE:HD11	2:D:140:ILE:N	2.29	0.45
2:D:4:ILE:HB	2:D:9:ILE:CD1	2.47	0.45
1:E:104:GLN:CB	1:E:153:SER:HB2	2.46	0.45
1:A:127:TYR:N	1:A:173:ASN:ND2	2.64	0.45
2:B:65:LYS:CB	2:B:65:LYS:NZ	2.76	0.45
1:C:249:PHE:CE1	1:E:244:VAL:CG2	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:LYS:CE	1:C:411:ILE:HB	2.47	0.45
1:C:68:ARG:H	1:C:68:ARG:HG2	1.48	0.45
1:A:252:VAL:HG21	1:E:249:PHE:CD2	2.51	0.45
2:F:141:ASP:HB3	2:F:144:ILE:HG12	1.98	0.45
2:F:7:LEU:HB2	2:F:36:VAL:HG11	1.99	0.45
1:A:374:ILE:O	1:A:395:LYS:HA	2.17	0.45
2:B:154:PHE:O	2:B:156:PHE:CD2	2.70	0.45
1:E:246:TYR:HA	1:E:251:LYS:O	2.16	0.45
1:E:1:GLU:CG	1:E:2:LYS:H	2.29	0.45
2:F:126:ALA:HB3	2:F:129:LEU:CD2	2.47	0.45
2:B:131:VAL:HG21	2:B:139:ILE:N	2.31	0.45
2:B:62:ALA:O	2:B:65:LYS:HB3	2.16	0.45
1:C:329:ASP:HA	1:C:340:LEU:HD22	1.98	0.45
1:C:88:LEU:HD23	1:C:88:LEU:N	2.30	0.45
2:D:119:ALA:O	2:D:120:SER:C	2.54	0.45
1:E:281:LYS:O	1:E:285:TYR:OH	2.31	0.45
2:F:57:SER:O	2:F:61:ILE:HD13	2.17	0.45
1:A:296:MET:HE3	1:A:296:MET:HB2	1.84	0.45
1:A:38:LYS:HD3	1:A:38:LYS:O	2.17	0.45
1:A:38:LYS:HZ3	1:A:40:LYS:HD2	1.81	0.45
2:B:120:SER:OG	2:B:121:GLU:N	2.49	0.45
2:B:126:ALA:O	2:B:129:LEU:CD1	2.65	0.45
1:C:256:LEU:HD12	1:C:257:ASP:N	2.31	0.45
1:C:58:ARG:HD2	1:C:347:TYR:OH	2.16	0.45
1:C:38:LYS:CD	1:C:38:LYS:O	2.65	0.45
2:D:131:VAL:HG21	2:D:139:ILE:CB	2.43	0.45
2:F:4:ILE:HG22	2:F:13:PHE:CE2	2.51	0.45
1:E:34:PHE:HE2	2:F:96:LEU:HD13	1.82	0.45
1:A:319:GLY:CA	1:A:354:HIS:HD2	2.30	0.45
2:B:118:LEU:O	2:B:119:ALA:C	2.55	0.45
2:B:119:ALA:O	2:B:120:SER:C	2.54	0.45
2:B:68:ASP:HB3	2:B:70:ILE:HB	1.98	0.45
1:C:424:THR:HG22	2:D:14:VAL:CG1	2.47	0.45
1:C:75:LYS:O	1:C:78:ASP:HB2	2.17	0.45
1:E:31:LYS:HZ2	1:E:411:ILE:HB	1.80	0.45
1:E:66:PHE:CE1	1:E:70:ALA:HB2	2.52	0.45
2:B:50:ASN:O	2:B:53:GLN:HB2	2.18	0.44
1:C:192:SER:C	1:C:194:ASN:H	2.20	0.44
1:E:121:HIS:C	1:E:123:ALA:H	2.21	0.44
1:E:31:LYS:NZ	1:E:31:LYS:CB	2.80	0.44
1:E:425:THR:HB	2:F:16:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:42:GLU:HG2	2:F:42:GLU:H	1.58	0.44
2:B:126:ALA:HB3	2:B:129:LEU:CD2	2.47	0.44
2:B:41:ALA:C	2:B:43:LYS:H	2.20	0.44
1:C:294:LEU:HD21	1:C:296:MET:CE	2.47	0.44
1:C:74:ALA:O	1:C:75:LYS:C	2.54	0.44
1:C:7:LEU:CD2	2:D:118:LEU:HD13	2.47	0.44
1:E:224:TYR:CE1	1:E:274:GLN:HB3	2.52	0.44
1:E:149:SER:HB3	1:E:304:ASP:O	2.17	0.44
1:E:93:PHE:CD1	1:E:93:PHE:N	2.85	0.44
2:F:149:CYS:HA	2:F:152:PHE:HB3	1.98	0.44
2:F:4:ILE:HD12	2:F:5:ASP:H	1.81	0.44
2:F:61:ILE:H	2:F:61:ILE:CD1	2.30	0.44
1:A:68:ARG:H	1:A:68:ARG:HG2	1.51	0.44
2:B:141:ASP:HB3	2:B:144:ILE:CG1	2.47	0.44
2:B:4:ILE:HG23	2:B:13:PHE:CG	2.53	0.44
1:C:180:LYS:HD2	1:C:299:ARG:NH2	2.33	0.44
1:E:190:LYS:HA	1:E:190:LYS:HD3	1.74	0.44
1:E:28:THR:CB	3:Q:2:NAG:C8	2.96	0.44
1:E:374:ILE:O	1:E:395:LYS:HA	2.16	0.44
1:E:426:VAL:HG22	1:E:427:THR:N	2.32	0.44
1:A:322:ARG:CD	1:A:354:HIS:CE1	3.00	0.44
1:C:161:THR:HG23	1:C:203:PHE:HB2	1.99	0.44
1:C:296:MET:CA	1:C:296:MET:HE2	2.46	0.44
2:D:149:CYS:HA	2:D:152:PHE:HB3	2.00	0.44
1:E:234:ASN:HA	1:E:237:GLY:O	2.17	0.44
1:C:174:CYS:SG	1:C:178:PHE:HA	2.57	0.44
1:C:234:ASN:HA	1:C:237:GLY:O	2.17	0.44
1:C:25:LEU:HD23	1:C:418:PRO:HA	1.99	0.44
1:E:181:ASN:O	1:E:183:ALA:N	2.51	0.44
2:F:125:ARG:HB3	2:F:129:LEU:CD2	2.47	0.44
1:C:116:VAL:HG13	1:C:117:ASN:N	2.31	0.44
1:C:204:PHE:HE1	1:C:206:LEU:HD21	1.82	0.44
1:C:376:GLN:O	1:C:376:GLN:HG3	2.18	0.44
1:E:174:CYS:SG	1:E:178:PHE:HA	2.57	0.44
1:E:322:ARG:HD2	1:E:354:HIS:CE1	2.52	0.44
2:F:67:ASN:N	2:F:67:ASN:OD1	2.50	0.44
1:A:216:LYS:CD	1:A:305:MET:H	2.15	0.44
1:A:387:THR:O	1:A:402:ALA:HA	2.18	0.44
1:A:3:ILE:HD11	2:B:140:ILE:O	2.17	0.44
1:C:121:HIS:C	1:C:123:ALA:N	2.69	0.44
1:C:36:LEU:HA	1:C:36:LEU:HD23	1.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:CG2	2:D:154:PHE:CE1	3.01	0.44
2:D:131:VAL:HG22	2:D:139:ILE:H	1.82	0.44
1:A:161:THR:HG23	1:A:203:PHE:HB2	2.00	0.44
1:A:36:LEU:HD23	1:A:36:LEU:HA	1.70	0.44
1:A:38:LYS:CD	1:A:38:LYS:O	2.66	0.44
2:D:97:GLY:O	2:D:100:ARG:HB3	2.17	0.44
1:E:28:THR:HG21	3:Q:2:NAG:C8	2.43	0.44
1:E:42:GLY:HA2	1:E:363:LEU:HD22	1.99	0.44
2:F:111:LEU:HA	2:F:111:LEU:HD23	1.77	0.44
1:E:20:GLY:C	4:P:1:NAG:H83	2.38	0.44
1:A:38:LYS:HA	1:A:388:GLU:OE2	2.18	0.44
2:D:141:ASP:HB3	2:D:144:ILE:CG1	2.48	0.44
1:E:21:PHE:CD2	2:F:102:LEU:HD23	2.53	0.44
2:F:59:ILE:H	2:F:59:ILE:HG12	1.47	0.44
1:A:3:ILE:HD11	2:B:140:ILE:N	2.33	0.43
1:A:422:THR:C	1:A:424:THR:H	2.20	0.43
2:B:155:LYS:O	2:B:156:PHE:HB2	2.18	0.43
1:C:219:LEU:C	1:C:219:LEU:CD2	2.86	0.43
1:C:318:TRP:HA	1:C:318:TRP:CE3	2.53	0.43
1:C:331:ALA:O	1:C:335:THR:CG2	2.66	0.43
1:E:216:LYS:CD	1:E:305:MET:H	2.17	0.43
1:E:318:TRP:CB	1:E:322:ARG:HG3	2.46	0.43
2:F:154:PHE:O	2:F:155:LYS:C	2.56	0.43
2:F:41:ALA:C	2:F:43:LYS:H	2.21	0.43
1:C:141:ASN:HD22	1:C:279:GLN:HE21	1.65	0.43
1:C:38:LYS:HD3	1:C:38:LYS:O	2.18	0.43
1:C:408:ILE:HD12	1:C:409:PRO:HD2	1.99	0.43
2:D:55:LEU:HD21	1:E:422:THR:HG22	1.99	0.43
1:E:230:LYS:O	1:E:233:TYR:N	2.51	0.43
1:E:261:SER:OG	1:E:262:PRO:HD2	2.18	0.43
2:F:119:ALA:O	2:F:120:SER:C	2.56	0.43
2:F:132:GLU:HG2	2:F:138:TRP:CE3	2.53	0.43
1:A:266:ASN:HD22	1:A:266:ASN:N	2.14	0.43
1:A:13:SER:CB	2:B:18:GLU:O	2.67	0.43
1:C:104:GLN:CB	1:C:153:SER:HB2	2.46	0.43
2:B:102:LEU:HB3	1:C:21:PHE:CE1	2.53	0.43
1:C:294:LEU:CD1	1:C:296:MET:HE3	2.31	0.43
1:C:52:ILE:HG12	1:C:53:GLY:N	2.32	0.43
2:D:9:ILE:HG21	2:D:13:PHE:CB	2.48	0.43
1:E:19:ASN:CG	4:P:2:NDG:C8	2.86	0.43
1:E:5:ILE:HG23	2:F:26:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:42:GLU:H	2:D:42:GLU:HG2	1.59	0.43
2:D:4:ILE:HG22	2:D:13:PHE:HB3	1.99	0.43
2:D:4:ILE:CB	2:D:9:ILE:HG13	2.48	0.43
2:F:132:GLU:CG	2:F:138:TRP:CE3	3.01	0.43
1:A:410:LYS:C	1:A:411:ILE:HD13	2.39	0.43
1:A:416:LEU:HB2	2:B:52:ILE:HD13	2.01	0.43
1:C:28:THR:HB	3:L:2:NAG:C8	2.48	0.43
1:C:401:LEU:N	1:C:401:LEU:HD12	2.33	0.43
1:C:410:LYS:C	1:C:411:ILE:HD13	2.38	0.43
2:D:111:LEU:HA	2:D:111:LEU:HD23	1.80	0.43
2:D:41:ALA:C	2:D:43:LYS:N	2.72	0.43
2:D:102:LEU:HD11	2:F:102:LEU:HD21	1.98	0.43
2:F:147:GLN:O	2:F:150:GLN:HB2	2.19	0.43
4:K:2:NDG:O3	4:K:3:MAN:C5	2.47	0.43
1:A:294:LEU:CD1	1:A:296:MET:HE3	2.37	0.43
1:A:404:LYS:HG2	1:A:404:LYS:H	1.32	0.43
1:A:80:PHE:HB2	1:A:82:PHE:HE2	1.81	0.43
2:D:59:ILE:HG12	2:D:59:ILE:H	1.52	0.43
1:E:266:ASN:ND2	1:E:266:ASN:C	2.70	0.43
2:F:147:GLN:O	2:F:150:GLN:N	2.51	0.43
2:B:61:ILE:CD1	2:B:61:ILE:H	2.32	0.43
1:C:158:LEU:HD21	1:C:298:GLU:CA	2.45	0.43
1:C:206:LEU:HB3	1:C:218:HIS:CD2	2.53	0.43
1:C:230:LYS:O	1:C:233:TYR:N	2.52	0.43
1:C:354:HIS:C	1:C:355:HIS:ND1	2.72	0.43
1:C:44:SER:OG	1:C:45:VAL:N	2.51	0.43
1:C:426:VAL:HG23	2:D:4:ILE:HG23	1.93	0.43
2:D:61:ILE:H	2:D:61:ILE:HD12	1.82	0.43
1:E:266:ASN:ND2	1:E:266:ASN:O	2.52	0.43
1:A:88:LEU:N	1:A:88:LEU:HD23	2.34	0.43
2:B:77:ILE:H	2:B:77:ILE:HD12	1.83	0.43
1:C:190:LYS:HD2	1:C:192:SER:OG	2.18	0.43
1:A:249:PHE:CE1	1:C:244:VAL:HG21	2.53	0.43
1:C:377:SER:CB	1:C:392:LEU:H	2.10	0.43
1:E:366:GLY:C	1:E:368:ASP:H	2.21	0.43
1:E:392:LEU:HA	1:E:393:PRO:HD2	1.56	0.43
1:E:387:THR:O	1:E:402:ALA:HA	2.19	0.43
1:A:121:HIS:C	1:A:123:ALA:N	2.72	0.43
1:A:317:ILE:HG22	1:A:324:SER:HB3	1.99	0.43
1:A:398:ARG:HH11	1:A:398:ARG:CG	2.32	0.43
2:B:131:VAL:CG1	2:B:139:ILE:H	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:ALA:HA	1:C:415:LEU:O	2.19	0.43
2:D:107:ILE:HD13	2:D:107:ILE:HA	1.83	0.43
2:D:126:ALA:O	2:D:129:LEU:CD1	2.66	0.43
1:E:194:ASN:ND2	1:E:194:ASN:O	2.52	0.43
1:E:223:CYS:HA	1:E:274:GLN:O	2.18	0.43
1:E:38:LYS:O	1:E:38:LYS:CD	2.67	0.43
1:A:294:LEU:CD2	1:A:294:LEU:C	2.87	0.43
2:B:115:LEU:HD23	2:B:115:LEU:HA	1.74	0.43
2:D:55:LEU:HD12	2:D:111:LEU:HG	2.01	0.43
2:D:147:GLN:O	2:D:150:GLN:HB2	2.19	0.43
2:D:39:GLU:OE1	2:D:155:LYS:HE3	2.19	0.43
1:E:241:TYR:CD2	1:E:242:PHE:N	2.87	0.43
1:E:253:VAL:O	1:E:278:LEU:HD21	2.19	0.43
1:E:404:LYS:HB2	1:E:406:GLU:HG2	2.00	0.43
1:A:135:LYS:HD3	1:A:327:ALA:HB3	2.00	0.42
1:A:209:GLN:HG2	1:A:214:GLU:HA	2.00	0.42
1:A:231:GLU:HA	1:A:234:ASN:HB2	2.01	0.42
2:B:147:GLN:O	2:B:150:GLN:HB2	2.17	0.42
1:C:318:TRP:CG	1:C:322:ARG:HG3	2.54	0.42
1:C:42:GLY:HA2	1:C:363:LEU:HD22	2.00	0.42
2:D:129:LEU:HD22	2:D:153:ILE:HG23	2.00	0.42
2:D:9:ILE:HG21	2:D:13:PHE:CG	2.53	0.42
1:E:338:CYS:O	2:F:78:ARG:NH2	2.52	0.42
1:C:329:ASP:HA	1:C:340:LEU:CD2	2.49	0.42
2:D:67:ASN:O	2:D:68:ASP:O	2.37	0.42
1:A:219:LEU:C	1:A:219:LEU:CD2	2.87	0.42
2:D:132:GLU:CG	2:D:138:TRP:CE3	3.02	0.42
1:E:162:ILE:N	1:E:162:ILE:CD1	2.82	0.42
1:C:249:PHE:CE1	1:E:244:VAL:HG21	2.54	0.42
1:E:156:ASN:HA	1:E:299:ARG:HG2	2.01	0.42
2:F:141:ASP:O	2:F:144:ILE:HG12	2.19	0.42
1:A:423:ASP:CG	2:F:47:LYS:NZ	2.73	0.42
1:A:161:THR:C	1:A:162:ILE:HD12	2.40	0.42
1:E:296:MET:HB2	1:E:296:MET:HE3	1.83	0.42
1:E:319:GLY:N	1:E:354:HIS:CD2	2.81	0.42
1:E:36:LEU:HA	1:E:36:LEU:HD23	1.69	0.42
1:E:398:ARG:CG	1:E:398:ARG:HH11	2.32	0.42
1:E:56:ASP:HB3	1:E:57:SER:H	1.29	0.42
1:E:85:GLY:O	1:E:99:VAL:CG1	2.68	0.42
1:A:11:VAL:HG12	2:B:16:ILE:HA	2.01	0.42
1:A:158:LEU:HD22	1:A:158:LEU:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:PHE:HE1	1:C:260:VAL:O	2.03	0.42
1:A:229:SER:C	1:A:231:GLU:OE1	2.58	0.42
1:A:373:CYS:HG	1:A:399:CYS:CB	2.32	0.42
1:A:74:ALA:O	1:A:75:LYS:C	2.56	0.42
1:C:198:LYS:O	1:C:199:GLU:C	2.58	0.42
2:D:93:LEU:HA	2:D:93:LEU:HD23	1.68	0.42
1:E:398:ARG:HG2	1:E:398:ARG:HH11	1.85	0.42
2:F:129:LEU:HD22	2:F:153:ILE:HG23	2.01	0.42
2:F:68:ASP:HB3	2:F:70:ILE:HB	2.01	0.42
1:A:190:LYS:HE2	1:A:192:SER:OG	2.20	0.42
2:B:104:VAL:HG12	2:B:105:GLY:N	2.33	0.42
1:C:209:GLN:HG2	1:C:214:GLU:HA	2.01	0.42
1:C:374:ILE:O	1:C:395:LYS:HA	2.19	0.42
1:C:422:THR:C	1:C:424:THR:H	2.23	0.42
1:E:158:LEU:CD2	1:E:298:GLU:HA	2.43	0.42
1:E:392:LEU:HA	1:E:392:LEU:HD23	1.72	0.42
2:F:122:ILE:HB	2:F:138:TRP:HH2	1.83	0.42
1:A:189:VAL:HG23	1:A:195:LYS:O	2.19	0.42
1:A:315:GLN:HG3	1:A:317:ILE:HD13	2.01	0.42
1:A:401:LEU:HD12	1:A:401:LEU:N	2.33	0.42
2:B:41:ALA:HB1	2:B:155:LYS:HA	2.02	0.42
1:C:149:SER:HB3	1:C:304:ASP:O	2.19	0.42
1:C:15:PHE:CD2	1:C:16:SER:N	2.87	0.42
1:C:190:LYS:HD3	1:C:190:LYS:HA	1.75	0.42
2:D:126:ALA:HB3	2:D:129:LEU:CD2	2.50	0.42
1:E:47:ASN:C	1:E:49:SER:H	2.22	0.42
1:A:85:GLY:O	1:A:99:VAL:CG1	2.67	0.42
1:A:13:SER:HB2	2:B:18:GLU:O	2.20	0.42
2:B:4:ILE:HG22	2:B:9:ILE:CG1	2.49	0.42
1:C:31:LYS:NZ	1:C:31:LYS:HB2	2.32	0.42
1:C:38:LYS:H	1:C:38:LYS:CD	2.26	0.42
2:D:131:VAL:HG21	2:D:139:ILE:N	2.34	0.42
2:D:147:GLN:O	2:D:148:SER:C	2.57	0.42
2:D:45:PHE:O	2:D:47:LYS:N	2.53	0.42
1:E:266:ASN:N	1:E:266:ASN:HD22	2.18	0.42
1:E:38:LYS:HD3	1:E:38:LYS:O	2.20	0.42
1:A:72:VAL:HG23	1:A:73:SER:O	2.19	0.42
1:C:253:VAL:O	1:C:278:LEU:HD21	2.20	0.42
2:D:30:LYS:CE	2:D:32:SER:HB3	2.49	0.42
1:E:158:LEU:HD21	1:E:298:GLU:CA	2.43	0.42
1:E:304:ASP:OD1	1:E:306:LYS:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:31:LYS:CE	1:E:411:ILE:HB	2.49	0.42
1:E:18:HIS:HD2	1:E:412:PRO:HD3	1.85	0.42
2:F:61:ILE:N	2:F:61:ILE:CD1	2.83	0.42
2:F:67:ASN:O	2:F:68:ASP:O	2.38	0.42
2:F:99:ILE:O	2:F:99:ILE:HG12	2.20	0.42
1:A:166:VAL:HG22	1:A:167:THR:N	2.35	0.42
1:A:192:SER:C	1:A:194:ASN:H	2.22	0.42
1:C:181:ASN:O	1:C:182:PRO:C	2.55	0.42
1:C:304:ASP:OD1	1:C:306:LYS:HB2	2.20	0.42
1:C:417:ILE:HG12	2:D:24:TYR:CZ	2.55	0.42
1:E:294:LEU:CD2	1:E:295:LEU:N	2.80	0.42
1:E:31:LYS:HZ2	1:E:31:LYS:C	2.24	0.42
1:C:195:LYS:HA	1:C:195:LYS:HD2	1.41	0.41
1:C:241:TYR:CG	1:C:242:PHE:N	2.87	0.41
1:C:319:GLY:CA	1:C:354:HIS:HD2	2.32	0.41
2:D:157:ASN:O	2:D:159:THR:HG23	2.20	0.41
1:E:181:ASN:O	1:E:182:PRO:C	2.55	0.41
1:E:190:LYS:HA	1:E:191:PRO:HD2	1.82	0.41
1:E:366:GLY:C	1:E:368:ASP:N	2.73	0.41
1:A:10:GLN:HG2	2:B:17:VAL:HG22	2.02	0.41
1:A:33:MET:HE3	1:A:409:PRO:HB2	2.02	0.41
1:A:5:ILE:HG22	1:A:6:CYS:N	2.34	0.41
2:B:149:CYS:O	2:B:153:ILE:N	2.41	0.41
1:C:171:ALA:N	1:C:177:SER:O	2.49	0.41
1:C:281:LYS:O	1:C:285:TYR:OH	2.26	0.41
2:D:132:GLU:HG2	2:D:138:TRP:CE3	2.55	0.41
2:D:149:CYS:O	2:D:153:ILE:HG12	2.21	0.41
2:F:155:LYS:O	2:F:156:PHE:HB2	2.20	0.41
1:A:304:ASP:OD1	1:A:306:LYS:N	2.53	0.41
2:B:123:THR:OG1	2:B:138:TRP:HZ3	2.02	0.41
2:D:51:ASP:O	2:D:55:LEU:HG	2.20	0.41
1:E:219:LEU:C	1:E:219:LEU:CD2	2.88	0.41
1:E:45:VAL:O	1:E:46:LEU:HD23	2.21	0.41
2:F:107:ILE:O	2:F:108:SER:C	2.59	0.41
2:F:50:ASN:O	2:F:53:GLN:HB2	2.20	0.41
1:A:95:PRO:HA	1:A:179:LEU:HD23	2.01	0.41
1:A:18:HIS:ND1	1:A:18:HIS:N	2.68	0.41
1:A:75:LYS:O	1:A:78:ASP:HB2	2.20	0.41
2:B:132:GLU:CG	2:B:138:TRP:CE3	3.04	0.41
2:B:80:LEU:HD12	2:B:80:LEU:HA	1.88	0.41
2:D:68:ASP:HB3	2:D:70:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:160:LYS:HG3	1:E:162:ILE:CD1	2.50	0.41
1:E:192:SER:C	1:E:194:ASN:H	2.24	0.41
1:E:72:VAL:HG23	1:E:73:SER:O	2.20	0.41
2:F:21:ILE:HD12	2:F:21:ILE:N	2.33	0.41
1:A:257:ASP:CG	1:A:259:ARG:HE	2.24	0.41
1:A:56:ASP:HB3	1:A:57:SER:H	1.26	0.41
2:B:140:ILE:HD12	2:B:141:ASP:N	2.31	0.41
2:B:41:ALA:C	2:B:43:LYS:N	2.74	0.41
1:C:33:MET:HE3	1:C:409:PRO:HB2	2.02	0.41
2:F:131:VAL:HG21	2:F:139:ILE:N	2.34	0.41
2:F:157:ASN:O	2:F:159:THR:HG23	2.20	0.41
1:A:145:LEU:HA	1:A:145:LEU:HD12	1.88	0.41
2:B:99:ILE:HD13	2:B:99:ILE:C	2.41	0.41
1:C:66:PHE:HE1	1:C:70:ALA:HB2	1.86	0.41
2:D:61:ILE:HG22	2:D:62:ALA:N	2.35	0.41
2:D:65:LYS:CB	2:D:65:LYS:NZ	2.74	0.41
1:E:201:LEU:C	1:E:201:LEU:CD2	2.89	0.41
1:E:377:SER:CB	1:E:392:LEU:H	2.11	0.41
2:F:126:ALA:O	2:F:129:LEU:CD1	2.68	0.41
1:E:330:GLN:NE2	3:S:2:NAG:H83	2.35	0.41
1:A:398:ARG:HH11	1:A:398:ARG:HG2	1.85	0.41
1:E:40:LYS:N	1:E:379:TRP:O	2.51	0.41
1:E:404:LYS:HG2	1:E:404:LYS:H	1.34	0.41
1:A:224:TYR:CE1	1:A:274:GLN:HB3	2.56	0.41
2:B:125:ARG:C	2:B:129:LEU:HD11	2.40	0.41
2:B:39:GLU:HG2	2:B:40:SER:N	2.34	0.41
2:B:51:ASP:O	2:B:55:LEU:HG	2.20	0.41
1:C:158:LEU:CD2	1:C:158:LEU:N	2.83	0.41
1:C:190:LYS:HE2	1:C:192:SER:OG	2.20	0.41
1:C:194:ASN:O	1:C:194:ASN:ND2	2.54	0.41
1:C:34:PHE:HE2	2:D:96:LEU:CD1	2.29	0.41
2:B:113:GLU:HB3	1:C:421:GLY:HA3	2.03	0.41
2:D:146:ASP:O	2:D:147:GLN:C	2.58	0.41
2:D:154:PHE:O	2:D:156:PHE:CD2	2.74	0.41
2:F:55:LEU:HD12	2:F:111:LEU:HG	2.02	0.41
2:F:61:ILE:H	2:F:61:ILE:HD12	1.86	0.41
3:G:1:NAG:H5	3:G:2:NAG:C7	2.50	0.41
1:A:102:LEU:HD21	1:A:104:GLN:NE2	2.35	0.41
1:A:329:ASP:O	1:A:330:GLN:C	2.58	0.41
1:A:31:LYS:CE	1:A:411:ILE:HB	2.49	0.41
2:B:149:CYS:HA	2:B:152:PHE:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:ASN:O	2:B:68:ASP:O	2.38	0.41
1:C:102:LEU:HD21	1:C:104:GLN:NE2	2.35	0.41
1:C:191:PRO:O	1:C:194:ASN:N	2.50	0.41
1:E:18:HIS:ND1	1:E:18:HIS:N	2.68	0.41
1:E:354:HIS:C	1:E:355:HIS:ND1	2.73	0.41
2:F:134:SER:OG	2:F:137:CYS:HB2	2.21	0.41
4:K:2:NDG:C4	4:K:3:MAN:C3	2.97	0.41
1:A:411:ILE:HD13	1:A:411:ILE:N	2.36	0.41
2:B:59:ILE:HG12	2:B:59:ILE:H	1.49	0.41
1:C:190:LYS:HA	1:C:191:PRO:HD2	1.80	0.41
1:C:231:GLU:N	1:C:231:GLU:OE2	2.52	0.41
2:D:119:ALA:HA	2:D:138:TRP:CH2	2.55	0.41
2:D:125:ARG:HB3	2:D:129:LEU:CD2	2.45	0.41
2:D:80:LEU:HA	2:D:80:LEU:HD12	1.93	0.41
1:E:202:ALA:HB3	1:E:296:MET:HE1	2.03	0.41
1:E:366:GLY:O	1:E:368:ASP:N	2.54	0.41
1:E:44:SER:OG	1:E:45:VAL:N	2.54	0.41
1:A:155:VAL:O	1:A:299:ARG:HG2	2.21	0.41
2:B:5:ASP:CG	2:B:9:ILE:CG2	2.89	0.41
1:C:25:LEU:HD23	1:C:25:LEU:HA	1.86	0.41
1:C:216:LYS:CD	1:C:305:MET:H	2.18	0.41
2:D:21:ILE:HD12	2:D:21:ILE:N	2.29	0.41
2:D:5:ASP:N	2:D:9:ILE:HD12	2.33	0.41
1:E:315:GLN:HG3	1:E:317:ILE:HD13	2.03	0.41
1:E:319:GLY:CA	1:E:354:HIS:HD2	2.33	0.41
1:A:100:ASP:OD1	1:A:100:ASP:C	2.60	0.40
1:A:11:VAL:N	2:B:15:ALA:O	2.38	0.40
1:C:158:LEU:CD2	1:C:298:GLU:HA	2.47	0.40
1:C:392:LEU:HD23	1:C:392:LEU:HA	1.81	0.40
1:E:27:ALA:HA	1:E:415:LEU:O	2.22	0.40
1:E:38:LYS:H	1:E:38:LYS:CD	2.28	0.40
1:E:406:GLU:H	1:E:406:GLU:CD	2.24	0.40
1:E:74:ALA:O	1:E:75:LYS:C	2.59	0.40
2:F:41:ALA:C	2:F:43:LYS:N	2.75	0.40
2:F:51:ASP:O	2:F:55:LEU:HG	2.20	0.40
2:F:93:LEU:HD23	2:F:93:LEU:HA	1.70	0.40
3:T:1:NAG:O4	3:T:2:NAG:O7	2.39	0.40
1:A:310:PRO:HB3	1:A:396:PHE:CE1	2.56	0.40
2:B:118:LEU:HA	2:B:118:LEU:HD23	1.94	0.40
2:B:119:ALA:O	2:B:122:ILE:N	2.55	0.40
1:E:189:VAL:HG23	1:E:195:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:LEU:HA	1:E:25:LEU:HD23	1.86	0.40
1:E:375:SER:HB2	1:E:395:LYS:HB3	2.03	0.40
1:E:391:LEU:HA	1:E:391:LEU:HD23	1.84	0.40
2:F:39:GLU:OE1	2:F:155:LYS:HE3	2.22	0.40
1:A:18:HIS:HD2	1:A:412:PRO:HD3	1.87	0.40
1:A:31:LYS:CB	1:A:31:LYS:NZ	2.85	0.40
2:B:132:GLU:HG2	2:B:138:TRP:CE3	2.56	0.40
1:C:189:VAL:HG23	1:C:195:LYS:O	2.22	0.40
2:D:134:SER:OG	2:D:137:CYS:HB2	2.21	0.40
1:E:1:GLU:HA	2:F:141:ASP:C	2.41	0.40
1:E:236:ARG:NH2	1:E:293:PHE:HZ	2.20	0.40
2:F:147:GLN:HG3	2:F:151:ASN:OD1	2.21	0.40
1:A:249:PHE:CE2	1:C:252:VAL:CG2	3.04	0.40
1:A:420:SER:HB2	2:B:12:LEU:O	2.21	0.40
2:B:128:ASP:O	2:B:140:ILE:HD11	2.21	0.40
2:B:129:LEU:HD22	2:B:153:ILE:HG23	2.04	0.40
2:B:133:VAL:HB	2:B:134:SER:H	1.65	0.40
2:B:26:LEU:HA	2:B:26:LEU:HD12	1.95	0.40
1:C:363:LEU:HA	1:C:363:LEU:HD23	1.71	0.40
2:D:118:LEU:HA	2:D:118:LEU:HD23	1.89	0.40
2:D:118:LEU:O	2:D:119:ALA:C	2.58	0.40
1:E:417:ILE:HA	2:F:24:TYR:OH	2.21	0.40
3:R:1:NAG:H61	3:R:2:NAG:C7	2.52	0.40
1:A:195:LYS:HA	1:A:195:LYS:HD2	1.47	0.40
2:D:11:VAL:HG13	2:D:11:VAL:O	2.20	0.40
2:D:123:THR:OG1	2:D:138:TRP:HZ3	2.04	0.40
2:D:41:ALA:HB1	2:D:155:LYS:HA	2.03	0.40
1:E:158:LEU:CD2	1:E:158:LEU:N	2.84	0.40
1:E:161:THR:HG23	1:E:203:PHE:HB2	2.02	0.40
1:E:242:PHE:CD1	1:E:242:PHE:C	2.94	0.40
1:E:58:ARG:HD2	1:E:347:TYR:OH	2.20	0.40
1:E:25:LEU:HD23	1:E:418:PRO:HA	2.03	0.40
1:E:87:SER:O	1:E:88:LEU:C	2.59	0.40
2:F:30:LYS:HD2	2:F:32:SER:N	2.08	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	425/432 (98%)	359 (84%)	49 (12%)	17 (4%)	3	21
1	C	425/432 (98%)	359 (84%)	50 (12%)	16 (4%)	3	22
1	E	425/432 (98%)	358 (84%)	51 (12%)	16 (4%)	3	22
2	B	160/175 (91%)	113 (71%)	32 (20%)	15 (9%)	0	3
2	D	160/175 (91%)	111 (69%)	32 (20%)	17 (11%)	0	2
2	F	160/175 (91%)	115 (72%)	29 (18%)	16 (10%)	0	3
All	All	1755/1821 (96%)	1415 (81%)	243 (14%)	97 (6%)	2	14

All (97) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	48	GLN
1	A	66	PHE
1	A	393	PRO
2	B	18	GLU
2	B	42	GLU
2	B	68	ASP
2	B	126	ALA
2	B	130	ALA
2	B	132	GLU
2	B	155	LYS
1	C	2	LYS
1	C	47	ASN
1	C	48	GLN
1	C	66	PHE
1	C	393	PRO
2	D	18	GLU
2	D	42	GLU
2	D	68	ASP
2	D	126	ALA

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Mol	Chain	Res	Type
2	D	130	ALA
2	D	132	GLU
2	D	155	LYS
2	D	161	PRO
2	D	163	PRO
2	D	164	THR
1	E	47	ASN
1	E	48	GLN
1	E	66	PHE
1	E	393	PRO
2	F	18	GLU
2	F	68	ASP
2	F	126	ALA
2	F	130	ALA
2	F	132	GLU
2	F	155	LYS
2	F	161	PRO
2	F	162	VAL
2	F	164	THR
1	A	64	SER
1	A	422	THR
2	B	67	ASN
2	B	133	VAL
2	B	156	PHE
1	C	64	SER
1	C	422	THR
2	D	67	ASN
2	D	133	VAL
1	E	64	SER
1	E	422	THR
2	F	42	GLU
2	F	67	ASN
2	F	133	VAL
2	F	156	PHE
1	A	2	LYS
1	A	177	SER
2	B	46	GLU
2	B	161	PRO
1	C	122	ALA
1	C	177	SER
1	C	407	SER
2	D	46	GLU

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Mol	Chain	Res	Type
2	D	156	PHE
1	E	122	ALA
1	E	177	SER
1	E	407	SER
2	F	46	GLU
1	A	14	SER
1	A	407	SER
2	B	162	VAL
1	C	14	SER
1	C	230	LYS
2	D	66	LEU
1	E	14	SER
1	E	230	LYS
1	A	4	LYS
1	A	122	ALA
1	A	181	ASN
2	B	164	THR
1	C	181	ASN
2	D	6	ASP
1	E	127	TYR
2	F	6	ASP
1	A	127	TYR
1	E	181	ASN
1	A	3	ILE
1	A	250	GLY
2	F	61	ILE
1	C	3	ILE
2	D	61	ILE
1	A	67	PRO
2	B	61	ILE
1	C	291	PRO
1	E	3	ILE
1	E	67	PRO
1	E	291	PRO
1	C	67	PRO

### 5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	369/374 (99%)	269 (73%)	100 (27%)	0	1
1	C	368/374 (98%)	265 (72%)	103 (28%)	0	1
1	E	369/374 (99%)	265 (72%)	104 (28%)	0	1
2	B	134/147 (91%)	78 (58%)	56 (42%)	0	0
2	D	134/147 (91%)	82 (61%)	52 (39%)	0	0
2	F	134/147 (91%)	81 (60%)	53 (40%)	0	0
All	All	1508/1563 (96%)	1040 (69%)	468 (31%)	0	0

All (468) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	7	LEU
1	A	13	SER
1	A	14	SER
1	A	16	SER
1	A	17	LEU
1	A	18	HIS
1	A	31	LYS
1	A	32	ARG
1	A	38	LYS
1	A	40	LYS
1	A	46	LEU
1	A	47	ASN
1	A	49	SER
1	A	56	ASP
1	A	57	SER
1	A	58	ARG
1	A	59	THR
1	A	61	LYS
1	A	64	SER
1	A	68	ARG
1	A	82	PHE
1	A	88	LEU
1	A	98	LYS
1	A	99	VAL
1	A	102	LEU
1	A	109	HIS
1	A	125	ASN

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Mol	Chain	Res	Type
1	A	136	LEU
1	A	145	LEU
1	A	153	SER
1	A	154	LEU
1	A	158	LEU
1	A	160	LYS
1	A	161	THR
1	A	165	GLN
1	A	167	THR
1	A	173	ASN
1	A	174	CYS
1	A	175	ASN
1	A	180	LYS
1	A	189	VAL
1	A	190	LYS
1	A	192	SER
1	A	195	LYS
1	A	198	LYS
1	A	200	ASN
1	A	201	LEU
1	A	204	PHE
1	A	208	THR
1	A	209	GLN
1	A	219	LEU
1	A	230	LYS
1	A	231	GLU
1	A	236	ARG
1	A	238	CYS
1	A	240	ASN
1	A	248	SER
1	A	252	VAL
1	A	266	ASN
1	A	267	SER
1	A	270	THR
1	A	272	THR
1	A	274	GLN
1	A	280	LEU
1	A	286	SER
1	A	288	ARG
1	A	290	SER
1	A	292	ARG
1	A	294	LEU

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Mol	Chain	Res	Type
1	A	299	ARG
1	A	302	CYS
1	A	306	LYS
1	A	316	SER
1	A	317	ILE
1	A	322	ARG
1	A	328	VAL
1	A	329	ASP
1	A	330	GLN
1	A	335	THR
1	A	342	GLN
1	A	343	LYS
1	A	348	ILE
1	A	365	SER
1	A	372	ARG
1	A	373	CYS
1	A	377	SER
1	A	380	VAL
1	A	382	GLU
1	A	384	SER
1	A	387	THR
1	A	388	GLU
1	A	395	LYS
1	A	398	ARG
1	A	404	LYS
1	A	408	ILE
1	A	416	LEU
1	A	419	THR
1	A	423	ASP
1	A	425	THR
2	B	4	ILE
2	B	5	ASP
2	B	6	ASP
2	B	7	LEU
2	B	9	ILE
2	B	11	VAL
2	B	12	LEU
2	B	13	PHE
2	B	14	VAL
2	B	19	THR
2	B	21	ILE
2	B	25	LEU

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Mol	Chain	Res	Type
2	B	26	LEU
2	B	29	ARG
2	B	30	LYS
2	B	31	GLU
2	B	43	LYS
2	B	47	LYS
2	B	52	ILE
2	B	56	LYS
2	B	57	SER
2	B	58	SER
2	B	59	ILE
2	B	65	LYS
2	B	68	ASP
2	B	69	ARG
2	B	70	ILE
2	B	71	SER
2	B	77	ILE
2	B	80	LEU
2	B	82	LEU
2	B	88	ARG
2	B	89	SER
2	B	92	LEU
2	B	98	ILE
2	B	99	ILE
2	B	102	LEU
2	B	109	ILE
2	B	111	LEU
2	B	112	GLN
2	B	114	SER
2	B	117	GLU
2	B	123	THR
2	B	125	ARG
2	B	128	ASP
2	B	129	LEU
2	B	131	VAL
2	B	132	GLU
2	B	138	TRP
2	B	140	ILE
2	B	143	ASN
2	B	144	ILE
2	B	148	SER
2	B	155	LYS

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Mol	Chain	Res	Type
2	B	159	THR
2	B	162	VAL
1	C	7	LEU
1	C	13	SER
1	C	14	SER
1	C	16	SER
1	C	17	LEU
1	C	18	HIS
1	C	31	LYS
1	C	32	ARG
1	C	38	LYS
1	C	40	LYS
1	C	46	LEU
1	C	47	ASN
1	C	49	SER
1	C	56	ASP
1	C	57	SER
1	C	58	ARG
1	C	59	THR
1	C	61	LYS
1	C	63	ASN
1	C	64	SER
1	C	68	ARG
1	C	82	PHE
1	C	88	LEU
1	C	98	LYS
1	C	99	VAL
1	C	102	LEU
1	C	109	HIS
1	C	120	PRO
1	C	125	ASN
1	C	136	LEU
1	C	145	LEU
1	C	153	SER
1	C	154	LEU
1	C	158	LEU
1	C	160	LYS
1	C	161	THR
1	C	165	GLN
1	C	167	THR
1	C	170	THR
1	C	173	ASN

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Mol	Chain	Res	Type
1	C	174	CYS
1	C	175	ASN
1	C	180	LYS
1	C	189	VAL
1	C	190	LYS
1	C	192	SER
1	C	195	LYS
1	C	198	LYS
1	C	200	ASN
1	C	201	LEU
1	C	204	PHE
1	C	208	THR
1	C	209	GLN
1	C	219	LEU
1	C	230	LYS
1	C	231	GLU
1	C	236	ARG
1	C	238	CYS
1	C	240	ASN
1	C	248	SER
1	C	252	VAL
1	C	266	ASN
1	C	267	SER
1	C	270	THR
1	C	272	THR
1	C	274	GLN
1	C	280	LEU
1	C	286	SER
1	C	288	ARG
1	C	290	SER
1	C	292	ARG
1	C	294	LEU
1	C	299	ARG
1	C	302	CYS
1	C	306	LYS
1	C	316	SER
1	C	317	ILE
1	C	322	ARG
1	C	328	VAL
1	C	329	ASP
1	C	330	GLN
1	C	335	THR

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Mol	Chain	Res	Type
1	C	342	GLN
1	C	343	LYS
1	C	348	ILE
1	C	365	SER
1	C	372	ARG
1	C	373	CYS
1	C	377	SER
1	C	380	VAL
1	C	382	GLU
1	C	384	SER
1	C	387	THR
1	C	388	GLU
1	C	395	LYS
1	C	398	ARG
1	C	404	LYS
1	C	408	ILE
1	C	416	LEU
1	C	419	THR
1	C	423	ASP
1	C	425	THR
1	C	427	THR
2	D	7	LEU
2	D	9	ILE
2	D	11	VAL
2	D	12	LEU
2	D	14	VAL
2	D	19	THR
2	D	21	ILE
2	D	25	LEU
2	D	26	LEU
2	D	29	ARG
2	D	30	LYS
2	D	31	GLU
2	D	43	LYS
2	D	47	LYS
2	D	52	ILE
2	D	56	LYS
2	D	57	SER
2	D	58	SER
2	D	59	ILE
2	D	65	LYS
2	D	68	ASP

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Mol	Chain	Res	Type
2	D	69	ARG
2	D	70	ILE
2	D	71	SER
2	D	77	ILE
2	D	78	ARG
2	D	80	LEU
2	D	82	LEU
2	D	88	ARG
2	D	89	SER
2	D	92	LEU
2	D	98	ILE
2	D	99	ILE
2	D	102	LEU
2	D	109	ILE
2	D	111	LEU
2	D	112	GLN
2	D	114	SER
2	D	117	GLU
2	D	123	THR
2	D	125	ARG
2	D	128	ASP
2	D	129	LEU
2	D	131	VAL
2	D	132	GLU
2	D	138	TRP
2	D	140	ILE
2	D	143	ASN
2	D	144	ILE
2	D	148	SER
2	D	155	LYS
2	D	159	THR
1	E	7	LEU
1	E	13	SER
1	E	14	SER
1	E	16	SER
1	E	17	LEU
1	E	18	HIS
1	E	31	LYS
1	E	32	ARG
1	E	38	LYS
1	E	40	LYS
1	E	46	LEU

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Mol	Chain	Res	Type
1	E	47	ASN
1	E	49	SER
1	E	56	ASP
1	E	57	SER
1	E	58	ARG
1	E	59	THR
1	E	61	LYS
1	E	63	ASN
1	E	64	SER
1	E	68	ARG
1	E	82	PHE
1	E	88	LEU
1	E	98	LYS
1	E	99	VAL
1	E	100	ASP
1	E	102	LEU
1	E	109	HIS
1	E	120	PRO
1	E	125	ASN
1	E	136	LEU
1	E	145	LEU
1	E	153	SER
1	E	154	LEU
1	E	158	LEU
1	E	160	LYS
1	E	161	THR
1	E	165	GLN
1	E	167	THR
1	E	173	ASN
1	E	174	CYS
1	E	175	ASN
1	E	180	LYS
1	E	189	VAL
1	E	190	LYS
1	E	192	SER
1	E	195	LYS
1	E	198	LYS
1	E	200	ASN
1	E	201	LEU
1	E	204	PHE
1	E	208	THR
1	E	209	GLN

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Mol	Chain	Res	Type
1	E	219	LEU
1	E	220	VAL
1	E	230	LYS
1	E	231	GLU
1	E	236	ARG
1	E	238	CYS
1	E	240	ASN
1	E	248	SER
1	E	252	VAL
1	E	266	ASN
1	E	267	SER
1	E	270	THR
1	E	272	THR
1	E	274	GLN
1	E	280	LEU
1	E	286	SER
1	E	288	ARG
1	E	290	SER
1	E	292	ARG
1	E	294	LEU
1	E	299	ARG
1	E	302	CYS
1	E	306	LYS
1	E	316	SER
1	E	317	ILE
1	E	322	ARG
1	E	328	VAL
1	E	329	ASP
1	E	330	GLN
1	E	335	THR
1	E	342	GLN
1	E	343	LYS
1	E	348	ILE
1	E	365	SER
1	E	372	ARG
1	E	373	CYS
1	E	377	SER
1	E	380	VAL
1	E	382	GLU
1	E	384	SER
1	E	387	THR
1	E	388	GLU

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Mol	Chain	Res	Type
1	E	395	LYS
1	E	398	ARG
1	E	404	LYS
1	E	408	ILE
1	E	416	LEU
1	E	419	THR
1	E	423	ASP
1	E	425	THR
1	E	427	THR
2	F	6	ASP
2	F	9	ILE
2	F	11	VAL
2	F	12	LEU
2	F	14	VAL
2	F	19	THR
2	F	21	ILE
2	F	25	LEU
2	F	26	LEU
2	F	29	ARG
2	F	30	LYS
2	F	31	GLU
2	F	43	LYS
2	F	47	LYS
2	F	52	ILE
2	F	56	LYS
2	F	57	SER
2	F	58	SER
2	F	59	ILE
2	F	65	LYS
2	F	68	ASP
2	F	69	ARG
2	F	70	ILE
2	F	71	SER
2	F	77	ILE
2	F	80	LEU
2	F	82	LEU
2	F	85	GLU
2	F	88	ARG
2	F	89	SER
2	F	92	LEU
2	F	98	ILE
2	F	99	ILE

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Mol	Chain	Res	Type
2	F	102	LEU
2	F	109	ILE
2	F	111	LEU
2	F	112	GLN
2	F	114	SER
2	F	117	GLU
2	F	123	THR
2	F	125	ARG
2	F	128	ASP
2	F	129	LEU
2	F	131	VAL
2	F	132	GLU
2	F	138	TRP
2	F	140	ILE
2	F	143	ASN
2	F	144	ILE
2	F	148	SER
2	F	155	LYS
2	F	159	THR
2	F	164	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	18	HIS
1	A	63	ASN
1	A	104	GLN
1	A	141	ASN
1	A	209	GLN
1	A	234	ASN
1	A	240	ASN
1	A	266	ASN
1	A	315	GLN
1	A	330	GLN
1	A	342	GLN
1	A	354	HIS
1	A	376	GLN
2	B	112	GLN
2	B	143	ASN
2	B	150	GLN
2	B	157	ASN

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Mol	Chain	Res	Type
1	C	8	GLN
1	C	10	GLN
1	C	18	HIS
1	C	63	ASN
1	C	104	GLN
1	C	141	ASN
1	C	173	ASN
1	C	209	GLN
1	C	234	ASN
1	C	240	ASN
1	C	266	ASN
1	C	315	GLN
1	C	330	GLN
1	C	342	GLN
1	C	354	HIS
1	C	376	GLN
2	D	112	GLN
2	D	150	GLN
2	D	157	ASN
1	E	8	GLN
1	E	10	GLN
1	E	18	HIS
1	E	63	ASN
1	E	104	GLN
1	E	141	ASN
1	E	173	ASN
1	E	209	GLN
1	E	234	ASN
1	E	240	ASN
1	E	266	ASN
1	E	315	GLN
1	E	330	GLN
1	E	342	GLN
1	E	354	HIS
1	E	376	GLN
2	F	112	GLN
2	F	143	ASN
2	F	150	GLN
2	F	157	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

45 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	G	1	1,3	14,14,15	0.69	0	17,19,21	1.29	2 (11%)
3	NAG	G	2	3	14,14,15	0.70	0	17,19,21	1.71	2 (11%)
3	BMA	G	3	3	11,11,12	1.13	0	15,15,17	0.77	0
3	NAG	H	1	1,3	14,14,15	0.67	0	17,19,21	1.17	2 (11%)
3	NAG	H	2	3	14,14,15	0.62	0	17,19,21	0.79	1 (5%)
3	BMA	H	3	3	11,11,12	0.92	1 (9%)	15,15,17	0.43	0
3	NAG	I	1	1,3	14,14,15	0.66	0	17,19,21	1.07	2 (11%)
3	NAG	I	2	3	14,14,15	0.65	0	17,19,21	1.09	2 (11%)
3	BMA	I	3	3	11,11,12	0.96	1 (9%)	15,15,17	0.78	1 (6%)
3	NAG	J	1	1,3	14,14,15	0.74	0	17,19,21	1.15	1 (5%)
3	NAG	J	2	3	14,14,15	0.54	0	17,19,21	0.80	1 (5%)
3	BMA	J	3	3	11,11,12	0.82	0	15,15,17	0.44	0
4	NAG	K	1	2,4	14,14,15	0.52	0	17,19,21	1.30	2 (11%)
4	NDG	K	2	4	14,14,15	0.93	1 (7%)	17,19,21	1.52	2 (11%)
4	MAN	K	3	4	11,11,12	0.85	0	15,15,17	0.40	0
3	NAG	L	1	1,3	14,14,15	0.58	0	17,19,21	1.63	3 (17%)
3	NAG	L	2	3	14,14,15	0.66	0	17,19,21	0.84	1 (5%)
3	BMA	L	3	3	11,11,12	0.82	0	15,15,17	0.53	0
3	NAG	M	1	1,3	14,14,15	0.76	0	17,19,21	1.22	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	M	2	3	14,14,15	0.68	0	17,19,21	0.89	1 (5%)
3	BMA	M	3	3	11,11,12	0.90	0	15,15,17	0.63	0
5	NAG	N	1	1,5	14,14,15	0.96	0	17,19,21	0.94	1 (5%)
5	NDG	N	2	5	14,14,15	0.94	1 (7%)	17,19,21	0.90	0
5	BMA	N	3	5	11,11,12	0.96	0	15,15,17	0.71	0
3	NAG	O	1	1,3	14,14,15	0.77	0	17,19,21	1.35	2 (11%)
3	NAG	O	2	3	14,14,15	0.62	0	17,19,21	1.06	1 (5%)
3	BMA	O	3	3	11,11,12	0.62	0	15,15,17	0.80	1 (6%)
4	NAG	P	1	2,4	14,14,15	0.80	0	17,19,21	1.21	2 (11%)
4	NDG	P	2	4	14,14,15	1.03	1 (7%)	17,19,21	1.23	2 (11%)
4	MAN	P	3	4	11,11,12	0.90	0	15,15,17	0.44	0
3	NAG	Q	1	1,3	14,14,15	0.86	1 (7%)	17,19,21	1.26	3 (17%)
3	NAG	Q	2	3	14,14,15	0.60	0	17,19,21	0.98	1 (5%)
3	BMA	Q	3	3	11,11,12	0.93	0	15,15,17	0.38	0
3	NAG	R	1	1,3	14,14,15	0.64	0	17,19,21	0.88	1 (5%)
3	NAG	R	2	3	14,14,15	0.90	0	17,19,21	0.76	0
3	BMA	R	3	3	11,11,12	0.83	0	15,15,17	0.54	0
3	NAG	S	1	1,3	14,14,15	0.54	0	17,19,21	0.88	0
3	NAG	S	2	3	14,14,15	0.78	0	17,19,21	1.31	3 (17%)
3	BMA	S	3	3	11,11,12	0.94	1 (9%)	15,15,17	0.70	0
3	NAG	T	1	1,3	14,14,15	0.57	0	17,19,21	0.99	2 (11%)
3	NAG	T	2	3	14,14,15	0.55	0	17,19,21	0.71	0
3	BMA	T	3	3	11,11,12	0.96	1 (9%)	15,15,17	0.45	0
4	NAG	U	1	2,4	14,14,15	0.49	0	17,19,21	1.46	2 (11%)
4	NDG	U	2	4	14,14,15	1.08	1 (7%)	17,19,21	1.92	4 (23%)
4	MAN	U	3	4	11,11,12	0.92	0	15,15,17	0.68	1 (6%)

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
3	NAG	G	1	1,3	1/1/5/7	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	1/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	BMA	I	3	3	-	2/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	BMA	J	3	3	-	2/2/19/22	0/1/1/1
4	NAG	K	1	2,4	-	1/6/23/26	0/1/1/1
4	NDG	K	2	4	-	3/6/23/26	0/1/1/1
4	MAN	K	3	4	-	2/2/19/22	0/1/1/1
3	NAG	L	1	1,3	1/1/5/7	1/6/23/26	0/1/1/1
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
3	BMA	L	3	3	-	0/2/19/22	0/1/1/1
3	NAG	M	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
3	BMA	M	3	3	-	2/2/19/22	0/1/1/1
5	NAG	N	1	1,5	-	0/6/23/26	0/1/1/1
5	NDG	N	2	5	-	0/6/23/26	0/1/1/1
5	BMA	N	3	5	-	0/2/19/22	0/1/1/1
3	NAG	O	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
3	BMA	O	3	3	-	2/2/19/22	0/1/1/1
4	NAG	P	1	2,4	-	0/6/23/26	0/1/1/1
4	NDG	P	2	4	-	0/6/23/26	0/1/1/1
4	MAN	P	3	4	-	2/2/19/22	0/1/1/1
3	NAG	Q	1	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	2/6/23/26	0/1/1/1
3	BMA	Q	3	3	-	1/2/19/22	0/1/1/1
3	NAG	R	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	R	2	3	-	2/6/23/26	0/1/1/1
3	BMA	R	3	3	-	2/2/19/22	0/1/1/1
3	NAG	S	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	S	2	3	-	2/6/23/26	0/1/1/1
3	BMA	S	3	3	-	2/2/19/22	0/1/1/1
3	NAG	T	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	T	2	3	-	0/6/23/26	0/1/1/1
3	BMA	T	3	3	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	U	1	2,4	-	0/6/23/26	0/1/1/1
4	NDG	U	2	4	-	2/6/23/26	0/1/1/1
4	MAN	U	3	4	-	0/2/19/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	U	2	NDG	C1-C2	3.05	1.56	1.52
4	K	2	NDG	C1-C2	2.85	1.56	1.52
3	I	3	BMA	C4-C5	2.56	1.58	1.53
4	P	2	NDG	C1-C2	2.52	1.56	1.52
3	Q	1	NAG	C1-C2	2.42	1.56	1.52
3	T	3	BMA	C2-C3	2.32	1.55	1.52
3	S	3	BMA	C2-C3	2.25	1.55	1.52
5	N	2	NDG	O5-C5	2.13	1.47	1.43
3	H	3	BMA	C2-C3	2.05	1.55	1.52

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	C4-C3-C2	-5.37	103.15	111.02
4	U	2	NDG	C3-C4-C5	-5.33	100.73	110.24
3	L	1	NAG	C4-C3-C2	-5.01	103.67	111.02
4	K	2	NDG	C3-C4-C5	-4.47	102.27	110.24
4	U	1	NAG	C3-C4-C5	-3.56	103.90	110.24
3	O	1	NAG	C2-N2-C7	-3.54	117.86	122.90
3	O	2	NAG	C2-N2-C7	-3.26	118.27	122.90
3	M	1	NAG	C2-N2-C7	-3.21	118.33	122.90
3	G	2	NAG	C2-N2-C7	-3.16	118.41	122.90
3	O	1	NAG	O5-C1-C2	-3.00	106.55	111.29
4	U	2	NDG	C6-C5-C4	2.97	119.96	113.00
4	P	1	NAG	C2-N2-C7	-2.92	118.75	122.90
3	L	1	NAG	C1-O5-C5	2.83	116.02	112.19
4	P	1	NAG	C3-C4-C5	-2.76	105.31	110.24
3	G	1	NAG	C4-C3-C2	-2.76	106.97	111.02
4	U	1	NAG	C6-C5-C4	2.74	119.42	113.00
3	S	2	NAG	C2-N2-C7	-2.73	119.02	122.90
3	G	1	NAG	C2-N2-C7	-2.72	119.03	122.90
3	R	1	NAG	C2-N2-C7	-2.72	119.03	122.90
3	L	1	NAG	C2-N2-C7	-2.67	119.10	122.90
4	U	2	NDG	C4-C3-C2	-2.66	107.12	111.02
4	K	1	NAG	C3-C4-C5	-2.65	105.51	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1	NAG	O5-C5-C6	-2.64	103.06	107.20
3	M	1	NAG	O5-C1-C2	-2.62	107.14	111.29
4	P	2	NDG	C4-C3-C2	-2.59	107.23	111.02
4	K	2	NDG	C6-C5-C4	2.53	118.93	113.00
3	L	2	NAG	C2-N2-C7	-2.41	119.47	122.90
4	K	1	NAG	C2-N2-C7	-2.39	119.50	122.90
3	M	2	NAG	C2-N2-C7	-2.38	119.51	122.90
3	J	1	NAG	C2-N2-C7	-2.38	119.52	122.90
3	T	1	NAG	C2-N2-C7	-2.36	119.54	122.90
3	S	2	NAG	C3-C4-C5	2.36	114.45	110.24
5	N	1	NAG	C2-N2-C7	-2.34	119.58	122.90
3	I	2	NAG	C2-N2-C7	-2.33	119.58	122.90
3	I	1	NAG	C2-N2-C7	-2.32	119.60	122.90
4	P	2	NDG	C2-N2-C7	-2.28	119.66	122.90
3	H	1	NAG	C2-N2-C7	-2.27	119.67	122.90
3	Q	1	NAG	C1-C2-N2	2.26	114.34	110.49
3	T	1	NAG	C4-C3-C2	-2.26	107.71	111.02
3	I	2	NAG	C3-C4-C5	2.22	114.21	110.24
4	U	2	NDG	O4-C4-C5	2.20	114.75	109.30
3	O	3	BMA	C2-C3-C4	-2.19	107.11	110.89
4	U	3	MAN	C1-C2-C3	2.19	112.35	109.67
3	Q	1	NAG	C2-N2-C7	-2.18	119.80	122.90
3	I	1	NAG	C1-C2-N2	2.14	114.14	110.49
3	Q	2	NAG	C2-N2-C7	-2.13	119.87	122.90
3	H	2	NAG	C2-N2-C7	-2.10	119.92	122.90
3	S	2	NAG	O5-C1-C2	-2.08	108.00	111.29
3	I	3	BMA	C3-C4-C5	2.05	113.89	110.24
3	J	2	NAG	C2-N2-C7	-2.02	120.03	122.90
3	Q	1	NAG	O7-C7-C8	-2.00	118.34	122.06

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	L	1	NAG	C1
3	G	1	NAG	C1
3	Q	1	NAG	C1

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	K	2	NDG	C3-C2-N2-C7
4	U	2	NDG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
3	R	3	BMA	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6
3	T	3	BMA	O5-C5-C6-O6
3	I	3	BMA	O5-C5-C6-O6
3	S	3	BMA	O5-C5-C6-O6
3	M	3	BMA	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
4	P	3	MAN	O5-C5-C6-O6
4	K	3	MAN	O5-C5-C6-O6
3	Q	2	NAG	O5-C5-C6-O6
3	L	2	NAG	C4-C5-C6-O6
3	R	3	BMA	C4-C5-C6-O6
4	K	2	NDG	C4-C5-C6-O6
3	R	2	NAG	O5-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
3	M	3	BMA	C4-C5-C6-O6
3	Q	2	NAG	C4-C5-C6-O6
3	R	1	NAG	O5-C5-C6-O6
3	R	2	NAG	C4-C5-C6-O6
3	S	3	BMA	C4-C5-C6-O6
3	T	3	BMA	C4-C5-C6-O6
3	R	1	NAG	C4-C5-C6-O6
3	O	3	BMA	O5-C5-C6-O6
3	I	3	BMA	C4-C5-C6-O6
3	L	1	NAG	O5-C5-C6-O6
4	K	2	NDG	O5-C5-C6-O6
3	H	3	BMA	C4-C5-C6-O6
4	K	3	MAN	C4-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	O	3	BMA	C4-C5-C6-O6
3	S	1	NAG	O5-C5-C6-O6
3	M	1	NAG	O5-C5-C6-O6
3	J	3	BMA	O5-C5-C6-O6
3	M	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	J	3	BMA	C4-C5-C6-O6
3	Q	3	BMA	O5-C5-C6-O6
3	S	1	NAG	C4-C5-C6-O6
3	H	3	BMA	O5-C5-C6-O6
3	S	2	NAG	C4-C5-C6-O6
3	S	2	NAG	O5-C5-C6-O6
3	G	3	BMA	O5-C5-C6-O6

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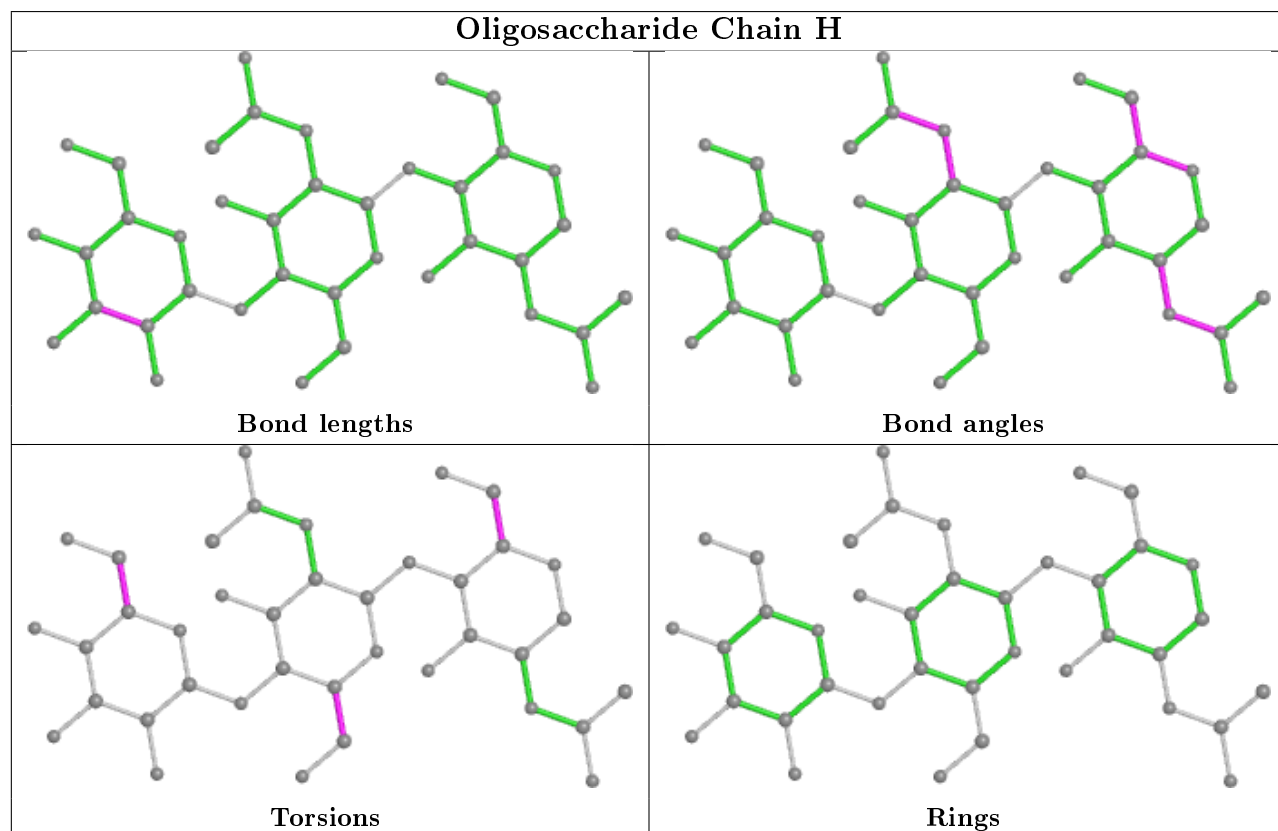
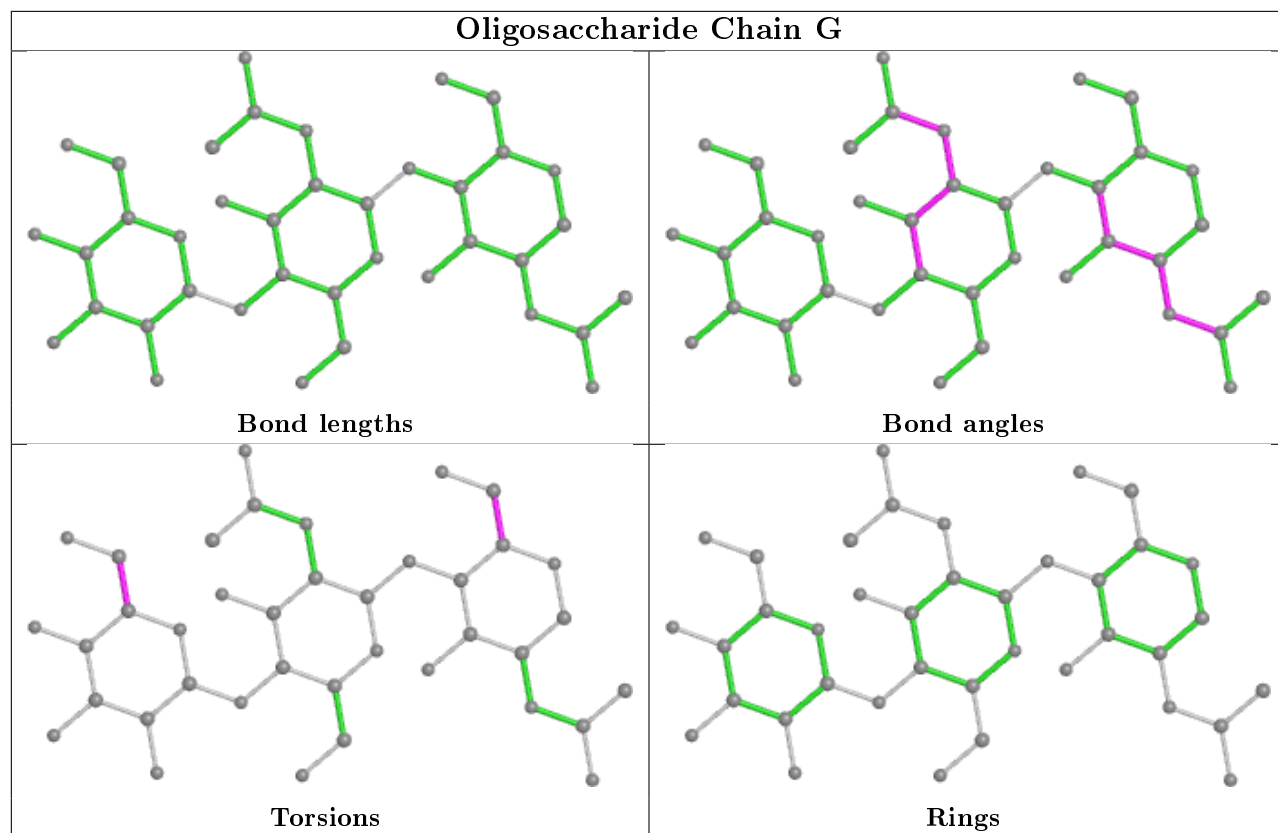
Mol	Chain	Res	Type	Atoms
3	G	1	NAG	O5-C5-C6-O6
4	P	3	MAN	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
4	U	2	NDG	C4-C5-C6-O6
4	K	1	NAG	C4-C5-C6-O6
3	T	1	NAG	C4-C5-C6-O6
3	T	1	NAG	O5-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
3	J	2	NAG	O5-C5-C6-O6

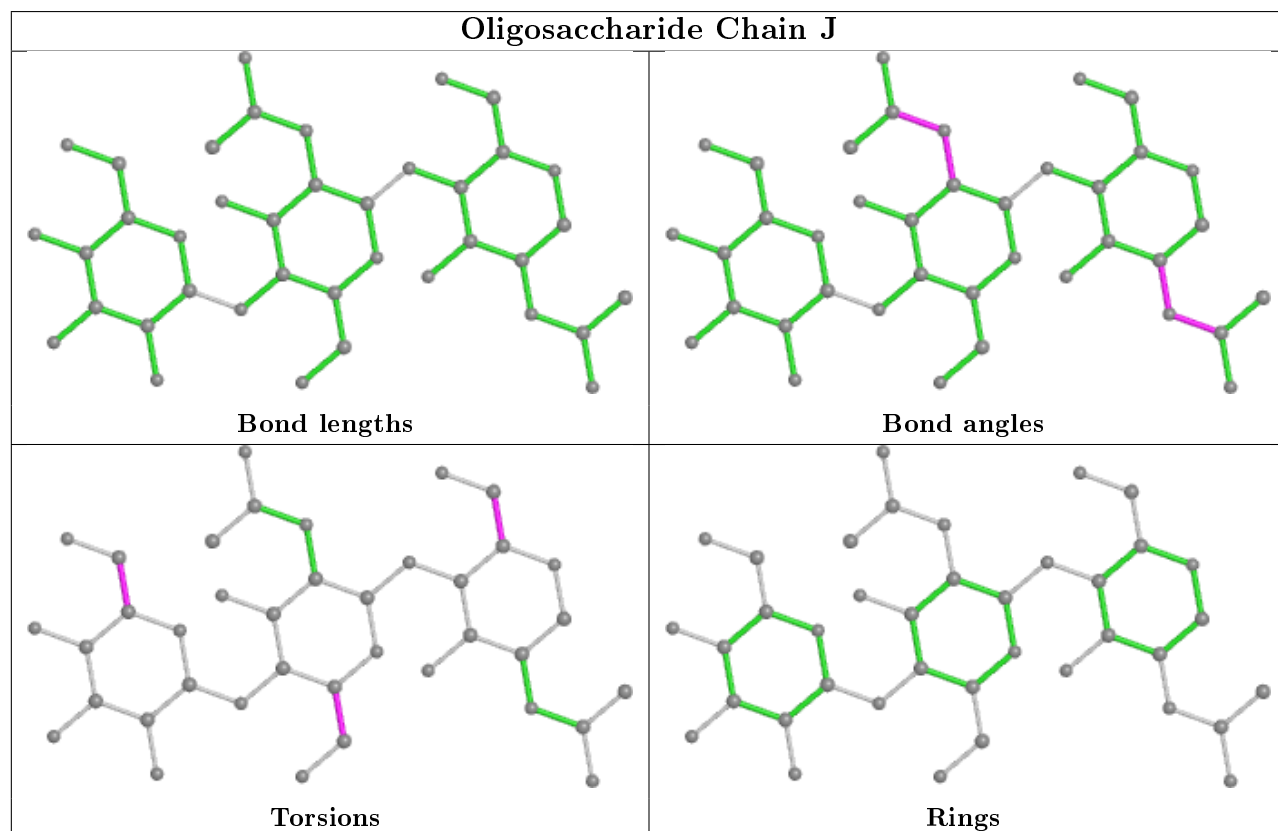
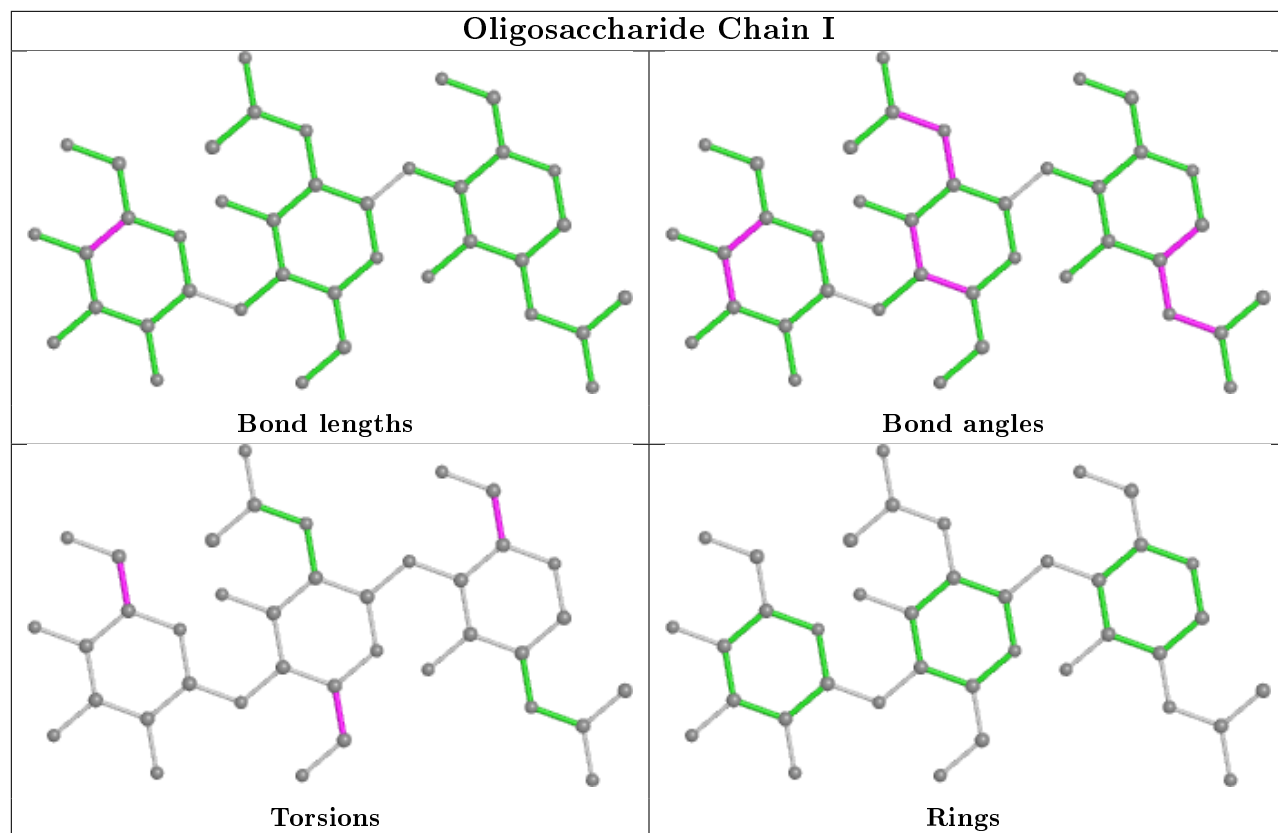
There are no ring outliers.

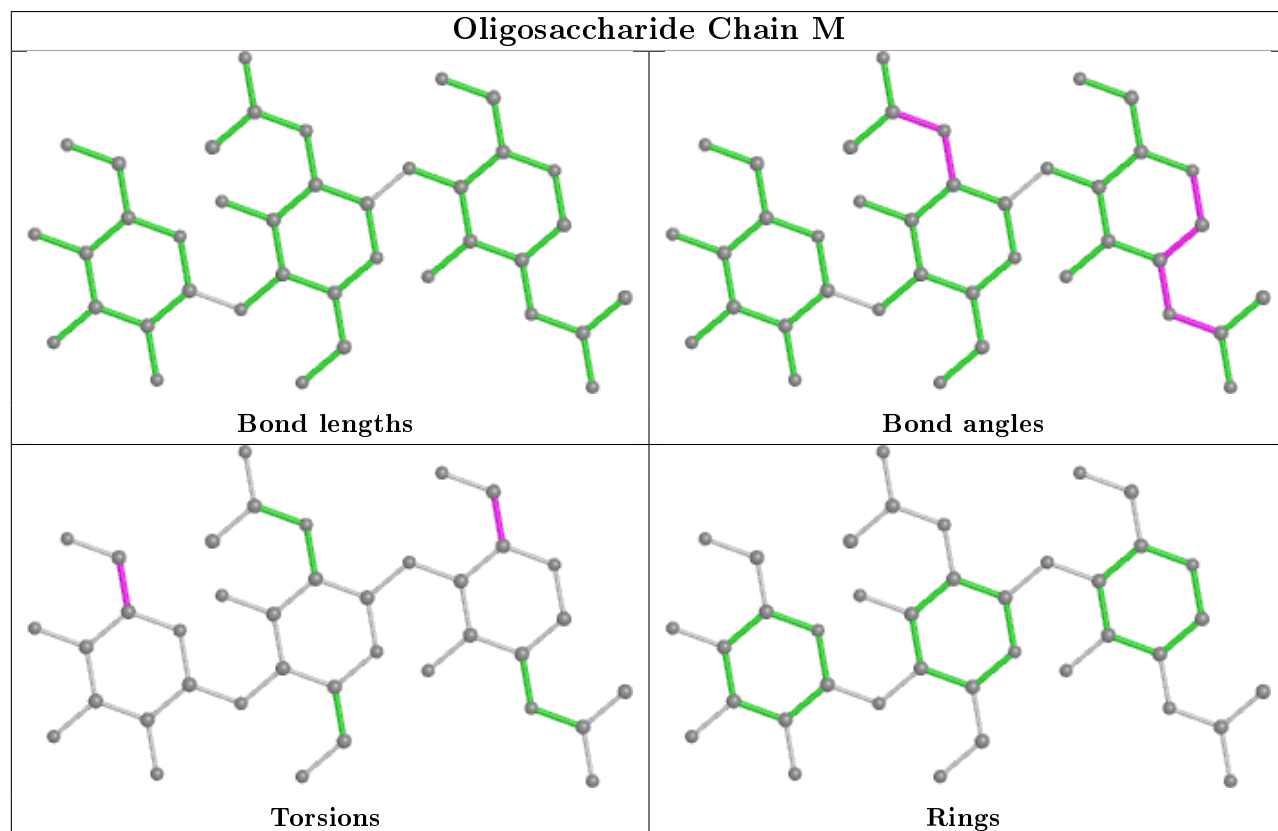
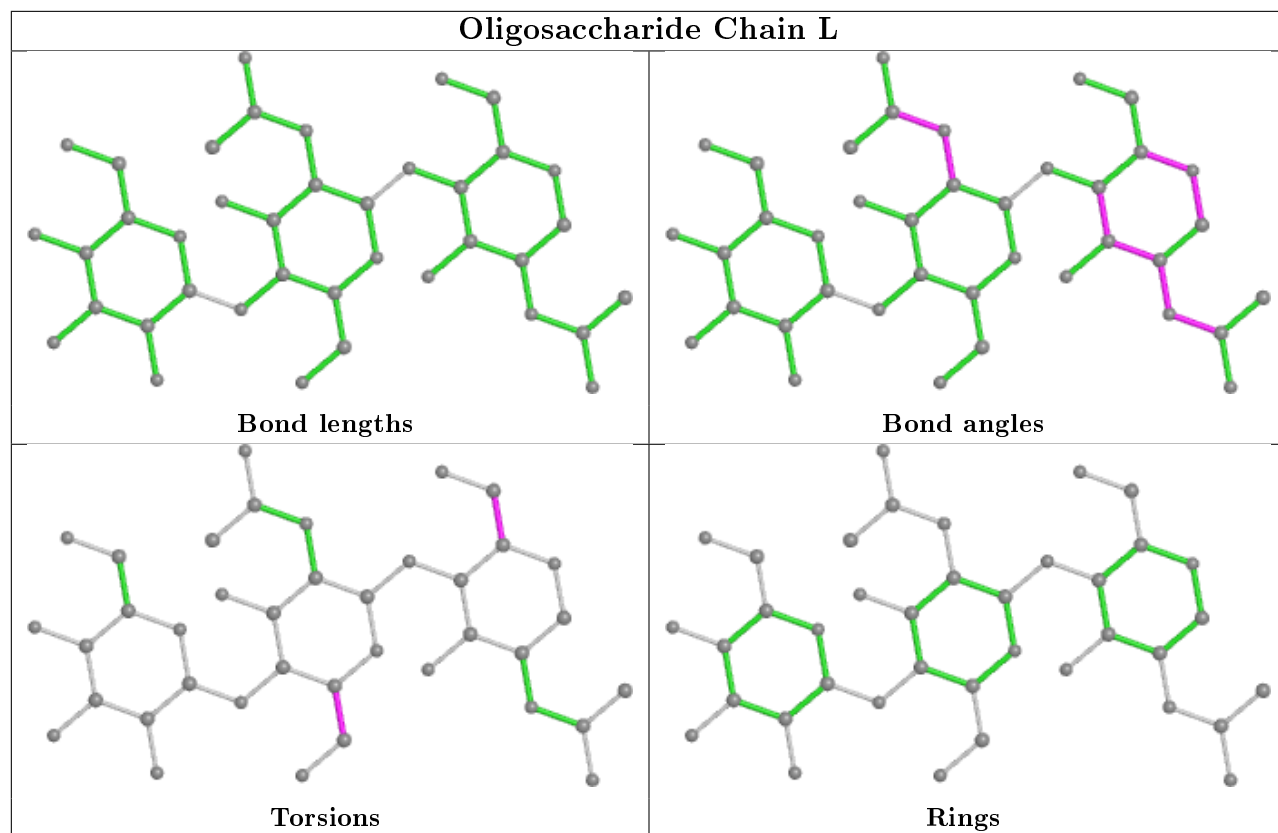
18 monomers are involved in 39 short contacts:

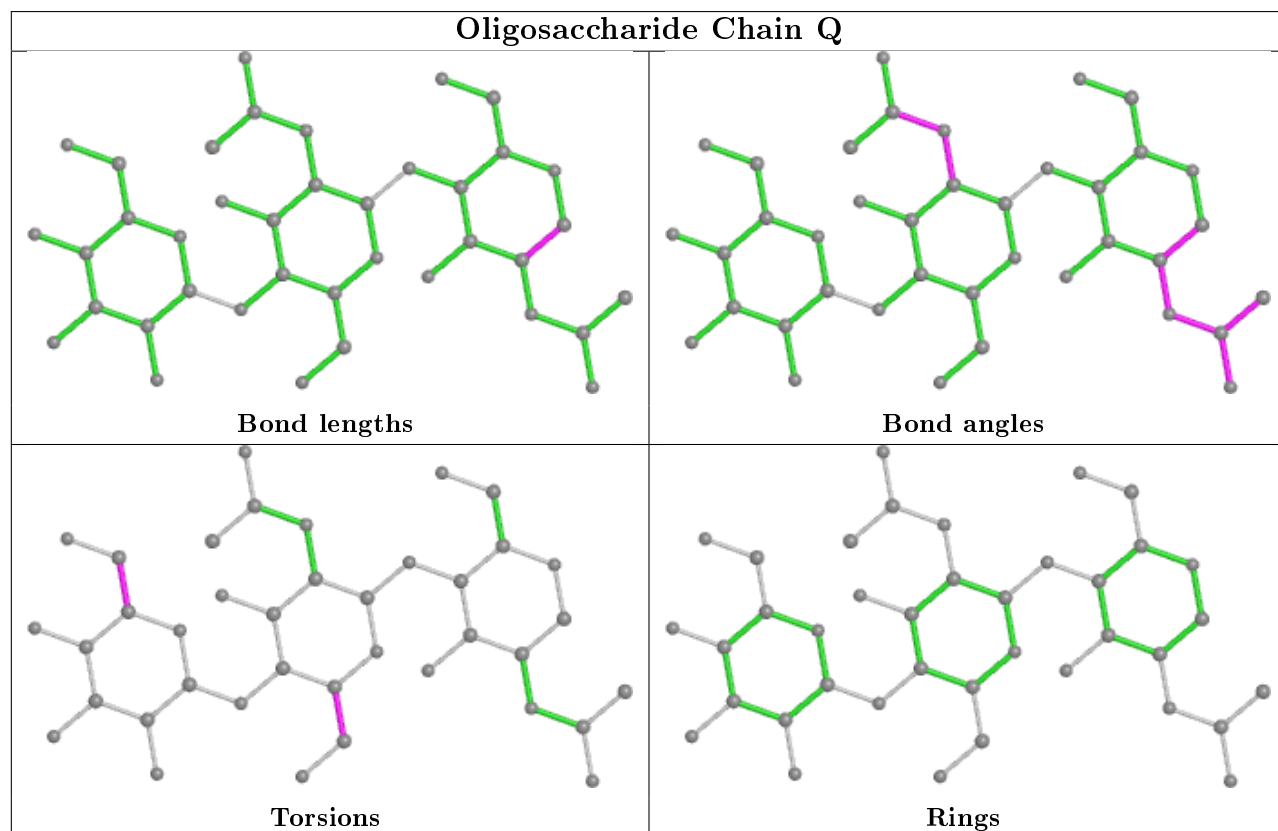
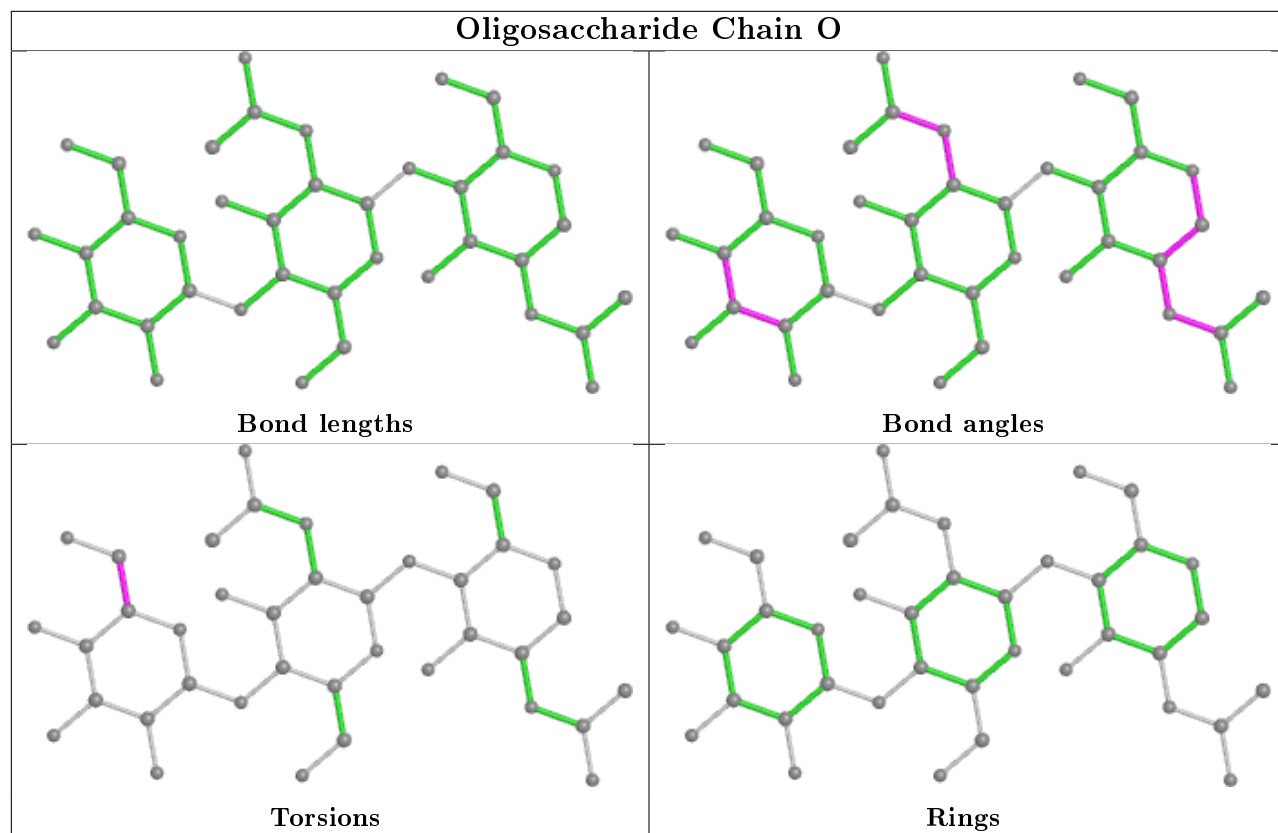
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	2	NAG	1	0
3	Q	2	NAG	6	0
4	U	3	MAN	1	0
3	G	2	NAG	1	0
3	T	1	NAG	2	0
3	L	1	NAG	2	0
3	G	1	NAG	2	0
4	P	3	MAN	1	0
3	T	2	NAG	2	0
4	P	1	NAG	1	0
4	P	2	NDG	4	0
3	S	2	NAG	1	0
4	K	2	NDG	11	0
3	R	1	NAG	1	0
3	R	2	NAG	1	0
4	K	3	MAN	7	0
4	U	2	NDG	8	0
4	U	1	NAG	3	0

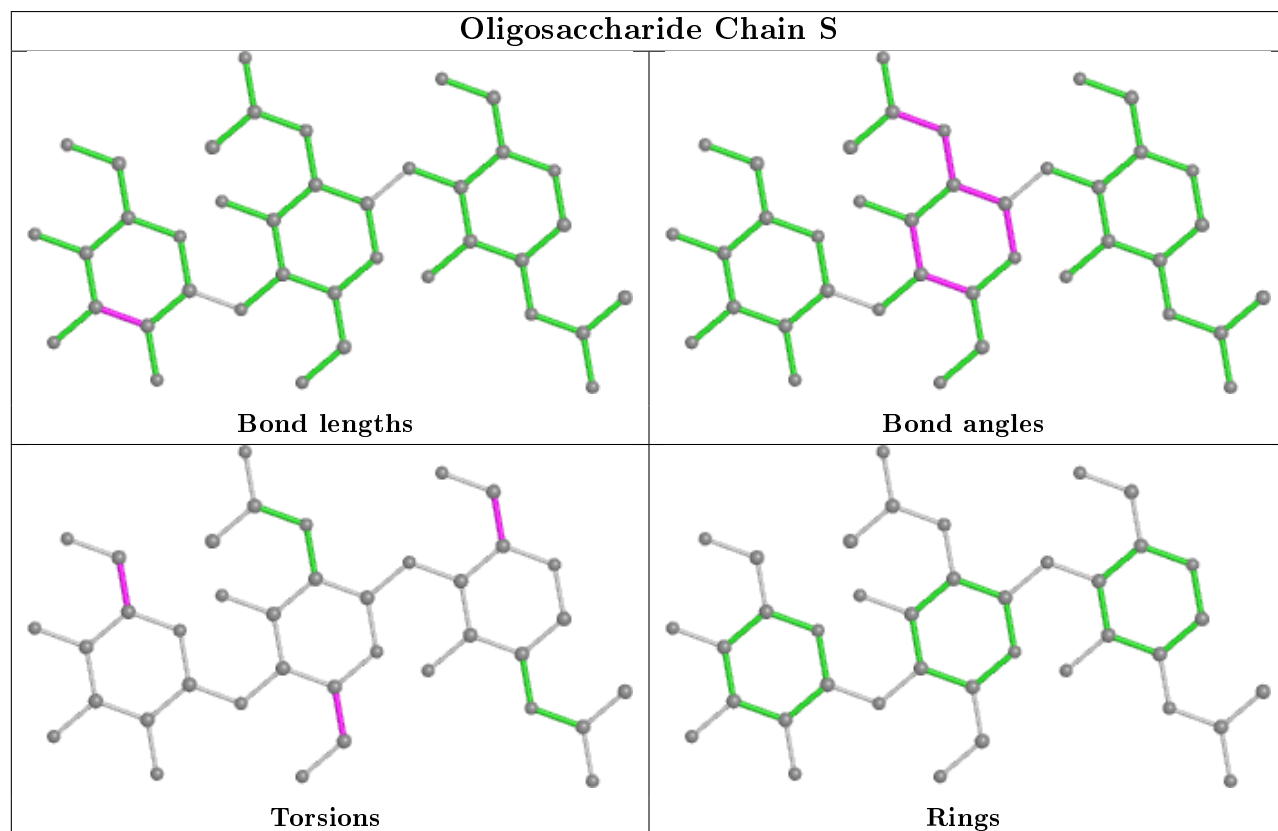
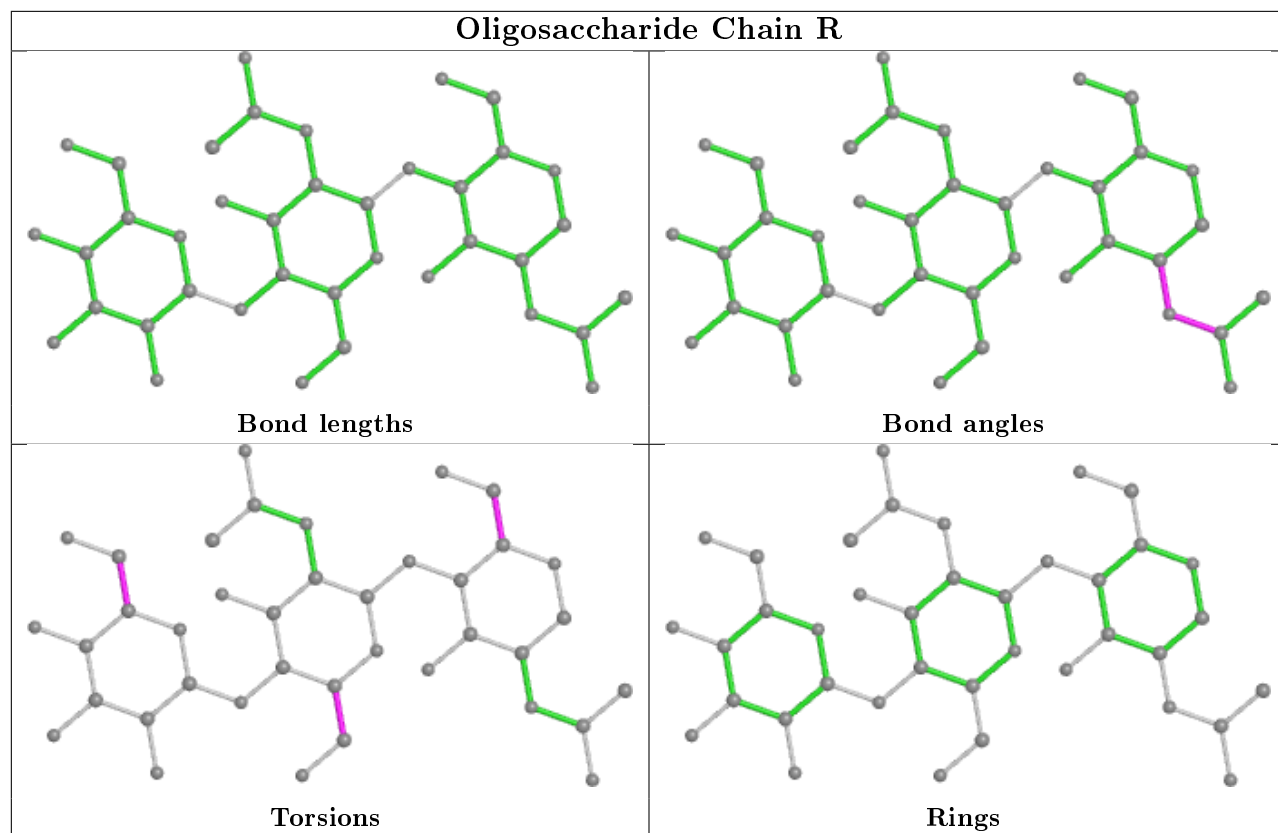
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

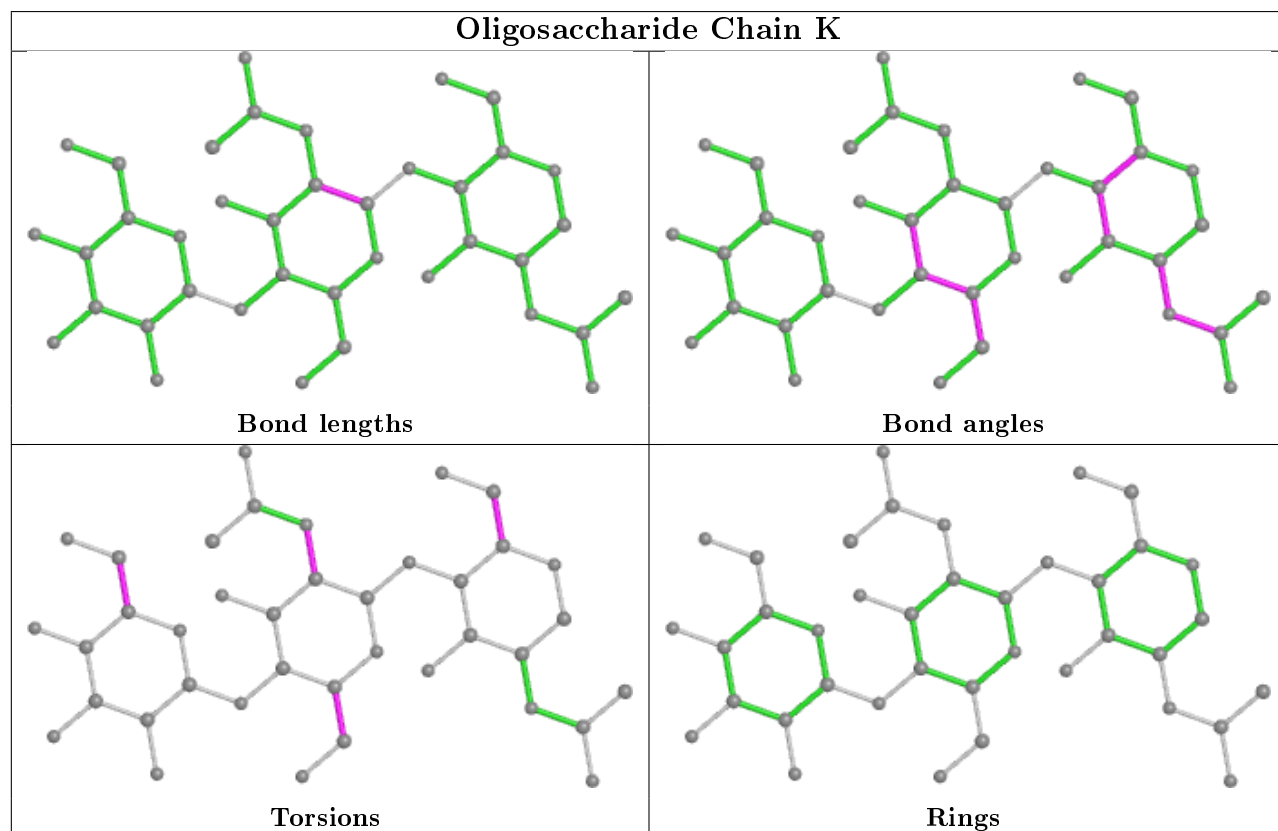
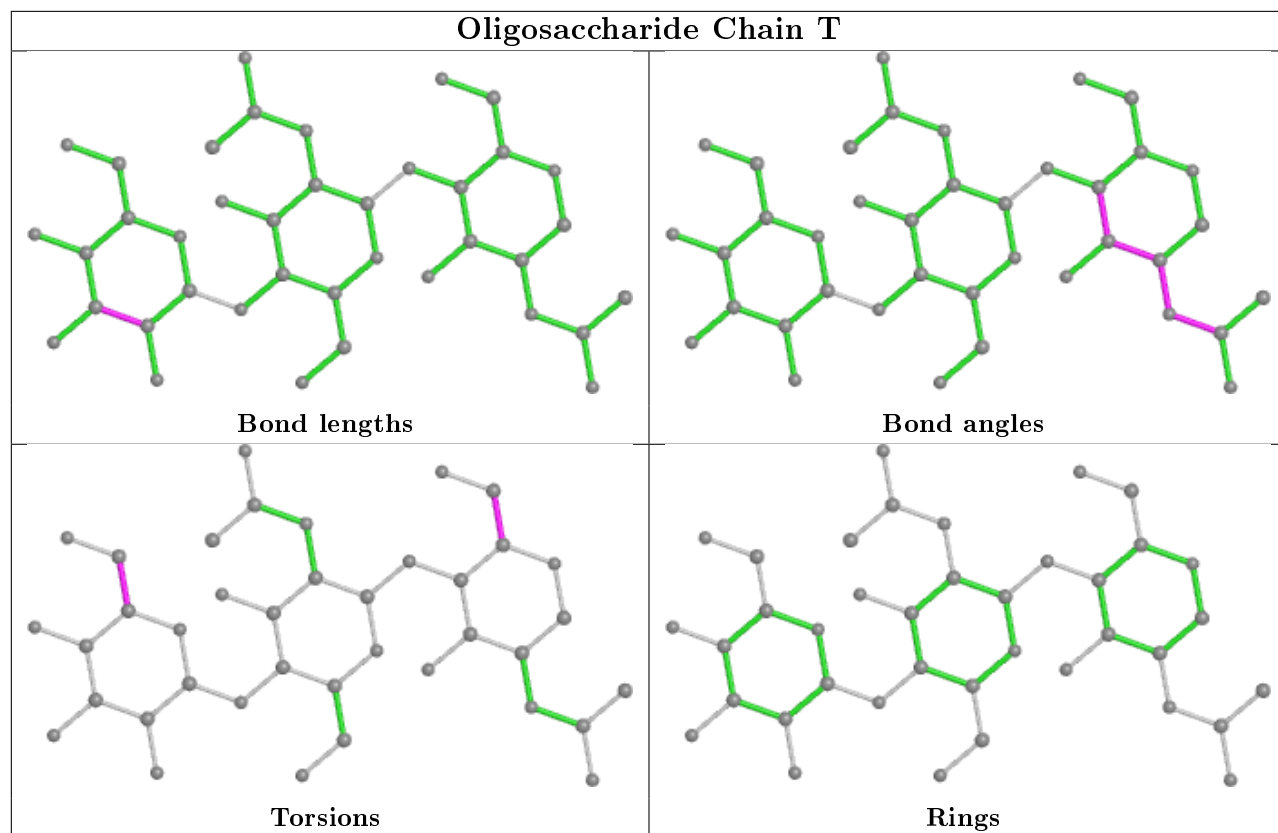


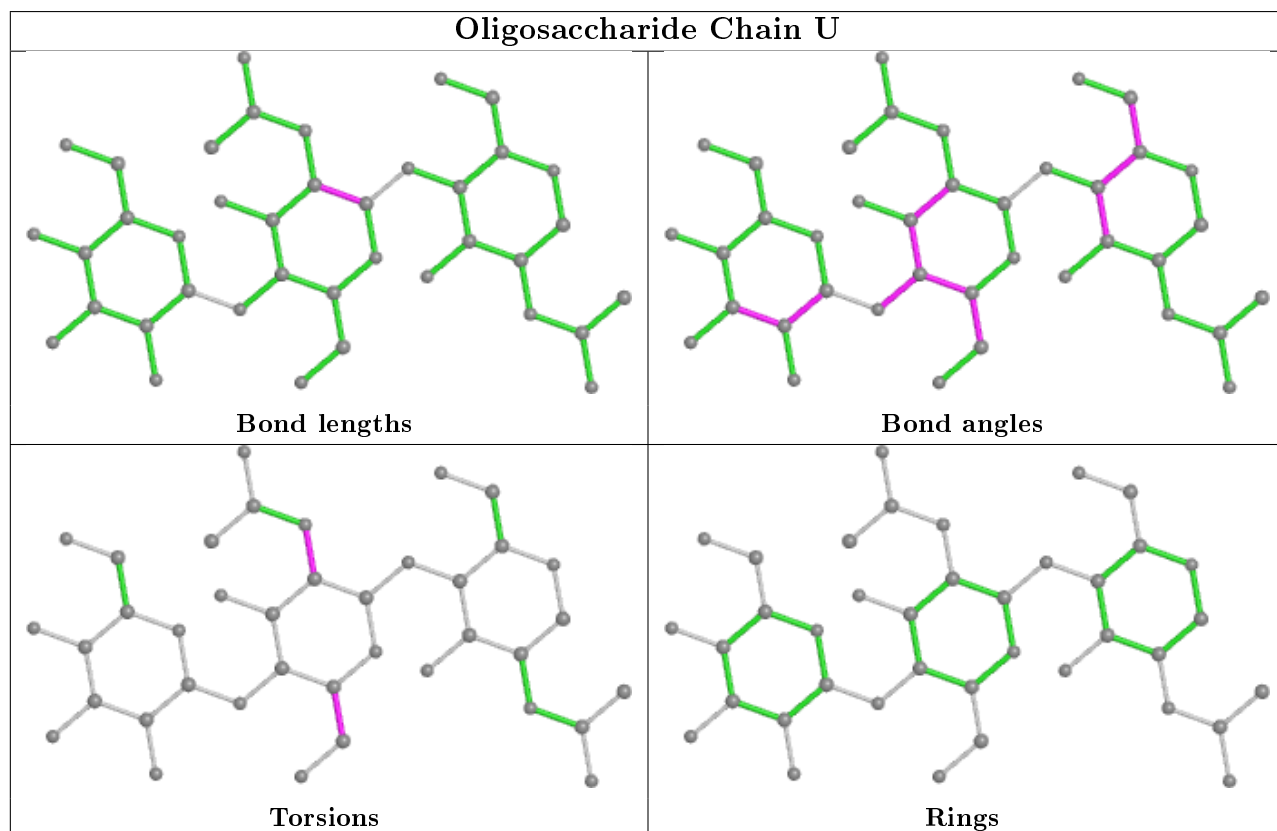
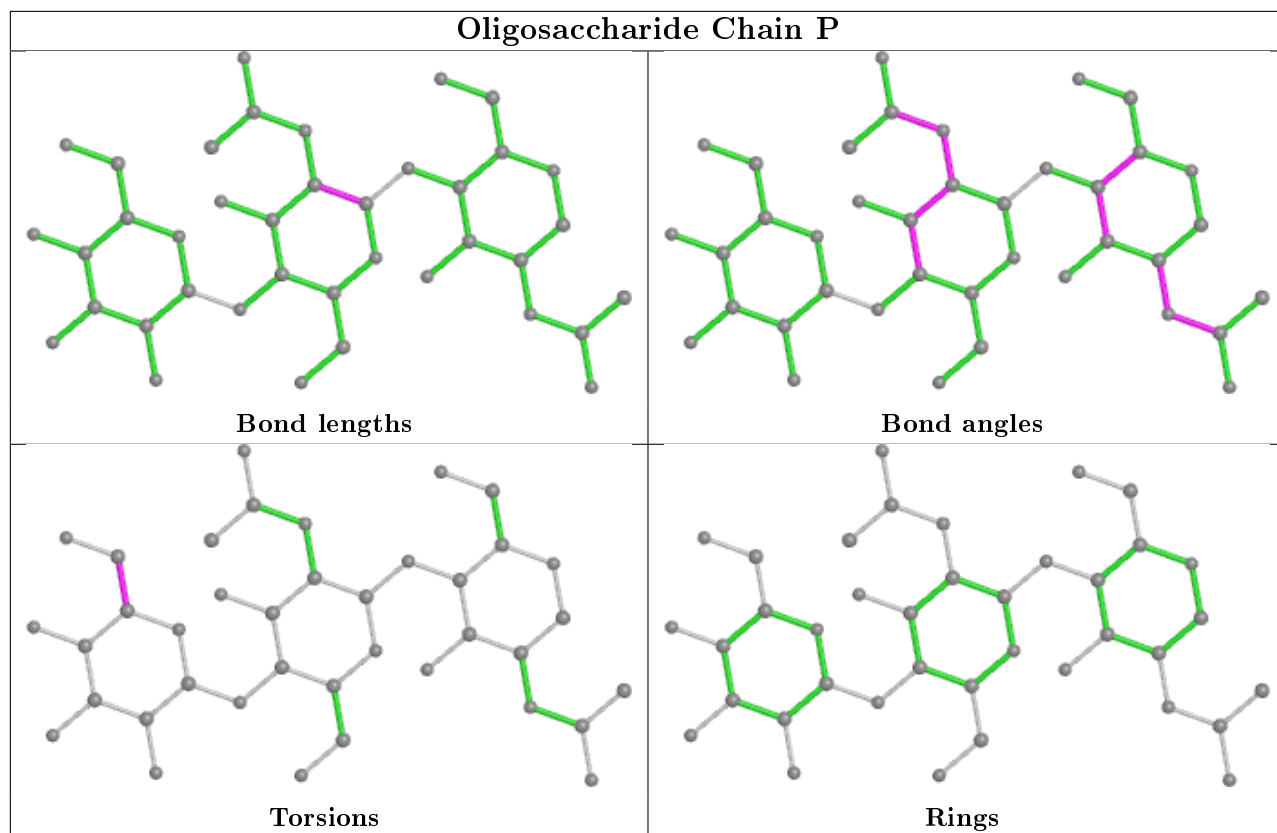


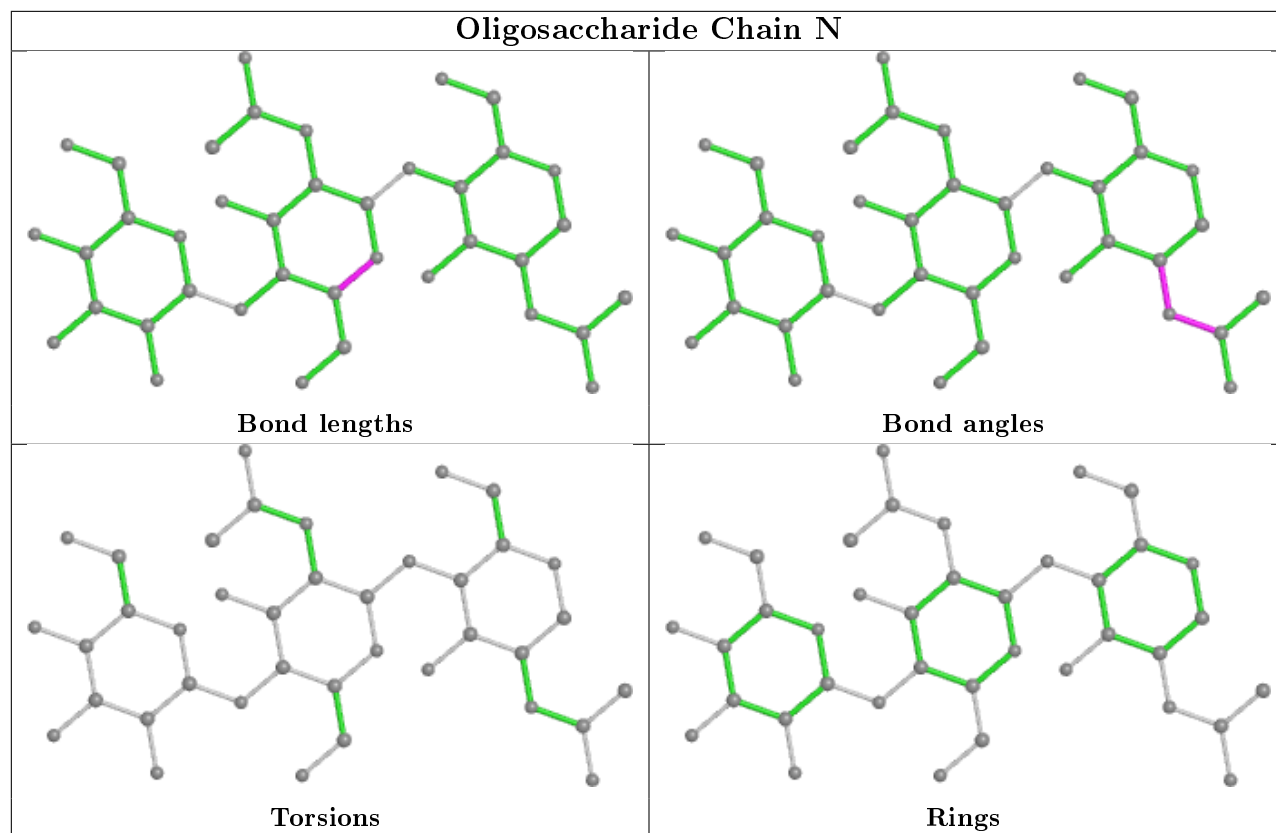












## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.