



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 02:15 PM BST

PDB ID : 2AJD  
Title : Porcine dipeptidyl peptidase IV (CD26) in complex with L-Pro-boro-L-Pro (boroPro)  
Authors : Engel, M.; Hoffmann, T.; Manhart, S.; Heiser, U.; Chambre, S.; Huber, R.; Demuth, H.U.; Bode, W.  
Deposited on : 2005-08-01  
Resolution : 2.56 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

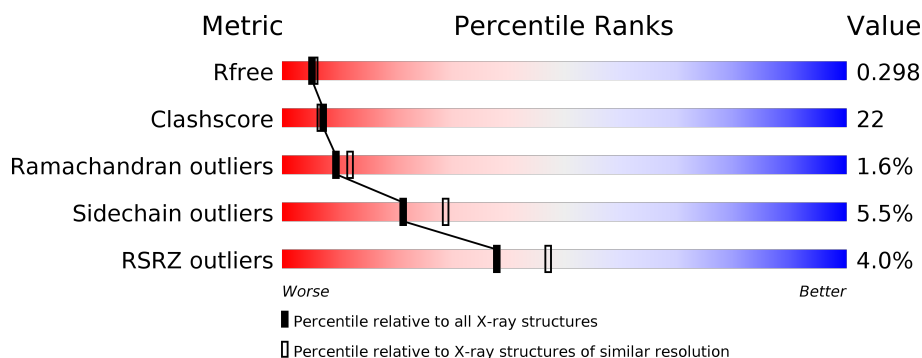
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.56 Å.

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






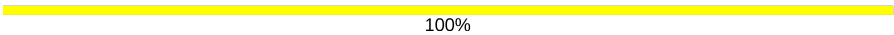

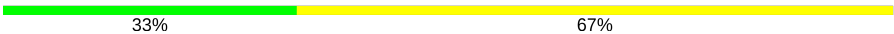

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1279 (2.58-2.54)
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312 (2.58-2.54)
Sidechain outliers	138945	1312 (2.58-2.54)
RSRZ outliers	127900	1269 (2.58-2.54)

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

Mol	Chain	Length	Quality of chain
1	A	728	<div> <div>2%</div> <div>61%</div> <div>36%</div> <div>.</div> </div>
1	B	728	<div> <div>2%</div> <div>60%</div> <div>37%</div> <div>.</div> </div>
1	C	728	<div> <div>9%</div> <div>47%</div> <div>48%</div> <div>.</div> </div>
1	D	728	<div> <div>2%</div> <div>61%</div> <div>36%</div> <div>.</div> </div>
2	E	2	<div> <div>100%</div> </div>
2	F	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	H	2	 50%50%
2	I	2	 50%50%
2	K	2	 50%50%
2	L	2	 100%
2	M	2	 50%50%
3	G	3	 33%67%
3	J	3	 67%33%

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	BMA	G	3	-	-	-	X
3	BMA	J	3	-	-	-	X
4	NAG	B	767(A)	-	-	-	X
4	NAG	D	767(A)	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 25139 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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	80	0	0
			5966	3825	986	1132	23			
1	B	728	Total	C	N	O	S	42	0	0
			5966	3825	986	1132	23			
1	C	728	Total	C	N	O	S	83	0	0
			5966	3825	986	1132	23			
1	D	728	Total	C	N	O	S	36	0	0
			5966	3825	986	1132	23			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	M	2	Total	C	N	O	0	0	0
			28	16	2	10			

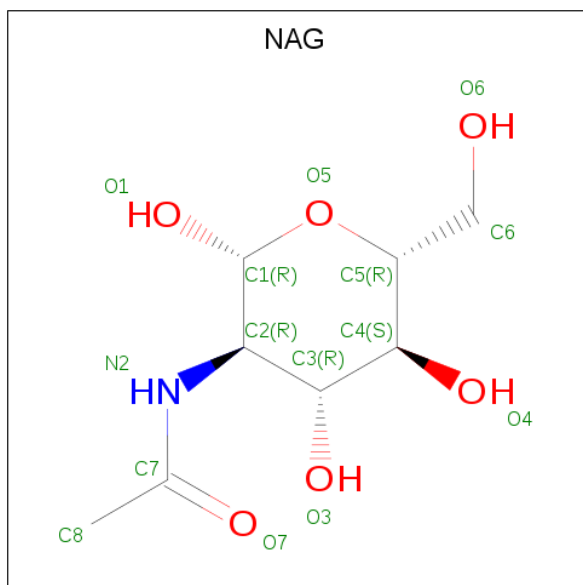
- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b

eta-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	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



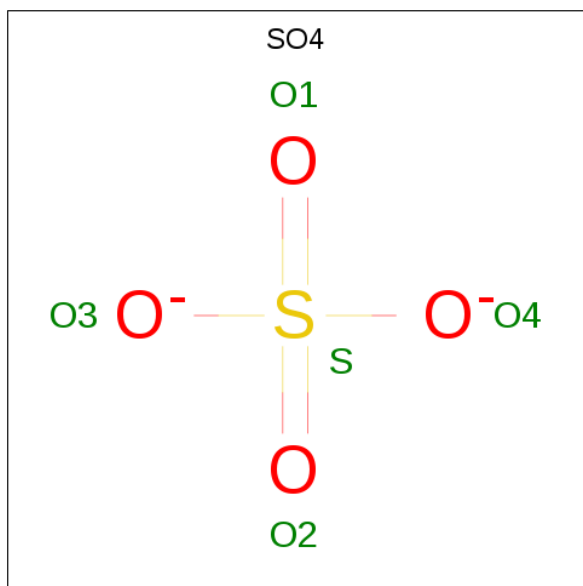
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	3	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



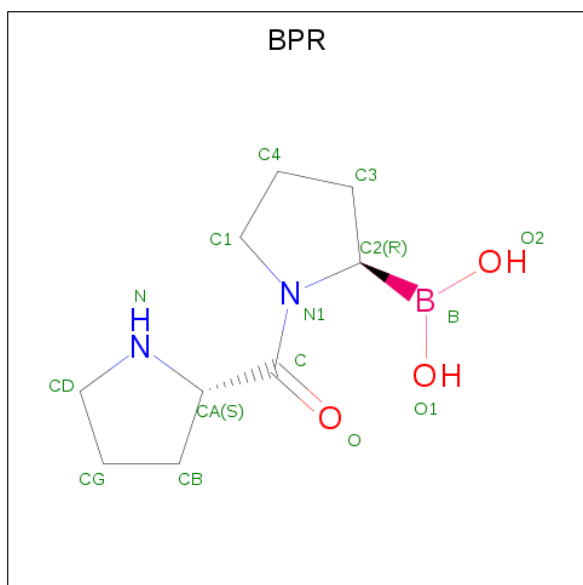
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is (2R)-N-[(2R)-2-(DIHYDROXYBORYL)-1-L-PROLYLPYRROLIDIN-2-YL]-N-[(5R)-5-(DIHYDROXYBORYL)-1-L-PROLYLPYRROLIDIN-2-YL]-L-PROLINAMIDE (three-letter code: BPR) (formula: C<sub>9</sub>H<sub>17</sub>BN<sub>2</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	B	C	N	O	0	0
			15	1	9	2	3		
6	B	1	Total	B	C	N	O	0	0
			15	1	9	2	3		
6	C	1	Total	B	C	N	O	0	0
			15	1	9	2	3		
6	D	1	Total	B	C	N	O	0	0
			15	1	9	2	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	163	Total	O	0	0
			163	163		
7	B	224	Total	O	0	0
			224	224		

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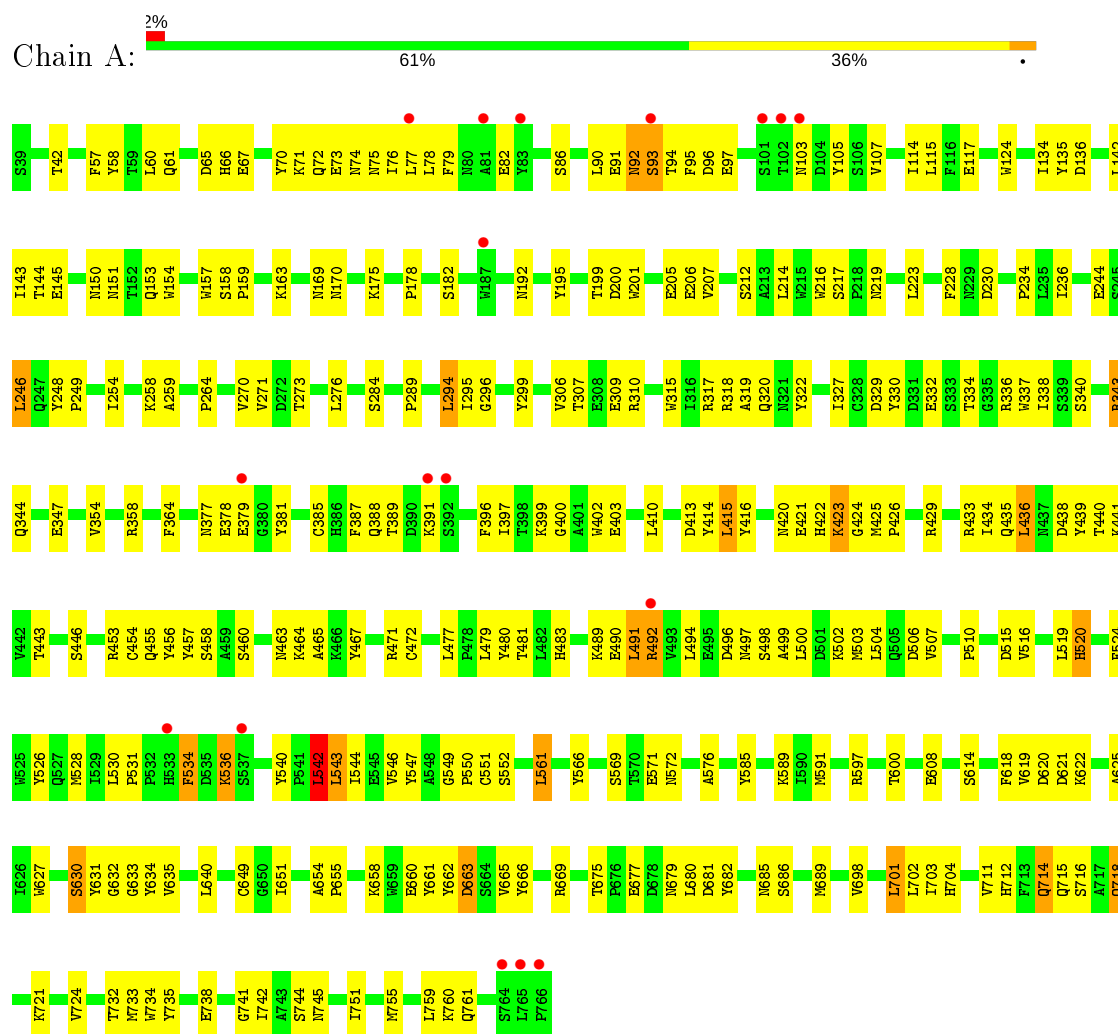
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	138	Total 138	O 138	0	0
7	D	186	Total 186	O 186	0	0



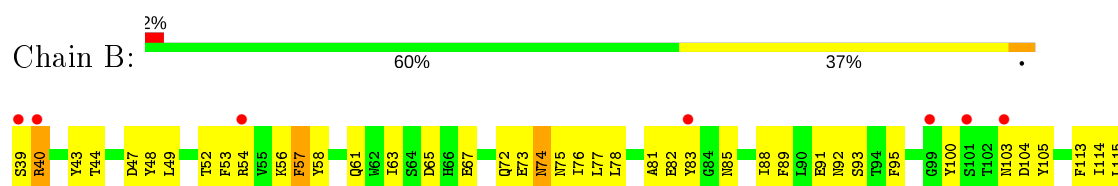
### 3 Residue-property plots

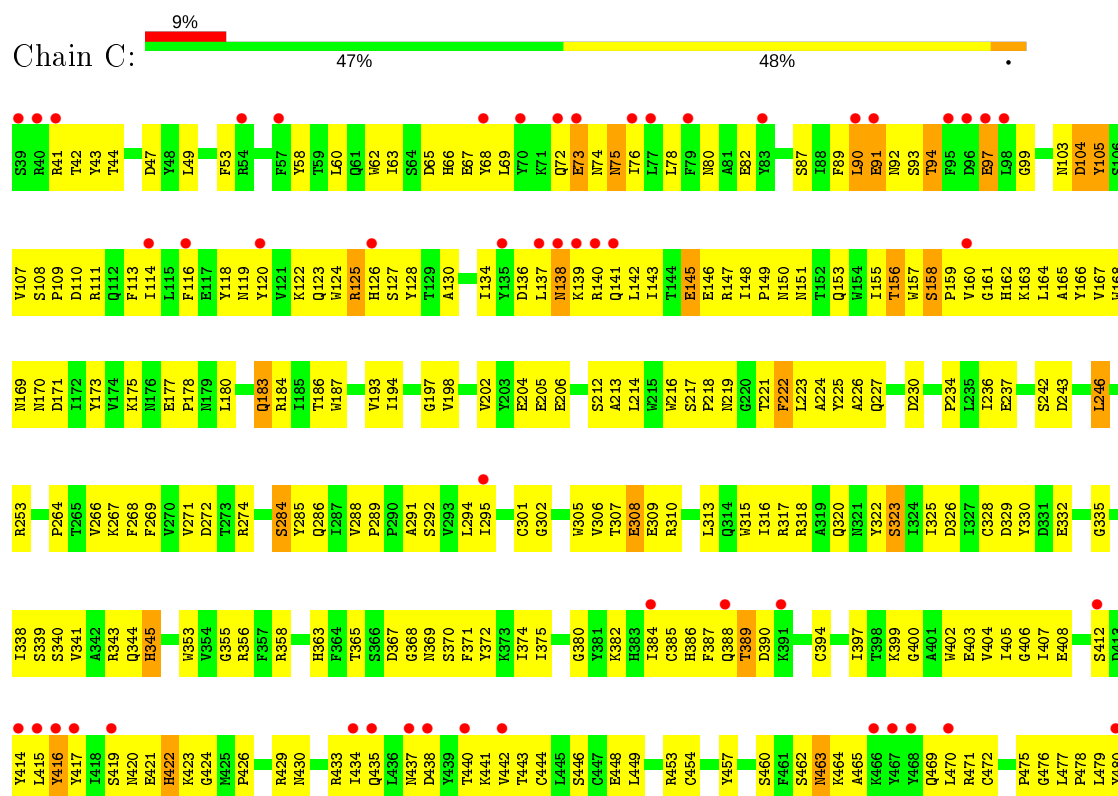
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

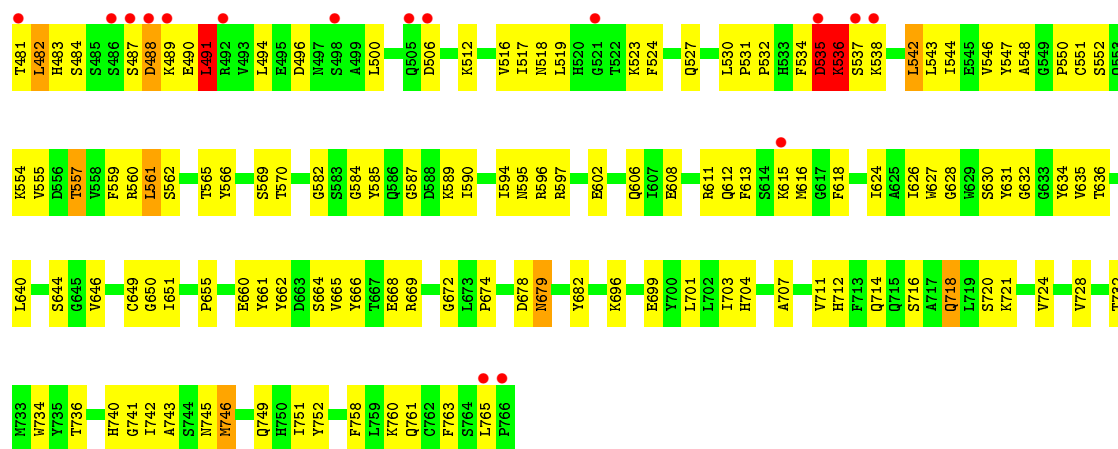
#### • Molecule 1: Dipeptidyl peptidase 4



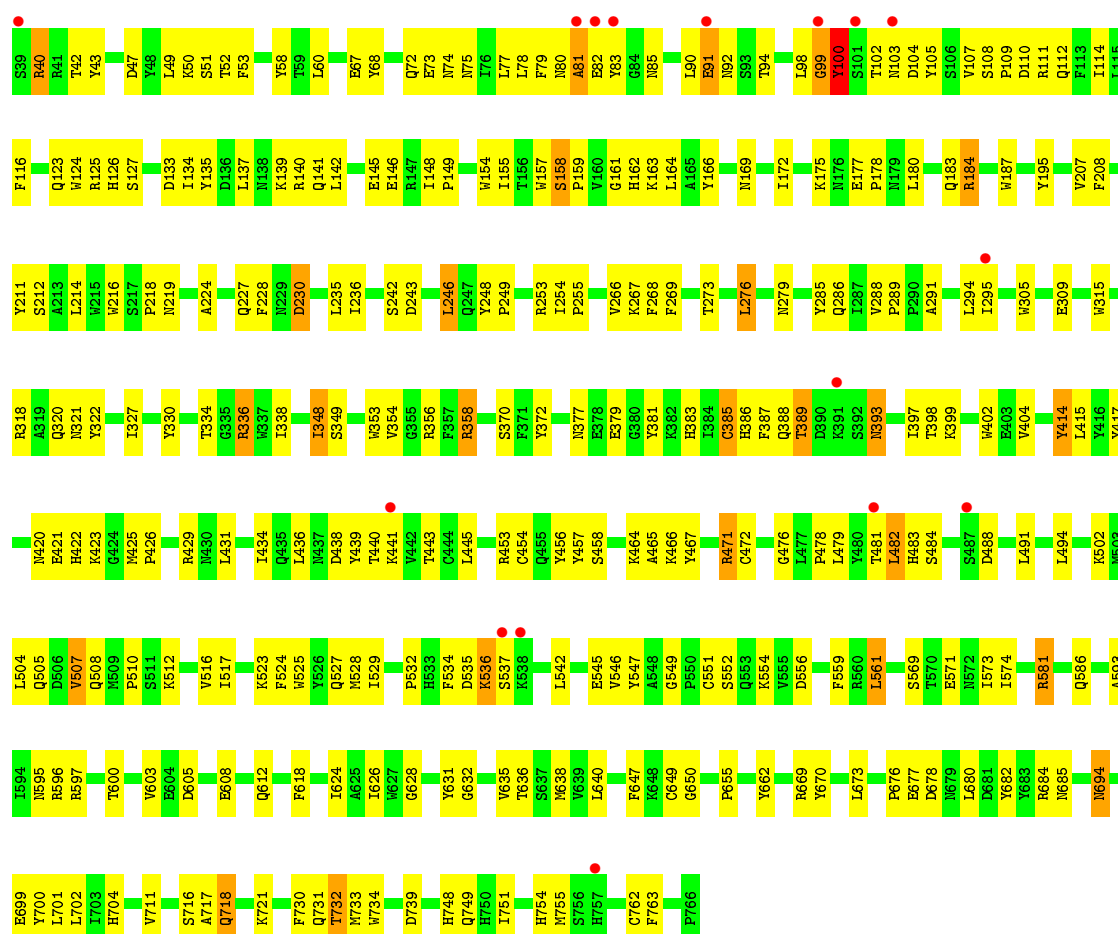
#### • Molecule 1: Dipeptidyl peptidase 4







• Molecule 1: Dipeptidyl peptidase 4



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



MAG1  
MAG2

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

Chain F:  100%MAG1  
MAG2

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

Chain H:  50% 50%MAG1  
MAG2

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

Chain I:  50% 50%MAG1  
MAG2

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

Chain K:  50% 50%MAG1  
MAG2

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

Chain L:  100%MAG1  
MAG2

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

Chain M:  50% 50%MAG1  
MAG2

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

Chain G:  33% 67%

MAG1  
MAG2  
BMA3

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

Chain J:  67% 33%

MAG1  
MAG2  
BMA3

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.40Å 122.07Å 134.03Å 111.41° 95.27° 94.52°	Depositor
Resolution (Å)	19.99 – 2.56 20.01 – 2.56	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.99-2.56) 97.0 (20.01-2.56)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.56Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.246 , 0.312 0.231 , 0.298	Depositor DCC
$R_{free}$ test set	5808 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 51.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	25139	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, BPR, NAG, SO4

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	0.47	0/6141	0.71	1/8353 (0.0%)
1	B	0.50	0/6141	0.73	1/8353 (0.0%)
1	C	0.45	0/6141	0.70	0/8353
1	D	0.49	0/6141	0.73	1/8353 (0.0%)
All	All	0.48	0/24564	0.72	3/33412 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	656	VAL	N-CA-C	-5.96	94.92	111.00
1	A	542	LEU	CA-CB-CG	5.41	127.74	115.30
1	D	529	ILE	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	256	TYR	Sidechain
1	C	285	TYR	Sidechain
1	D	700	TYR	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5966	0	5662	237	0
1	B	5966	0	5662	215	0
1	C	5966	0	5661	359	0
1	D	5966	0	5661	255	0
2	E	28	0	25	0	0
2	F	28	0	25	4	0
2	H	28	0	25	4	0
2	I	28	0	25	2	0
2	K	28	0	25	0	0
2	L	28	0	25	0	0
2	M	28	0	25	4	0
3	G	39	0	34	1	0
3	J	39	0	34	1	0
4	A	56	0	52	1	0
4	B	56	0	52	1	0
4	C	70	0	65	6	0
4	D	28	0	26	1	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	A	15	0	17	2	0
6	B	15	0	17	3	0
6	C	15	0	17	4	0
6	D	15	0	17	1	0
7	A	163	0	0	14	0
7	B	224	0	0	14	0
7	C	138	0	0	21	0
7	D	186	0	0	13	0
All	All	25139	0	23152	1057	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 22.

All (1057) 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:C:536:LYS:HG2	1:C:537:SER:H	1.09	1.18
1:D:600:THR:HG22	2:M:1:NAG:H83	1.42	1.02
1:B:82:GLU:HG2	1:B:467:TYR:OH	1.65	0.95
1:D:393:ASN:HD22	1:D:393:ASN:H	1.11	0.92
1:A:453:ARG:HH21	1:A:479:LEU:HB2	1.36	0.91
1:C:536:LYS:HG2	1:C:537:SER:N	1.86	0.91
1:C:519:LEU:HD22	1:C:608:GLU:OE1	1.72	0.89
1:D:581:ARG:HB2	1:D:605:ASP:OD2	1.74	0.88
1:D:320:GLN:OE1	1:D:669:ARG:HD3	1.75	0.87
1:A:492:ARG:HH21	1:A:492:ARG:HB3	1.40	0.86
1:A:67:GLU:HB3	1:A:78:LEU:HD11	1.56	0.86
1:A:377:ASN:HB2	1:A:381:TYR:H	1.40	0.86
1:C:382:LYS:H	1:C:403:GLU:HG2	1.39	0.85
1:C:536:LYS:CG	1:C:537:SER:H	1.88	0.85
1:C:696:LYS:HG2	1:C:728:VAL:HG22	1.57	0.84
1:C:471:ARG:HG2	1:C:480:TYR:CD2	2.13	0.84
1:C:516:VAL:HG11	1:C:523:LYS:HB2	1.60	0.84
1:C:516:VAL:HG12	1:C:517:ILE:H	1.41	0.84
1:C:184:ARG:HD3	1:C:186:THR:O	1.77	0.84
1:C:718:GLN:HE21	1:C:718:GLN:HA	1.43	0.83
1:C:76:ILE:HD12	1:C:90:LEU:HD11	1.59	0.82
1:D:516:VAL:HG11	1:D:523:LYS:HB2	1.61	0.81
1:A:336:ARG:HH11	1:A:336:ARG:HG3	1.46	0.81
1:C:612:GLN:O	1:C:615:LYS:HG2	1.80	0.81
1:B:184:ARG:HD3	1:B:186:THR:O	1.81	0.81
1:C:343:ARG:HH11	1:C:343:ARG:HG3	1.46	0.81
1:A:377:ASN:HB3	1:A:379:GLU:H	1.46	0.80
1:B:175:LYS:NZ	1:B:178:PRO:HA	1.97	0.80
1:D:718:GLN:HE22	1:D:721:LYS:NZ	1.81	0.79
1:C:438:ASP:OD2	1:C:441:LYS:HG3	1.82	0.79
1:D:718:GLN:HE22	1:D:721:LYS:HZ1	1.32	0.78
1:D:327:ILE:HD13	1:D:389:THR:HG23	1.66	0.78
1:B:113:PHE:HE2	1:B:162:HIS:ND1	1.82	0.77
1:A:460:SER:HB2	1:A:471:ARG:HH21	1.48	0.76
1:C:221:THR:HB	1:C:222:PHE:CD2	2.20	0.76
1:C:516:VAL:HG12	1:C:517:ILE:N	2.00	0.76
1:C:75:ASN:ND2	1:C:92:ASN:HB2	2.01	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:ARG:HH11	1:D:40:ARG:HB2	1.50	0.75
1:A:92:ASN:O	1:A:94:THR:N	2.19	0.75
1:A:438:ASP:OD1	1:A:440:THR:HB	1.87	0.74
1:C:109:PRO:HG2	1:C:161:GLY:O	1.87	0.74
1:C:137:LEU:HA	7:C:1579:HOH:O	1.86	0.74
1:D:718:GLN:HE21	1:D:718:GLN:HA	1.52	0.74
1:B:73:GLU:O	1:B:74:ASN:HB2	1.87	0.74
1:A:159:PRO:HG2	1:A:217:SER:O	1.88	0.74
1:C:666:TYR:CE2	6:C:801:BPR:HB1	2.23	0.74
1:A:414:TYR:CD2	1:A:433:ARG:HD2	2.22	0.73
1:B:175:LYS:HZ3	1:B:178:PRO:HA	1.53	0.73
1:B:393:ASN:H	1:B:393:ASN:HD22	1.35	0.73
1:C:330:TYR:CE1	1:C:335:GLY:HA2	2.24	0.73
1:D:377:ASN:HD21	1:D:383:HIS:CD2	2.06	0.73
1:D:184:ARG:NH1	1:D:187:TRP:HA	2.03	0.73
1:B:356:ARG:HD3	1:B:551:CYS:SG	2.29	0.72
1:B:428:GLY:O	1:B:429:ARG:HD3	1.89	0.72
1:A:413:ASP:O	1:A:436:LEU:HB2	1.90	0.72
1:C:67:GLU:HB3	1:C:78:LEU:HD11	1.72	0.72
1:C:289:PRO:HB3	1:C:315:TRP:CD2	2.25	0.72
1:C:104:ASP:HA	7:C:1617:HOH:O	1.88	0.71
1:C:435:GLN:NE2	1:C:441:LYS:HD2	2.05	0.71
1:A:438:ASP:OD1	1:A:441:LYS:HG3	1.91	0.70
1:C:134:ILE:HD13	1:C:178:PRO:HB3	1.71	0.70
1:A:320:GLN:OE1	1:A:669:ARG:HD3	1.91	0.70
1:C:662:TYR:CE2	6:C:801:BPR:H12	2.26	0.70
1:B:114:ILE:HG23	1:B:135:TYR:HB3	1.73	0.70
1:A:542:LEU:HD11	1:A:544:ILE:HD11	1.72	0.70
1:D:377:ASN:ND2	1:D:383:HIS:HD2	1.89	0.70
1:C:416:TYR:N	1:C:416:TYR:CD1	2.58	0.70
1:D:114:ILE:HG23	1:D:135:TYR:HB3	1.73	0.70
1:C:470:LEU:HD12	1:C:483:HIS:CE1	2.26	0.70
1:A:438:ASP:HB3	1:A:441:LYS:HD2	1.73	0.69
1:A:230:ASP:OD1	1:A:264:PRO:HB3	1.92	0.69
1:C:664:SER:O	1:C:668:GLU:HG3	1.92	0.69
1:C:590:ILE:HG13	7:C:1555:HOH:O	1.92	0.69
1:B:457:TYR:CD2	1:B:470:LEU:HD13	2.27	0.69
1:D:377:ASN:HD21	1:D:383:HIS:HD2	1.40	0.69
1:C:471:ARG:HG2	1:C:480:TYR:HD2	1.55	0.69
1:D:393:ASN:ND2	1:D:393:ASN:H	1.89	0.69
1:B:133:ASP:HB3	1:B:142:LEU:HD21	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:676:PRO:HG2	1:D:677:GLU:OE1	1.93	0.69
1:A:718:GLN:HA	1:A:718:GLN:HE21	1.58	0.68
1:B:218:PRO:HB2	7:B:1586:HOH:O	1.92	0.68
1:A:531:PRO:HB3	1:A:572:ASN:HD22	1.59	0.68
1:B:143:ILE:H	1:B:143:ILE:HD12	1.58	0.68
1:C:87:SER:OG	4:C:767(A):NAG:H81	1.93	0.68
1:B:125:ARG:HH11	1:B:125:ARG:HG3	1.59	0.68
1:B:457:TYR:CE2	1:B:470:LEU:HD13	2.29	0.68
1:B:65:ASP:HB2	1:B:466:LYS:HD2	1.75	0.68
1:C:63:ILE:HD11	1:C:111:ARG:NH1	2.08	0.68
1:C:701:LEU:HD11	1:C:703:ILE:HD11	1.75	0.68
1:D:536:LYS:HB3	1:D:536:LYS:NZ	2.09	0.68
1:D:75:ASN:HD21	1:D:92:ASN:ND2	1.91	0.68
1:C:289:PRO:HG2	1:C:294:LEU:CD2	2.24	0.68
1:A:71:LYS:HD2	1:A:105:TYR:HE2	1.59	0.68
1:D:600:THR:HG22	2:M:1:NAG:C8	2.22	0.68
1:A:201:TRP:CH2	1:A:205:GLU:HG2	2.29	0.67
1:A:309:GLU:HG2	1:A:330:TYR:HB3	1.76	0.67
1:C:159:PRO:HB2	1:C:218:PRO:O	1.94	0.67
1:A:490:GLU:O	1:A:492:ARG:N	2.27	0.67
1:C:222:PHE:CD2	1:C:222:PHE:N	2.63	0.67
1:C:225:TYR:CE1	1:C:269:PHE:HB2	2.30	0.67
1:C:292:SER:HA	1:C:295:ILE:HD11	1.74	0.67
1:C:517:ILE:HB	1:C:612:GLN:HE22	1.58	0.67
1:B:219:ASN:N	1:B:308:GLU:OE2	2.19	0.67
1:B:751:ILE:O	1:B:755:MET:HG3	1.94	0.67
1:C:76:ILE:HB	1:C:90:LEU:CD1	2.24	0.67
1:B:39:SER:O	1:B:40:ARG:HB2	1.93	0.67
1:B:516:VAL:HG11	1:B:523:LYS:HB2	1.76	0.67
1:C:374:ILE:HD11	1:C:406:GLY:HA2	1.76	0.66
1:D:704:HIS:HD2	1:D:716:SER:OG	1.78	0.66
1:A:246:LEU:HD22	1:A:248:TYR:H	1.60	0.66
1:C:743:ALA:HB1	7:C:1589:HOH:O	1.95	0.66
1:A:496:ASP:OD2	1:A:498:SER:HB3	1.96	0.66
1:B:83:TYR:CE2	4:B:767(A):NAG:H62	2.30	0.66
1:B:660:GLU:HG3	1:B:683:TYR:HD1	1.60	0.66
1:A:675:THR:HB	1:A:677:GLU:OE1	1.96	0.66
1:B:487:SER:OG	1:B:489:LYS:HB3	1.96	0.66
1:A:403:GLU:OE1	1:A:585:TYR:HA	1.97	0.65
1:D:402:TRP:CD2	1:D:421:GLU:HB2	2.31	0.65
1:B:378:GLU:CD	1:B:378:GLU:H	1.99	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1:NAG:H61	2:F:2:NAG:H82	1.78	0.65
1:B:54:ARG:O	1:B:500:LEU:HD13	1.96	0.65
1:B:334:THR:OG1	1:B:336:ARG:HG2	1.96	0.65
1:B:403:GLU:OE1	1:B:585:TYR:HA	1.95	0.65
1:B:481:THR:OG1	1:B:483:HIS:HE1	1.78	0.65
1:D:100:TYR:HE1	1:D:102:THR:HG1	1.45	0.65
1:D:169:ASN:HD22	1:D:169:ASN:N	1.94	0.65
1:C:516:VAL:HG13	1:C:524:PHE:O	1.96	0.65
1:D:289:PRO:HB3	1:D:315:TRP:CD2	2.31	0.65
1:C:704:HIS:HD2	1:C:716:SER:OG	1.81	0.64
1:D:414:TYR:HA	1:D:436:LEU:HD13	1.79	0.64
1:B:327:ILE:CD1	1:B:389:THR:HG23	2.28	0.64
1:C:422:HIS:HA	7:C:1628:HOH:O	1.96	0.64
1:C:153:GLN:HE22	1:C:170:ASN:ND2	1.96	0.64
1:C:718:GLN:HE21	1:C:718:GLN:CA	2.10	0.64
1:D:242:SER:HB3	1:D:246:LEU:HD12	1.80	0.64
1:A:388:GLN:HB2	1:A:391:LYS:HB2	1.78	0.64
1:C:242:SER:HB3	1:C:246:LEU:HD12	1.78	0.64
1:C:416:TYR:HD1	1:C:416:TYR:H	1.43	0.64
1:C:221:THR:HB	1:C:222:PHE:CE2	2.32	0.64
1:D:288:VAL:CG1	1:D:289:PRO:HD2	2.27	0.64
1:D:731:GLN:OE1	7:D:1507:HOH:O	2.14	0.64
1:C:291:ALA:O	1:C:295:ILE:HG13	1.97	0.64
1:C:746:MET:CE	1:C:746:MET:H	2.11	0.64
1:B:660:GLU:HG3	1:B:683:TYR:CD1	2.32	0.64
1:A:214:LEU:HD22	1:A:223:LEU:HD11	1.80	0.64
1:C:134:ILE:HG21	1:C:178:PRO:HB3	1.80	0.64
1:C:491:LEU:H	1:C:491:LEU:CD2	2.11	0.63
1:D:40:ARG:HB2	1:D:40:ARG:NH1	2.13	0.63
1:D:484:SER:O	1:D:488:ASP:HA	1.99	0.63
1:B:143:ILE:N	1:B:143:ILE:HD12	2.13	0.63
1:C:535:ASP:C	1:C:536:LYS:HD3	2.18	0.63
1:C:316:ILE:HG22	1:C:323:SER:HB2	1.79	0.63
1:A:704:HIS:HE1	1:A:711:VAL:O	1.81	0.63
1:C:184:ARG:HD2	1:C:187:TRP:CE2	2.33	0.63
1:A:327:ILE:CD1	1:A:389:THR:HG23	2.29	0.63
1:D:640:LEU:HD11	1:D:650:GLY:HA3	1.79	0.63
1:B:516:VAL:HG11	1:B:523:LYS:HD2	1.80	0.63
1:C:535:ASP:O	1:C:536:LYS:HB3	1.98	0.63
7:C:1562:HOH:O	1:D:243:ASP:HA	1.98	0.63
1:C:718:GLN:NE2	1:C:718:GLN:HA	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:343:ARG:HG3	1:C:343:ARG:NH1	2.12	0.62
1:C:453:ARG:HG2	1:C:453:ARG:O	1.99	0.62
1:B:516:VAL:CG1	1:B:523:LYS:HB2	2.28	0.62
1:C:484:SER:HB2	1:C:491:LEU:HD21	1.81	0.62
1:C:631:TYR:O	1:C:634:TYR:HB3	1.99	0.62
1:B:113:PHE:CE2	1:B:162:HIS:ND1	2.67	0.62
1:C:435:GLN:HG2	1:C:437:ASN:OD1	1.99	0.62
1:C:678:ASP:OD1	1:C:679:ASN:N	2.32	0.62
1:B:614:SER:HA	1:B:619:VAL:HG11	1.80	0.62
1:B:654:ALA:HA	1:B:704:HIS:CD2	2.34	0.62
1:D:266:VAL:HG22	1:D:267:LYS:N	2.14	0.62
1:D:516:VAL:HG13	1:D:524:PHE:O	1.99	0.62
1:A:422:HIS:NE2	1:A:423:LYS:HD3	2.14	0.62
1:A:234:PRO:HB2	1:B:248:TYR:CZ	2.34	0.62
1:D:291:ALA:O	1:D:295:ILE:HG13	1.99	0.62
1:C:429:ARG:HB2	1:C:457:TYR:H	1.65	0.62
1:D:457:TYR:HA	1:D:471:ARG:O	2.00	0.62
1:A:107:VAL:HG22	1:A:114:ILE:HG13	1.82	0.61
1:A:65:ASP:HA	1:A:463:ASN:HB2	1.82	0.61
1:C:416:TYR:N	1:C:416:TYR:HD1	1.95	0.61
1:C:438:ASP:OD2	1:C:440:THR:HB	2.00	0.61
1:D:377:ASN:HB3	1:D:379:GLU:H	1.64	0.61
1:A:378:GLU:CD	1:A:378:GLU:H	2.03	0.61
1:B:402:TRP:CD2	1:B:421:GLU:HB2	2.36	0.61
1:C:272:ASP:OD2	1:C:274:ARG:HB2	2.00	0.61
1:C:718:GLN:HE22	1:C:721:LYS:NZ	1.99	0.61
1:A:704:HIS:HD2	1:A:716:SER:OG	1.84	0.61
1:A:336:ARG:NH2	1:A:338:ILE:HD11	2.15	0.61
1:C:536:LYS:N	1:C:536:LYS:HD3	2.15	0.61
1:B:134:ILE:HG21	1:B:178:PRO:HB3	1.83	0.61
1:C:90:LEU:O	1:C:90:LEU:HD13	2.01	0.60
1:D:81:ALA:O	1:D:82:GLU:HB3	2.00	0.60
1:C:307:THR:C	1:C:309:GLU:H	2.04	0.60
3:G:2:NAG:O6	3:G:3:BMA:H2	2.00	0.60
1:A:271:VAL:HG22	1:A:284:SER:HB3	1.82	0.60
1:A:453:ARG:NH2	1:A:479:LEU:HB2	2.12	0.60
1:C:317:ARG:NH1	1:C:322:TYR:CD2	2.70	0.60
1:C:640:LEU:HD11	1:C:650:GLY:HA3	1.84	0.60
1:D:288:VAL:HG13	1:D:289:PRO:HD2	1.83	0.60
1:D:762:CYS:HA	7:D:1584:HOH:O	2.00	0.60
1:C:463:ASN:HD22	1:C:463:ASN:N	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:PRO:HD2	7:B:1521:HOH:O	2.00	0.60
1:A:91:GLU:C	1:A:92:ASN:O	2.39	0.60
1:D:502:LYS:O	1:D:505:GLN:HG2	2.01	0.60
1:B:410:LEU:HD13	1:B:415:LEU:HD22	1.83	0.60
1:C:487:SER:C	1:C:489:LYS:H	2.05	0.60
1:C:512:LYS:HE3	1:C:527:GLN:NE2	2.17	0.60
1:C:547:TYR:HD2	1:C:552:SER:HB2	1.67	0.60
1:C:613:PHE:HA	1:C:616:MET:HE3	1.83	0.60
1:A:114:ILE:HG22	1:A:135:TYR:HB3	1.84	0.60
1:C:374:ILE:CD1	1:C:406:GLY:HA2	2.30	0.60
1:C:87:SER:CB	4:C:767(A):NAG:H81	2.31	0.60
1:D:372:TYR:CE2	1:D:386:HIS:HD2	2.20	0.60
1:B:397:ILE:HG13	1:B:398:THR:HG23	1.83	0.59
1:C:430:ASN:HB2	7:C:1527:HOH:O	2.02	0.59
1:A:435:GLN:HB3	1:A:441:LYS:HB2	1.84	0.59
1:D:100:TYR:HE1	1:D:102:THR:OG1	1.85	0.59
1:D:98:LEU:HD22	1:D:142:LEU:HD12	1.84	0.59
1:A:295:ILE:HG23	1:A:296:GLY:N	2.16	0.59
1:C:402:TRP:HA	7:C:1560:HOH:O	2.01	0.59
1:D:662:TYR:CE2	6:D:801:BPR:H12	2.36	0.59
1:B:522:THR:HG21	1:B:590:ILE:HD11	1.83	0.59
1:C:138:ASN:C	1:C:140:ARG:H	2.06	0.59
1:C:491:LEU:HD22	1:C:491:LEU:H	1.66	0.59
1:A:82:GLU:HG2	1:A:467:TYR:OH	2.02	0.59
1:D:40:ARG:HB3	1:D:508:GLN:HG3	1.83	0.59
1:C:236:ILE:HD13	1:C:712:HIS:ND1	2.18	0.59
1:C:403:GLU:OE1	1:C:585:TYR:HA	2.02	0.59
1:A:435:GLN:NE2	1:A:441:LYS:HD3	2.17	0.59
1:A:543:LEU:HD21	1:A:627:TRP:HD1	1.67	0.59
1:D:155:ILE:HG13	1:D:166:TYR:HB3	1.85	0.59
1:D:94:THR:O	1:D:98:LEU:HG	2.01	0.59
1:C:153:GLN:OE1	1:C:167:VAL:HG12	2.02	0.59
1:C:589:LYS:HB3	7:C:1555:HOH:O	2.02	0.59
1:A:78:LEU:HD12	1:A:79:PHE:N	2.17	0.59
1:A:718:GLN:HE22	1:A:721:LYS:NZ	2.01	0.59
1:B:429:ARG:HG3	1:B:429:ARG:HH11	1.68	0.59
1:B:696:LYS:HG2	1:B:728:VAL:HG22	1.85	0.59
1:A:500:LEU:HA	1:A:503:MET:HE3	1.85	0.58
1:D:385:CYS:HB3	1:D:387:PHE:CE1	2.37	0.58
1:B:718:GLN:HE21	1:B:718:GLN:HA	1.68	0.58
1:D:484:SER:HB2	1:D:491:LEU:HD21	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:ILE:HD13	1:B:389:THR:HG23	1.84	0.58
1:C:651:ILE:HG23	1:C:701:LEU:HD12	1.86	0.58
1:D:472:CYS:O	1:D:478:PRO:HA	2.04	0.58
1:A:685:ASN:O	2:F:1:NAG:H82	2.04	0.58
1:A:295:ILE:CG2	1:A:296:GLY:N	2.67	0.58
1:A:481:THR:OG1	1:A:483:HIS:HE1	1.86	0.58
1:A:534:PHE:CE1	1:A:540:TYR:CE1	2.92	0.58
1:C:307:THR:O	1:C:309:GLU:N	2.37	0.58
1:A:402:TRP:CD2	1:A:421:GLU:HB2	2.39	0.58
1:A:415:LEU:HB3	1:A:434:ILE:CG2	2.33	0.58
1:B:173:TYR:CE2	1:B:184:ARG:HG3	2.39	0.58
1:C:487:SER:O	1:C:489:LYS:N	2.37	0.57
1:A:477:LEU:HD22	1:A:500:LEU:HD23	1.85	0.57
1:C:732:THR:CG2	1:D:733:MET:HA	2.35	0.57
1:D:114:ILE:CG2	1:D:135:TYR:HB3	2.34	0.57
1:D:60:LEU:C	1:D:60:LEU:HD12	2.25	0.57
1:B:327:ILE:HB	1:B:343:ARG:HB3	1.86	0.57
1:D:536:LYS:HZ3	1:D:536:LYS:HB3	1.68	0.57
1:A:703:ILE:HG12	1:A:733:MET:HB3	1.86	0.57
1:B:143:ILE:CD1	1:B:143:ILE:H	2.18	0.57
1:C:565:THR:O	1:C:569:SER:HB3	2.03	0.57
1:A:327:ILE:HB	1:A:343:ARG:HG2	1.85	0.57
1:C:159:PRO:HD3	1:C:216:TRP:HB3	1.84	0.57
1:A:340:SER:O	1:A:344:GLN:HG3	2.05	0.57
1:A:464:LYS:O	1:A:465:ALA:HB3	2.05	0.57
1:B:75:ASN:ND2	1:B:92:ASN:H	2.02	0.57
1:A:534:PHE:CD2	1:A:536:LYS:HD2	2.39	0.57
1:B:214:LEU:HD12	1:B:214:LEU:O	2.05	0.57
1:D:532:PRO:HD3	1:D:569:SER:HA	1.86	0.57
1:A:631:TYR:O	1:A:634:TYR:HB3	2.05	0.57
1:B:370:SER:HB2	1:B:387:PHE:O	2.05	0.57
1:B:77:LEU:HD23	1:B:88:ILE:HA	1.86	0.57
1:C:372:TYR:CE2	1:C:386:HIS:CG	2.93	0.57
1:C:372:TYR:HE2	1:C:386:HIS:CG	2.22	0.57
1:C:546:VAL:HG21	1:C:635:VAL:HG11	1.87	0.57
1:B:232:GLU:CB	1:B:262:GLU:HG2	2.35	0.56
1:C:301:CYS:SG	1:C:316:ILE:HG12	2.45	0.56
1:D:169:ASN:HB2	7:D:1515:HOH:O	2.04	0.56
1:C:602:GLU:O	1:C:606:GLN:HG2	2.05	0.56
1:D:536:LYS:O	1:D:537:SER:CB	2.51	0.56
1:D:438:ASP:OD2	1:D:441:LYS:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:ASN:ND2	1:B:393:ASN:H	2.01	0.56
1:B:159:PRO:HG2	1:B:217:SER:O	2.04	0.56
1:C:184:ARG:HD2	1:C:187:TRP:CD2	2.41	0.56
1:C:43:TYR:OH	1:C:561:LEU:HB3	2.05	0.56
1:C:460:SER:HB3	1:C:469:GLN:HB3	1.86	0.56
1:D:536:LYS:O	1:D:537:SER:HB2	2.05	0.56
1:A:327:ILE:HD13	1:A:389:THR:HG23	1.87	0.56
1:C:316:ILE:CG2	1:C:323:SER:HB2	2.36	0.56
1:D:289:PRO:HB3	1:D:315:TRP:CE2	2.41	0.56
1:B:546:VAL:HG23	7:B:1516:HOH:O	2.04	0.56
1:C:269:PHE:CE2	1:C:286:GLN:HG3	2.40	0.56
1:C:483:HIS:CE1	1:C:490:GLU:HG3	2.41	0.56
1:C:417:TYR:HE1	1:C:419:SER:HB3	1.71	0.56
1:D:139:LYS:HG3	1:D:141:GLN:HG3	1.88	0.56
1:D:454:CYS:HB3	1:D:457:TYR:CZ	2.41	0.56
1:C:160:VAL:HG13	1:C:218:PRO:O	2.05	0.55
1:C:194:ILE:HD12	4:C:769(A):NAG:H82	1.87	0.55
1:D:718:GLN:HA	1:D:718:GLN:NE2	2.20	0.55
1:D:600:THR:CG2	2:M:1:NAG:H83	2.27	0.55
1:C:415:LEU:HD23	1:C:415:LEU:C	2.26	0.55
1:A:378:GLU:CD	1:A:378:GLU:N	2.60	0.55
1:A:519:LEU:HD22	1:A:608:GLU:HG2	1.89	0.55
1:A:718:GLN:HA	1:A:718:GLN:NE2	2.21	0.55
1:B:44:THR:O	1:B:47:ASP:HB2	2.07	0.55
1:D:482:LEU:HD13	1:D:491:LEU:HD12	1.88	0.55
1:C:63:ILE:HG21	1:C:69:LEU:HG	1.89	0.55
1:D:183:GLN:HB2	7:D:1574:HOH:O	2.07	0.55
1:D:75:ASN:ND2	1:D:92:ASN:H	2.04	0.55
1:A:500:LEU:HA	1:A:503:MET:CE	2.37	0.55
1:B:125:ARG:NH1	1:B:125:ARG:HG3	2.20	0.55
1:B:379:GLU:OE2	1:B:399:LYS:NZ	2.39	0.55
1:C:177:GLU:CB	1:C:180:LEU:HD23	2.37	0.55
1:C:443:THR:HG22	1:C:444:CYS:N	2.22	0.55
1:B:72:GLN:HG2	1:B:73:GLU:HG2	1.89	0.55
1:C:479:LEU:HD12	1:C:496:ASP:HA	1.88	0.55
1:D:164:LEU:HB2	1:D:175:LYS:HB2	1.88	0.55
1:C:320:GLN:OE1	1:C:669:ARG:HD3	2.06	0.55
1:C:666:TYR:HE2	6:C:801:BPR:HB1	1.70	0.55
1:B:67:GLU:HB3	1:B:78:LEU:HD11	1.89	0.54
1:B:91:GLU:C	1:B:93:SER:H	2.09	0.54
1:C:194:ILE:CD1	4:C:769(A):NAG:H82	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:ARG:HH11	1:C:358:ARG:HG2	1.72	0.54
1:C:108:SER:HB3	1:C:157:TRP:CE3	2.42	0.54
1:C:234:PRO:HB2	1:D:248:TYR:CZ	2.42	0.54
1:D:718:GLN:NE2	1:D:721:LYS:NZ	2.53	0.54
1:C:136:ASP:HB2	1:C:143:ILE:HD11	1.88	0.54
1:C:536:LYS:HE3	1:C:538:LYS:HB2	1.89	0.54
1:A:295:ILE:CG2	1:A:296:GLY:H	2.21	0.54
1:A:397:ILE:HD12	1:A:434:ILE:HD13	1.89	0.54
1:B:377:ASN:HA	1:B:396:PHE:CZ	2.42	0.54
1:B:513:LYS:HE2	1:B:530:LEU:HD11	1.90	0.54
1:C:472:CYS:O	1:C:478:PRO:HA	2.06	0.54
1:B:410:LEU:HD13	1:B:415:LEU:CD2	2.38	0.54
1:C:288:VAL:HG12	1:C:294:LEU:HD11	1.88	0.54
1:D:49:LEU:HD22	1:D:749:GLN:HA	1.88	0.54
1:A:306:VAL:HB	1:A:310:ARG:HG2	1.90	0.54
1:A:336:ARG:NH1	1:A:336:ARG:HG3	2.21	0.54
1:A:479:LEU:HD12	1:A:496:ASP:HA	1.90	0.54
1:A:91:GLU:O	1:A:92:ASN:O	2.26	0.54
1:C:143:ILE:HG21	1:C:178:PRO:O	2.08	0.54
1:C:582:GLY:HA3	1:C:594:ILE:HD13	1.90	0.54
1:C:760:LYS:HB3	1:C:765:LEU:O	2.06	0.54
1:D:47:ASP:HA	1:D:52:THR:HG23	1.89	0.54
1:A:400:GLY:HA3	1:A:402:TRP:NE1	2.22	0.54
1:D:334:THR:OG1	1:D:336:ARG:HG3	2.08	0.54
1:B:420:ASN:ND2	1:B:426:PRO:HA	2.23	0.54
1:B:515:ASP:HB3	1:B:526:TYR:CE2	2.42	0.54
1:C:145:GLU:O	1:C:146:GLU:HB2	2.08	0.54
1:C:325:ILE:O	1:C:344:GLN:HA	2.08	0.54
1:B:134:ILE:O	1:B:142:LEU:HD23	2.07	0.53
1:C:292:SER:O	1:C:295:ILE:HD12	2.08	0.53
1:D:372:TYR:CE2	1:D:386:HIS:CD2	2.96	0.53
1:A:439:TYR:HE1	7:A:1568:HOH:O	1.90	0.53
1:B:704:HIS:HE1	1:B:711:VAL:O	1.90	0.53
1:C:156:THR:HG21	1:C:214:LEU:HD11	1.90	0.53
1:A:270:VAL:HG11	1:A:337:TRP:CE2	2.43	0.53
1:A:310:ARG:NE	1:A:329:ASP:OD1	2.27	0.53
1:B:420:ASN:HD22	1:B:426:PRO:HA	1.73	0.53
1:C:127:SER:HB3	1:C:204:GLU:OE1	2.08	0.53
1:C:41:ARG:HA	7:C:1515:HOH:O	2.08	0.53
1:C:435:GLN:HB3	1:C:438:ASP:O	2.08	0.53
1:D:159:PRO:HD3	1:D:216:TRP:CB	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:377:ASN:HD22	1:D:381:TYR:HB2	1.74	0.53
1:A:143:ILE:HD12	1:A:143:ILE:N	2.24	0.53
1:B:237:GLU:HG2	1:B:253:ARG:HG2	1.89	0.53
1:D:334:THR:CB	1:D:336:ARG:HG3	2.39	0.53
1:D:523:LYS:HZ3	1:D:525:TRP:HE1	1.55	0.53
1:D:82:GLU:HA	1:D:491:LEU:HD13	1.89	0.53
1:A:319:ALA:O	1:A:320:GLN:HB2	2.09	0.53
1:A:528:MET:HG2	1:A:576:ALA:HB2	1.89	0.53
1:C:484:SER:O	1:C:488:ASP:HA	2.09	0.53
7:C:1506:HOH:O	1:D:249:PRO:HD2	2.09	0.53
1:B:103:ASN:O	1:B:104:ASP:HB2	2.09	0.53
1:B:58:TYR:CD2	1:B:494:LEU:HB3	2.44	0.53
1:C:536:LYS:CE	1:C:538:LYS:HB2	2.38	0.53
1:B:600:THR:HG22	2:H:1:NAG:HN2	1.73	0.53
1:B:105:TYR:HA	1:B:115:LEU:O	2.09	0.53
1:C:111:ARG:O	1:C:137:LEU:HD12	2.09	0.53
1:C:302:GLY:HA2	7:C:1537:HOH:O	2.08	0.53
1:C:454:CYS:HB3	1:C:457:TYR:CE1	2.43	0.53
1:D:694:ASN:N	1:D:694:ASN:HD22	2.06	0.53
1:B:429:ARG:HG3	1:B:429:ARG:NH1	2.24	0.53
1:D:443:THR:HG22	1:D:445:LEU:HD23	1.91	0.53
1:A:718:GLN:HE22	1:A:721:LYS:HZ1	1.55	0.53
1:C:415:LEU:O	1:C:434:ILE:HG22	2.08	0.53
1:C:49:LEU:HD22	1:C:749:GLN:HA	1.90	0.53
1:A:718:GLN:HE21	1:A:718:GLN:CA	2.18	0.52
1:C:109:PRO:HG3	1:C:158:SER:O	2.08	0.52
1:C:224:ALA:HB1	1:C:268:PHE:CZ	2.44	0.52
1:C:516:VAL:CG1	1:C:517:ILE:H	2.16	0.52
1:D:98:LEU:HD13	1:D:100:TYR:OH	2.09	0.52
1:D:372:TYR:CZ	1:D:386:HIS:HD2	2.26	0.52
1:D:404:VAL:HG13	1:D:417:TYR:CD1	2.44	0.52
1:C:167:VAL:HA	1:C:171:ASP:O	2.09	0.52
1:D:90:LEU:HD11	1:D:94:THR:HG21	1.92	0.52
1:A:458:SER:OG	1:A:471:ARG:HD2	2.08	0.52
1:A:751:ILE:O	1:A:755:MET:HG3	2.08	0.52
1:C:649:CYS:HB3	1:C:699:GLU:HB2	1.89	0.52
1:C:65:ASP:HB2	1:C:463:ASN:O	2.09	0.52
1:A:686:SER:HA	2:F:1:NAG:H82	1.91	0.52
1:C:662:TYR:CZ	6:C:801:BPR:H12	2.45	0.52
1:D:158:SER:OG	1:D:163:LYS:HB2	2.08	0.52
1:A:246:LEU:CD2	1:A:248:TYR:H	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:GLU:HB3	1:B:262:GLU:HG2	1.90	0.52
1:B:546:VAL:HG22	1:B:547:TYR:N	2.24	0.52
1:B:687:THR:HG22	7:B:1575:HOH:O	2.09	0.52
1:A:454:CYS:HB3	1:A:457:TYR:CZ	2.45	0.52
1:C:109:PRO:O	1:C:111:ARG:HG3	2.10	0.52
1:C:353:TRP:HZ3	1:C:595:ASN:HD22	1.54	0.52
1:C:60:LEU:HD12	1:C:60:LEU:C	2.30	0.52
1:C:197:GLY:C	1:C:213:ALA:HB3	2.30	0.52
1:C:414:TYR:CG	1:C:433:ARG:HD2	2.44	0.52
1:C:596:ARG:HD2	7:C:1524:HOH:O	2.10	0.52
1:C:720:SER:O	1:C:724:VAL:HG23	2.10	0.52
1:D:159:PRO:HD3	1:D:216:TRP:HB3	1.90	0.52
1:D:73:GLU:O	1:D:74:ASN:HB2	2.10	0.52
1:D:748:HIS:HD2	7:D:1558:HOH:O	1.91	0.52
1:C:155:ILE:HG13	1:C:166:TYR:HB3	1.92	0.52
1:C:237:GLU:HG2	1:C:253:ARG:HG2	1.92	0.52
1:C:616:MET:HB3	1:C:618:PHE:CE2	2.45	0.52
1:D:172:ILE:HD13	1:D:214:LEU:HD21	1.91	0.52
1:D:358:ARG:HA	7:D:1683:HOH:O	2.10	0.52
1:B:183:GLN:HE22	1:B:278:PRO:HA	1.75	0.52
1:B:258:LYS:NZ	1:B:714:GLN:OE1	2.43	0.52
1:D:140:ARG:HH11	1:D:140:ARG:HG2	1.74	0.52
1:D:517:ILE:HB	1:D:612:GLN:HE22	1.75	0.52
1:D:523:LYS:HG3	1:D:523:LYS:O	2.10	0.52
1:A:410:LEU:HD11	1:A:436:LEU:HD21	1.92	0.52
1:B:206:GLU:OE1	6:B:801:BPR:HD2	2.10	0.52
1:C:289:PRO:HG2	1:C:294:LEU:HD21	1.92	0.52
1:A:158:SER:HA	1:A:216:TRP:CD1	2.45	0.51
1:A:738:GLU:OE2	1:A:744:SER:HB3	2.10	0.51
1:D:571:GLU:OE1	1:D:571:GLU:HA	2.10	0.51
1:B:500:LEU:HG	1:B:504:LEU:CD1	2.40	0.51
1:D:83:TYR:HB2	1:D:85:ASN:OD1	2.10	0.51
1:D:266:VAL:CG2	1:D:267:LYS:N	2.74	0.51
1:C:627:TRP:HB2	1:C:651:ILE:HB	1.92	0.51
1:A:724:VAL:HG22	1:B:750:HIS:CG	2.45	0.51
1:A:377:ASN:HB2	1:A:381:TYR:N	2.18	0.51
1:C:363:HIS:O	1:C:371:PHE:HB2	2.10	0.51
1:C:58:TYR:CE1	1:C:494:LEU:HD13	2.45	0.51
1:D:377:ASN:ND2	1:D:383:HIS:CD2	2.71	0.51
1:B:761:GLN:HG2	1:B:762:CYS:N	2.26	0.51
1:C:365:THR:O	1:C:368:GLY:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:636:THR:HG21	1:C:651:ILE:O	2.11	0.51
1:D:273:THR:HA	1:D:276:LEU:HD22	1.93	0.51
1:D:516:VAL:CG1	1:D:523:LYS:HB2	2.38	0.51
1:A:489:LYS:HG3	1:A:491:LEU:H	1.74	0.51
1:B:402:TRP:HA	7:B:1508:HOH:O	2.09	0.51
1:C:222:PHE:HD2	1:C:222:PHE:N	2.09	0.51
1:D:472:CYS:HB3	1:D:479:LEU:HB3	1.92	0.51
1:C:219:ASN:H	1:C:308:GLU:CD	2.12	0.51
1:A:246:LEU:HD22	1:A:248:TYR:N	2.24	0.51
1:A:589:LYS:HB2	7:A:1642:HOH:O	2.10	0.51
1:A:61:GLN:HA	7:A:1550:HOH:O	2.11	0.51
1:A:654:ALA:HA	1:A:704:HIS:CD2	2.46	0.51
1:B:516:VAL:HG12	1:B:517:ILE:N	2.25	0.51
1:C:518:ASN:HB3	7:C:1614:HOH:O	2.10	0.51
1:C:90:LEU:C	1:C:90:LEU:HD22	2.32	0.51
1:C:481:THR:OG1	1:C:483:HIS:HE1	1.92	0.50
1:A:415:LEU:C	1:A:415:LEU:HD13	2.30	0.50
1:A:675:THR:C	1:A:680:LEU:HB2	2.32	0.50
1:B:658:LYS:HB3	1:B:661:TYR:CD2	2.46	0.50
1:C:704:HIS:CE1	1:C:711:VAL:O	2.63	0.50
1:D:334:THR:HB	1:D:336:ARG:HG3	1.92	0.50
1:B:516:VAL:CG1	1:B:517:ILE:N	2.75	0.50
1:D:107:VAL:HG12	1:D:114:ILE:HB	1.93	0.50
1:D:458:SER:OG	1:D:471:ARG:HB2	2.12	0.50
1:D:718:GLN:HE21	1:D:718:GLN:CA	2.14	0.50
1:C:214:LEU:HD12	1:C:214:LEU:O	2.11	0.50
1:C:701:LEU:CD1	1:C:703:ILE:HD11	2.40	0.50
1:D:516:VAL:HG12	1:D:517:ILE:N	2.27	0.50
2:H:1:NAG:H61	2:H:2:NAG:H82	1.94	0.50
1:A:199:THR:HA	1:A:228:PHE:CE2	2.47	0.50
1:D:123:GLN:HG2	1:D:124:TRP:N	2.27	0.50
1:D:273:THR:O	1:D:276:LEU:HB2	2.11	0.50
1:A:547:TYR:HE2	7:A:1607:HOH:O	1.93	0.50
1:C:120:TYR:HA	1:C:130:ALA:HB2	1.92	0.50
1:C:150:ASN:O	1:C:151:ASN:HB2	2.10	0.50
1:A:551:CYS:O	1:A:551:CYS:SG	2.70	0.50
1:B:114:ILE:CG2	1:B:135:TYR:HB3	2.41	0.50
1:C:741:GLY:O	1:C:742:ILE:C	2.50	0.50
7:B:1604:HOH:O	2:H:1:NAG:H82	2.11	0.50
1:C:547:TYR:HD2	1:C:552:SER:CB	2.24	0.50
1:D:415:LEU:C	1:D:415:LEU:HD23	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:99:GLY:O	1:D:100:TYR:HB3	2.12	0.50
1:A:327:ILE:HD12	1:A:389:THR:HG23	1.94	0.50
1:D:175:LYS:HE3	1:D:177:GLU:O	2.12	0.50
1:A:158:SER:HB3	1:A:163:LYS:HB2	1.94	0.49
1:A:741:GLY:O	1:A:742:ILE:C	2.50	0.49
1:B:519:LEU:HD21	1:B:608:GLU:HB3	1.94	0.49
1:B:693:GLU:OE1	1:B:696:LYS:HE3	2.11	0.49
1:C:307:THR:C	1:C:309:GLU:N	2.66	0.49
1:C:375:ILE:HG12	1:C:385:CYS:HB2	1.93	0.49
1:C:400:GLY:C	7:C:1546:HOH:O	2.50	0.49
1:C:707:ALA:HB2	7:C:1520:HOH:O	2.11	0.49
1:A:492:ARG:CB	1:A:492:ARG:HH21	2.19	0.49
1:B:73:GLU:O	1:B:74:ASN:CB	2.59	0.49
1:C:159:PRO:HD3	1:C:216:TRP:CB	2.43	0.49
1:C:628:GLY:HA3	1:C:632:GLY:O	2.12	0.49
1:B:658:LYS:HD3	1:B:661:TYR:CZ	2.47	0.49
1:C:517:ILE:HB	1:C:612:GLN:NE2	2.27	0.49
1:C:475:PRO:HA	1:C:557:THR:O	2.12	0.49
1:C:651:ILE:HD11	1:C:758:PHE:HD2	1.77	0.49
1:D:434:ILE:HD11	1:D:439:TYR:HB3	1.93	0.49
1:A:571:GLU:HA	1:A:571:GLU:OE1	2.12	0.49
1:C:536:LYS:HE3	1:C:538:LYS:N	2.27	0.49
1:A:640:LEU:HB3	1:A:698:VAL:HG21	1.95	0.49
1:C:148:ILE:HD13	1:C:155:ILE:CD1	2.42	0.49
1:B:280:ALA:HB2	1:D:285:TYR:HD1	1.77	0.49
1:D:547:TYR:HD2	1:D:552:SER:HB2	1.76	0.49
1:B:65:ASP:HB2	1:B:466:LYS:CD	2.41	0.49
1:D:682:TYR:OH	2:M:2:NAG:H83	2.13	0.49
1:B:289:PRO:HG2	1:B:294:LEU:HG	1.94	0.49
1:D:512:LYS:HA	1:D:528:MET:O	2.12	0.49
1:D:549:GLY:HA2	1:D:631:TYR:CE1	2.48	0.49
1:A:429:ARG:HB2	1:A:457:TYR:H	1.78	0.49
1:B:57:PHE:HA	1:B:480:TYR:CE1	2.48	0.49
1:C:388:GLN:O	1:C:390:ASP:N	2.46	0.49
1:C:516:VAL:O	1:C:517:ILE:HG23	2.13	0.49
1:A:65:ASP:CA	1:A:463:ASN:HB2	2.42	0.48
1:B:405:ILE:HG13	1:B:429:ARG:HD2	1.95	0.48
1:B:76:ILE:O	1:B:89:PHE:HB3	2.13	0.48
1:C:289:PRO:HD2	1:C:294:LEU:HD21	1.95	0.48
1:D:294:LEU:O	1:D:294:LEU:HD23	2.13	0.48
1:D:438:ASP:OD2	1:D:440:THR:HB	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:VAL:HG11	1:A:337:TRP:CZ2	2.48	0.48
1:C:125:ARG:NH2	1:C:205:GLU:OE2	2.47	0.48
1:C:345:HIS:ND1	1:C:345:HIS:N	2.60	0.48
1:C:384:ILE:HG13	1:C:404:VAL:HG21	1.94	0.48
1:D:43:TYR:HE1	1:D:53:PHE:HD2	1.60	0.48
1:A:515:ASP:HB3	1:A:526:TYR:CE2	2.48	0.48
1:A:689:MET:HE3	1:B:244:GLU:HG3	1.95	0.48
1:A:96:ASP:HA	7:A:1510:HOH:O	2.13	0.48
1:B:219:ASN:ND2	7:B:1534:HOH:O	2.44	0.48
1:B:61:GLN:O	1:B:63:ILE:HG23	2.13	0.48
1:B:596:ARG:NH2	1:B:679:ASN:HB2	2.28	0.48
1:C:386:HIS:C	1:C:386:HIS:CD2	2.87	0.48
1:C:420:ASN:ND2	1:C:426:PRO:HA	2.28	0.48
1:A:571:GLU:CD	1:A:760:LYS:HD3	2.33	0.48
1:B:438:ASP:OD2	1:B:441:LYS:HE3	2.13	0.48
1:C:177:GLU:HB3	1:C:180:LEU:HD23	1.96	0.48
1:C:197:GLY:O	1:C:213:ALA:N	2.42	0.48
1:C:562:SER:O	1:C:565:THR:HB	2.13	0.48
1:D:453:ARG:HG3	1:D:476:GLY:HA3	1.95	0.48
1:A:347:GLU:OE2	1:A:354:VAL:HG13	2.13	0.48
1:B:603:VAL:HG22	1:B:635:VAL:HG13	1.95	0.48
1:D:110:ASP:O	1:D:111:ARG:HB2	2.13	0.48
1:D:289:PRO:HA	7:D:1603:HOH:O	2.13	0.48
4:A:768(A):NAG:N2	7:A:1651:HOH:O	2.31	0.48
1:D:236:ILE:HD12	7:D:1557:HOH:O	2.13	0.48
1:D:628:GLY:HA3	1:D:632:GLY:O	2.13	0.48
1:D:77:LEU:HB2	1:D:79:PHE:CE2	2.48	0.48
1:A:453:ARG:NH2	1:A:479:LEU:HD13	2.29	0.48
1:D:67:GLU:HB3	1:D:78:LEU:HD11	1.95	0.48
1:A:415:LEU:CD1	1:A:415:LEU:C	2.82	0.48
1:C:542:LEU:HB3	1:C:624:ILE:HG23	1.96	0.48
1:D:321:ASN:HA	1:D:354:VAL:HG23	1.95	0.48
1:D:546:VAL:HG21	1:D:635:VAL:HG11	1.96	0.48
1:A:246:LEU:HD22	1:A:248:TYR:O	2.14	0.48
1:A:206:GLU:OE2	1:A:663:ASP:OD2	2.32	0.48
1:C:114:ILE:O	1:C:114:ILE:HG23	2.14	0.48
1:C:704:HIS:HE1	1:C:711:VAL:O	1.97	0.48
1:D:224:ALA:HB1	1:D:268:PHE:CZ	2.49	0.48
1:C:90:LEU:HD22	1:C:90:LEU:O	2.13	0.47
1:B:155:ILE:HG13	1:B:166:TYR:HB3	1.96	0.47
1:C:356:ARG:NH1	1:C:382:LYS:HG2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:519:LEU:HD22	1:C:608:GLU:CD	2.31	0.47
1:D:127:SER:HB3	1:D:211:TYR:CD1	2.48	0.47
1:A:236:ILE:HG12	1:A:712:HIS:CE1	2.49	0.47
1:A:93:SER:C	1:A:95:PHE:N	2.67	0.47
1:B:230:ASP:OD2	1:B:255:PRO:HB2	2.14	0.47
1:C:108:SER:HB3	1:C:157:TRP:CZ3	2.50	0.47
1:C:429:ARG:HG2	1:C:429:ARG:HH11	1.79	0.47
1:C:75:ASN:HD21	1:C:92:ASN:HB2	1.74	0.47
1:A:614:SER:HA	1:A:619:VAL:HG11	1.97	0.47
1:B:263:ASN:ND2	1:B:318:ARG:CZ	2.76	0.47
1:C:108:SER:HB3	1:C:157:TRP:CD2	2.49	0.47
1:C:405:ILE:HG13	1:C:429:ARG:CD	2.44	0.47
1:C:746:MET:H	1:C:746:MET:HE3	1.78	0.47
1:D:183:GLN:HG2	1:D:276:LEU:HG	1.96	0.47
1:D:162:HIS:HD2	1:D:178:PRO:HD3	1.80	0.47
1:D:535:ASP:C	1:D:536:LYS:O	2.51	0.47
1:C:317:ARG:HB3	7:C:1624:HOH:O	2.13	0.47
1:A:289:PRO:HG2	1:A:294:LEU:HG	1.96	0.47
1:A:455:GLN:HA	7:A:1575:HOH:O	2.14	0.47
1:A:79:PHE:CD1	1:A:86:SER:HB3	2.49	0.47
1:A:90:LEU:HD23	1:A:91:GLU:O	2.15	0.47
1:C:288:VAL:CG1	1:C:289:PRO:HD2	2.44	0.47
1:A:724:VAL:HG22	1:B:750:HIS:CD2	2.49	0.47
1:C:463:ASN:C	1:C:465:ALA:H	2.18	0.47
1:D:103:ASN:O	1:D:104:ASP:HB2	2.13	0.47
1:D:235:LEU:HA	1:D:254:ILE:O	2.15	0.47
1:D:523:LYS:NZ	1:D:525:TRP:HE1	2.13	0.47
1:B:127:SER:HB3	1:B:211:TYR:CG	2.49	0.47
1:C:80:ASN:OD1	1:C:82:GLU:HB3	2.15	0.47
1:A:438:ASP:C	1:A:440:THR:H	2.18	0.47
1:A:625:ALA:HB2	1:A:649:CYS:SG	2.55	0.47
1:D:739:ASP:HB2	7:D:1550:HOH:O	2.14	0.47
1:A:591:MET:CE	7:A:1522:HOH:O	2.62	0.47
1:B:177:GLU:HB2	1:B:180:LEU:HB2	1.96	0.47
1:C:184:ARG:HH11	1:C:187:TRP:HA	1.79	0.47
1:D:218:PRO:HD3	1:D:305:TRP:HB3	1.97	0.47
1:A:114:ILE:CG2	1:A:135:TYR:HB3	2.45	0.46
1:A:547:TYR:HD2	1:A:552:SER:CB	2.28	0.46
1:C:516:VAL:CG1	1:C:517:ILE:N	2.71	0.46
1:D:72:GLN:HE21	1:D:77:LEU:HD12	1.79	0.46
1:A:175:LYS:HG2	1:A:182:SER:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:658:LYS:HB3	1:A:661:TYR:CD2	2.50	0.46
1:B:100:TYR:HE2	1:B:133:ASP:OD2	1.98	0.46
1:B:199:THR:HA	1:B:228:PHE:CE2	2.51	0.46
1:A:658:LYS:HB3	1:A:661:TYR:CE2	2.50	0.46
1:A:681:ASP:HA	7:A:1544:HOH:O	2.15	0.46
1:B:83:TYR:HB2	1:B:85:ASN:OD1	2.16	0.46
1:C:356:ARG:CZ	1:C:382:LYS:HG2	2.45	0.46
1:D:348:ILE:HG13	1:D:349:SER:N	2.28	0.46
1:C:301:CYS:HB3	1:C:316:ILE:HD11	1.97	0.46
1:C:547:TYR:HB2	1:C:554:LYS:HD3	1.98	0.46
1:D:423:LYS:HB3	1:D:425:MET:HG3	1.98	0.46
1:A:415:LEU:HB3	1:A:434:ILE:HG23	1.97	0.46
1:A:542:LEU:HD22	1:A:543:LEU:N	2.30	0.46
1:C:126:HIS:O	1:C:128:TYR:HD2	1.98	0.46
1:C:142:LEU:C	1:C:142:LEU:HD23	2.36	0.46
1:C:345:HIS:CD2	1:C:371:PHE:HZ	2.32	0.46
1:C:72:GLN:O	1:C:74:ASN:N	2.48	0.46
4:C:768(A):NAG:O3	4:C:768(A):NAG:H83	2.16	0.46
1:D:110:ASP:OD2	1:D:162:HIS:ND1	2.49	0.46
1:D:184:ARG:HD2	1:D:187:TRP:CZ3	2.51	0.46
1:C:183:GLN:HB2	1:C:183:GLN:HE21	1.54	0.46
1:C:226:ALA:HA	1:C:267:LYS:O	2.16	0.46
1:C:550:PRO:HD2	1:C:631:TYR:CE2	2.50	0.46
1:D:169:ASN:N	1:D:169:ASN:ND2	2.61	0.46
1:D:216:TRP:HZ3	1:D:273:THR:HG21	1.81	0.46
1:D:288:VAL:HG12	1:D:289:PRO:HD2	1.98	0.46
1:D:47:ASP:HA	1:D:52:THR:CG2	2.46	0.46
1:A:630:SER:HA	1:A:654:ALA:O	2.16	0.46
1:B:256:TYR:CE2	1:B:712:HIS:NE2	2.84	0.46
1:B:403:GLU:OE1	1:B:585:TYR:CA	2.64	0.46
1:C:407:ILE:HG22	1:C:408:GLU:N	2.31	0.46
1:D:110:ASP:HB2	1:D:112:GLN:HE21	1.81	0.46
1:A:310:ARG:HD2	7:A:1659:HOH:O	2.15	0.46
1:C:114:ILE:HG12	1:C:116:PHE:CE2	2.51	0.46
1:C:230:ASP:OD1	1:C:264:PRO:HB3	2.16	0.46
1:C:266:VAL:HG22	1:C:267:LYS:N	2.31	0.46
1:D:109:PRO:HG2	1:D:161:GLY:O	2.16	0.46
1:D:184:ARG:HH11	1:D:187:TRP:HA	1.80	0.46
1:A:714:GLN:HG2	1:A:715:GLN:N	2.29	0.46
1:A:759:LEU:HA	1:A:759:LEU:HD23	1.66	0.46
1:C:136:ASP:HB2	1:C:143:ILE:CD1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:HIS:CE1	1:A:711:VAL:O	2.65	0.45
1:B:571:GLU:HA	1:B:571:GLU:OE1	2.15	0.45
1:B:91:GLU:C	1:B:93:SER:N	2.70	0.45
1:C:271:VAL:HG22	1:C:284:SER:OG	2.15	0.45
1:C:43:TYR:O	1:C:570:THR:OG1	2.34	0.45
1:C:627:TRP:HA	1:C:651:ILE:O	2.17	0.45
1:D:547:TYR:HD2	1:D:552:SER:CB	2.30	0.45
1:A:134:ILE:O	1:A:143:ILE:HD13	2.16	0.45
1:A:504:LEU:C	1:A:506:ASP:H	2.20	0.45
1:B:232:GLU:HB2	1:B:262:GLU:HG2	1.97	0.45
1:C:62:TRP:CG	1:C:462:SER:HA	2.51	0.45
1:C:712:HIS:C	1:C:714:GLN:N	2.69	0.45
1:B:686:SER:HA	2:H:1:NAG:H81	1.98	0.45
1:A:124:TRP:HA	1:A:124:TRP:CE3	2.51	0.45
1:A:597:ARG:HH21	1:A:600:THR:HB	1.81	0.45
1:B:208:PHE:C	1:B:210:ALA:N	2.68	0.45
1:B:692:ALA:O	1:B:728:VAL:HG21	2.17	0.45
1:B:95:PHE:HE1	1:B:116:PHE:CE2	2.34	0.45
1:C:382:LYS:N	1:C:403:GLU:HG2	2.20	0.45
1:C:463:ASN:O	1:C:464:LYS:HB2	2.16	0.45
1:C:356:ARG:HB3	1:C:551:CYS:SG	2.57	0.45
1:D:134:ILE:HG21	1:D:178:PRO:HB3	1.98	0.45
1:D:546:VAL:CG2	1:D:547:TYR:N	2.78	0.45
1:A:499:ALA:O	1:A:502:LYS:HB3	2.17	0.45
1:A:660:GLU:HG3	7:A:1564:HOH:O	2.17	0.45
1:B:420:ASN:HB2	1:B:426:PRO:HA	1.98	0.45
1:B:443:THR:HG22	1:B:444:CYS:N	2.32	0.45
1:C:148:ILE:HD13	1:C:155:ILE:HD11	1.97	0.45
1:C:375:ILE:HD11	1:C:385:CYS:SG	2.56	0.45
1:D:680:LEU:HD11	1:D:684:ARG:HE	1.81	0.45
1:D:704:HIS:CD2	1:D:716:SER:OG	2.65	0.45
1:A:142:LEU:HD23	1:A:143:ILE:O	2.16	0.45
1:B:388:GLN:HG3	7:B:1676:HOH:O	2.17	0.45
1:B:56:LYS:HG3	7:B:1681:HOH:O	2.16	0.45
1:C:193:VAL:HG12	1:C:194:ILE:HG12	1.98	0.45
1:C:536:LYS:CG	1:C:537:SER:N	2.58	0.45
1:C:76:ILE:HB	1:C:90:LEU:HD13	1.98	0.45
1:D:573:ILE:HD13	1:D:763:PHE:CD2	2.52	0.45
1:B:214:LEU:C	1:B:214:LEU:HD12	2.37	0.45
1:B:308:GLU:HG2	7:B:1586:HOH:O	2.16	0.45
1:B:513:LYS:HE2	1:B:513:LYS:HB3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:676:PRO:HG2	1:B:677:GLU:OE2	2.17	0.45
1:C:340:SER:O	1:C:344:GLN:HG3	2.17	0.45
1:C:454:CYS:HB3	1:C:457:TYR:CZ	2.52	0.45
1:D:135:TYR:CD2	1:D:137:LEU:HD23	2.52	0.45
1:D:148:ILE:HG23	1:D:149:PRO:HD2	1.99	0.45
1:D:80:ASN:O	1:D:81:ALA:O	2.35	0.45
1:A:195:TYR:N	1:A:195:TYR:CD1	2.84	0.45
1:A:364:PHE:HB2	7:A:1654:HOH:O	2.16	0.45
1:B:49:LEU:HD22	1:B:749:GLN:HA	1.99	0.45
1:C:227:GLN:O	1:C:266:VAL:HA	2.17	0.45
1:C:306:VAL:CG2	1:C:310:ARG:HG2	2.46	0.45
1:C:66:HIS:CD2	1:C:67:GLU:HG3	2.52	0.45
1:D:40:ARG:O	1:D:508:GLN:NE2	2.50	0.45
1:C:597:ARG:NH1	2:I:2:NAG:O7	2.49	0.45
1:A:534:PHE:HZ	1:A:618:PHE:CG	2.35	0.45
1:B:208:PHE:O	1:B:209:SER:C	2.55	0.45
1:B:301:CYS:SG	1:B:314:GLN:HG2	2.57	0.45
1:C:288:VAL:CG1	1:C:294:LEU:HD11	2.45	0.45
1:C:326:ASP:OD1	1:C:339:SER:OG	2.35	0.45
1:C:43:TYR:HE1	1:C:53:PHE:HD2	1.63	0.45
1:C:559:PHE:C	1:C:560:ARG:HG3	2.37	0.45
1:C:380:GLY:O	1:C:587:GLY:HA2	2.16	0.45
1:D:269:PHE:CE2	1:D:286:GLN:HG3	2.52	0.45
1:A:504:LEU:O	1:A:507:VAL:HG12	2.17	0.45
1:B:184:ARG:O	1:B:185:ILE:HD13	2.17	0.45
1:C:107:VAL:HG12	1:C:108:SER:O	2.16	0.45
1:C:164:LEU:HB2	1:C:175:LYS:HB2	1.99	0.45
1:C:487:SER:C	1:C:489:LYS:N	2.70	0.45
1:C:668:GLU:HA	1:C:672:GLY:O	2.17	0.45
1:D:414:TYR:CA	1:D:436:LEU:HD13	2.45	0.45
1:A:420:ASN:HB2	1:A:426:PRO:HA	1.99	0.45
1:B:584:GLY:HA2	7:B:1503:HOH:O	2.16	0.45
1:C:661:TYR:OH	1:C:718:GLN:HG3	2.17	0.45
1:C:718:GLN:HE22	1:C:721:LYS:HZ1	1.65	0.45
1:D:42:THR:HB	1:D:569:SER:OG	2.17	0.45
1:A:273:THR:HA	1:A:276:LEU:HG	1.98	0.44
1:A:336:ARG:NH1	1:A:336:ARG:CG	2.76	0.44
1:B:714:GLN:HG2	1:B:715:GLN:N	2.32	0.44
1:C:167:VAL:HG21	1:C:198:VAL:HG13	1.98	0.44
1:C:219:ASN:N	1:C:308:GLU:OE2	2.40	0.44
1:C:482:LEU:HD23	1:C:483:HIS:H	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:377:ASN:C	1:D:379:GLU:N	2.68	0.44
1:D:464:LYS:O	1:D:465:ALA:HB3	2.17	0.44
1:A:438:ASP:CG	1:A:441:LYS:HG3	2.37	0.44
1:A:651:ILE:HG23	1:A:701:LEU:HB3	1.99	0.44
1:B:113:PHE:HE2	1:B:162:HIS:CE1	2.34	0.44
1:B:761:GLN:HB3	1:B:761:GLN:HE21	1.60	0.44
1:C:527:GLN:HB3	1:C:555:VAL:HG13	1.99	0.44
1:D:318:ARG:O	1:D:320:GLN:HG3	2.18	0.44
1:D:429:ARG:HB2	1:D:456:TYR:HA	1.99	0.44
1:D:635:VAL:O	1:D:638:MET:N	2.51	0.44
1:D:680:LEU:HD11	1:D:684:ARG:NE	2.32	0.44
1:B:177:GLU:HB2	1:B:180:LEU:HD23	1.99	0.44
1:B:384:ILE:HG13	1:B:404:VAL:HG21	2.00	0.44
1:B:500:LEU:HA	1:B:503:MET:CE	2.47	0.44
1:B:47:ASP:HA	1:B:52:THR:HG23	2.00	0.44
1:B:662:TYR:CE2	6:B:801:BPR:H12	2.51	0.44
1:B:734:TRP:CD1	1:B:734:TRP:C	2.91	0.44
1:C:322:TYR:CD1	1:C:322:TYR:C	2.91	0.44
1:A:306:VAL:HG12	1:A:307:THR:HG23	2.00	0.44
1:B:146:GLU:OE1	1:B:181:SER:HA	2.17	0.44
1:C:358:ARG:HG2	1:C:358:ARG:NH1	2.32	0.44
1:A:397:ILE:CD1	1:A:434:ILE:HD13	2.47	0.44
1:B:666:TYR:CE2	6:B:801:BPR:HB1	2.53	0.44
1:B:704:HIS:CE1	1:B:711:VAL:O	2.71	0.44
1:D:422:HIS:NE2	1:D:423:LYS:HD3	2.32	0.44
1:D:75:ASN:ND2	1:D:92:ASN:ND2	2.64	0.44
1:B:566:TYR:CE2	1:B:567:LEU:HD23	2.52	0.44
1:C:421:GLU:O	1:C:422:HIS:C	2.56	0.44
1:C:482:LEU:HB2	1:C:494:LEU:HD21	1.99	0.44
1:C:92:ASN:O	1:C:94:THR:N	2.49	0.44
1:D:377:ASN:C	1:D:379:GLU:H	2.16	0.44
1:A:543:LEU:HD21	1:A:627:TRP:CD1	2.51	0.44
1:A:76:ILE:O	1:A:77:LEU:HD23	2.18	0.44
1:B:387:PHE:CE2	1:B:394:CYS:HB3	2.53	0.44
1:B:434:ILE:HD11	1:B:439:TYR:HB3	1.99	0.44
1:B:524:PHE:CE2	1:B:590:ILE:HD12	2.53	0.44
1:D:105:TYR:CD1	1:D:105:TYR:C	2.91	0.44
1:A:620:ASP:O	1:A:622:LYS:N	2.51	0.44
1:B:718:GLN:HE22	1:B:721:LYS:NZ	2.16	0.44
1:C:108:SER:O	1:C:109:PRO:C	2.56	0.44
1:C:438:ASP:CG	1:C:440:THR:HB	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:TYR:CE1	1:C:53:PHE:HD2	2.36	0.44
1:D:422:HIS:O	1:D:423:LYS:HB2	2.17	0.44
1:D:512:LYS:HE3	1:D:527:GLN:CD	2.37	0.44
1:A:734:TRP:C	1:A:734:TRP:CD1	2.91	0.43
1:B:704:HIS:HD2	1:B:716:SER:OG	2.01	0.43
1:C:104:ASP:O	1:C:105:TYR:O	2.36	0.43
1:C:329:ASP:OD2	1:C:343:ARG:NH2	2.51	0.43
1:C:365:THR:HG21	1:C:370:SER:OG	2.18	0.43
1:C:736:THR:HB	1:D:721:LYS:HB2	2.00	0.43
1:D:751:ILE:O	1:D:755:MET:HG3	2.18	0.43
1:B:689:MET:HG2	1:B:722:ALA:HB2	2.00	0.43
1:C:306:VAL:HG21	1:C:310:ARG:HG2	1.99	0.43
1:C:548:ALA:HA	7:C:1608:HOH:O	2.17	0.43
1:C:734:TRP:H	1:D:732:THR:HG21	1.82	0.43
1:A:246:LEU:CD2	1:A:248:TYR:O	2.66	0.43
1:A:70:TYR:HB3	1:A:79:PHE:CE2	2.53	0.43
1:B:118:TYR:CE2	1:B:119:ASN:ND2	2.86	0.43
1:B:140:ARG:HG3	1:B:140:ARG:HH11	1.83	0.43
1:B:95:PHE:HE1	1:B:116:PHE:HE2	1.65	0.43
1:C:118:TYR:O	1:C:119:ASN:HB3	2.18	0.43
1:C:53:PHE:HB3	1:C:500:LEU:CD1	2.48	0.43
1:D:107:VAL:HG12	1:D:114:ILE:CB	2.48	0.43
1:D:127:SER:HB3	1:D:211:TYR:CG	2.53	0.43
1:D:73:GLU:OE2	3:J:1:NAG:H4	2.19	0.43
1:A:258:LYS:O	1:A:259:ALA:C	2.55	0.43
1:B:694:ASN:HA	1:B:697:GLN:NE2	2.32	0.43
1:C:397:ILE:HD12	1:C:434:ILE:HD13	1.99	0.43
1:C:44:THR:O	1:C:47:ASP:HB2	2.18	0.43
1:D:704:HIS:CE1	1:D:711:VAL:O	2.71	0.43
1:D:49:LEU:HB3	1:D:749:GLN:HG2	1.99	0.43
1:A:143:ILE:N	1:A:143:ILE:CD1	2.81	0.43
1:A:289:PRO:HB3	1:A:315:TRP:CD2	2.54	0.43
1:A:329:ASP:OD2	1:A:343:ARG:NH1	2.52	0.43
1:A:385:CYS:HA	1:A:396:PHE:HA	1.99	0.43
1:A:429:ARG:HG3	1:A:456:TYR:CE1	2.54	0.43
1:B:197:GLY:C	1:B:213:ALA:HB3	2.39	0.43
1:B:288:VAL:HG22	7:B:1598:HOH:O	2.18	0.43
1:B:526:TYR:HA	1:B:555:VAL:HG21	2.00	0.43
1:C:158:SER:OG	1:C:163:LYS:HB2	2.18	0.43
1:D:309:GLU:HB3	1:D:330:TYR:HB3	2.01	0.43
1:D:417:TYR:O	1:D:431:LEU:HD12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:TYR:CE1	1:D:494:LEU:HD13	2.53	0.43
1:D:504:LEU:HA	1:D:507:VAL:CG1	2.49	0.43
1:D:542:LEU:HD12	1:D:574:ILE:O	2.18	0.43
1:A:124:TRP:HA	1:A:124:TRP:HE3	1.84	0.43
1:A:453:ARG:HG2	1:A:454:CYS:SG	2.59	0.43
1:C:118:TYR:O	1:C:119:ASN:CB	2.66	0.43
1:C:422:HIS:O	1:C:424:GLY:N	2.52	0.43
1:C:644:SER:C	1:C:646:VAL:H	2.22	0.43
1:D:556:ASP:C	1:D:556:ASP:OD1	2.56	0.43
1:D:673:LEU:O	1:D:678:ASP:HB3	2.18	0.43
1:A:136:ASP:HB2	1:A:143:ILE:HD11	2.01	0.43
1:A:702:LEU:O	1:A:732:THR:HA	2.19	0.43
1:B:158:SER:OG	1:B:163:LYS:HB2	2.18	0.43
1:B:200:ASP:OD1	1:B:203:TYR:HB2	2.18	0.43
1:A:248:TYR:CZ	1:B:234:PRO:HB2	2.54	0.43
1:C:367:ASP:OD2	1:C:369:ASN:HB2	2.18	0.43
1:D:397:ILE:HG13	1:D:398:THR:HG23	2.00	0.43
1:A:499:ALA:O	1:A:503:MET:HE2	2.18	0.43
1:A:742:ILE:HG22	1:A:742:ILE:O	2.19	0.43
1:D:140:ARG:HG2	1:D:140:ARG:NH1	2.33	0.43
1:D:279:ASN:OD1	4:D:773(A):NAG:N2	2.52	0.43
1:D:481:THR:OG1	1:D:483:HIS:HE1	2.02	0.43
1:D:581:ARG:HG3	1:D:593:ALA:CB	2.48	0.43
1:D:72:GLN:NE2	1:D:77:LEU:HD12	2.32	0.43
1:D:72:GLN:O	1:D:73:GLU:HB2	2.18	0.43
1:D:75:ASN:HD22	1:D:91:GLU:HA	1.83	0.43
1:C:288:VAL:HG13	1:C:289:PRO:HD2	1.99	0.43
1:D:733:MET:HE2	1:D:754:HIS:CE1	2.54	0.43
1:D:734:TRP:CD1	1:D:734:TRP:C	2.92	0.43
1:A:334:THR:OG1	1:A:336:ARG:NH1	2.51	0.43
1:A:385:CYS:HB3	1:A:387:PHE:CE1	2.54	0.43
1:A:497:ASN:HA	7:A:1609:HOH:O	2.18	0.43
1:B:320:GLN:NE2	1:B:669:ARG:HB2	2.34	0.43
1:C:340:SER:CB	1:C:343:ARG:NH1	2.82	0.43
1:C:751:ILE:HG23	1:C:752:TYR:N	2.33	0.43
1:D:454:CYS:HB2	1:D:457:TYR:OH	2.19	0.43
1:B:266:VAL:HG22	1:B:267:LYS:N	2.33	0.42
1:C:165:ALA:HA	1:C:173:TYR:O	2.19	0.42
1:C:538:LYS:HE3	7:C:1635:HOH:O	2.19	0.42
1:D:207:VAL:HG12	1:D:208:PHE:HD1	1.84	0.42
1:D:586:GLN:HB2	7:D:1679:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ASN:HD21	1:A:117:GLU:CD	2.20	0.42
1:A:158:SER:CB	1:A:163:LYS:HB2	2.49	0.42
1:A:318:ARG:O	1:A:320:GLN:HG3	2.18	0.42
1:A:330:TYR:CE2	1:A:332:GLU:HA	2.54	0.42
1:A:631:TYR:CD1	1:A:635:VAL:HG23	2.54	0.42
1:B:402:TRP:CE3	1:B:421:GLU:HB2	2.54	0.42
1:C:330:TYR:HE1	1:C:335:GLY:HA2	1.80	0.42
1:C:544:ILE:O	1:C:626:ILE:HA	2.19	0.42
1:C:763:PHE:CB	1:C:765:LEU:HG	2.49	0.42
1:D:370:SER:HB3	1:D:388:GLN:NE2	2.33	0.42
1:D:429:ARG:HG3	1:D:456:TYR:CZ	2.53	0.42
1:D:626:ILE:HB	1:D:647:PHE:CE2	2.54	0.42
1:A:150:ASN:O	1:A:151:ASN:HB2	2.19	0.42
1:B:155:ILE:HD11	1:B:164:LEU:HD22	2.02	0.42
1:B:438:ASP:OD2	1:B:441:LYS:CE	2.67	0.42
1:C:437:ASN:OD1	1:C:438:ASP:N	2.51	0.42
1:D:183:GLN:O	1:D:183:GLN:HG3	2.19	0.42
1:D:322:TYR:C	1:D:322:TYR:CD1	2.93	0.42
1:A:200:ASP:HB2	7:A:1539:HOH:O	2.19	0.42
1:B:297:ASP:HA	7:B:1662:HOH:O	2.19	0.42
1:B:454:CYS:HB3	1:B:457:TYR:CZ	2.54	0.42
1:B:602:GLU:HG2	1:B:603:VAL:N	2.33	0.42
1:C:317:ARG:HD2	1:C:322:TYR:HB3	2.02	0.42
1:A:207:VAL:HG12	1:A:207:VAL:O	2.20	0.42
1:A:322:TYR:CD1	1:A:322:TYR:C	2.93	0.42
1:A:423:LYS:N	1:A:423:LYS:HD2	2.34	0.42
1:B:365:THR:HG23	1:B:370:SER:O	2.20	0.42
1:C:141:GLN:HE21	1:C:141:GLN:HB3	1.66	0.42
1:C:341:VAL:O	1:C:341:VAL:HG12	2.19	0.42
1:C:387:PHE:CD2	1:C:394:CYS:HB3	2.54	0.42
1:C:476:GLY:O	1:C:477:LEU:C	2.58	0.42
1:D:145:GLU:O	1:D:146:GLU:HB2	2.19	0.42
1:A:410:LEU:HD12	1:A:414:TYR:O	2.20	0.42
1:A:662:TYR:OH	6:A:801:BPR:C	2.68	0.42
1:A:735:TYR:OH	1:A:751:ILE:HA	2.20	0.42
1:B:177:GLU:HA	1:B:178:PRO:HD3	1.90	0.42
1:B:334:THR:OG1	1:B:336:ARG:CG	2.65	0.42
1:B:510:PRO:HB2	1:B:530:LEU:O	2.19	0.42
1:B:631:TYR:O	1:B:634:TYR:HB3	2.19	0.42
1:B:664:SER:O	1:B:668:GLU:HB2	2.20	0.42
1:D:420:ASN:ND2	1:D:426:PRO:HA	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:LEU:HD12	1:A:561:LEU:HA	1.88	0.42
1:A:666:TYR:CE2	6:A:801:BPR:HB1	2.55	0.42
1:B:500:LEU:HG	1:B:504:LEU:HD11	2.01	0.42
1:C:330:TYR:CZ	1:C:335:GLY:HA2	2.53	0.42
1:D:649:CYS:HB3	1:D:699:GLU:HB2	2.01	0.42
1:D:730:PHE:N	1:D:730:PHE:CD1	2.88	0.42
1:A:446:SER:HB2	1:A:457:TYR:CE1	2.54	0.42
1:A:516:VAL:HA	1:A:524:PHE:O	2.20	0.42
1:A:703:ILE:HG23	1:A:733:MET:O	2.20	0.42
1:B:491:LEU:O	1:B:492:ARG:HB3	2.18	0.42
1:D:532:PRO:CD	1:D:569:SER:HA	2.50	0.42
1:A:423:LYS:O	1:A:425:MET:N	2.53	0.42
1:B:136:ASP:HB2	1:B:143:ILE:HD11	2.01	0.42
1:B:165:ALA:HB2	1:B:216:TRP:CZ2	2.55	0.42
1:B:53:PHE:HE1	1:B:503:MET:HB3	1.85	0.42
1:B:658:LYS:HB3	1:B:661:TYR:CE2	2.55	0.42
1:C:168:TRP:O	1:C:169:ASN:HB2	2.20	0.42
1:C:236:ILE:HG13	1:C:237:GLU:N	2.35	0.42
1:C:53:PHE:HB3	1:C:500:LEU:HD11	2.02	0.42
1:C:682:TYR:CE2	2:I:1:NAG:H5	2.55	0.42
1:A:159:PRO:HD3	1:A:216:TRP:CB	2.49	0.42
1:A:169:ASN:HD22	1:A:169:ASN:N	2.17	0.42
1:A:415:LEU:HD13	1:A:416:TYR:N	2.35	0.42
1:A:434:ILE:HD11	1:A:439:TYR:HA	2.01	0.42
1:A:633:GLY:HA3	1:A:655:PRO:HB3	2.01	0.42
1:A:72:GLN:HG2	1:A:73:GLU:HG3	2.02	0.42
1:A:75:ASN:HB3	1:A:92:ASN:N	2.35	0.42
1:B:515:ASP:HB3	1:B:526:TYR:CZ	2.55	0.42
1:B:81:ALA:O	1:B:492:ARG:NH2	2.52	0.42
1:C:318:ARG:N	7:C:1624:HOH:O	2.53	0.42
1:C:310:ARG:NE	1:C:329:ASP:OD1	2.51	0.42
1:C:370:SER:HA	1:C:389:THR:H	1.84	0.42
1:B:236:ILE:HG12	1:B:712:HIS:CE1	2.55	0.41
1:B:626:ILE:HG23	1:B:636:THR:HG23	2.02	0.41
1:C:242:SER:OG	1:C:243:ASP:N	2.52	0.41
1:D:195:TYR:O	1:D:227:GLN:HA	2.19	0.41
1:D:372:TYR:CZ	1:D:386:HIS:CD2	3.08	0.41
1:A:453:ARG:HH21	1:A:479:LEU:CB	2.21	0.41
1:B:405:ILE:N	1:B:418:ILE:O	2.49	0.41
1:C:217:SER:HB3	1:C:305:TRP:CZ2	2.55	0.41
1:C:446:SER:HA	1:C:449:LEU:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:490:GLU:O	1:C:491:LEU:C	2.58	0.41
1:C:506:ASP:OD1	1:C:506:ASP:O	2.38	0.41
1:C:68:TYR:C	1:C:68:TYR:CD1	2.93	0.41
1:C:763:PHE:HB3	1:C:765:LEU:HG	2.02	0.41
1:D:276:LEU:HD12	7:D:1664:HOH:O	2.19	0.41
1:D:327:ILE:CD1	1:D:389:THR:HG23	2.43	0.41
1:D:436:LEU:O	1:D:439:TYR:CE1	2.73	0.41
1:D:596:ARG:N	1:D:670:TYR:O	2.49	0.41
1:A:549:GLY:O	1:A:550:PRO:C	2.59	0.41
1:A:714:GLN:HA	1:B:241:TYR:CE2	2.56	0.41
1:B:374:ILE:CD1	1:B:406:GLY:HA2	2.50	0.41
1:B:547:TYR:HD2	1:B:549:GLY:H	1.66	0.41
1:C:328:CYS:HA	1:C:338:ILE:O	2.20	0.41
1:C:546:VAL:HG22	1:C:547:TYR:N	2.35	0.41
1:D:534:PHE:HZ	1:D:618:PHE:CG	2.38	0.41
1:B:118:TYR:CD2	1:B:119:ASN:ND2	2.88	0.41
1:C:110:ASP:O	1:C:111:ARG:HB2	2.21	0.41
1:C:234:PRO:HB2	1:D:248:TYR:OH	2.20	0.41
1:C:530:LEU:HA	1:C:531:PRO:HD3	1.98	0.41
1:C:542:LEU:HD22	1:C:543:LEU:N	2.35	0.41
1:C:736:THR:HG23	1:D:717:ALA:HB1	2.02	0.41
1:D:466:LYS:HG2	1:D:467:TYR:CE2	2.55	0.41
1:D:68:TYR:C	1:D:68:TYR:CD1	2.93	0.41
1:C:122:LYS:HG2	1:C:123:GLN:N	2.36	0.41
1:C:223:LEU:HA	1:C:223:LEU:HD12	1.90	0.41
1:D:246:LEU:HD22	1:D:248:TYR:O	2.20	0.41
1:A:422:HIS:CE1	1:A:423:LYS:HD3	2.56	0.41
1:A:42:THR:HB	1:A:569:SER:OG	2.21	0.41
1:A:60:LEU:C	1:A:60:LEU:HD12	2.41	0.41
1:A:75:ASN:HD22	1:A:92:ASN:ND2	2.19	0.41
1:B:153:GLN:HE22	1:B:170:ASN:ND2	2.18	0.41
1:B:410:LEU:HD11	1:B:436:LEU:HD21	2.03	0.41
1:B:411:THR:CG2	1:B:465:ALA:HB3	2.51	0.41
1:B:43:TYR:HE2	1:B:48:TYR:HB2	1.86	0.41
1:B:524:PHE:CB	1:B:578:PHE:CE1	3.03	0.41
1:B:612:GLN:HE21	1:B:612:GLN:HB3	1.69	0.41
1:D:230:ASP:OD2	1:D:255:PRO:HB2	2.21	0.41
1:D:542:LEU:HB3	1:D:624:ILE:HG12	2.02	0.41
1:C:732:THR:HG22	1:D:733:MET:HA	2.01	0.41
1:A:682:TYR:OH	2:F:2:NAG:H81	2.21	0.41
1:A:154:TRP:HD1	1:A:214:LEU:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:PHE:HA	1:A:480:TYR:CE1	2.55	0.41
1:B:357:PHE:O	1:B:358:ARG:HB3	2.21	0.41
1:B:524:PHE:HB2	1:B:578:PHE:CE1	2.55	0.41
1:C:114:ILE:CG2	1:C:137:LEU:HD21	2.51	0.41
1:C:664:SER:HB2	1:C:668:GLU:CD	2.40	0.41
1:D:133:ASP:HB3	1:D:142:LEU:HD21	2.02	0.41
1:D:545:GLU:HG2	1:D:554:LYS:NZ	2.35	0.41
1:D:559:PHE:CZ	1:D:561:LEU:HD13	2.55	0.41
1:D:60:LEU:HD22	1:D:68:TYR:CD2	2.56	0.41
1:D:624:ILE:HB	7:D:1593:HOH:O	2.19	0.41
1:A:74:ASN:O	1:A:92:ASN:HB3	2.21	0.41
1:B:748:HIS:O	1:B:751:ILE:HG22	2.21	0.41
1:C:113:PHE:HE2	1:C:162:HIS:CD2	2.38	0.41
1:C:343:ARG:CG	1:C:343:ARG:NH1	2.82	0.41
1:C:711:VAL:HG23	1:C:740:HIS:CE1	2.56	0.41
1:D:125:ARG:HD2	1:D:126:HIS:NE2	2.36	0.41
1:D:429:ARG:HG3	1:D:456:TYR:CE1	2.55	0.41
1:D:635:VAL:O	1:D:636:THR:C	2.58	0.41
1:A:153:GLN:HE22	1:A:170:ASN:ND2	2.18	0.41
1:A:157:TRP:HE3	1:A:163:LYS:O	2.04	0.41
1:A:414:TYR:CG	1:A:433:ARG:HD2	2.54	0.41
1:C:471:ARG:HG2	1:C:480:TYR:CE2	2.55	0.41
1:C:97:GLU:OE1	1:C:97:GLU:N	2.46	0.41
1:D:381:TYR:N	1:D:381:TYR:CD1	2.89	0.41
1:D:510:PRO:HD3	1:D:569:SER:HB2	2.02	0.41
1:A:299:TYR:CZ	1:A:665:VAL:HG22	2.56	0.41
1:B:168:TRP:HZ2	7:B:1627:HOH:O	2.04	0.41
1:B:285:TYR:CE1	1:B:336:ARG:HB3	2.55	0.41
1:C:149:PRO:HB2	1:C:168:TRP:CD1	2.56	0.41
1:C:595:ASN:O	1:C:596:ARG:HB2	2.20	0.41
1:C:734:TRP:CE3	1:D:732:THR:HG23	2.56	0.41
1:D:135:TYR:CE2	1:D:137:LEU:HD23	2.56	0.41
1:D:338:ILE:HA	7:D:1518:HOH:O	2.20	0.41
1:D:353:TRP:CE3	1:D:595:ASN:ND2	2.88	0.41
1:C:435:GLN:HE22	1:C:441:LYS:HD2	1.81	0.41
1:D:102:THR:HG21	1:D:116:PHE:CD2	2.56	0.41
1:D:195:TYR:HB2	1:D:228:PHE:HB2	2.02	0.41
1:D:58:TYR:CD1	1:D:494:LEU:HD13	2.56	0.41
1:D:50:LYS:O	1:D:51:SER:C	2.58	0.41
1:A:236:ILE:HG22	1:A:254:ILE:O	2.21	0.40
1:A:58:TYR:CD2	1:A:494:LEU:HB3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:VAL:O	1:A:632:GLY:HA3	2.20	0.40
1:B:118:TYR:O	1:B:119:ASN:HB2	2.20	0.40
1:B:148:ILE:HD13	1:B:155:ILE:CD1	2.51	0.40
1:B:148:ILE:HD13	1:B:155:ILE:HD12	2.03	0.40
1:C:87:SER:HB3	4:C:767(A):NAG:H81	2.01	0.40
1:D:216:TRP:CZ3	1:D:273:THR:HG21	2.56	0.40
1:D:356:ARG:HG2	1:D:551:CYS:SG	2.60	0.40
1:A:317:ARG:HD2	1:A:322:TYR:HB3	2.02	0.40
1:B:325:ILE:HD11	1:B:373:LYS:HE2	2.03	0.40
1:C:206:GLU:HB2	1:C:665:VAL:HG11	2.03	0.40
1:C:532:PRO:HD3	1:C:569:SER:HA	2.03	0.40
1:D:597:ARG:HG3	1:D:597:ARG:O	2.21	0.40
1:A:103:ASN:ND2	1:A:117:GLU:OE2	2.36	0.40
1:A:704:HIS:CD2	1:A:716:SER:OG	2.71	0.40
1:C:170:ASN:HD22	1:C:170:ASN:N	2.19	0.40
1:C:42:THR:N	7:C:1515:HOH:O	2.50	0.40
1:C:442:VAL:O	1:C:442:VAL:HG13	2.21	0.40
1:C:470:LEU:HD12	1:C:483:HIS:NE2	2.34	0.40
1:C:89:PHE:HE1	1:C:137:LEU:HD13	1.86	0.40
1:A:377:ASN:HD22	1:A:381:TYR:HB2	1.86	0.40
1:C:415:LEU:HD23	1:C:415:LEU:O	2.21	0.40
1:C:584:GLY:O	1:C:585:TYR:HB2	2.21	0.40
1:C:72:GLN:HG2	1:C:73:GLU:HG3	2.02	0.40
1:C:91:GLU:HB3	1:C:92:ASN:H	1.69	0.40
1:A:438:ASP:CG	1:A:441:LYS:HE3	2.42	0.40
1:A:510:PRO:HD3	1:A:569:SER:HB2	2.03	0.40
1:A:530:LEU:HA	1:A:531:PRO:HD3	1.97	0.40
1:B:95:PHE:CE1	1:B:116:PHE:HE2	2.39	0.40
1:B:140:ARG:HH11	1:B:140:ARG:CG	2.34	0.40
1:B:142:LEU:O	1:B:144:THR:HG23	2.22	0.40
1:C:123:GLN:HG2	1:C:124:TRP:CD2	2.56	0.40
1:C:307:THR:OG1	1:C:310:ARG:HB3	2.21	0.40
1:C:345:HIS:CD2	1:C:371:PHE:CZ	3.10	0.40
1:C:626:ILE:HG23	1:C:636:THR:HG23	2.04	0.40
1:D:108:SER:HB3	1:D:157:TRP:CZ3	2.56	0.40
1:D:154:TRP:CD2	1:D:212:SER:HB3	2.56	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	726/728 (100%)	655 (90%)	60 (8%)	11 (2%)	10	13
1	B	726/728 (100%)	658 (91%)	60 (8%)	8 (1%)	14	19
1	C	726/728 (100%)	610 (84%)	93 (13%)	23 (3%)	4	3
1	D	726/728 (100%)	664 (92%)	58 (8%)	4 (1%)	25	33
All	All	2904/2912 (100%)	2587 (89%)	271 (9%)	46 (2%)	9	12

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	97	GLU
1	A	491	LEU
1	B	140	ARG
1	C	91	GLU
1	C	103	ASN
1	C	104	ASP
1	C	105	TYR
1	C	423	LYS
1	C	488	ASP
1	C	536	LYS
1	D	81	ALA
1	A	92	ASN
1	A	424	GLY
1	B	438	ASP
1	B	538	LYS
1	C	97	GLU
1	C	308	GLU
1	C	389	THR
1	C	535	ASP
1	D	99	GLY
1	A	244	GLU
1	A	621	ASP

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Mol	Chain	Res	Type
1	B	678	ASP
1	C	73	GLU
1	C	93	SER
1	C	139	LYS
1	C	355	GLY
1	C	491	LEU
1	C	534	PHE
1	D	100	TYR
1	D	389	THR
1	A	93	SER
1	B	520	HIS
1	C	94	THR
1	C	422	HIS
1	B	40	ARG
1	B	138	ASN
1	C	138	ASN
1	C	332	GLU
1	A	66	HIS
1	A	520	HIS
1	A	534	PHE
1	B	465	ALA
1	C	99	GLY
1	C	674	PRO
1	A	178	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	652/652 (100%)	621 (95%)	31 (5%)	25	34
1	B	652/652 (100%)	610 (94%)	42 (6%)	17	22
1	C	652/652 (100%)	614 (94%)	38 (6%)	20	26
1	D	652/652 (100%)	619 (95%)	33 (5%)	24	32
All	All	2608/2608 (100%)	2464 (94%)	144 (6%)	21	29

All (144) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LEU
1	A	144	THR
1	A	145	GLU
1	A	192	ASN
1	A	212	SER
1	A	219	ASN
1	A	246	LEU
1	A	294	LEU
1	A	343	ARG
1	A	358	ARG
1	A	399	LYS
1	A	415	LEU
1	A	423	LYS
1	A	436	LEU
1	A	443	THR
1	A	472	CYS
1	A	492	ARG
1	A	520	HIS
1	A	536	LYS
1	A	542	LEU
1	A	543	LEU
1	A	561	LEU
1	A	566	TYR
1	A	630	SER
1	A	663	ASP
1	A	679	ASN
1	A	701	LEU
1	A	714	GLN
1	A	718	GLN
1	A	745	ASN
1	A	761	GLN
1	B	57	PHE
1	B	74	ASN
1	B	142	LEU
1	B	158	SER
1	B	162	HIS
1	B	212	SER
1	B	230	ASP
1	B	243	ASP
1	B	246	LEU
1	B	256	TYR
1	B	284	SER

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Mol	Chain	Res	Type
1	B	293	VAL
1	B	323	SER
1	B	336	ARG
1	B	340	SER
1	B	385	CYS
1	B	393	ASN
1	B	415	LEU
1	B	418	ILE
1	B	423	LYS
1	B	435	GLN
1	B	448	GLU
1	B	450	ASN
1	B	470	LEU
1	B	472	CYS
1	B	520	HIS
1	B	535	ASP
1	B	536	LYS
1	B	542	LEU
1	B	543	LEU
1	B	561	LEU
1	B	621	ASP
1	B	627	TRP
1	B	630	SER
1	B	685	ASN
1	B	701	LEU
1	B	702	LEU
1	B	714	GLN
1	B	718	GLN
1	B	732	THR
1	B	759	LEU
1	B	761	GLN
1	C	75	ASN
1	C	90	LEU
1	C	125	ARG
1	C	145	GLU
1	C	147	ARG
1	C	156	THR
1	C	158	SER
1	C	183	GLN
1	C	202	VAL
1	C	212	SER
1	C	222	PHE

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Mol	Chain	Res	Type
1	C	246	LEU
1	C	284	SER
1	C	313	LEU
1	C	323	SER
1	C	345	HIS
1	C	399	LYS
1	C	412	SER
1	C	416	TYR
1	C	448	GLU
1	C	463	ASN
1	C	482	LEU
1	C	491	LEU
1	C	535	ASP
1	C	536	LYS
1	C	542	LEU
1	C	557	THR
1	C	561	LEU
1	C	566	TYR
1	C	611	ARG
1	C	630	SER
1	C	655	PRO
1	C	660	GLU
1	C	679	ASN
1	C	718	GLN
1	C	745	ASN
1	C	746	MET
1	C	761	GLN
1	D	40	ARG
1	D	91	GLU
1	D	100	TYR
1	D	158	SER
1	D	180	LEU
1	D	184	ARG
1	D	219	ASN
1	D	230	ASP
1	D	246	LEU
1	D	253	ARG
1	D	276	LEU
1	D	336	ARG
1	D	348	ILE
1	D	358	ARG
1	D	385	CYS

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Mol	Chain	Res	Type
1	D	393	ASN
1	D	399	LYS
1	D	414	TYR
1	D	471	ARG
1	D	482	LEU
1	D	507	VAL
1	D	536	LYS
1	D	561	LEU
1	D	581	ARG
1	D	603	VAL
1	D	608	GLU
1	D	655	PRO
1	D	685	ASN
1	D	694	ASN
1	D	701	LEU
1	D	702	LEU
1	D	718	GLN
1	D	732	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	75	ASN
1	A	141	GLN
1	A	150	ASN
1	A	169	ASN
1	A	170	ASN
1	A	176	ASN
1	A	183	GLN
1	A	192	ASN
1	A	247	GLN
1	A	386	HIS
1	A	435	GLN
1	A	483	HIS
1	A	505	GLN
1	A	572	ASN
1	A	612	GLN
1	A	679	ASN
1	A	694	ASN
1	A	704	HIS
1	A	718	GLN

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Mol	Chain	Res	Type
1	A	745	ASN
1	A	761	GLN
1	B	61	GLN
1	B	75	ASN
1	B	119	ASN
1	B	169	ASN
1	B	170	ASN
1	B	176	ASN
1	B	179	ASN
1	B	183	GLN
1	B	247	GLN
1	B	314	GLN
1	B	369	ASN
1	B	393	ASN
1	B	430	ASN
1	B	435	GLN
1	B	450	ASN
1	B	463	ASN
1	B	483	HIS
1	B	505	GLN
1	B	520	HIS
1	B	572	ASN
1	B	606	GLN
1	B	612	GLN
1	B	679	ASN
1	B	694	ASN
1	B	704	HIS
1	B	718	GLN
1	B	748	HIS
1	B	761	GLN
1	C	72	GLN
1	C	74	ASN
1	C	112	GLN
1	C	141	GLN
1	C	169	ASN
1	C	170	ASN
1	C	176	ASN
1	C	192	ASN
1	C	247	GLN
1	C	435	GLN
1	C	463	ASN
1	C	483	HIS

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Mol	Chain	Res	Type
1	C	505	GLN
1	C	508	GLN
1	C	572	ASN
1	C	612	GLN
1	C	679	ASN
1	C	694	ASN
1	C	704	HIS
1	C	718	GLN
1	C	761	GLN
1	D	72	GLN
1	D	75	ASN
1	D	112	GLN
1	D	138	ASN
1	D	141	GLN
1	D	169	ASN
1	D	170	ASN
1	D	176	ASN
1	D	183	GLN
1	D	192	ASN
1	D	247	GLN
1	D	369	ASN
1	D	377	ASN
1	D	383	HIS
1	D	386	HIS
1	D	388	GLN
1	D	393	ASN
1	D	430	ASN
1	D	463	ASN
1	D	483	HIS
1	D	505	GLN
1	D	533	HIS
1	D	612	GLN
1	D	679	ASN
1	D	694	ASN
1	D	704	HIS
1	D	718	GLN
1	D	731	GLN
1	D	745	ASN
1	D	748	HIS

### 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 ⓘ

20 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$
2	NAG	E	1	1,2	14,14,15	0.38	0	17,19,21	0.76	1 (5%)
2	NAG	E	2	2	14,14,15	0.50	0	17,19,21	0.76	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.59	0	17,19,21	0.77	0
2	NAG	F	2	2	14,14,15	0.61	0	17,19,21	0.72	0
3	NAG	G	1	1,3	14,14,15	0.67	0	17,19,21	0.70	0
3	NAG	G	2	3	14,14,15	0.72	0	17,19,21	0.79	0
3	BMA	G	3	3	11,11,12	0.66	0	15,15,17	0.30	0
2	NAG	H	1	1,2	14,14,15	0.58	0	17,19,21	0.67	0
2	NAG	H	2	2	14,14,15	0.79	1 (7%)	17,19,21	0.69	0
2	NAG	I	1	1,2	14,14,15	0.82	1 (7%)	17,19,21	0.76	0
2	NAG	I	2	2	14,14,15	0.67	0	17,19,21	0.65	0
3	NAG	J	1	1,3	14,14,15	0.51	0	17,19,21	0.68	0
3	NAG	J	2	3	14,14,15	0.55	0	17,19,21	0.64	0
3	BMA	J	3	3	11,11,12	0.61	0	15,15,17	0.23	0
2	NAG	K	1	1,2	14,14,15	0.59	0	17,19,21	0.71	0
2	NAG	K	2	2	14,14,15	0.60	0	17,19,21	0.88	1 (5%)
2	NAG	L	1	1,2	14,14,15	0.52	0	17,19,21	0.97	1 (5%)
2	NAG	L	2	2	14,14,15	0.64	0	17,19,21	0.79	1 (5%)
2	NAG	M	1	1,2	14,14,15	0.63	0	17,19,21	0.79	0
2	NAG	M	2	2	14,14,15	0.65	0	17,19,21	1.14	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	4/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	BMA	G	3	3	-	2/2/19/22	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	6/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	J	2	3	-	3/6/23/26	0/1/1/1
3	BMA	J	3	3	-	1/2/19/22	0/1/1/1
2	NAG	K	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	4/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1
2	NAG	M	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	M	2	2	-	3/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	2	NAG	C1-C2	2.19	1.55	1.52
2	I	1	NAG	C1-C2	2.14	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	NAG	C2-N2-C7	-2.53	119.30	122.90
2	K	2	NAG	C2-N2-C7	-2.49	119.35	122.90
2	L	1	NAG	C2-N2-C7	-2.33	119.59	122.90
2	L	2	NAG	C2-N2-C7	-2.13	119.87	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	2	NAG	O5-C1-C2	-2.12	107.94	111.29
2	E	1	NAG	C2-N2-C7	-2.09	119.92	122.90
2	M	2	NAG	C4-C3-C2	-2.03	108.04	111.02

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	2	NAG	C8-C7-N2-C2
2	K	2	NAG	O7-C7-N2-C2
2	L	1	NAG	C8-C7-N2-C2
2	L	1	NAG	O7-C7-N2-C2
2	L	2	NAG	C8-C7-N2-C2
2	L	2	NAG	O7-C7-N2-C2
3	J	2	NAG	C3-C2-N2-C7
3	J	2	NAG	C8-C7-N2-C2
3	J	2	NAG	O7-C7-N2-C2
2	H	2	NAG	C3-C2-N2-C7
2	H	2	NAG	O7-C7-N2-C2
2	M	2	NAG	C8-C7-N2-C2
2	M	2	NAG	O7-C7-N2-C2
2	H	2	NAG	C8-C7-N2-C2
2	M	1	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	J	1	NAG	C8-C7-N2-C2
3	J	1	NAG	O7-C7-N2-C2
2	K	1	NAG	O5-C5-C6-O6
2	M	1	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
2	F	2	NAG	O5-C5-C6-O6
3	G	3	BMA	O5-C5-C6-O6
2	M	2	NAG	C1-C2-N2-C7
2	F	2	NAG	C4-C5-C6-O6
2	K	1	NAG	C4-C5-C6-O6
3	G	3	BMA	C4-C5-C6-O6
2	F	2	NAG	C8-C7-N2-C2
2	E	1	NAG	C4-C5-C6-O6
2	K	2	NAG	O5-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
2	M	1	NAG	C8-C7-N2-C2

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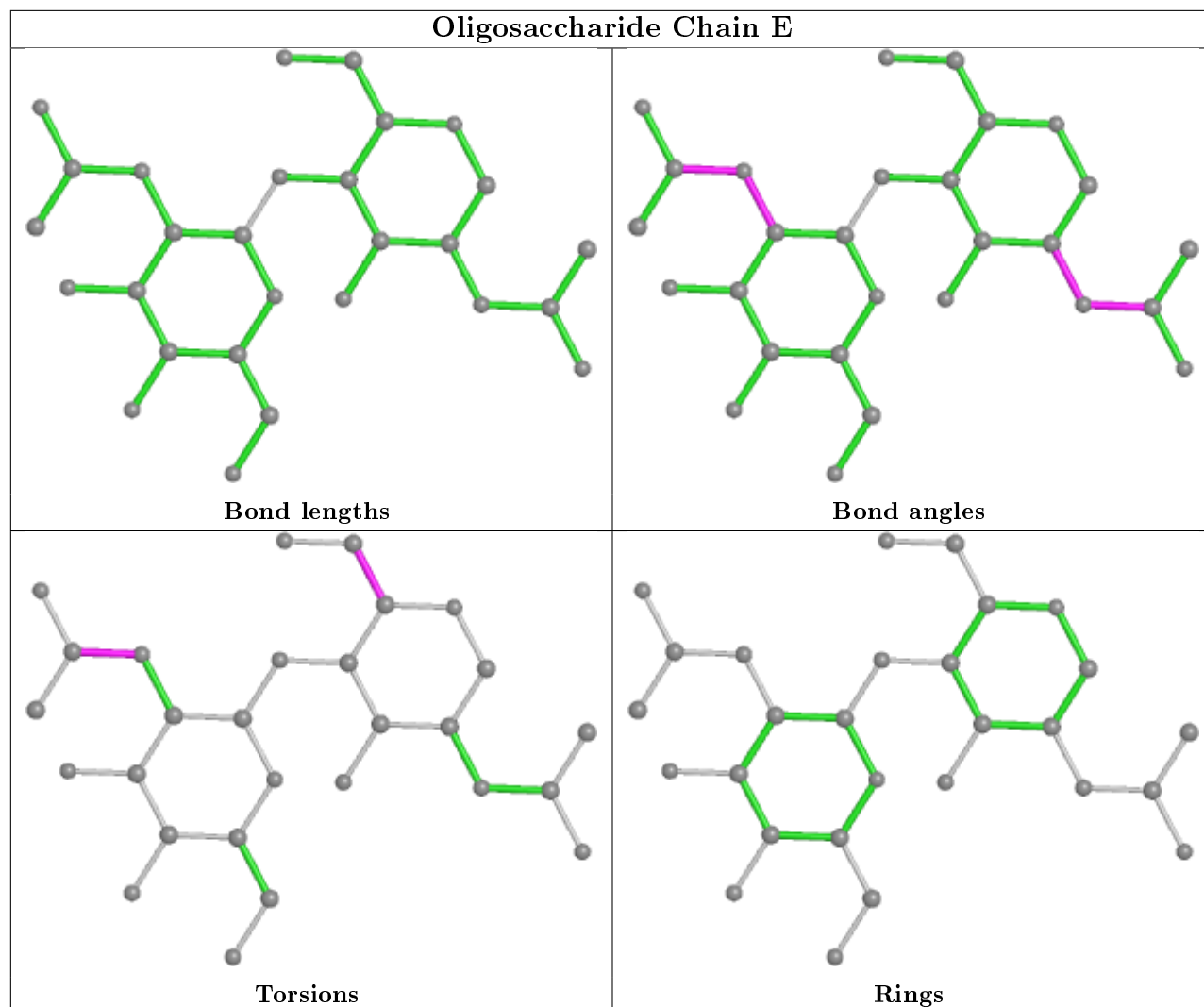
Mol	Chain	Res	Type	Atoms
2	K	2	NAG	C4-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	F	2	NAG	O7-C7-N2-C2
2	E	1	NAG	O5-C5-C6-O6
2	M	1	NAG	O7-C7-N2-C2
2	E	2	NAG	C8-C7-N2-C2
2	L	1	NAG	C4-C5-C6-O6
2	L	1	NAG	O5-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
2	E	2	NAG	O7-C7-N2-C2
3	J	3	BMA	C4-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	H	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O5-C5-C6-O6
2	H	1	NAG	O7-C7-N2-C2
2	H	2	NAG	C1-C2-N2-C7

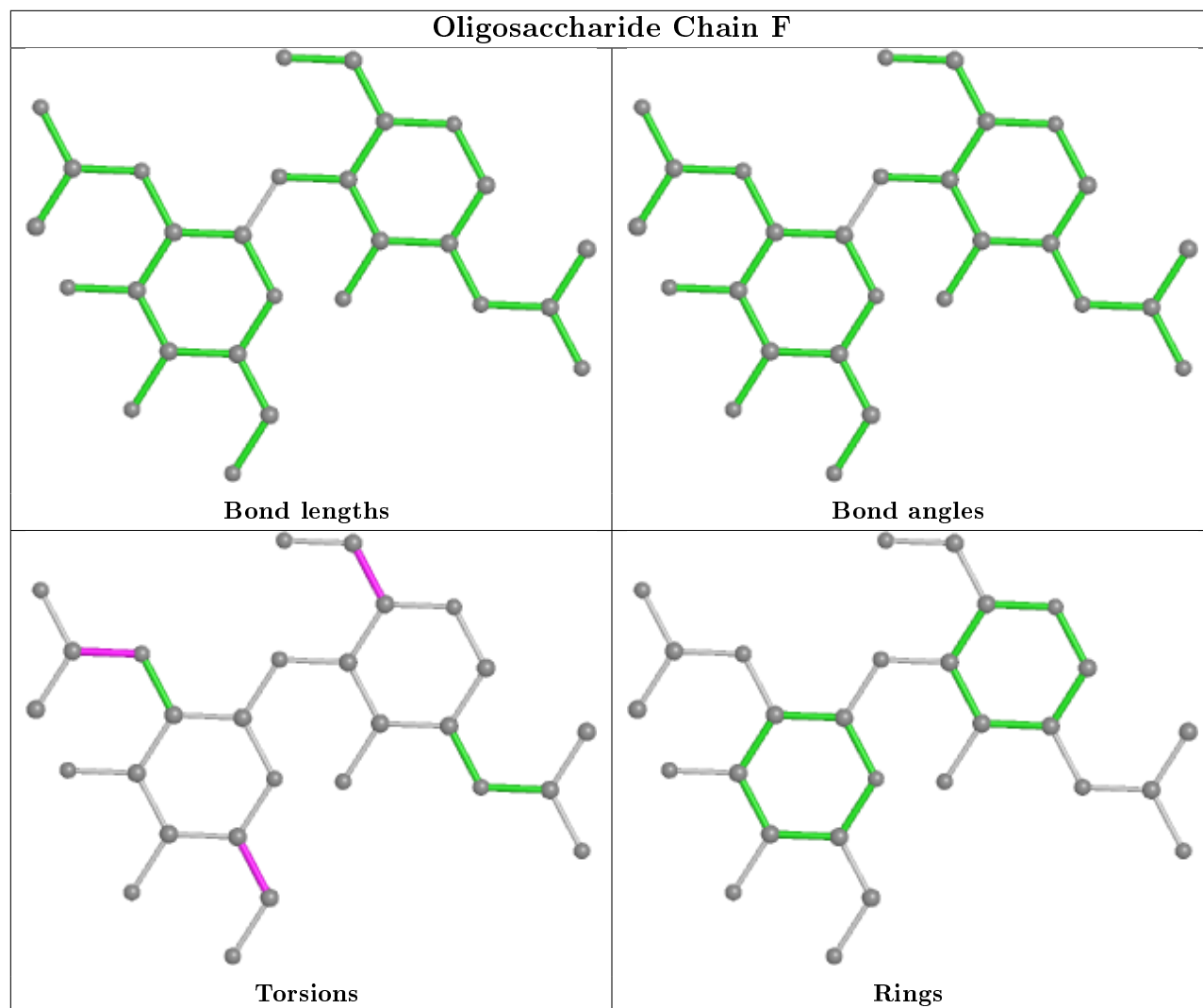
There are no ring outliers.

11 monomers are involved in 16 short contacts:

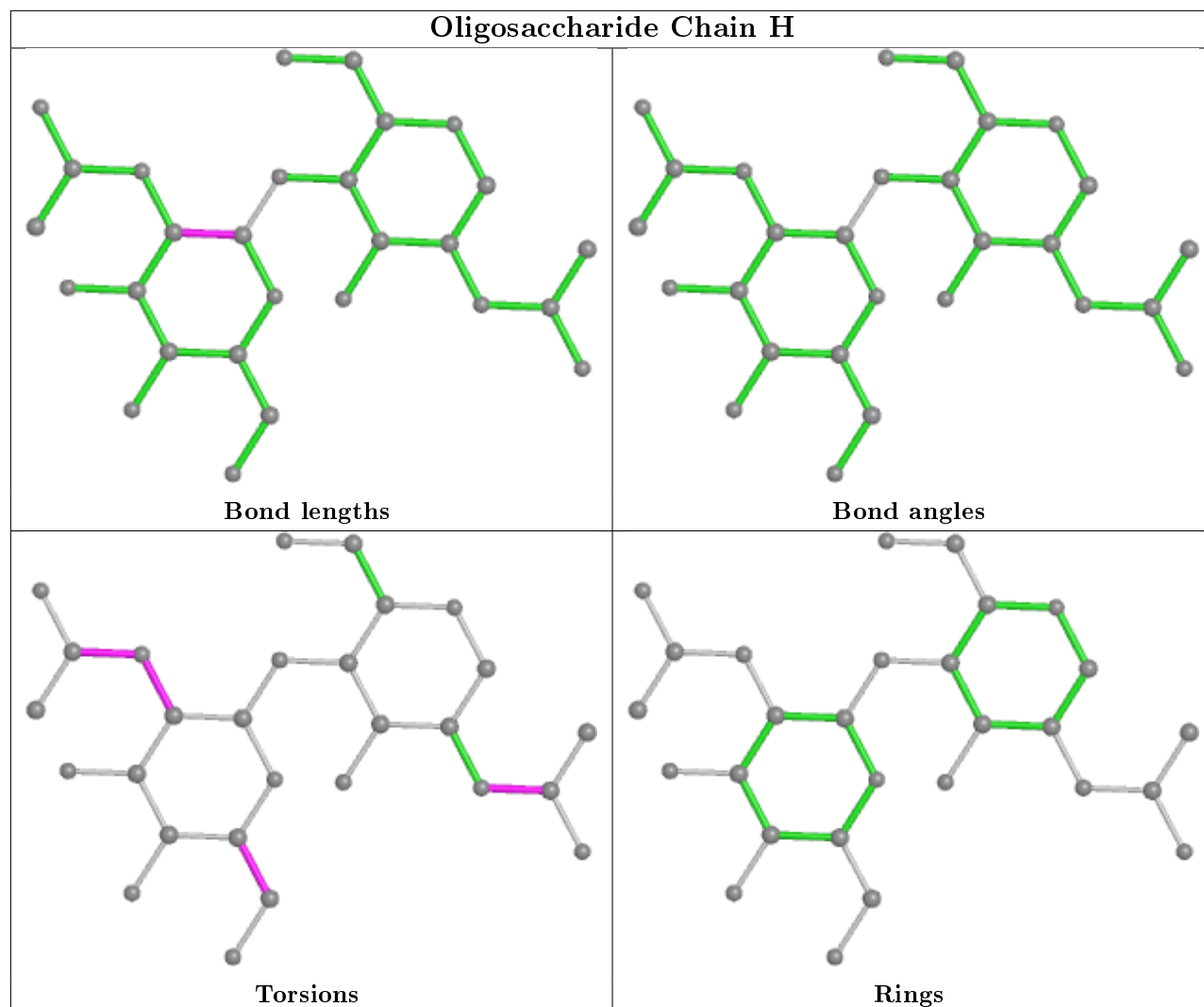
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	M	1	NAG	3	0
3	J	1	NAG	1	0
2	I	1	NAG	1	0
2	M	2	NAG	1	0
2	H	1	NAG	4	0
2	H	2	NAG	1	0
2	F	2	NAG	2	0
3	G	2	NAG	1	0
3	G	3	BMA	1	0
2	F	1	NAG	3	0
2	I	2	NAG	1	0

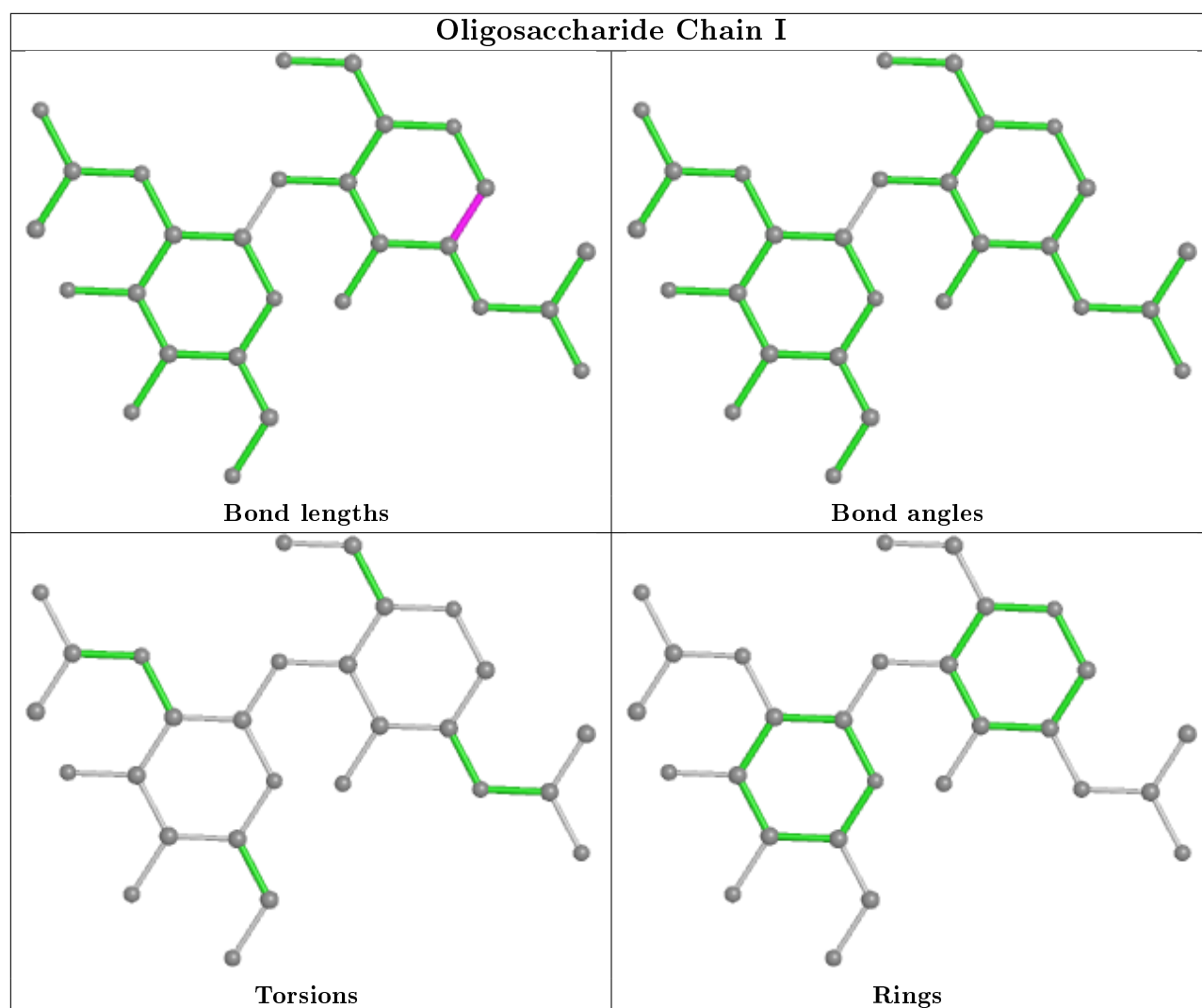
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

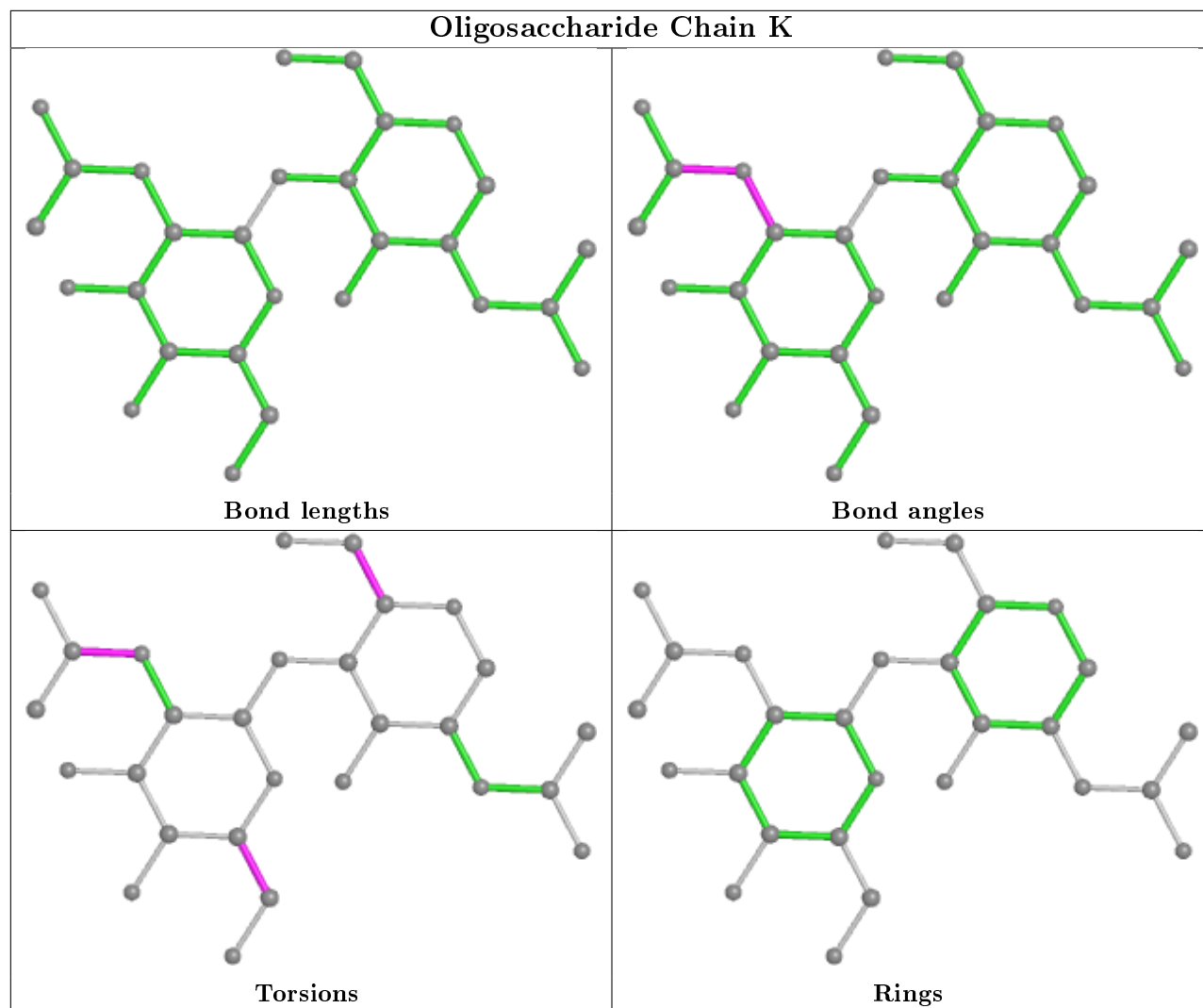


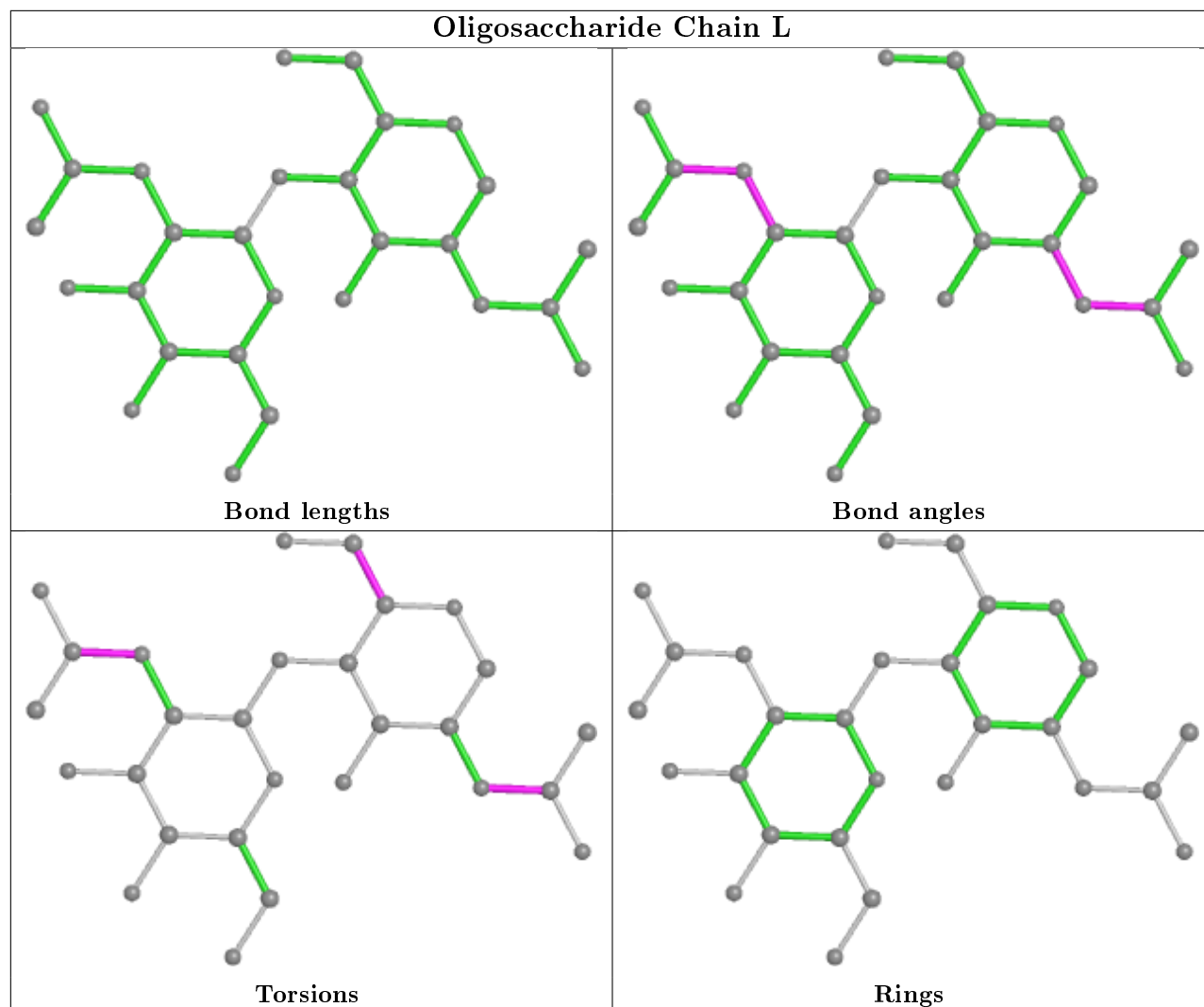


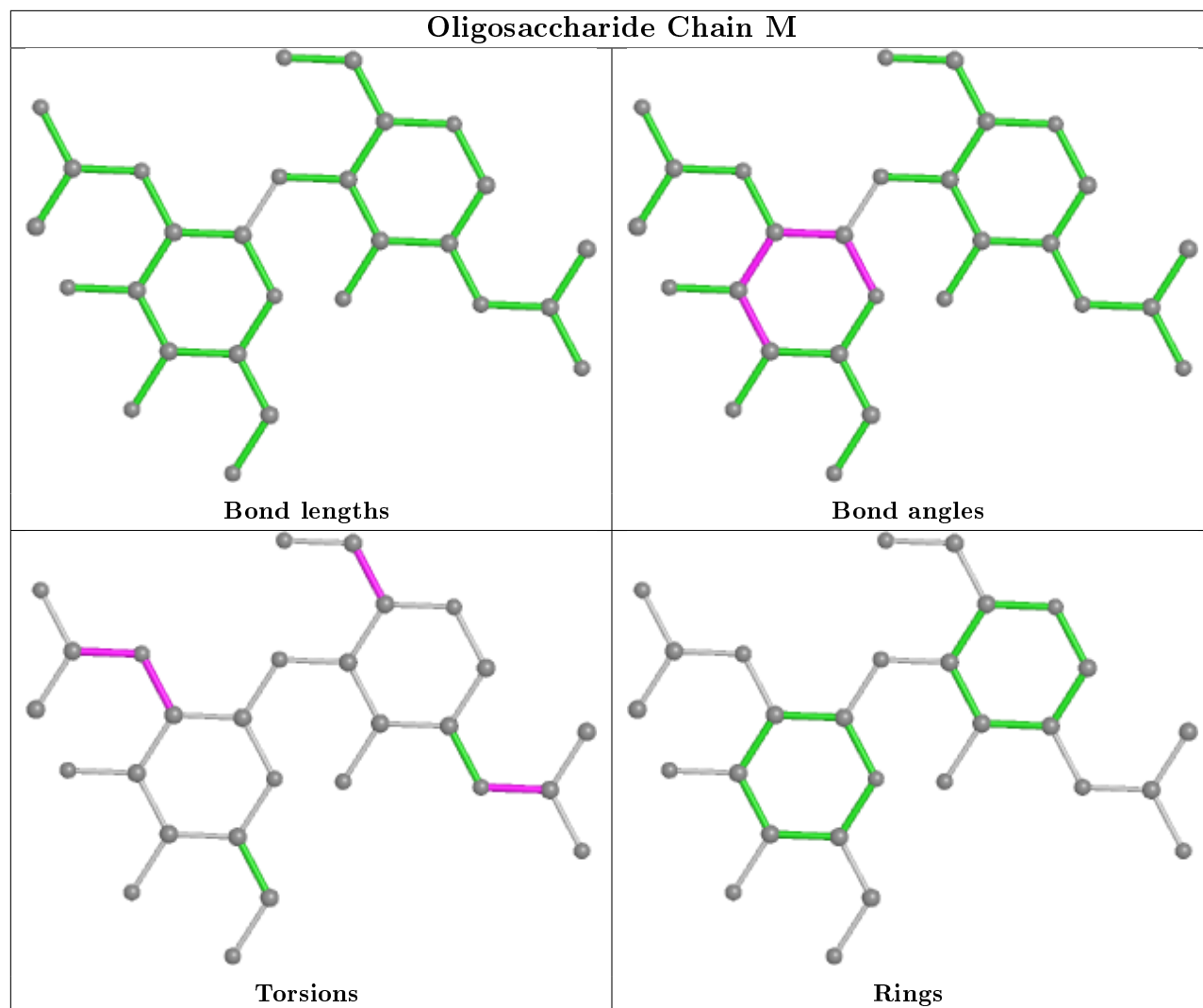


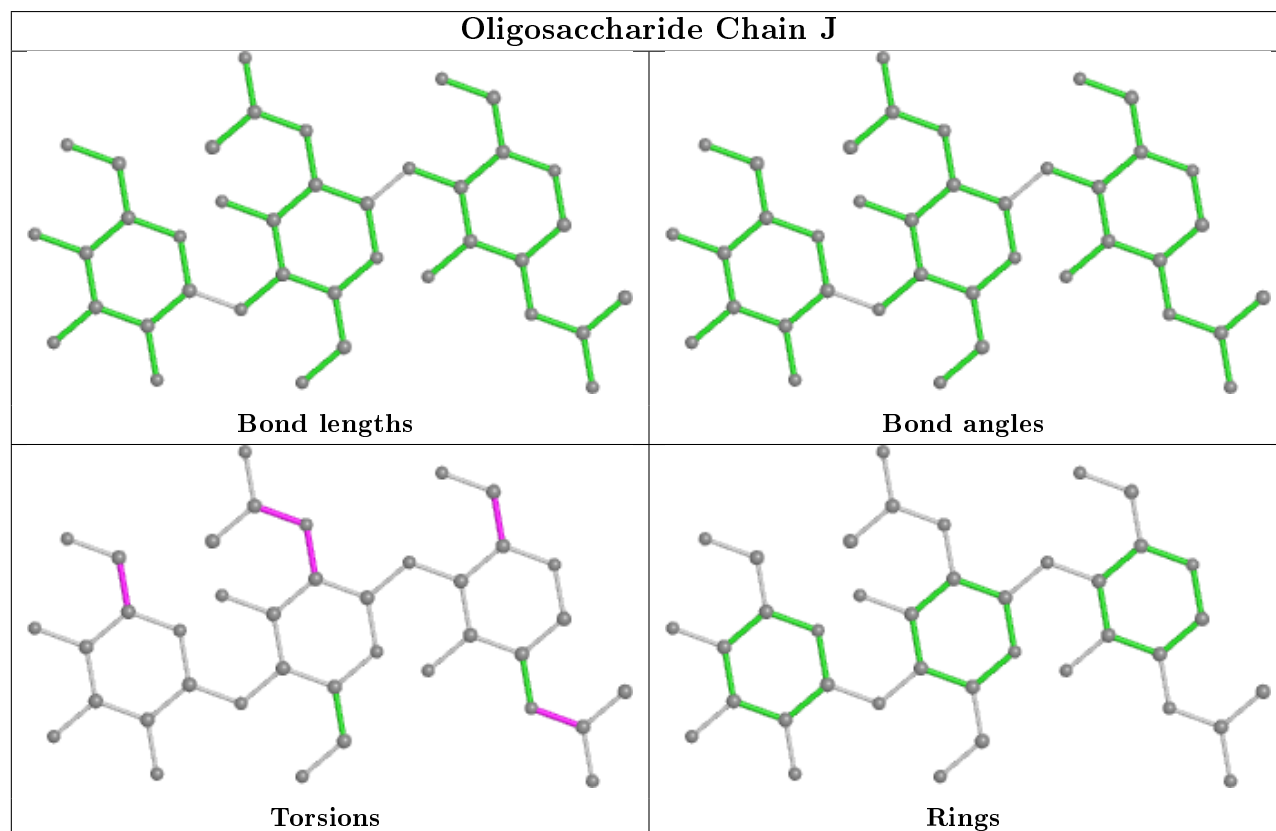
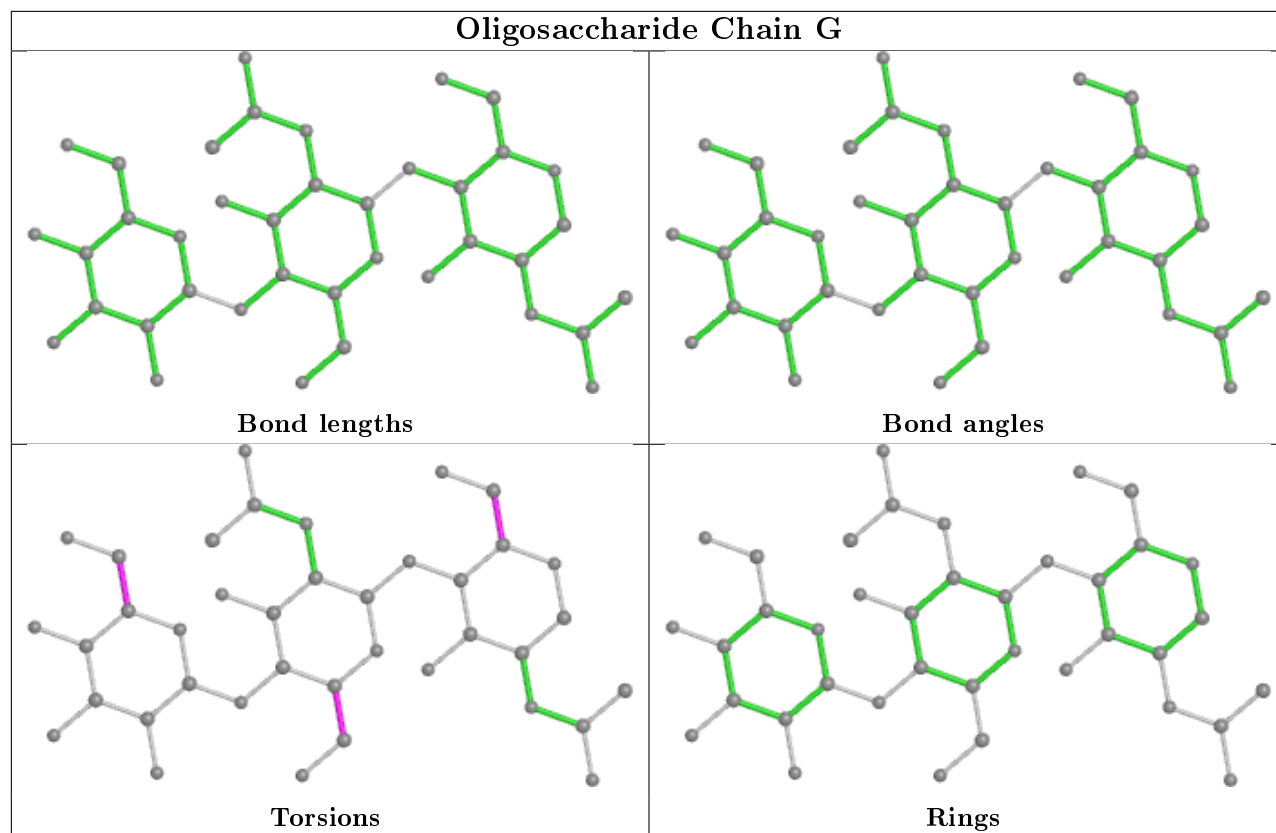












## 5.6 Ligand geometry

23 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	C	770(A)	1	14,14,15	0.70	0	17,19,21	0.61	0
4	NAG	A	768(A)	1	14,14,15	0.59	0	17,19,21	0.96	2 (11%)
6	BPR	B	801	1	12,16,16	0.68	0	15,22,22	0.73	0
4	NAG	D	773(A)	1	14,14,15	0.63	0	17,19,21	0.66	0
4	NAG	B	767(A)	1	14,14,15	0.77	0	17,19,21	0.60	0
6	BPR	D	801	1	12,16,16	0.48	0	15,22,22	0.56	0
4	NAG	A	767(A)	1	14,14,15	0.53	0	17,19,21	0.70	0
4	NAG	B	772(A)	1	14,14,15	0.66	0	17,19,21	0.58	0
6	BPR	A	801	1	12,16,16	0.57	0	15,22,22	0.71	0
6	BPR	C	801	1	12,16,16	0.73	0	15,22,22	0.93	1 (6%)
5	SO4	B	1501	-	4,4,4	0.43	0	6,6,6	0.70	0
4	NAG	B	771(A)	1	14,14,15	0.64	0	17,19,21	0.74	0
4	NAG	C	768(A)	1	14,14,15	0.55	0	17,19,21	0.63	0
4	NAG	C	769(A)	1	14,14,15	0.54	0	17,19,21	0.77	0
4	NAG	C	767(A)	1	14,14,15	0.59	0	17,19,21	0.60	0
5	SO4	C	1502	-	4,4,4	0.47	0	6,6,6	0.76	0
4	NAG	C	771(A)	1	14,14,15	0.65	0	17,19,21	0.90	0
4	NAG	A	771(A)	1	14,14,15	0.66	0	17,19,21	0.62	0
5	SO4	A	1500	-	4,4,4	0.34	0	6,6,6	0.69	0
4	NAG	A	772(A)	1	14,14,15	0.52	0	17,19,21	0.94	1 (5%)
5	SO4	D	1503	-	4,4,4	0.52	0	6,6,6	0.65	0
4	NAG	B	773(A)	1	14,14,15	0.50	0	17,19,21	1.03	1 (5%)
4	NAG	D	767(A)	1	14,14,15	0.64	0	17,19,21	0.63	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BPR	B	801	1	-	0/8/29/29	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BPR	D	801	1	-	1/8/29/29	0/2/2/2
4	NAG	B	772(A)	1	-	3/6/23/26	0/1/1/1
4	NAG	C	770(A)	1	-	4/6/23/26	0/1/1/1
6	BPR	A	801	1	-	0/8/29/29	0/2/2/2
6	BPR	C	801	1	-	0/8/29/29	0/2/2/2
4	NAG	C	771(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	B	773(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	A	771(A)	1	-	3/6/23/26	0/1/1/1
4	NAG	B	771(A)	1	-	0/6/23/26	0/1/1/1
4	NAG	C	768(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	A	772(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	A	768(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	A	767(A)	1	-	2/6/23/26	0/1/1/1
4	NAG	D	767(A)	1	-	2/6/23/26	0/1/1/1
4	NAG	D	773(A)	1	-	5/6/23/26	0/1/1/1
4	NAG	B	767(A)	1	-	4/6/23/26	0/1/1/1
4	NAG	C	769(A)	1	-	2/6/23/26	0/1/1/1
4	NAG	C	767(A)	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	801	BPR	C-CA-N	2.73	116.67	111.74
4	B	773(A)	NAG	C2-N2-C7	-2.58	119.23	122.90
4	A	772(A)	NAG	C2-N2-C7	-2.51	119.33	122.90
4	A	768(A)	NAG	C2-N2-C7	-2.27	119.67	122.90
4	A	768(A)	NAG	C4-C3-C2	-2.03	108.05	111.02

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	770(A)	NAG	C8-C7-N2-C2
4	C	770(A)	NAG	O7-C7-N2-C2
4	A	768(A)	NAG	C8-C7-N2-C2
4	A	768(A)	NAG	O7-C7-N2-C2
4	D	773(A)	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	D	773(A)	NAG	O7-C7-N2-C2
4	B	767(A)	NAG	C8-C7-N2-C2
4	B	767(A)	NAG	O7-C7-N2-C2
4	A	767(A)	NAG	C8-C7-N2-C2
4	A	767(A)	NAG	O7-C7-N2-C2
4	B	772(A)	NAG	C8-C7-N2-C2
4	B	772(A)	NAG	O7-C7-N2-C2
4	C	768(A)	NAG	C8-C7-N2-C2
4	C	768(A)	NAG	O7-C7-N2-C2
4	C	771(A)	NAG	C8-C7-N2-C2
4	C	771(A)	NAG	O7-C7-N2-C2
4	A	771(A)	NAG	C8-C7-N2-C2
4	A	771(A)	NAG	O7-C7-N2-C2
4	C	771(A)	NAG	C4-C5-C6-O6
4	C	767(A)	NAG	O5-C5-C6-O6
4	A	772(A)	NAG	O5-C5-C6-O6
4	C	771(A)	NAG	O5-C5-C6-O6
4	C	767(A)	NAG	C4-C5-C6-O6
4	C	768(A)	NAG	C4-C5-C6-O6
4	A	772(A)	NAG	C4-C5-C6-O6
4	C	768(A)	NAG	O5-C5-C6-O6
4	C	770(A)	NAG	C4-C5-C6-O6
4	D	767(A)	NAG	C4-C5-C6-O6
4	D	773(A)	NAG	O5-C5-C6-O6
4	A	768(A)	NAG	O5-C5-C6-O6
4	C	770(A)	NAG	O5-C5-C6-O6
4	A	772(A)	NAG	C8-C7-N2-C2
4	D	767(A)	NAG	O5-C5-C6-O6
4	B	773(A)	NAG	O5-C5-C6-O6
4	D	773(A)	NAG	C4-C5-C6-O6
4	A	771(A)	NAG	O5-C5-C6-O6
4	A	772(A)	NAG	O7-C7-N2-C2
4	C	769(A)	NAG	C4-C5-C6-O6
4	B	773(A)	NAG	C8-C7-N2-C2
4	C	767(A)	NAG	C8-C7-N2-C2
4	B	767(A)	NAG	C4-C5-C6-O6
4	A	768(A)	NAG	C4-C5-C6-O6
4	B	773(A)	NAG	O7-C7-N2-C2
4	C	767(A)	NAG	O7-C7-N2-C2
4	B	767(A)	NAG	O5-C5-C6-O6
4	C	769(A)	NAG	O5-C5-C6-O6
6	D	801	BPR	O-C-N1-C1

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Mol	Chain	Res	Type	Atoms
4	D	773(A)	NAG	C1-C2-N2-C7
4	B	772(A)	NAG	O5-C5-C6-O6
4	B	773(A)	NAG	C4-C5-C6-O6

There are no ring outliers.

10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	768(A)	NAG	1	0
6	B	801	BPR	3	0
4	D	773(A)	NAG	1	0
4	B	767(A)	NAG	1	0
6	D	801	BPR	1	0
6	A	801	BPR	2	0
6	C	801	BPR	4	0
4	C	768(A)	NAG	1	0
4	C	769(A)	NAG	2	0
4	C	767(A)	NAG	3	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	724/728 (99%)	0.07	17 (2%) 60 68	9, 36, 61, 94	13 (1%)
1	B	728/728 (100%)	-0.10	15 (2%) 63 71	7, 31, 59, 76	12 (1%)
1	C	723/728 (99%)	0.48	67 (9%) 8 12	12, 43, 85, 108	12 (1%)
1	D	728/728 (100%)	-0.00	16 (2%) 62 70	12, 33, 66, 86	10 (1%)
All	All	2903/2912 (99%)	0.11	115 (3%) 38 47	7, 35, 69, 108	47 (1%)

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	98	LEU	12.3
1	C	83	TYR	9.2
1	C	766	PRO	6.7
1	A	101	SER	6.4
1	D	83	TYR	5.9
1	C	39	SER	5.5
1	A	103	ASN	5.4
1	D	82	GLU	5.4
1	C	505	GLN	4.6
1	C	72	GLN	4.4
1	B	39	SER	4.3
1	C	73	GLU	4.3
1	A	102	THR	4.3
1	D	99	GLY	4.3
1	C	97	GLU	4.3
1	B	99	GLY	4.2
1	D	39	SER	4.2
1	B	103	ASN	4.1
1	C	70	TYR	4.0
1	C	535	ASP	3.8
1	C	138	ASN	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	91	GLU	3.8
1	A	765	LEU	3.8
1	C	41	ARG	3.7
1	C	139	LYS	3.7
1	C	487	SER	3.5
1	C	468	TYR	3.5
1	D	487	SER	3.5
1	C	90	LEU	3.5
1	C	506	ASP	3.5
1	B	537	SER	3.5
1	A	392	SER	3.4
1	C	140	ARG	3.4
1	C	537	SER	3.4
1	C	467	TYR	3.3
1	C	141	GLN	3.3
1	D	295	ILE	3.3
1	C	412	SER	3.3
1	C	160	VAL	3.2
1	D	81	ALA	3.2
1	C	417	TYR	3.1
1	C	79	PHE	3.1
1	C	137	LEU	3.1
1	D	101	SER	3.1
1	B	83	TYR	3.1
1	A	766	PRO	3.1
1	B	487	SER	3.1
1	C	77	LEU	3.0
1	D	103	ASN	3.0
1	C	438	ASP	3.0
1	C	391	LYS	3.0
1	C	442	VAL	2.9
1	A	187	TRP	2.9
1	B	766	PRO	2.9
1	C	492	ARG	2.8
1	B	488	ASP	2.8
1	C	95	PHE	2.8
1	C	96	ASP	2.8
1	C	765	LEU	2.8
1	C	295	ILE	2.7
1	A	492	ARG	2.7
1	C	388	GLN	2.7
1	C	440	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	101	SER	2.6
1	D	537	SER	2.6
1	C	414	TYR	2.6
1	C	488	ASP	2.6
1	A	83	TYR	2.6
1	C	76	ILE	2.6
1	B	498	SER	2.6
1	C	415	LEU	2.5
1	C	434	ILE	2.5
1	C	437	ASN	2.5
1	C	57	PHE	2.5
1	C	498	SER	2.5
1	C	538	LYS	2.5
1	D	538	LYS	2.5
1	D	481	THR	2.4
1	C	489	LYS	2.4
1	C	68	TYR	2.4
1	C	40	ARG	2.4
1	C	54	ARG	2.3
1	B	401	ALA	2.3
1	C	481	THR	2.3
1	A	379	GLU	2.3
1	C	384	ILE	2.3
1	C	416	TYR	2.3
1	A	533	HIS	2.3
1	C	470	LEU	2.3
1	A	764	SER	2.2
1	B	54	ARG	2.2
1	C	135	TYR	2.2
1	D	91	GLU	2.2
1	C	114	ILE	2.2
1	C	116	PHE	2.2
1	C	435	GLN	2.2
1	C	120	TYR	2.2
1	C	486	SER	2.2
1	C	126	HIS	2.2
1	B	615	LYS	2.2
1	C	615	LYS	2.2
1	A	81	ALA	2.2
1	B	489	LYS	2.1
1	D	441	LYS	2.1
1	C	419	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	391	LYS	2.1
1	A	77	LEU	2.1
1	D	757	HIS	2.1
1	A	93	SER	2.1
1	A	391	LYS	2.1
1	B	40	ARG	2.1
1	A	537	SER	2.0
1	C	480	TYR	2.0
1	C	521	GLY	2.0
1	C	466	LYS	2.0

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

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

## 6.3 Carbohydrates [i](#)

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

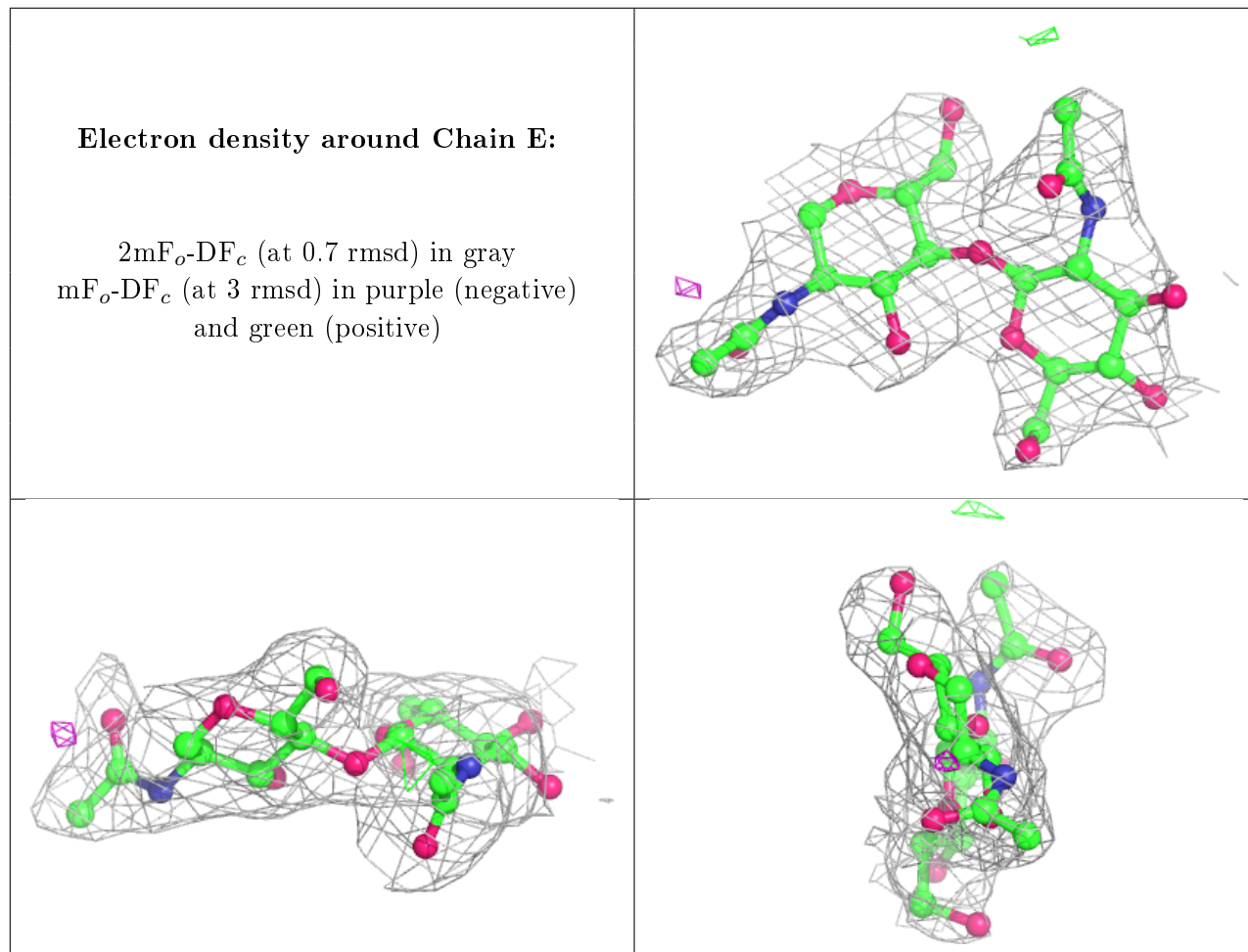
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	BMA	G	3	11/12	0.41	0.47	82,84,85,86	0
3	BMA	J	3	11/12	0.44	0.44	103,104,105,105	0
2	NAG	M	2	14/15	0.70	0.35	55,58,64,67	0
3	NAG	J	2	14/15	0.70	0.39	96,98,100,102	0
3	NAG	J	1	14/15	0.74	0.30	84,87,91,92	0
2	NAG	L	2	14/15	0.76	0.35	59,64,66,67	0
3	NAG	G	2	14/15	0.77	0.31	71,72,74,78	0
2	NAG	K	2	14/15	0.80	0.31	52,55,56,58	0
2	NAG	I	2	14/15	0.80	0.32	48,53,55,56	0
2	NAG	L	1	14/15	0.84	0.18	43,46,50,57	0
2	NAG	I	1	14/15	0.85	0.21	44,47,50,51	0
2	NAG	E	2	14/15	0.86	0.28	50,54,56,58	0
2	NAG	H	2	14/15	0.86	0.31	57,59,60,60	0
2	NAG	M	1	14/15	0.87	0.18	35,41,45,50	0
3	NAG	G	1	14/15	0.88	0.17	62,65,66,67	0
2	NAG	F	1	14/15	0.88	0.14	40,44,47,48	0
2	NAG	H	1	14/15	0.88	0.18	46,51,54,54	0
2	NAG	F	2	14/15	0.89	0.30	49,51,53,54	0

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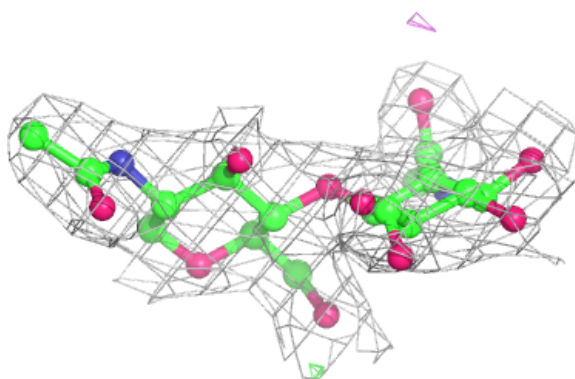
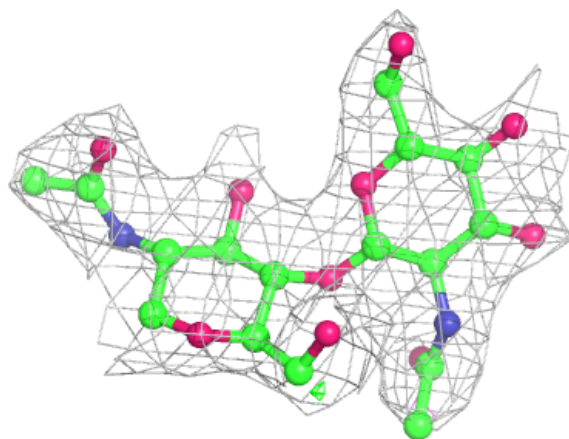
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	E	1	14/15	0.92	0.15	32,39,44,48	0
2	NAG	K	1	14/15	0.93	0.12	29,36,41,46	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around Chain F:**

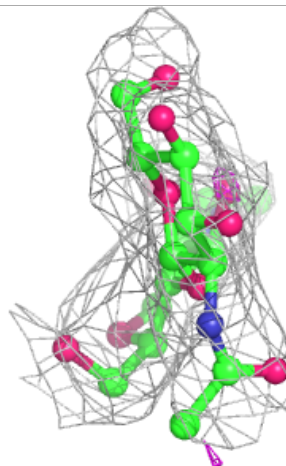
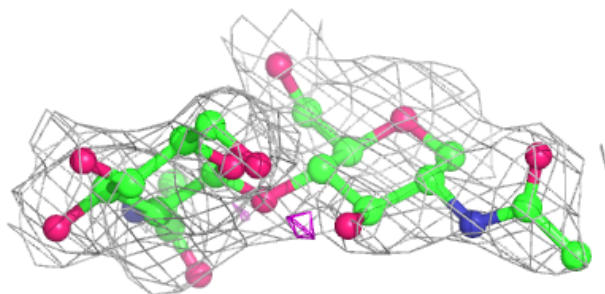
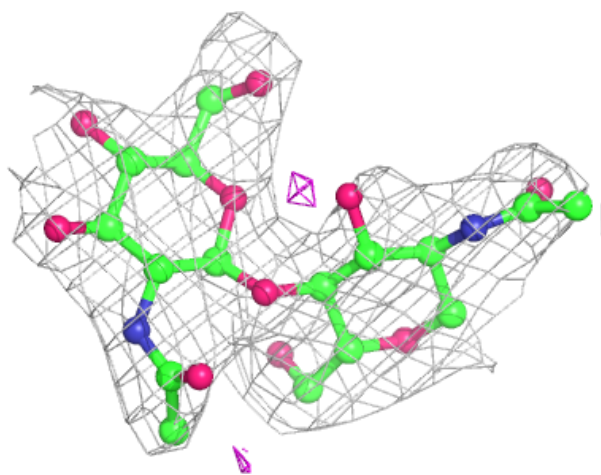
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





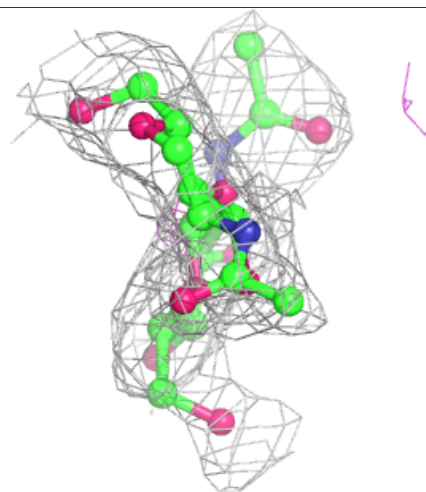
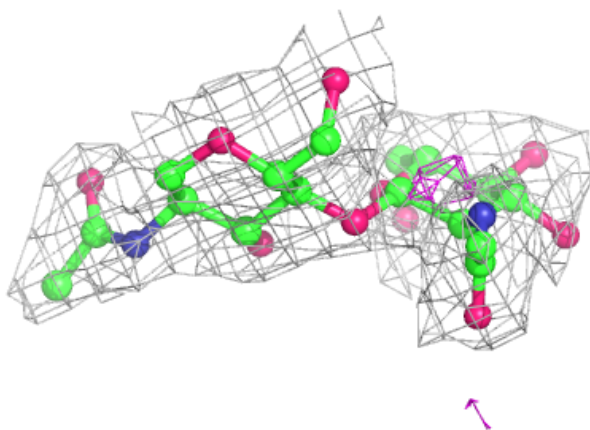
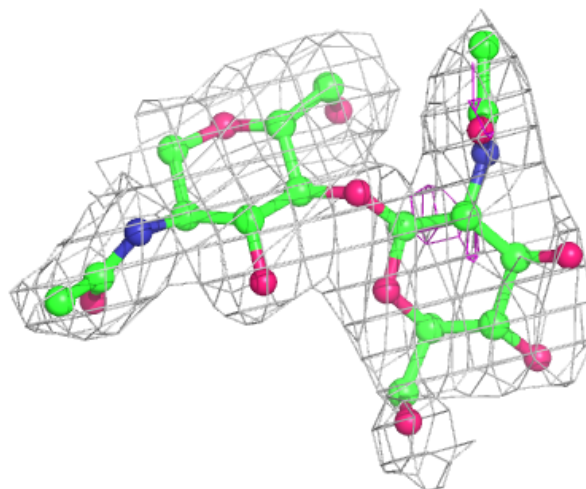
**Electron density around Chain H:**

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



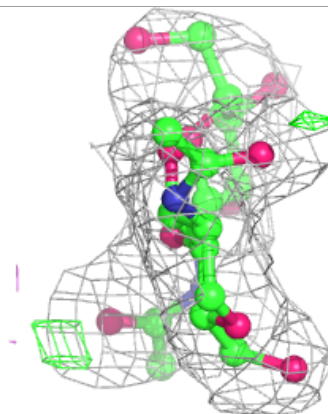
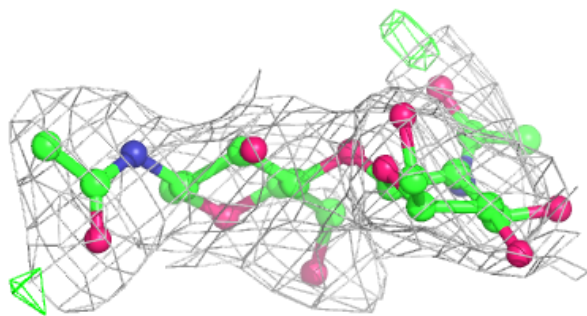
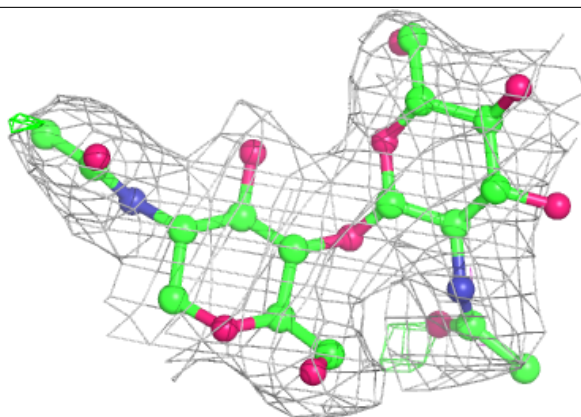
**Electron density around Chain I:**

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

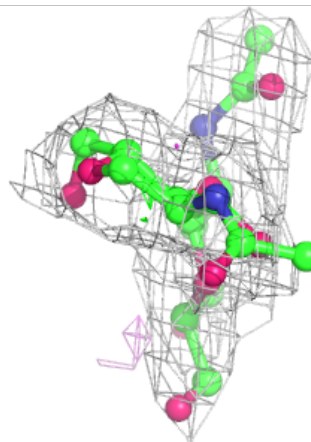
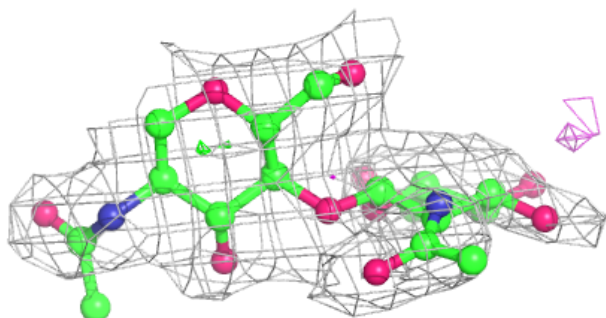
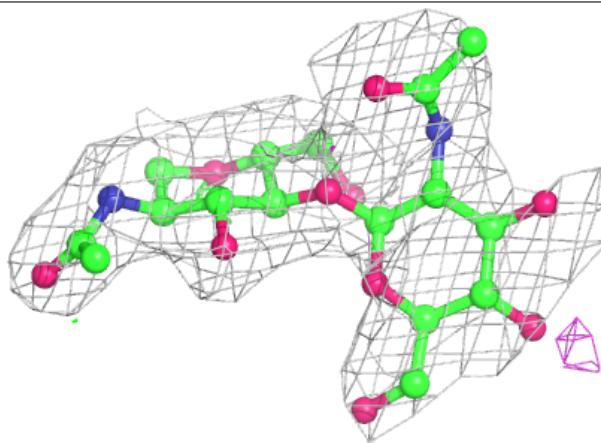


**Electron density around Chain K:**

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

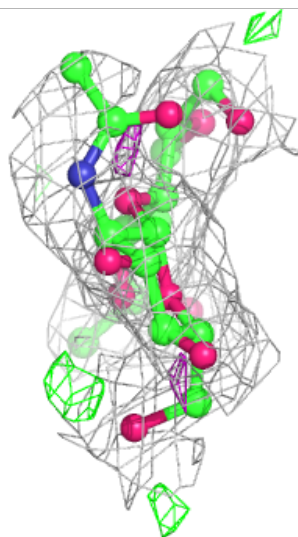
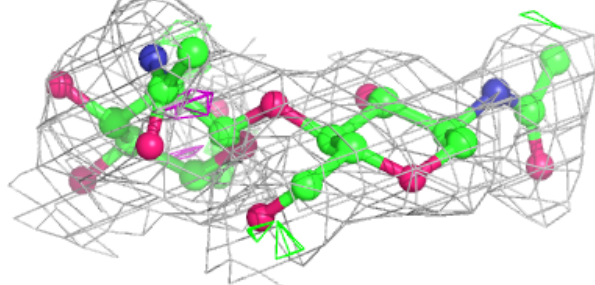
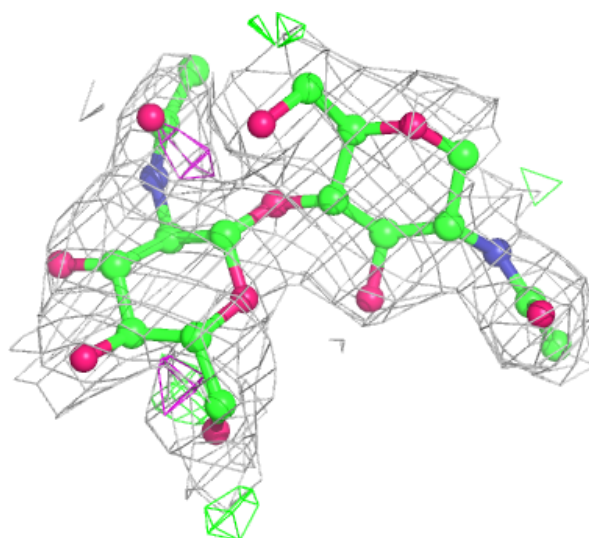
**Electron density around Chain L:**

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



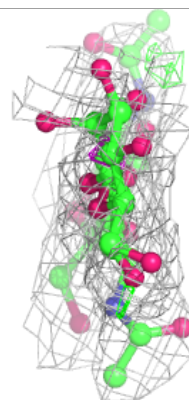
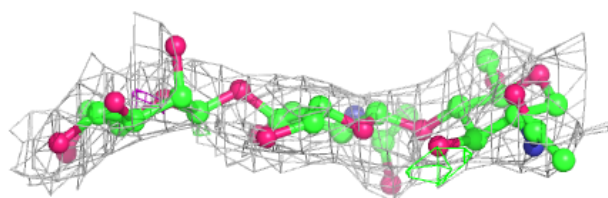
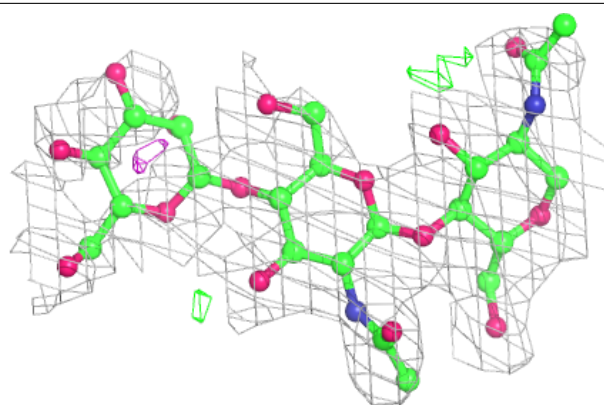
**Electron density around Chain M:**

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

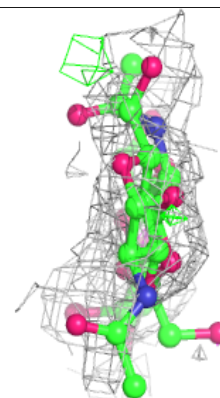
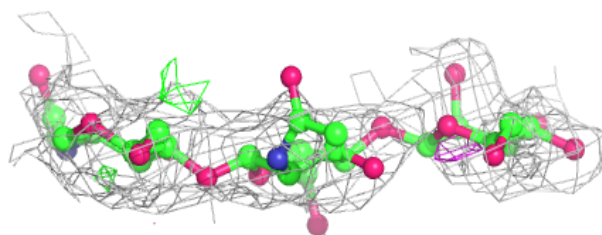
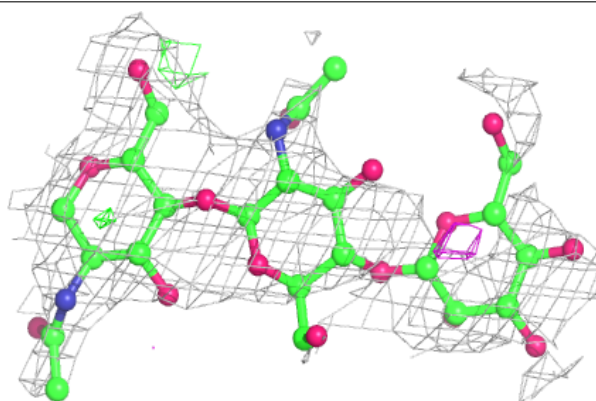


**Electron density around Chain G:**

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

**Electron density around Chain J:**

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



## 6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	D	767(A)	14/15	0.38	0.54	97,99,101,102	0
4	NAG	C	768(A)	14/15	0.62	0.34	100,101,101,101	0
4	NAG	B	767(A)	14/15	0.68	0.43	76,77,79,79	0
4	NAG	A	771(A)	14/15	0.71	0.28	47,50,53,53	3
4	NAG	D	773(A)	14/15	0.71	0.26	55,58,66,66	0
4	NAG	A	767(A)	14/15	0.74	0.37	84,86,87,88	0
4	NAG	C	767(A)	14/15	0.77	0.36	93,95,96,96	0
4	NAG	A	768(A)	14/15	0.79	0.22	82,83,85,85	0
4	NAG	C	771(A)	14/15	0.81	0.18	56,59,62,62	0
4	NAG	C	770(A)	14/15	0.81	0.23	55,58,60,61	0
4	NAG	B	772(A)	14/15	0.81	0.27	50,53,58,59	0
4	NAG	B	773(A)	14/15	0.89	0.14	38,41,42,43	0
4	NAG	A	772(A)	14/15	0.91	0.19	44,46,48,51	0
5	SO4	C	1502	5/5	0.93	0.15	44,46,49,49	0
6	BPR	B	801	15/15	0.93	0.13	14,17,20,21	0
4	NAG	B	771(A)	14/15	0.93	0.16	23,30,34,37	0
4	NAG	C	769(A)	14/15	0.94	0.13	33,35,38,39	0
6	BPR	D	801	15/15	0.94	0.13	22,25,27,28	0
6	BPR	A	801	15/15	0.95	0.14	26,28,30,30	0
6	BPR	C	801	15/15	0.96	0.12	16,21,22,22	0
5	SO4	D	1503	5/5	0.98	0.09	46,46,47,47	0
5	SO4	B	1501	5/5	0.99	0.10	37,38,40,40	0
5	SO4	A	1500	5/5	0.99	0.17	45,45,46,46	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.