



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 26, 2026 – 02:20 AM UTC

PDB ID : 4M4R / pdb_00004m4r
Title : EphA4 ectodomain complex with ephrin a5
Authors : Xu, K.; Tsvetkova-Robev, D.; Xu, Y.; Goldgur, Y.; Chan, Y.-P.; Himanen, J.P.; Nikolov, D.B.
Deposited on : 2013-08-07
Resolution : 3.13 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

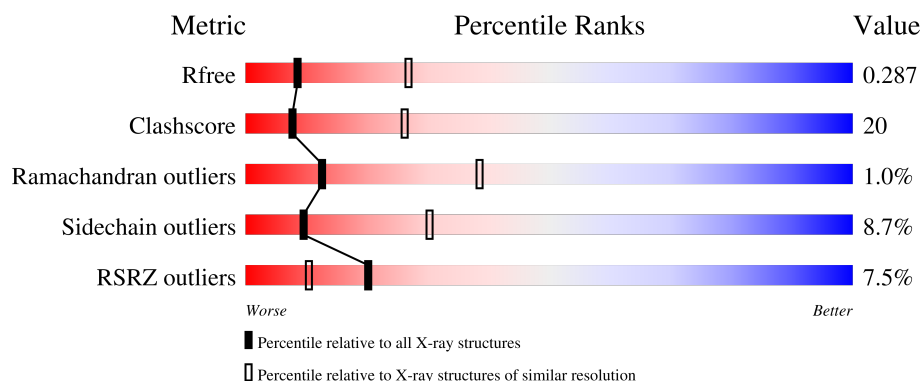
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.13 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}	180053	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	518	13% 70% 26% .
1	C	518	7% 68% 25% 6%
1	E	518	7% 70% 25% ..
1	G	518	10% 68% 28% .
2	B	141	% 60% 32% 6% .

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Mol	Chain	Length	Quality of chain
2	D	141	
2	F	141	
2	H	141	
3	I	2	
3	J	2	
3	K	2	
3	L	2	
3	M	2	
3	N	2	
3	O	2	
3	P	2	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	K	1	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20947 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 Ephrin type-A receptor 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	516	Total	C	N	O	S	0	0	0
			4014	2502	694	792	26			
1	C	516	Total	C	N	O	S	0	0	0
			4014	2502	694	792	26			
1	E	516	Total	C	N	O	S	0	0	0
			4014	2502	694	792	26			
1	G	516	Total	C	N	O	S	0	0	0
			4014	2502	694	792	26			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ALA	-	expression tag	UNP P54764
C	26	ALA	-	expression tag	UNP P54764
E	26	ALA	-	expression tag	UNP P54764
G	26	ALA	-	expression tag	UNP P54764

- Molecule 2 is a protein called Ephrin-A5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	141	Total	C	N	O	S	0	0	0
			1165	745	201	211	8			
2	D	140	Total	C	N	O	S	0	0	0
			1160	742	200	210	8			
2	F	138	Total	C	N	O	S	0	0	0
			1150	736	198	208	8			
2	H	138	Total	C	N	O	S	0	0	0
			1150	736	198	208	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	25	ALA	-	expression tag	UNP P52803
B	26	ALA	-	expression tag	UNP P52803
D	25	ALA	-	expression tag	UNP P52803
D	26	ALA	-	expression tag	UNP P52803
F	25	ALA	-	expression tag	UNP P52803
F	26	ALA	-	expression tag	UNP P52803
H	25	ALA	-	expression tag	UNP P52803
H	26	ALA	-	expression tag	UNP P52803

- Molecule 3 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
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

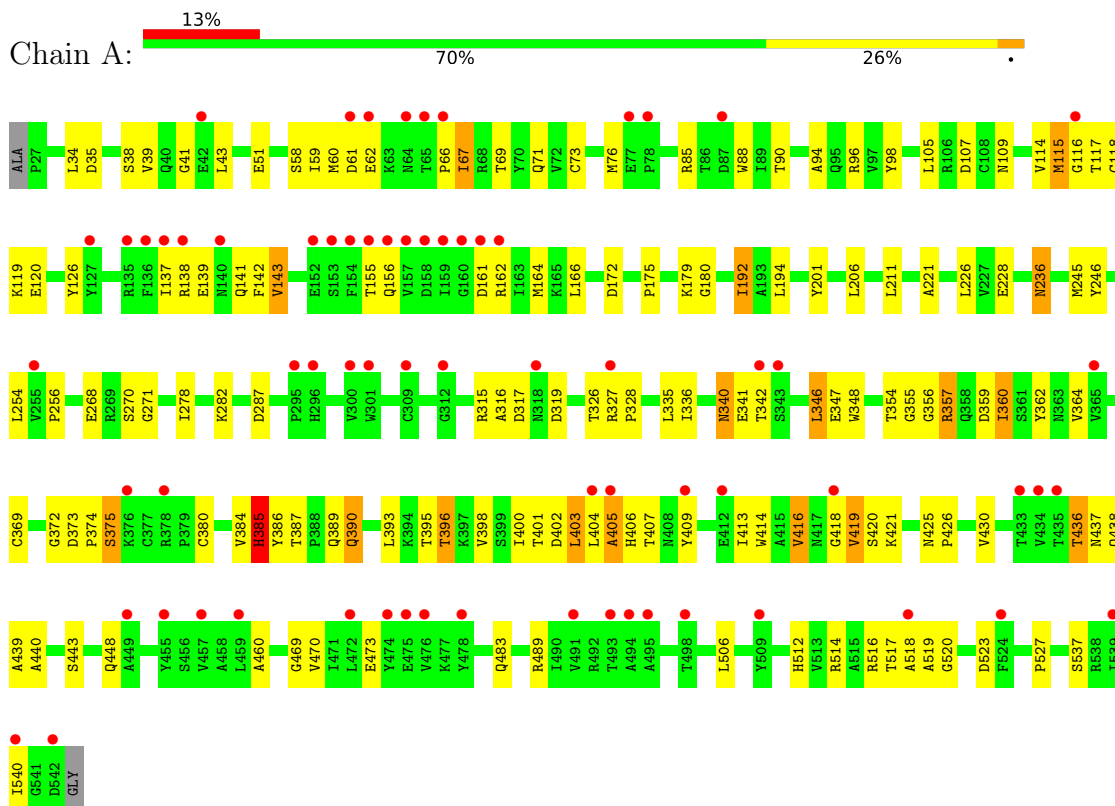


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		

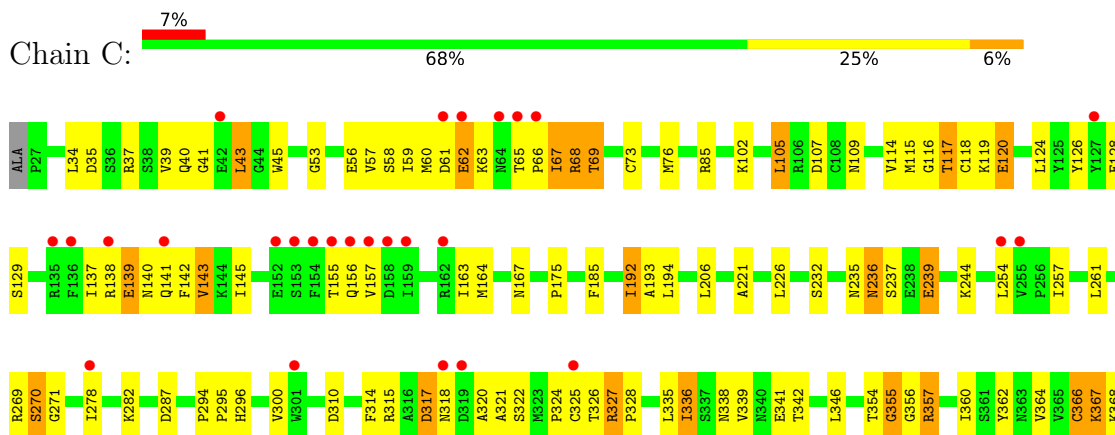
3 Residue-property plots [i](#)

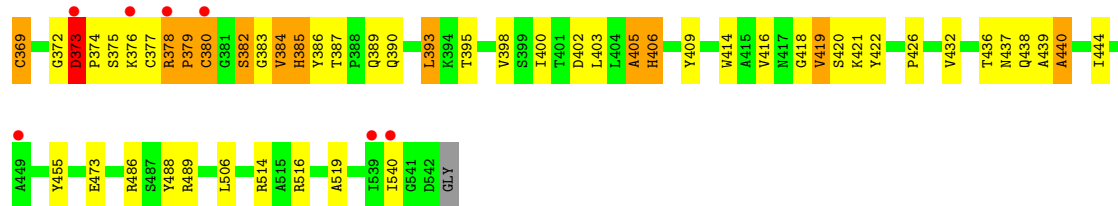
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ephrin type-A receptor 4

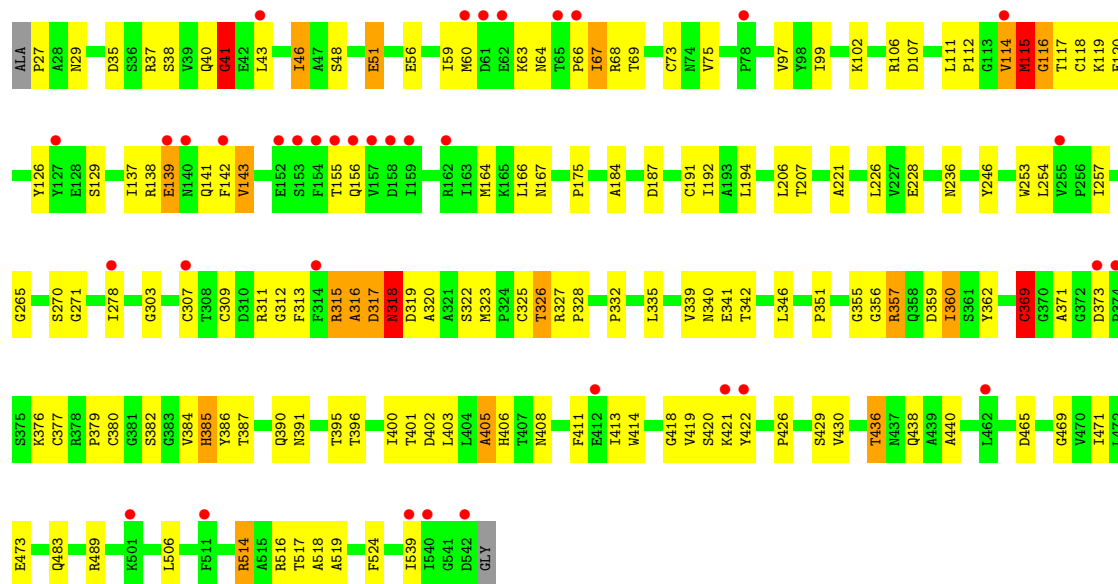


• Molecule 1: Ephrin type-A receptor 4

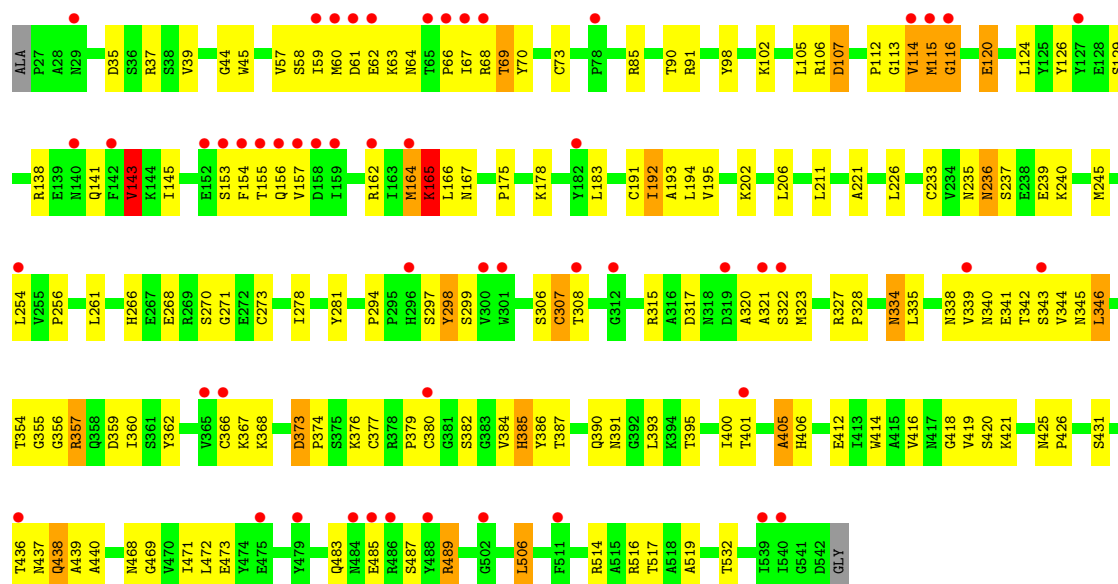




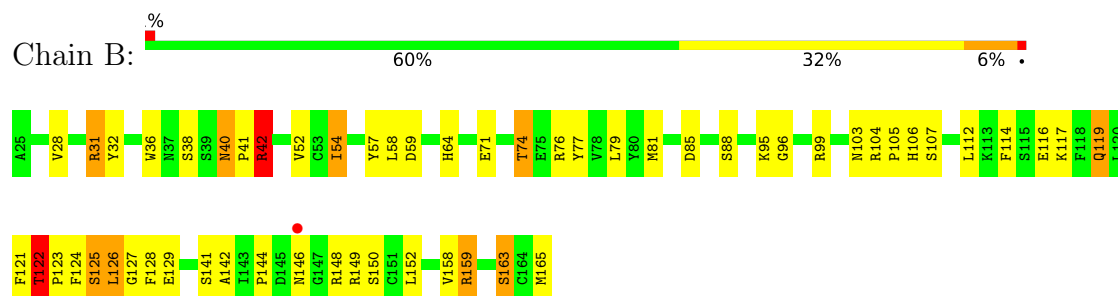
• Molecule 1: Ephrin type-A receptor 4



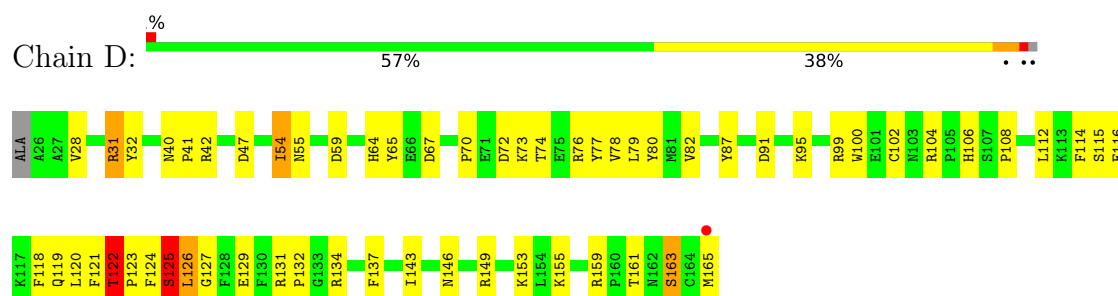
• Molecule 1: Ephrin type-A receptor 4



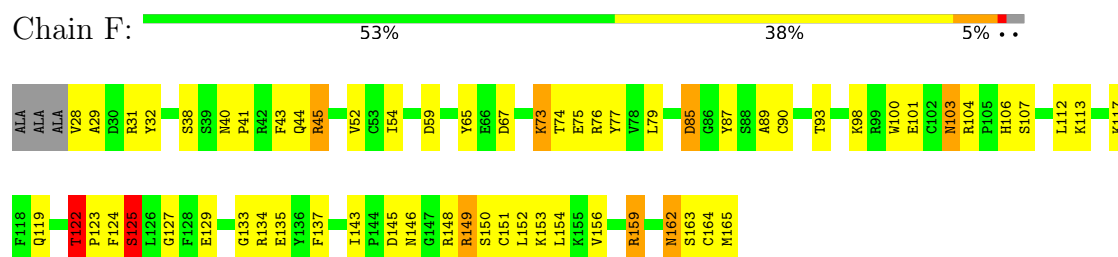
- Molecule 2: Ephrin-A5



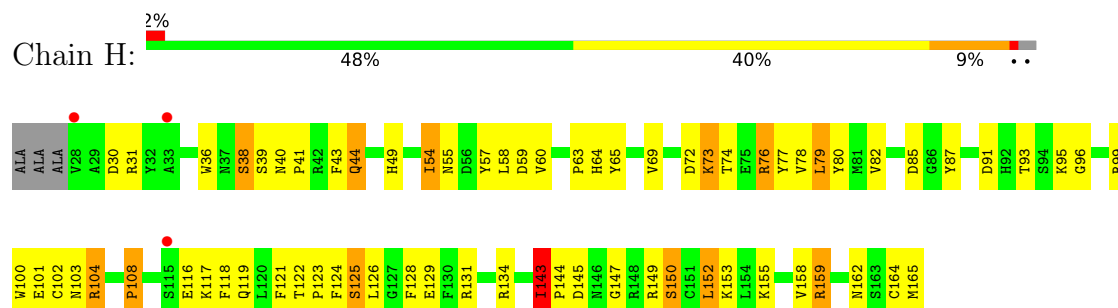
- Molecule 2: Ephrin-A5



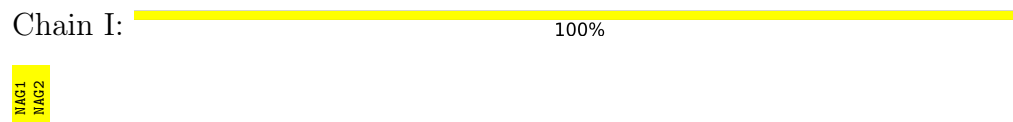
- Molecule 2: Ephrin-A5



- Molecule 2: Ephrin-A5



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



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

Chain J:  50% 50%

MAG1
MAG2

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

Chain K:  50% 50%

MAG1
MAG2

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

Chain L:  50% 50%

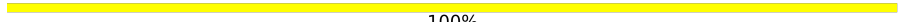
MAG1
MAG2

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

Chain M:  100%

MAG1
MAG2

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

Chain N:  100%

MAG1
MAG2

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

Chain O:  50% 50%

MAG1
MAG2

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

Chain P:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	207.54Å 46.69Å 262.31Å 90.00° 98.45° 90.00°	Depositor
Resolution (Å)	30.00 – 3.13 30.00 – 3.13	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.00-3.13) 99.2 (30.00-3.13)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.11Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.244 , 0.290 0.241 , 0.287	Depositor DCC
R_{free} test set	4633 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 100.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	20947	wwPDB-VP
Average B, all atoms (Å ²)	148.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.89	2/4100 (0.0%)	1.06	9/5579 (0.2%)
1	C	0.96	5/4100 (0.1%)	1.17	18/5579 (0.3%)
1	E	0.85	0/4100	1.06	16/5579 (0.3%)
1	G	0.75	0/4100	1.03	13/5579 (0.2%)
2	B	1.13	2/1204 (0.2%)	1.28	9/1631 (0.6%)
2	D	1.13	3/1199 (0.3%)	1.18	2/1624 (0.1%)
2	F	0.93	1/1189 (0.1%)	1.14	3/1610 (0.2%)
2	H	0.86	2/1189 (0.2%)	1.07	5/1610 (0.3%)
All	All	0.90	15/21181 (0.1%)	1.10	75/28791 (0.3%)

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	E	0	1
2	H	0	1
All	All	0	2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	125	SER	CA-C	-9.03	1.41	1.52
2	D	125	SER	CA-C	-7.03	1.43	1.52
1	A	192	ILE	C-O	-6.27	1.17	1.23
1	C	406	HIS	CG-CD2	6.00	1.42	1.35
2	D	118	PHE	C-O	5.97	1.30	1.23
1	C	105	LEU	C-O	-5.88	1.17	1.24
2	D	31	ARG	CA-C	5.72	1.59	1.52
1	C	327	ARG	CA-C	5.62	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	119	GLN	C-O	5.52	1.30	1.23
2	H	143	ILE	CA-C	5.44	1.58	1.52
2	F	125	SER	CA-C	-5.36	1.45	1.52
1	A	71	GLN	N-CA	-5.34	1.39	1.45
1	C	185	PHE	C-O	5.33	1.30	1.24
1	C	69	THR	C-O	5.27	1.30	1.23
2	H	125	SER	CA-C	-5.14	1.45	1.52

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	440	ALA	CA-C-N	13.74	133.63	120.03
1	C	440	ALA	C-N-CA	13.74	133.63	120.03
2	B	28	VAL	N-CA-C	-13.23	99.73	112.96
1	G	114	VAL	N-CA-C	11.72	124.84	113.71
1	E	440	ALA	CA-C-N	11.56	132.29	119.92
1	E	440	ALA	C-N-CA	11.56	132.29	119.92
1	C	405	ALA	N-CA-C	10.29	122.57	111.36
1	G	440	ALA	CA-C-N	10.23	131.57	120.11
1	G	440	ALA	C-N-CA	10.23	131.57	120.11
2	F	122	THR	CB-CA-C	-9.28	95.25	109.08
2	B	122	THR	CB-CA-C	-8.75	95.24	109.41
1	A	440	ALA	CA-C-N	8.49	129.61	120.11
1	A	440	ALA	C-N-CA	8.49	129.61	120.11
1	A	405	ALA	N-CA-C	7.98	120.76	111.02
2	D	122	THR	CB-CA-C	-7.90	97.70	108.68
1	E	326	THR	N-CA-C	7.87	120.87	109.14
1	G	405	ALA	N-CA-C	7.66	119.42	111.14
2	B	149	ARG	N-CA-C	-7.66	103.66	113.16
1	E	114	VAL	N-CA-C	7.57	120.47	113.20
1	C	385	HIS	N-CA-C	-7.29	97.52	109.40
1	E	67	ILE	CB-CA-C	-7.29	101.20	111.19
1	C	355	GLY	N-CA-C	7.28	123.71	114.25
1	C	40	GLN	N-CA-C	7.27	120.08	111.71
1	G	195	VAL	N-CA-C	7.26	117.39	110.42
2	H	143	ILE	CB-CA-C	7.05	124.19	111.36
1	C	69	THR	CA-C-N	-6.80	111.93	122.87
1	C	69	THR	C-N-CA	-6.80	111.93	122.87
2	B	40	ASN	CA-C-N	6.68	128.19	119.84
2	B	40	ASN	C-N-CA	6.68	128.19	119.84
2	H	159	ARG	CA-C-N	6.44	126.45	119.89
2	H	159	ARG	C-N-CA	6.44	126.45	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	42	ARG	N-CA-C	-6.32	105.43	113.01
2	D	55	ASN	N-CA-C	6.26	120.50	112.86
2	B	159	ARG	CA-C-N	6.26	126.27	119.89
2	B	159	ARG	C-N-CA	6.26	126.27	119.89
1	G	298	TYR	N-CA-C	6.26	119.70	109.06
1	C	163	ILE	CB-CA-C	-6.19	101.60	110.83
1	E	117	THR	N-CA-C	-6.14	104.86	112.72
2	F	149	ARG	N-CA-C	-6.07	105.70	113.23
1	E	118	CYS	N-CA-C	6.00	118.89	109.96
1	G	143	VAL	N-CA-C	5.96	116.46	108.11
1	C	117	THR	N-CA-C	5.93	121.02	113.55
2	H	73	LYS	N-CA-C	-5.92	105.14	112.90
1	E	421	LYS	N-CA-C	-5.80	105.47	112.54
1	E	99	ILE	CB-CA-C	-5.77	103.87	110.73
1	A	115	MET	N-CA-C	5.76	118.06	109.59
1	E	184	ALA	N-CA-C	5.72	118.09	109.23
1	C	378	ARG	CB-CA-C	5.69	117.39	108.63
2	B	163	SER	N-CA-C	-5.63	106.76	113.97
1	C	336	ILE	CB-CA-C	5.61	118.52	110.33
1	C	379	PRO	CA-C-N	-5.59	116.55	126.45
1	C	379	PRO	C-N-CA	-5.59	116.55	126.45
1	E	316	ALA	N-CA-C	5.55	122.62	110.80
1	C	327	ARG	CB-CA-C	5.53	117.63	109.22
1	C	385	HIS	CA-C-N	5.53	131.65	121.70
1	C	385	HIS	C-N-CA	5.53	131.65	121.70
1	G	421	LYS	N-CA-C	-5.51	105.81	112.54
1	G	44	GLY	N-CA-C	-5.51	100.12	113.18
1	C	53	GLY	N-CA-C	-5.50	100.14	113.18
1	E	318	ASN	N-CA-C	-5.41	102.31	110.70
1	A	425	ASN	CA-C-N	5.35	126.52	119.84
1	A	425	ASN	C-N-CA	5.35	126.52	119.84
2	F	137	PHE	N-CA-C	5.34	118.11	109.40
1	A	520	GLY	N-CA-C	5.27	117.55	110.43
1	A	385	HIS	CA-C-N	5.17	131.01	121.70
1	A	385	HIS	C-N-CA	5.17	131.01	121.70
1	E	115	MET	CA-CB-CG	5.14	124.39	114.10
1	E	41	GLY	N-CA-C	-5.13	101.03	113.18
1	E	115	MET	CG-SD-CE	5.11	112.15	100.90
2	H	30	ASP	N-CA-C	5.10	117.80	109.59
1	G	165	LYS	N-CA-C	-5.08	99.98	110.80
1	G	116	GLY	N-CA-C	-5.06	107.67	114.25
1	E	369	CYS	N-CA-C	5.04	117.38	108.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	425	ASN	CA-C-N	5.03	124.81	119.28
1	G	425	ASN	C-N-CA	5.03	124.81	119.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	116	GLY	Peptide
2	H	143	ILE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4014	0	3868	177	0
1	C	4014	0	3873	185	0
1	E	4014	0	3870	154	1
1	G	4014	0	3870	198	1
2	B	1165	0	1082	46	0
2	D	1160	0	1077	38	0
2	F	1150	0	1067	53	0
2	H	1150	0	1067	63	0
3	I	28	0	23	0	0
3	J	28	0	25	1	0
3	K	28	0	25	0	0
3	L	28	0	25	1	0
3	M	28	0	25	3	0
3	N	28	0	25	0	0
3	O	28	0	25	1	0
3	P	28	0	25	3	0
4	A	14	0	13	0	0
4	E	14	0	12	0	0
4	G	14	0	13	1	0
All	All	20947	0	20010	816	1

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 20.

All (816) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:HIS:CE1	1:A:438:GLN:HB3	1.53	1.40
1:C:118:CYS:CB	1:G:115:MET:HE3	1.53	1.35
1:C:372:GLY:C	1:C:374:PRO:HD3	1.54	1.31
1:A:406:HIS:HE1	1:A:438:GLN:CB	1.47	1.28
1:A:60:MET:HE1	1:A:66:PRO:CA	1.64	1.28
1:G:294:PRO:HG3	1:G:322:SER:O	1.31	1.24
1:C:117:THR:N	1:G:115:MET:SD	2.11	1.24
1:G:299:SER:N	1:G:307:CYS:SG	2.10	1.24
1:A:341:GLU:HA	1:A:437:ASN:CB	1.69	1.22
1:G:294:PRO:CG	1:G:322:SER:O	1.89	1.19
1:G:298:TYR:C	1:G:307:CYS:SG	2.25	1.19
1:A:60:MET:CE	1:A:66:PRO:HA	1.75	1.17
1:G:385:HIS:HA	1:G:386:TYR:HB2	1.26	1.16
1:A:114:VAL:O	1:E:115:MET:CB	1.93	1.16
1:G:294:PRO:HG3	1:G:322:SER:C	1.70	1.16
1:A:60:MET:HE1	1:A:66:PRO:CB	1.75	1.16
2:H:143:ILE:HG23	2:H:144:PRO:CD	1.76	1.15
1:G:298:TYR:HA	1:G:307:CYS:SG	1.88	1.13
1:A:341:GLU:CA	1:A:437:ASN:HB3	1.78	1.12
1:A:115:MET:CA	1:E:115:MET:HB2	1.78	1.11
1:C:57:VAL:HG13	1:C:59:ILE:CD1	1.81	1.11
1:C:118:CYS:HB3	1:G:115:MET:HE3	1.22	1.11
1:E:385:HIS:HA	1:E:386:TYR:HB2	1.32	1.10
1:A:115:MET:C	1:E:115:MET:SD	2.34	1.09
1:A:73:CYS:HB2	2:B:123:PRO:HG3	1.35	1.09
2:H:143:ILE:HG23	2:H:144:PRO:HD3	1.33	1.09
1:A:60:MET:HE1	1:A:66:PRO:HA	1.23	1.08
1:G:298:TYR:CA	1:G:307:CYS:SG	2.41	1.08
1:C:372:GLY:O	1:C:374:PRO:CD	2.03	1.07
1:A:116:GLY:N	1:E:115:MET:SD	2.27	1.07
1:C:73:CYS:HB2	2:D:123:PRO:HG3	1.33	1.07
1:A:335:LEU:CD1	1:A:346:LEU:HD21	1.84	1.06
2:B:74:THR:HG22	2:B:76:ARG:HH11	1.14	1.06
1:C:295:PRO:HG2	1:C:324:PRO:HB3	1.37	1.06
1:G:335:LEU:HD11	1:G:346:LEU:HD21	1.35	1.05
1:A:114:VAL:O	1:E:115:MET:CG	2.05	1.05
1:A:60:MET:HE1	1:A:66:PRO:HB3	1.38	1.04
1:G:294:PRO:HG3	1:G:322:SER:CA	1.89	1.03
1:A:342:THR:CG2	1:A:403:LEU:O	2.08	1.02
1:C:372:GLY:C	1:C:374:PRO:CD	2.32	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:THR:HG23	1:A:403:LEU:O	1.57	1.01
1:A:373:ASP:N	1:A:374:PRO:HD2	1.75	1.01
1:A:385:HIS:HA	1:A:386:TYR:HB2	1.41	1.01
1:A:115:MET:HA	1:E:115:MET:HB2	1.05	1.01
1:C:118:CYS:CB	1:G:115:MET:CE	2.37	1.01
1:A:335:LEU:HD11	1:A:346:LEU:HD21	1.42	1.00
1:A:341:GLU:HA	1:A:437:ASN:HB3	1.03	1.00
1:C:57:VAL:HG13	1:C:59:ILE:HD12	1.41	1.00
1:A:115:MET:HA	1:E:115:MET:CB	1.92	0.99
1:A:118:CYS:H	1:E:115:MET:HG2	1.27	0.99
1:G:281:TYR:OH	1:G:322:SER:HB2	1.62	0.99
1:C:372:GLY:O	1:C:374:PRO:HD2	1.59	0.97
1:A:406:HIS:CE1	1:A:469:GLY:HA2	1.99	0.96
1:G:405:ALA:O	1:G:436:THR:HB	1.63	0.96
1:C:39:VAL:CG1	1:C:43:LEU:HB2	1.94	0.96
1:C:118:CYS:HB3	1:G:115:MET:CE	1.94	0.96
1:C:118:CYS:H	1:G:115:MET:CE	1.79	0.95
1:G:338:ASN:HB3	1:G:345:ASN:HB2	1.49	0.94
2:H:64:HIS:H	3:P:1:NAG:H81	1.33	0.94
1:E:342:THR:HG21	1:E:403:LEU:O	1.69	0.93
1:A:116:GLY:H	1:E:115:MET:H	1.11	0.92
1:A:114:VAL:C	1:E:115:MET:HE2	1.94	0.92
1:E:342:THR:CG2	1:E:403:LEU:O	2.18	0.92
1:E:59:ILE:HG22	1:E:60:MET:N	1.85	0.92
1:G:335:LEU:CD1	1:G:346:LEU:HD21	1.99	0.91
2:B:122:THR:HG22	2:B:124:PHE:H	1.34	0.91
1:C:58:SER:O	1:C:59:ILE:HG13	1.69	0.90
2:H:143:ILE:CG2	2:H:144:PRO:HD2	2.02	0.90
1:A:406:HIS:CE1	1:A:438:GLN:CB	2.33	0.90
2:H:143:ILE:CG2	2:H:144:PRO:CD	2.49	0.89
1:A:341:GLU:HA	1:A:437:ASN:CG	1.98	0.88
1:E:405:ALA:O	1:E:436:THR:HB	1.72	0.88
1:C:118:CYS:CA	1:G:115:MET:HE3	2.04	0.88
1:C:118:CYS:HB2	1:G:115:MET:HE3	1.54	0.88
1:A:114:VAL:O	1:E:115:MET:HB3	1.74	0.87
2:D:122:THR:HG21	2:D:127:GLY:HA3	1.56	0.87
1:A:117:THR:OG1	1:E:115:MET:HE3	1.74	0.86
1:G:294:PRO:HG3	1:G:322:SER:HA	1.55	0.86
1:E:59:ILE:CG2	1:E:60:MET:N	2.36	0.86
1:C:39:VAL:HG11	1:C:43:LEU:HB2	1.55	0.85
1:C:155:THR:HG22	1:C:156:GLN:N	1.90	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:PRO:CG	1:C:324:PRO:HB3	2.05	0.85
1:C:57:VAL:HG13	1:C:59:ILE:HD11	1.55	0.85
1:C:118:CYS:N	1:G:115:MET:HE3	1.92	0.85
1:E:67:ILE:HG22	1:E:68:ARG:N	1.89	0.85
1:C:115:MET:HE2	1:G:113:GLY:O	1.77	0.85
1:A:406:HIS:CE1	1:A:469:GLY:CA	2.59	0.84
1:C:372:GLY:O	1:C:374:PRO:HD3	1.72	0.84
1:C:254:LEU:HD13	1:G:226:LEU:HD12	1.57	0.84
1:E:335:LEU:CD1	1:E:346:LEU:HD21	2.08	0.84
1:C:118:CYS:H	1:G:115:MET:HE3	1.40	0.83
1:A:114:VAL:O	1:E:115:MET:HB2	1.78	0.83
1:A:116:GLY:H	1:E:115:MET:N	1.76	0.83
1:E:155:THR:HG22	1:E:156:GLN:N	1.94	0.82
2:B:74:THR:HG22	2:B:76:ARG:NH1	1.95	0.82
1:C:385:HIS:HA	1:C:386:TYR:HB2	1.61	0.82
1:C:335:LEU:HD11	1:C:346:LEU:HD21	1.62	0.82
1:G:344:VAL:HB	1:G:400:ILE:HB	1.63	0.81
1:G:335:LEU:HD11	1:G:346:LEU:CD2	2.09	0.80
2:H:64:HIS:N	3:P:1:NAG:H81	1.95	0.80
1:A:60:MET:HE2	1:A:66:PRO:HA	1.64	0.80
1:A:60:MET:CE	1:A:66:PRO:CA	2.45	0.80
2:H:119:GLN:NE2	2:H:122:THR:HG22	1.97	0.80
1:G:155:THR:HG22	1:G:156:GLN:H	1.46	0.79
1:C:254:LEU:HD13	1:G:226:LEU:CD1	2.12	0.79
2:B:122:THR:HG21	2:B:127:GLY:HA3	1.65	0.78
2:F:122:THR:HG22	2:F:124:PHE:H	1.46	0.78
2:H:76:ARG:HG2	2:H:103:ASN:HA	1.65	0.78
1:A:116:GLY:N	1:E:115:MET:H	1.82	0.78
1:C:116:GLY:H	1:G:115:MET:H	1.31	0.78
1:A:406:HIS:HE1	1:A:438:GLN:HB2	1.45	0.77
1:C:57:VAL:CG1	1:C:59:ILE:HD11	2.14	0.77
1:E:342:THR:HG22	1:E:342:THR:O	1.84	0.77
1:C:57:VAL:CG1	1:C:59:ILE:CD1	2.62	0.77
2:B:148:ARG:HB3	2:B:150:SER:O	1.83	0.77
1:A:373:ASP:N	1:A:374:PRO:CD	2.48	0.76
1:C:37:ARG:NH1	1:C:62:GLU:OE2	2.17	0.76
1:G:155:THR:HG22	1:G:156:GLN:N	2.00	0.76
1:C:118:CYS:HB2	1:G:115:MET:CE	2.11	0.76
1:A:35:ASP:HB3	1:A:38:SER:HB3	1.67	0.76
1:G:298:TYR:O	1:G:308:THR:N	2.19	0.76
1:C:382:SER:OG	1:C:384:VAL:HG13	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:VAL:O	1:G:115:MET:SD	2.45	0.75
1:G:294:PRO:CG	1:G:322:SER:HA	2.16	0.75
1:A:117:THR:HG1	1:E:115:MET:HE3	1.50	0.74
1:C:116:GLY:C	1:G:115:MET:SD	2.70	0.74
1:C:294:PRO:HG2	1:C:315:ARG:HH11	1.52	0.74
1:E:155:THR:HG22	1:E:156:GLN:H	1.51	0.74
1:C:373:ASP:N	1:C:374:PRO:HD3	2.01	0.73
1:C:438:GLN:O	1:C:519:ALA:HB2	1.87	0.73
2:H:76:ARG:HH21	2:H:143:ILE:HG21	1.53	0.73
1:E:46:ILE:HD13	1:E:46:ILE:N	2.02	0.73
1:E:371:ALA:HB2	3:M:1:NAG:C6	2.18	0.73
1:G:385:HIS:CA	1:G:386:TYR:HB2	2.13	0.73
1:C:116:GLY:N	1:G:115:MET:SD	2.61	0.73
2:H:143:ILE:HG22	2:H:144:PRO:HD2	1.70	0.73
1:A:389:GLN:HB2	1:A:393:LEU:HD13	1.71	0.73
1:A:116:GLY:N	1:E:115:MET:CG	2.52	0.72
1:A:155:THR:HG22	1:A:156:GLN:N	2.04	0.72
1:A:270:SER:OG	1:A:271:GLY:N	2.21	0.72
1:C:270:SER:OG	1:C:271:GLY:N	2.22	0.72
1:A:60:MET:CE	1:A:66:PRO:HB3	2.17	0.72
1:A:438:GLN:HE21	1:A:518:ALA:HB3	1.54	0.72
1:G:379:PRO:O	1:G:380:CYS:SG	2.48	0.72
2:H:76:ARG:NH2	2:H:143:ILE:HG21	2.05	0.72
1:G:226:LEU:HD21	1:G:254:LEU:HD12	1.70	0.71
1:G:61:ASP:OD2	1:G:67:ILE:HD12	1.91	0.71
1:E:315:ARG:HD3	1:E:323:MET:O	1.91	0.71
2:B:42:ARG:HB3	2:B:42:ARG:NH1	2.06	0.71
1:A:85:ARG:HD3	1:A:137:ILE:HG12	1.73	0.70
2:B:99:ARG:NH2	2:B:116:GLU:OE1	2.23	0.70
1:G:294:PRO:CD	1:G:322:SER:HA	2.22	0.70
1:A:35:ASP:O	1:A:39:VAL:HG23	1.92	0.70
1:A:406:HIS:ND1	1:A:469:GLY:HA2	2.06	0.69
1:E:438:GLN:NE2	1:E:518:ALA:HB3	2.06	0.69
2:D:122:THR:HG22	2:D:124:PHE:H	1.58	0.69
2:H:87:TYR:CE1	2:H:153:LYS:HB3	2.28	0.69
1:E:473:GLU:OE1	1:E:516:ARG:NH1	2.24	0.69
1:A:114:VAL:C	1:E:115:MET:HB2	2.18	0.69
1:C:341:GLU:O	1:C:436:THR:CG2	2.41	0.69
1:A:372:GLY:C	1:A:374:PRO:HD2	2.17	0.69
1:G:59:ILE:HG22	1:G:60:MET:N	2.08	0.69
1:G:298:TYR:C	1:G:307:CYS:CB	2.65	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:341:GLU:O	1:C:436:THR:HG23	1.93	0.68
1:C:155:THR:CG2	1:C:156:GLN:N	2.56	0.68
1:C:335:LEU:HD21	1:C:432:VAL:HG12	1.75	0.68
1:A:342:THR:HG22	1:A:342:THR:O	1.94	0.67
1:C:115:MET:CE	1:G:114:VAL:HA	2.23	0.67
1:C:328:PRO:HB3	1:C:420:SER:CB	2.24	0.67
1:C:354:THR:C	1:C:356:GLY:HA2	2.20	0.67
1:A:405:ALA:O	1:A:436:THR:HB	1.94	0.67
2:B:121:PHE:HA	2:B:129:GLU:OE2	1.95	0.67
1:C:60:MET:HE1	1:C:66:PRO:HB3	1.75	0.67
1:C:58:SER:C	1:C:59:ILE:HG13	2.20	0.67
2:F:41:PRO:O	2:F:44:GLN:HB2	1.95	0.67
1:A:439:ALA:HA	1:A:519:ALA:CB	2.25	0.67
1:E:438:GLN:O	1:E:519:ALA:HB2	1.95	0.67
2:F:98:LYS:HZ1	2:F:101:GLU:CD	2.03	0.67
1:A:114:VAL:O	1:E:115:MET:HG2	1.95	0.66
1:A:385:HIS:O	1:A:401:THR:N	2.26	0.66
1:E:73:CYS:HB2	2:F:123:PRO:HG3	1.75	0.66
1:E:46:ILE:N	1:E:46:ILE:CD1	2.57	0.66
1:G:107:ASP:OD1	1:G:153:SER:OG	2.11	0.66
2:B:42:ARG:HB3	2:B:42:ARG:HH11	1.60	0.66
1:A:39:VAL:HG12	1:A:41:GLY:O	1.96	0.66
1:C:68:ARG:HH22	2:D:115:SER:HB2	1.61	0.66
1:A:59:ILE:CG2	2:B:124:PHE:CE2	2.78	0.66
1:E:400:ILE:HD13	1:E:411:PHE:CE2	2.31	0.65
2:H:76:ARG:HB3	2:H:143:ILE:HG12	1.78	0.65
1:G:299:SER:HA	1:G:307:CYS:HA	1.78	0.65
1:C:114:VAL:O	1:G:115:MET:HE1	1.95	0.65
1:A:386:TYR:CD1	1:A:390:GLN:HG3	2.31	0.65
1:C:118:CYS:N	1:G:115:MET:SD	2.69	0.65
2:F:28:VAL:HG12	2:F:29:ALA:N	2.09	0.65
1:G:69:THR:CG2	1:G:70:TYR:N	2.59	0.65
1:C:66:PRO:C	1:C:67:ILE:HG22	2.21	0.65
1:E:342:THR:HG23	1:E:403:LEU:O	1.95	0.65
1:G:73:CYS:HB2	2:H:123:PRO:HG3	1.78	0.65
1:E:155:THR:CG2	1:E:156:GLN:H	2.10	0.65
1:G:164:MET:O	1:G:165:LYS:HB2	1.96	0.65
1:C:317:ASP:HB2	1:C:421:LYS:NZ	2.12	0.65
1:E:155:THR:CG2	1:E:156:GLN:N	2.60	0.65
1:G:37:ARG:HD3	1:G:67:ILE:HD13	1.80	0.64
1:C:473:GLU:OE1	1:C:516:ARG:NH1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:338:ASN:CB	1:G:345:ASN:HB2	2.25	0.64
1:A:406:HIS:CG	1:A:469:GLY:HA2	2.31	0.64
2:B:74:THR:O	2:B:76:ARG:NH1	2.31	0.64
1:A:117:THR:HG1	1:E:115:MET:CE	2.11	0.64
1:E:67:ILE:CG2	1:E:68:ARG:N	2.60	0.64
1:E:385:HIS:CA	1:E:386:TYR:HB2	2.17	0.64
1:G:294:PRO:HG2	1:G:322:SER:O	1.90	0.64
1:A:354:THR:HG23	1:A:356:GLY:HA3	1.79	0.64
2:H:55:ASN:N	2:H:118:PHE:O	2.25	0.64
1:C:115:MET:CG	1:G:115:MET:O	2.46	0.63
1:C:317:ASP:HB2	1:C:421:LYS:HZ3	1.62	0.63
1:G:69:THR:HG22	1:G:70:TYR:N	2.12	0.63
1:G:164:MET:O	1:G:165:LYS:CB	2.47	0.63
1:C:61:ASP:CG	1:C:67:ILE:HG21	2.23	0.63
1:A:438:GLN:NE2	1:A:518:ALA:HB3	2.13	0.63
1:G:162:ARG:NH1	2:H:126:LEU:HB3	2.14	0.63
1:C:34:LEU:HD12	1:C:35:ASP:N	2.14	0.63
2:F:32:TYR:CD2	2:F:52:VAL:HG12	2.33	0.63
1:G:335:LEU:CD1	1:G:346:LEU:CD2	2.73	0.63
1:C:43:LEU:HD11	1:C:45:TRP:HE1	1.63	0.62
2:H:119:GLN:HE21	2:H:122:THR:HG22	1.64	0.62
1:A:341:GLU:C	1:A:437:ASN:HB3	2.24	0.62
1:C:115:MET:HA	1:G:115:MET:O	1.99	0.62
2:H:104:ARG:NH1	2:H:108:PRO:HD3	2.14	0.62
1:A:59:ILE:HG21	2:B:124:PHE:CE2	2.34	0.62
1:G:67:ILE:HG22	1:G:68:ARG:N	2.14	0.62
1:C:294:PRO:HB3	1:C:322:SER:O	2.00	0.62
1:G:340:ASN:CG	1:G:341:GLU:H	2.07	0.62
2:B:36:TRP:HB3	2:B:77:TYR:OH	2.01	0.61
1:G:69:THR:HG23	1:G:194:LEU:O	2.01	0.61
1:C:68:ARG:NH2	2:D:115:SER:HB2	2.15	0.61
2:F:103:ASN:HB3	2:F:143:ILE:HD12	1.82	0.61
2:H:124:PHE:CE2	2:H:126:LEU:HB2	2.34	0.61
1:E:401:THR:HG22	1:E:402:ASP:N	2.15	0.61
2:B:76:ARG:NH2	2:B:144:PRO:HD3	2.15	0.61
1:C:39:VAL:HB	1:C:43:LEU:HD22	1.82	0.61
1:C:295:PRO:O	1:C:325:CYS:N	2.33	0.61
1:A:117:THR:OG1	1:E:115:MET:CE	2.46	0.61
1:A:43:LEU:O	1:A:43:LEU:HD12	2.01	0.61
2:H:121:PHE:HA	2:H:129:GLU:OE2	2.01	0.61
1:A:335:LEU:HD12	1:A:346:LEU:HD21	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:GLU:C	1:C:142:PHE:CE2	2.79	0.61
1:C:65:THR:O	1:C:67:ILE:HG22	2.00	0.60
2:F:32:TYR:HD2	2:F:52:VAL:HG12	1.66	0.60
1:E:40:GLN:C	1:E:41:GLY:O	2.44	0.60
1:E:371:ALA:HB2	3:M:1:NAG:H61	1.81	0.60
2:H:78:VAL:HG12	2:H:80:TYR:CE1	2.36	0.60
1:A:69:THR:HB	1:A:194:LEU:O	2.01	0.60
1:A:335:LEU:HD22	1:A:430:VAL:HG13	1.82	0.60
2:B:95:LYS:HE2	2:B:95:LYS:HA	1.83	0.60
1:E:175:PRO:HB3	1:E:221:ALA:HB1	1.84	0.60
1:E:307:CYS:HB2	1:E:315:ARG:HH22	1.66	0.60
1:A:61:ASP:OD2	1:A:67:ILE:HD13	2.01	0.60
1:C:39:VAL:HG21	1:C:43:LEU:HD13	1.83	0.60
1:A:403:LEU:HB2	1:A:409:TYR:OH	2.01	0.60
1:C:237:SER:HB2	1:C:261:LEU:O	2.01	0.60
1:C:314:PHE:HB2	1:C:419:VAL:HG11	1.84	0.60
1:C:39:VAL:HG11	1:C:43:LEU:CB	2.28	0.59
1:E:332:PRO:HG3	1:E:413:ILE:HG22	1.84	0.59
1:C:373:ASP:C	1:C:375:SER:H	2.10	0.59
1:C:155:THR:HG22	1:C:156:GLN:H	1.64	0.59
1:C:389:GLN:HB2	1:C:393:LEU:HD13	1.85	0.59
2:D:65:TYR:CD2	2:D:74:THR:HG22	2.36	0.59
1:G:328:PRO:HB3	1:G:420:SER:HB3	1.84	0.59
1:G:406:HIS:ND1	1:G:469:GLY:HA2	2.17	0.59
1:A:340:ASN:OD1	1:A:341:GLU:N	2.35	0.59
1:C:114:VAL:O	1:G:115:MET:CE	2.51	0.59
2:D:129:GLU:HB3	2:D:131:ARG:HH12	1.67	0.59
1:G:270:SER:OG	1:G:271:GLY:N	2.35	0.59
1:C:226:LEU:HD21	1:C:254:LEU:HD12	1.84	0.59
2:F:73:LYS:NZ	2:F:73:LYS:HA	2.17	0.59
1:A:386:TYR:H	1:A:400:ILE:HA	1.67	0.59
1:G:162:ARG:NH2	2:H:128:PHE:CZ	2.71	0.59
1:C:69:THR:HB	1:C:194:LEU:O	2.03	0.58
1:C:115:MET:HE3	1:G:114:VAL:HA	1.85	0.58
1:C:328:PRO:HB3	1:C:420:SER:HB3	1.84	0.58
1:E:382:SER:OG	1:E:384:VAL:HG13	2.03	0.58
1:A:406:HIS:CE1	1:A:469:GLY:HA3	2.39	0.58
1:G:386:TYR:CE1	1:G:390:GLN:HG3	2.38	0.58
1:G:390:GLN:O	1:G:391:ASN:ND2	2.36	0.58
1:C:342:THR:HB	1:C:403:LEU:O	2.04	0.58
1:G:61:ASP:O	1:G:63:LYS:N	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:117:LYS:HG2	2:H:119:GLN:HB3	1.86	0.58
1:E:63:LYS:O	1:E:64:ASN:HB2	2.03	0.58
1:A:109:ASN:OD1	1:E:116:GLY:O	2.22	0.58
1:A:357:ARG:NH1	1:A:418:GLY:H	2.02	0.58
1:E:357:ARG:HG3	1:E:359:ASP:OD1	2.04	0.58
1:A:384:VAL:HG12	1:A:402:ASP:O	2.04	0.58
1:G:373:ASP:N	1:G:374:PRO:HD2	2.19	0.58
1:C:294:PRO:HG2	1:C:315:ARG:NH1	2.17	0.57
1:C:115:MET:HG3	1:G:115:MET:O	2.04	0.57
2:D:64:HIS:H	3:L:1:NAG:H81	1.70	0.57
1:C:155:THR:CG2	1:C:156:GLN:H	2.17	0.57
1:G:245:MET:SD	1:G:256:PRO:HB3	2.44	0.57
1:C:105:LEU:HD21	1:C:120:GLU:HG3	1.85	0.57
1:G:112:PRO:O	1:G:114:VAL:HG13	2.04	0.57
1:G:405:ALA:O	1:G:436:THR:CB	2.46	0.57
1:A:175:PRO:HB3	1:A:221:ALA:HB1	1.87	0.57
2:F:152:LEU:HD12	2:F:152:LEU:H	1.69	0.57
1:A:115:MET:O	1:E:115:MET:SD	2.63	0.57
2:D:32:TYR:N	2:D:32:TYR:CD2	2.71	0.57
1:G:299:SER:CA	1:G:307:CYS:HA	2.35	0.57
1:C:314:PHE:N	1:C:326:THR:O	2.38	0.57
1:E:316:ALA:O	1:E:319:ASP:HB2	2.05	0.57
1:G:386:TYR:CD1	1:G:390:GLN:HG3	2.39	0.57
1:A:155:THR:CG2	1:A:156:GLN:N	2.68	0.57
1:C:403:LEU:HD13	1:C:409:TYR:CE1	2.40	0.57
2:F:65:TYR:CD2	2:F:74:THR:HG22	2.40	0.57
1:C:155:THR:HG22	1:C:157:VAL:H	1.70	0.56
1:E:270:SER:OG	1:E:271:GLY:N	2.36	0.56
1:E:328:PRO:HB3	1:E:420:SER:CB	2.35	0.56
1:G:193:ALA:HB2	2:H:123:PRO:HB2	1.87	0.56
1:E:317:ASP:OD1	1:E:422:TYR:OH	2.24	0.56
1:G:406:HIS:CG	1:G:469:GLY:HA2	2.40	0.56
2:H:99:ARG:NE	2:H:128:PHE:CE2	2.73	0.56
2:B:36:TRP:O	2:B:152:LEU:HD13	2.05	0.56
1:G:192:ILE:HG12	1:G:193:ALA:N	2.19	0.56
1:A:414:TRP:CH2	1:A:426:PRO:HA	2.41	0.56
1:C:61:ASP:OD1	1:C:67:ILE:HG21	2.05	0.56
1:C:68:ARG:HH22	2:D:115:SER:CB	2.19	0.56
2:F:162:ASN:OD1	2:F:162:ASN:N	2.37	0.56
1:C:386:TYR:HB3	1:C:390:GLN:HB2	1.86	0.56
2:H:77:TYR:H	2:H:102:CYS:HB2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:PRO:HB3	1:C:420:SER:HB2	1.88	0.56
1:G:155:THR:CG2	1:G:156:GLN:N	2.69	0.55
1:A:115:MET:N	1:E:115:MET:HB2	2.20	0.55
1:A:116:GLY:N	1:E:115:MET:CB	2.68	0.55
2:D:74:THR:OG1	2:D:76:ARG:NH1	2.38	0.55
2:H:87:TYR:HE1	2:H:153:LYS:HB3	1.68	0.55
1:C:244:LYS:HB2	1:C:257:ILE:HG13	1.88	0.55
1:E:59:ILE:CG2	1:E:60:MET:H	2.17	0.55
1:E:69:THR:HB	1:E:194:LEU:O	2.06	0.55
1:E:385:HIS:O	1:E:401:THR:HB	2.07	0.55
2:F:103:ASN:HB3	2:F:143:ILE:CD1	2.36	0.55
1:G:59:ILE:CG2	1:G:60:MET:N	2.68	0.55
1:G:129:SER:HB2	1:G:138:ARG:NH2	2.20	0.55
1:G:406:HIS:HB2	1:G:468:ASN:C	2.32	0.55
1:C:60:MET:CE	1:C:66:PRO:HB3	2.35	0.55
1:C:294:PRO:CG	1:C:315:ARG:HH11	2.19	0.55
2:F:104:ARG:HB2	2:F:112:LEU:HD22	1.88	0.55
1:A:354:THR:C	1:A:356:GLY:HA2	2.32	0.55
1:C:60:MET:HE1	1:C:66:PRO:CB	2.37	0.55
1:A:328:PRO:HB3	1:A:420:SER:CB	2.36	0.55
2:F:28:VAL:CG1	2:F:29:ALA:N	2.70	0.55
1:G:382:SER:OG	1:G:384:VAL:HG13	2.07	0.55
1:A:61:ASP:CG	1:A:67:ILE:HD13	2.32	0.55
1:A:406:HIS:CD2	1:A:469:GLY:HA2	2.41	0.55
1:C:355:GLY:N	1:C:356:GLY:HA2	2.22	0.55
1:C:382:SER:OG	1:C:383:GLY:N	2.39	0.55
1:E:355:GLY:N	1:E:356:GLY:HA2	2.22	0.55
1:C:421:LYS:HE3	1:C:422:TYR:CZ	2.42	0.55
1:E:37:ARG:CD	1:E:67:ILE:HD11	2.37	0.55
1:G:124:LEU:HG	1:G:145:ILE:HD12	1.89	0.55
1:A:512:HIS:HE1	1:A:527:PRO:HG3	1.72	0.54
1:G:37:ARG:HD3	1:G:67:ILE:CD1	2.36	0.54
1:C:115:MET:HE2	1:G:114:VAL:HA	1.88	0.54
2:F:65:TYR:CE2	2:F:74:THR:HB	2.42	0.54
1:A:114:VAL:C	1:E:115:MET:CE	2.76	0.54
1:E:342:THR:CG2	1:E:342:THR:O	2.55	0.54
1:C:105:LEU:CD2	1:C:120:GLU:HG3	2.37	0.54
1:A:161:ASP:O	1:A:162:ARG:CB	2.54	0.54
2:B:64:HIS:O	3:J:1:NAG:H83	2.08	0.54
1:G:385:HIS:HA	1:G:386:TYR:CB	2.15	0.54
1:A:406:HIS:NE2	1:A:469:GLY:HA2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:PRO:HG2	1:C:324:PRO:CB	2.25	0.54
1:E:379:PRO:O	1:E:380:CYS:SG	2.66	0.54
1:E:335:LEU:HD13	1:E:346:LEU:HD21	1.89	0.54
1:G:406:HIS:O	3:O:1:NAG:H81	2.08	0.54
2:B:57:TYR:CE1	2:B:117:LYS:HB2	2.43	0.54
1:C:296:HIS:HB2	1:C:325:CYS:HB2	1.90	0.54
2:F:164:CYS:O	2:F:165:MET:CG	2.56	0.54
2:H:82:VAL:HG12	2:H:95:LYS:O	2.08	0.54
2:B:31:ARG:NH1	2:B:59:ASP:OD2	2.40	0.53
1:C:390:GLN:O	1:C:390:GLN:HG2	2.08	0.53
2:D:126:LEU:N	2:D:126:LEU:HD23	2.22	0.53
1:E:386:TYR:CD1	1:E:390:GLN:HG3	2.43	0.53
1:A:448:GLN:HG2	1:A:460:ALA:O	2.09	0.53
2:B:99:ARG:HH22	2:B:116:GLU:CD	2.17	0.53
1:E:106:ARG:HB3	1:E:191:CYS:HB3	1.90	0.53
1:E:129:SER:HB2	1:E:138:ARG:NH2	2.22	0.53
1:E:112:PRO:O	1:E:114:VAL:HG13	2.08	0.53
1:C:114:VAL:HB	1:G:115:MET:HE1	1.91	0.53
1:E:328:PRO:HB3	1:E:420:SER:HB3	1.89	0.53
1:G:63:LYS:O	1:G:64:ASN:HB2	2.08	0.53
1:A:437:ASN:OD1	1:A:438:GLN:N	2.40	0.53
2:F:52:VAL:O	2:F:159:ARG:HG2	2.08	0.53
1:G:328:PRO:HB3	1:G:420:SER:CB	2.38	0.53
1:C:73:CYS:HB2	2:D:123:PRO:CG	2.23	0.53
1:A:126:TYR:CE1	1:A:143:VAL:HG22	2.44	0.53
1:C:379:PRO:O	1:C:380:CYS:CB	2.56	0.53
1:G:164:MET:O	1:G:165:LYS:HG3	2.08	0.53
1:G:175:PRO:HB3	1:G:221:ALA:HB1	1.89	0.53
1:G:386:TYR:H	1:G:400:ILE:HA	1.74	0.53
2:H:38:SER:C	2:H:40:ASN:H	2.17	0.53
1:E:164:MET:HE3	1:E:166:LEU:HB2	1.90	0.53
2:H:99:ARG:NH2	2:H:116:GLU:OE1	2.42	0.53
1:C:486:ARG:HD3	1:C:488:TYR:CZ	2.45	0.52
2:H:40:ASN:O	2:H:44:GLN:HG3	2.09	0.52
1:A:138:ARG:HD3	1:A:141:GLN:HB2	1.90	0.52
1:E:414:TRP:CH2	1:E:426:PRO:HA	2.44	0.52
2:F:38:SER:C	2:F:40:ASN:H	2.18	0.52
1:A:114:VAL:O	1:E:115:MET:SD	2.67	0.52
2:D:65:TYR:CE2	2:D:74:THR:HA	2.45	0.52
1:G:414:TRP:CH2	1:G:426:PRO:HA	2.44	0.52
1:A:228:GLU:HB2	1:A:246:TYR:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:ARG:HG2	1:C:67:ILE:HD12	1.92	0.52
1:C:357:ARG:HG3	1:C:357:ARG:HH11	1.73	0.52
1:C:439:ALA:C	1:C:519:ALA:HB3	2.33	0.52
2:F:43:PHE:CD1	2:F:152:LEU:HB3	2.44	0.52
1:G:439:ALA:C	1:G:519:ALA:HB3	2.35	0.52
2:D:100:TRP:CG	2:D:114:PHE:HB2	2.44	0.52
2:D:159:ARG:HD2	2:D:163:SER:HB2	1.91	0.52
2:F:148:ARG:HD2	2:F:150:SER:OG	2.10	0.52
1:G:357:ARG:HH12	1:G:418:GLY:CA	2.23	0.52
2:H:65:TYR:HE2	2:H:74:THR:HG1	1.58	0.52
2:H:74:THR:HG23	2:H:76:ARG:HH11	1.74	0.52
1:G:155:THR:CG2	1:G:156:GLN:H	2.17	0.52
1:A:59:ILE:HG22	1:A:60:MET:N	2.25	0.51
1:A:164:MET:HE3	1:A:166:LEU:HB2	1.92	0.51
1:E:326:THR:HG21	1:E:357:ARG:HE	1.75	0.51
1:G:45:TRP:HB3	1:G:85:ARG:O	2.10	0.51
1:G:298:TYR:O	1:G:307:CYS:C	2.53	0.51
1:G:57:VAL:HG22	1:G:58:SER:H	1.74	0.51
2:B:99:ARG:NH1	2:B:114:PHE:CZ	2.79	0.51
2:B:126:LEU:N	2:B:126:LEU:HD23	2.26	0.51
1:G:406:HIS:HB2	1:G:469:GLY:N	2.24	0.51
1:C:39:VAL:HG12	1:C:43:LEU:HB2	1.90	0.51
1:C:43:LEU:HD11	1:C:45:TRP:NE1	2.26	0.51
1:C:296:HIS:HA	1:C:310:ASP:OD2	2.11	0.51
2:F:145:ASP:OD1	2:F:146:ASN:N	2.44	0.51
1:C:62:GLU:CG	1:C:164:MET:HE1	2.39	0.51
1:C:115:MET:HG2	1:G:115:MET:O	2.10	0.51
1:C:124:LEU:HG	1:C:145:ILE:HD12	1.92	0.51
2:H:31:ARG:NH1	2:H:59:ASP:OD2	2.44	0.51
2:D:87:TYR:CE1	2:D:153:LYS:HD3	2.45	0.51
1:E:226:LEU:HD21	1:E:254:LEU:HD12	1.93	0.51
1:E:369:CYS:O	1:E:408:ASN:HB2	2.10	0.51
1:A:406:HIS:ND1	1:A:469:GLY:CA	2.73	0.51
1:G:35:ASP:O	1:G:39:VAL:HB	2.11	0.51
1:G:406:HIS:CG	1:G:406:HIS:O	2.63	0.51
1:A:34:LEU:HD12	1:A:35:ASP:N	2.26	0.51
1:A:59:ILE:HG23	2:B:124:PHE:CE2	2.46	0.51
1:A:60:MET:HE2	1:A:60:MET:HA	1.93	0.51
1:C:109:ASN:OD1	1:G:116:GLY:O	2.28	0.51
1:A:61:ASP:OD2	1:A:67:ILE:HG21	2.11	0.50
1:G:342:THR:HG23	1:G:401:THR:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:357:ARG:HG3	1:G:359:ASP:OD1	2.11	0.50
1:E:390:GLN:O	1:E:391:ASN:ND2	2.44	0.50
1:C:57:VAL:CG1	1:C:59:ILE:HD12	2.29	0.50
1:G:59:ILE:HG23	2:H:124:PHE:CE2	2.47	0.50
1:G:344:VAL:HG11	1:G:400:ILE:HD13	1.93	0.50
1:A:114:VAL:O	1:E:115:MET:CE	2.59	0.50
1:A:407:THR:O	1:A:436:THR:OG1	2.29	0.50
1:C:139:GLU:C	1:C:142:PHE:HE2	2.18	0.50
1:E:27:PRO:HB2	1:E:29:ASN:OD1	2.11	0.50
1:E:309:CYS:SG	1:E:315:ARG:HB2	2.52	0.50
1:E:318:ASN:OD1	1:E:318:ASN:N	2.44	0.50
2:H:63:PRO:HA	3:P:1:NAG:O7	2.12	0.50
1:A:385:HIS:HA	1:A:386:TYR:CB	2.28	0.50
2:B:159:ARG:HD3	2:B:163:SER:HB2	1.94	0.50
1:C:357:ARG:NH1	1:C:418:GLY:H	2.09	0.50
1:C:420:SER:C	1:C:422:TYR:N	2.67	0.50
2:F:28:VAL:HG12	2:F:29:ALA:H	1.77	0.50
1:G:344:VAL:HG12	1:G:345:ASN:N	2.26	0.50
2:H:147:GLY:C	2:H:149:ARG:H	2.19	0.50
1:A:346:LEU:HD23	1:A:347:GLU:N	2.27	0.50
1:C:56:GLU:HA	1:C:69:THR:O	2.12	0.50
1:C:368:LYS:O	1:C:377:CYS:HA	2.12	0.50
1:E:46:ILE:HD13	1:E:46:ILE:H	1.75	0.50
2:F:85:ASP:OD1	2:F:85:ASP:N	2.44	0.50
1:C:85:ARG:HD3	1:C:137:ILE:HG12	1.94	0.50
2:H:54:ILE:HG13	2:H:158:VAL:HG11	1.93	0.50
1:A:161:ASP:O	1:A:162:ARG:HB3	2.12	0.49
1:E:339:VAL:O	1:E:339:VAL:HG23	2.12	0.49
1:A:139:GLU:C	1:A:142:PHE:CE2	2.90	0.49
1:A:342:THR:HG21	1:A:403:LEU:O	2.07	0.49
1:G:105:LEU:HD21	1:G:120:GLU:HG3	1.94	0.49
1:A:114:VAL:C	1:E:115:MET:CB	2.74	0.49
1:A:328:PRO:HB3	1:A:420:SER:HB3	1.94	0.49
1:A:374:PRO:O	1:A:375:SER:HB2	2.13	0.49
1:E:59:ILE:O	1:E:66:PRO:HA	2.12	0.49
2:H:119:GLN:HE21	2:H:122:THR:CG2	2.25	0.49
1:A:59:ILE:CG2	1:A:60:MET:N	2.75	0.49
1:A:118:CYS:N	1:E:115:MET:HG2	2.10	0.49
1:A:357:ARG:HG3	1:A:359:ASP:OD1	2.12	0.49
1:A:473:GLU:HG2	1:A:516:ARG:HH11	1.77	0.49
1:C:126:TYR:CE1	1:C:143:VAL:HG22	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:320:ALA:C	1:E:322:SER:H	2.18	0.49
1:A:118:CYS:H	1:E:115:MET:CG	2.13	0.49
1:E:63:LYS:O	1:E:64:ASN:CB	2.59	0.49
1:G:367:LYS:HB3	1:G:377:CYS:HB2	1.94	0.49
2:H:65:TYR:HB2	2:H:69:VAL:HG21	1.94	0.49
1:A:58:SER:C	1:A:59:ILE:HG13	2.37	0.49
1:E:37:ARG:HD3	1:E:67:ILE:HD11	1.95	0.49
1:E:51:GLU:OE2	2:F:28:VAL:HG13	2.13	0.49
1:G:405:ALA:HB3	1:G:468:ASN:HB3	1.95	0.49
1:G:102:LYS:HD3	1:G:166:LEU:HD21	1.95	0.49
1:G:298:TYR:N	1:G:307:CYS:HB3	2.28	0.49
1:A:346:LEU:HD23	1:A:347:GLU:H	1.78	0.49
1:C:138:ARG:HD3	1:C:141:GLN:HB2	1.93	0.49
1:E:102:LYS:HA	1:E:167:ASN:O	2.13	0.49
1:E:316:ALA:C	1:E:319:ASP:HB2	2.37	0.49
3:M:2:NAG:H3	3:M:2:NAG:H83	1.94	0.49
1:A:61:ASP:OD1	1:A:67:ILE:HD13	2.13	0.48
1:A:164:MET:HB2	2:B:126:LEU:HG	1.95	0.48
1:E:320:ALA:C	1:E:322:SER:N	2.70	0.48
1:G:320:ALA:HB3	1:G:323:MET:HG3	1.93	0.48
1:E:313:PHE:HB3	1:E:325:CYS:HB3	1.95	0.48
1:G:157:VAL:HG12	1:G:157:VAL:O	2.14	0.48
1:A:116:GLY:H	1:E:115:MET:CB	2.26	0.48
1:E:59:ILE:HG23	1:E:60:MET:H	1.78	0.48
1:C:366:CYS:SG	1:C:367:LYS:N	2.86	0.48
1:E:228:GLU:HB2	1:E:246:TYR:CE1	2.49	0.48
2:F:28:VAL:CG1	2:F:29:ALA:H	2.25	0.48
2:F:67:ASP:HA	2:F:106:HIS:ND1	2.29	0.48
1:A:58:SER:O	1:A:59:ILE:HG13	2.13	0.48
1:A:211:LEU:HD21	1:A:268:GLU:HG3	1.95	0.48
1:E:40:GLN:O	1:E:41:GLY:O	2.31	0.48
1:G:355:GLY:N	1:G:356:GLY:HA2	2.28	0.48
1:G:436:THR:HG22	1:G:437:ASN:N	2.28	0.48
1:C:62:GLU:HB3	1:C:164:MET:HE1	1.95	0.48
1:C:39:VAL:CB	1:C:43:LEU:HB2	2.43	0.48
1:G:61:ASP:O	1:G:64:ASN:N	2.46	0.48
1:G:106:ARG:HB3	1:G:191:CYS:HB3	1.94	0.48
1:C:294:PRO:HG3	1:C:321:ALA:O	2.13	0.48
1:E:317:ASP:C	1:E:319:ASP:N	2.71	0.48
2:H:60:VAL:HG11	2:H:79:LEU:HD11	1.96	0.48
1:A:362:TYR:HA	1:A:414:TRP:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:294:PRO:CG	1:G:322:SER:C	2.58	0.48
1:G:294:PRO:HD3	1:G:322:SER:HA	1.96	0.48
2:B:99:ARG:NH1	2:B:114:PHE:HZ	2.12	0.47
1:C:373:ASP:O	1:C:375:SER:N	2.43	0.47
1:C:386:TYR:H	1:C:400:ILE:HA	1.79	0.47
2:F:100:TRP:CZ2	2:F:113:LYS:O	2.67	0.47
2:F:119:GLN:HE22	2:F:122:THR:HG23	1.79	0.47
1:G:211:LEU:HD21	1:G:268:GLU:HG3	1.94	0.47
1:A:114:VAL:O	1:E:115:MET:HE2	2.13	0.47
1:G:105:LEU:HD21	1:G:120:GLU:CG	2.45	0.47
1:C:239:GLU:O	1:C:239:GLU:HG3	2.13	0.47
1:E:406:HIS:CG	1:E:469:GLY:HA2	2.49	0.47
2:F:119:GLN:NE2	2:F:122:THR:HG23	2.29	0.47
1:G:338:ASN:HB3	1:G:345:ASN:CB	2.33	0.47
1:G:338:ASN:HB3	1:G:345:ASN:HD22	1.79	0.47
2:B:81:MET:O	2:B:96:GLY:HA3	2.14	0.47
1:E:357:ARG:HH12	1:E:418:GLY:CA	2.26	0.47
2:D:70:PRO:C	2:D:72:ASP:H	2.23	0.47
1:G:102:LYS:HA	1:G:167:ASN:O	2.15	0.47
1:G:67:ILE:CG2	1:G:68:ARG:N	2.77	0.47
1:G:340:ASN:CG	1:G:341:GLU:N	2.73	0.47
1:G:342:THR:HG23	1:G:401:THR:CG2	2.45	0.47
2:H:36:TRP:CE3	2:H:43:PHE:HZ	2.31	0.47
1:A:226:LEU:HD11	1:E:254:LEU:HD13	1.95	0.47
1:C:403:LEU:HD13	1:C:409:TYR:CZ	2.50	0.47
1:E:319:ASP:OD1	1:E:320:ALA:N	2.48	0.47
2:B:54:ILE:HD12	2:B:158:VAL:CG1	2.45	0.47
1:C:43:LEU:O	1:C:43:LEU:HG	2.14	0.47
1:C:62:GLU:CB	1:C:164:MET:HE1	2.45	0.47
1:C:320:ALA:C	1:C:322:SER:N	2.73	0.47
2:D:77:TYR:H	2:D:102:CYS:HB2	1.80	0.47
2:H:85:ASP:HB3	2:H:95:LYS:HE2	1.97	0.47
2:H:58:LEU:HB3	2:H:116:GLU:HB3	1.96	0.47
1:A:226:LEU:CD1	1:E:254:LEU:HD13	2.45	0.46
1:A:316:ALA:O	1:A:319:ASP:HB2	2.15	0.46
1:C:362:TYR:HA	1:C:414:TRP:O	2.14	0.46
2:F:65:TYR:CD2	2:F:74:THR:HB	2.50	0.46
2:F:87:TYR:HE1	2:F:153:LYS:HB2	1.80	0.46
1:A:98:TYR:CD2	1:A:172:ASP:HB3	2.51	0.46
1:A:115:MET:C	1:E:115:MET:HB2	2.38	0.46
1:A:386:TYR:CE1	1:A:390:GLN:HG3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:ASP:OD1	1:C:67:ILE:HD13	2.16	0.46
1:C:406:HIS:CG	1:C:406:HIS:O	2.67	0.46
2:D:76:ARG:HB2	2:D:143:ILE:HB	1.97	0.46
1:A:419:VAL:C	1:A:421:LYS:H	2.23	0.46
1:E:317:ASP:C	1:E:319:ASP:H	2.23	0.46
1:E:341:GLU:O	1:E:436:THR:HG22	2.14	0.46
1:A:254:LEU:HD23	1:A:254:LEU:HA	1.74	0.46
1:A:315:ARG:HD3	1:A:319:ASP:OD1	2.15	0.46
1:A:341:GLU:HA	1:A:437:ASN:ND2	2.31	0.46
1:E:138:ARG:O	1:E:142:PHE:CE2	2.68	0.46
1:G:57:VAL:HG22	1:G:58:SER:N	2.30	0.46
2:B:122:THR:HG22	2:B:124:PHE:N	2.16	0.46
1:C:379:PRO:O	1:C:380:CYS:SG	2.73	0.46
2:D:125:SER:C	2:D:126:LEU:HD23	2.41	0.46
1:A:226:LEU:HD21	1:A:254:LEU:HD12	1.98	0.46
1:C:116:GLY:C	1:G:115:MET:CG	2.88	0.46
1:G:357:ARG:HH12	1:G:418:GLY:HA3	1.79	0.46
1:A:155:THR:CG2	1:A:156:GLN:H	2.29	0.46
1:C:320:ALA:C	1:C:322:SER:H	2.23	0.46
2:D:74:THR:O	2:D:76:ARG:NH1	2.49	0.46
2:D:121:PHE:HA	2:D:129:GLU:OE2	2.16	0.46
1:E:406:HIS:CG	1:E:406:HIS:O	2.67	0.46
2:F:133:GLY:O	2:F:134:ARG:HG3	2.14	0.46
1:G:354:THR:C	1:G:356:GLY:HA2	2.40	0.46
1:A:115:MET:HA	1:E:115:MET:CA	2.44	0.46
1:A:385:HIS:CA	1:A:386:TYR:HB2	2.31	0.46
1:C:440:ALA:N	1:C:519:ALA:HB3	2.31	0.46
1:E:67:ILE:HG22	1:E:68:ARG:C	2.41	0.46
2:F:65:TYR:CD2	2:F:74:THR:CG2	2.99	0.46
1:G:297:SER:HB2	1:G:315:ARG:NH1	2.31	0.46
1:G:472:LEU:HG	1:G:517:THR:HA	1.98	0.46
2:B:85:ASP:HB2	2:B:95:LYS:HZ2	1.80	0.46
1:C:226:LEU:CD2	1:C:254:LEU:HD12	2.46	0.46
1:C:314:PHE:HB2	1:C:419:VAL:CG1	2.46	0.46
2:F:74:THR:OG1	2:F:76:ARG:NH1	2.49	0.46
2:F:162:ASN:HA	2:F:165:MET:HE3	1.98	0.46
2:H:43:PHE:CD1	2:H:152:LEU:HD12	2.51	0.46
1:A:155:THR:HG22	1:A:156:GLN:H	1.76	0.45
1:A:355:GLY:N	1:A:356:GLY:HA2	2.31	0.45
1:A:439:ALA:HA	1:A:519:ALA:HB1	1.98	0.45
2:B:99:ARG:NE	2:B:128:PHE:CE2	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:LEU:HD13	1:G:226:LEU:HD11	1.94	0.45
1:C:386:TYR:CD1	1:C:390:GLN:HG3	2.51	0.45
1:E:138:ARG:O	1:E:142:PHE:CD2	2.69	0.45
1:E:138:ARG:HD3	1:E:141:GLN:HB2	1.98	0.45
1:G:58:SER:HB2	2:H:100:TRP:CZ3	2.51	0.45
1:C:34:LEU:HD12	1:C:35:ASP:H	1.79	0.45
1:E:67:ILE:HD13	1:E:67:ILE:HG21	1.68	0.45
1:G:164:MET:HE3	2:H:124:PHE:CE1	2.51	0.45
2:H:74:THR:HG23	2:H:76:ARG:HD3	1.98	0.45
2:H:131:ARG:O	2:H:134:ARG:HB2	2.16	0.45
1:A:116:GLY:H	1:E:115:MET:CA	2.28	0.45
1:A:403:LEU:HB2	1:A:409:TYR:CZ	2.52	0.45
2:B:119:GLN:NE2	2:B:122:THR:HA	2.32	0.45
1:C:118:CYS:N	1:G:115:MET:CE	2.55	0.45
1:C:254:LEU:HD23	1:C:254:LEU:HA	1.85	0.45
1:C:270:SER:HG	1:C:271:GLY:H	1.60	0.45
1:A:88:TRP:CE2	1:A:180:GLY:HA3	2.52	0.45
1:A:126:TYR:CE1	1:A:143:VAL:CG2	3.00	0.45
1:A:364:VAL:HG21	1:A:398:VAL:HG11	1.97	0.45
1:E:48:SER:HB3	1:E:137:ILE:HD12	1.99	0.45
1:G:368:LYS:N	1:G:377:CYS:HB3	2.32	0.45
2:B:74:THR:HG21	2:B:105:PRO:HG2	1.96	0.45
1:G:344:VAL:CG1	1:G:345:ASN:N	2.78	0.45
1:E:357:ARG:HH12	1:E:418:GLY:HA3	1.82	0.45
1:G:412:GLU:HG2	1:G:431:SER:OG	2.16	0.45
1:C:61:ASP:OD2	1:C:67:ILE:HG21	2.17	0.45
2:B:148:ARG:CB	2:B:150:SER:O	2.60	0.45
2:D:99:ARG:NH2	2:D:116:GLU:OE1	2.50	0.45
1:E:139:GLU:H	1:E:139:GLU:HG2	1.51	0.45
1:G:59:ILE:O	1:G:66:PRO:HA	2.17	0.45
1:G:240:LYS:HD2	1:G:261:LEU:HD11	1.99	0.45
1:C:59:ILE:HG23	2:D:124:PHE:CE2	2.52	0.45
1:C:129:SER:HB2	1:C:138:ARG:NH2	2.32	0.44
1:E:265:GLY:O	1:E:303:GLY:HA2	2.17	0.44
2:F:117:LYS:HG2	2:F:119:GLN:HB3	1.99	0.44
2:F:146:ASN:HB2	2:F:148:ARG:HG2	1.98	0.44
1:G:487:SER:OG	1:G:489:ARG:HD2	2.16	0.44
1:E:59:ILE:HG22	1:E:60:MET:C	2.43	0.44
2:F:89:ALA:HB1	2:F:149:ARG:HH12	1.82	0.44
2:F:135:GLU:HA	2:F:156:VAL:O	2.18	0.44
1:G:226:LEU:CD2	1:G:254:LEU:HD12	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:75:VAL:HG21	1:E:111:LEU:HD13	1.98	0.44
1:E:401:THR:CG2	1:E:402:ASP:N	2.81	0.44
1:G:373:ASP:HB2	1:G:374:PRO:HD3	1.99	0.44
1:C:115:MET:HG2	1:G:114:VAL:C	2.42	0.44
1:E:335:LEU:HD11	1:E:346:LEU:HD21	1.95	0.44
1:C:364:VAL:HG21	1:C:398:VAL:HG11	2.00	0.44
2:D:76:ARG:HE	2:D:143:ILE:HG21	1.83	0.44
1:G:126:TYR:CE1	1:G:143:VAL:HG22	2.53	0.44
1:G:362:TYR:HA	1:G:414:TRP:O	2.18	0.44
1:G:366:CYS:SG	1:G:367:LYS:N	2.90	0.44
2:H:76:ARG:NH2	2:H:143:ILE:CG2	2.79	0.44
1:G:233:CYS:SG	1:G:239:GLU:HB3	2.58	0.44
1:G:506:LEU:HA	1:G:532:THR:O	2.17	0.44
1:A:62:GLU:HB3	1:A:164:MET:HE1	1.99	0.44
1:E:126:TYR:CE1	1:E:143:VAL:HG22	2.53	0.44
2:F:164:CYS:O	2:F:165:MET:HG2	2.16	0.44
1:A:94:ALA:HB2	1:A:201:TYR:CG	2.52	0.43
1:A:443:SER:HB3	1:A:523:ASP:HB2	2.00	0.43
2:D:159:ARG:HD2	2:D:163:SER:CB	2.48	0.43
1:E:414:TRP:CD2	1:E:429:SER:HB3	2.53	0.43
1:G:129:SER:HB2	1:G:138:ARG:HH22	1.83	0.43
1:G:339:VAL:HG22	1:G:343:SER:O	2.18	0.43
1:G:340:ASN:OD1	1:G:341:GLU:N	2.51	0.43
2:B:74:THR:HG22	2:B:74:THR:O	2.18	0.43
1:E:351:PRO:HD3	1:E:362:TYR:OH	2.18	0.43
1:A:245:MET:SD	1:A:256:PRO:HB3	2.59	0.43
1:A:373:ASP:H	1:A:374:PRO:HD2	1.72	0.43
1:A:537:SER:HB3	1:A:540:ILE:HD12	2.00	0.43
2:B:54:ILE:CD1	2:B:158:VAL:HG11	2.48	0.43
1:E:67:ILE:HG22	1:E:68:ARG:O	2.18	0.43
2:F:31:ARG:NH1	2:F:59:ASP:OD1	2.51	0.43
2:B:40:ASN:HA	2:B:41:PRO:HD3	1.78	0.43
1:C:60:MET:HE2	1:C:60:MET:HA	2.00	0.43
1:C:405:ALA:O	1:C:436:THR:HB	2.18	0.43
2:D:119:GLN:NE2	2:D:122:THR:HG23	2.33	0.43
1:G:473:GLU:OE1	1:G:516:ARG:NH1	2.51	0.43
1:A:59:ILE:O	1:A:60:MET:HE2	2.17	0.43
1:C:269:ARG:HG3	1:C:269:ARG:HH11	1.84	0.43
2:D:67:ASP:HA	2:D:106:HIS:CD2	2.53	0.43
2:D:82:VAL:O	2:D:137:PHE:HB2	2.18	0.43
1:G:306:SER:HA	1:G:321:ALA:HB1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:485:GLU:HG3	1:G:485:GLU:O	2.19	0.43
1:A:470:VAL:O	1:A:517:THR:HG22	2.19	0.43
1:C:296:HIS:O	1:C:325:CYS:HB2	2.19	0.43
1:E:335:LEU:HD22	1:E:430:VAL:HG13	2.01	0.43
1:A:473:GLU:HG2	1:A:516:ARG:NH1	2.34	0.43
1:G:226:LEU:HD23	1:G:226:LEU:HA	1.89	0.43
1:C:175:PRO:HB3	1:C:221:ALA:HB1	2.00	0.43
1:C:235:ASN:HA	1:C:236:ASN:HA	1.80	0.43
1:E:360:ILE:H	1:E:360:ILE:HG13	1.57	0.43
1:G:294:PRO:CG	1:G:322:SER:CA	2.75	0.43
2:B:36:TRP:CD1	2:B:77:TYR:CE2	3.07	0.43
2:F:122:THR:HG21	2:F:127:GLY:HA3	2.01	0.43
1:G:164:MET:O	1:G:165:LYS:CG	2.67	0.43
1:C:76:MET:HG3	1:C:114:VAL:HG12	2.00	0.42
2:D:78:VAL:HG12	2:D:80:TYR:CE1	2.54	0.42
2:F:159:ARG:HG2	2:F:159:ARG:H	1.35	0.42
1:G:162:ARG:HH22	2:H:128:PHE:HZ	1.64	0.42
1:A:439:ALA:C	1:A:519:ALA:HB3	2.43	0.42
2:F:75:GLU:HB3	2:F:77:TYR:CE2	2.54	0.42
1:G:98:TYR:CE1	1:G:202:LYS:HE3	2.53	0.42
1:C:192:ILE:CG1	1:C:193:ALA:N	2.82	0.42
1:C:295:PRO:CB	1:C:324:PRO:HB3	2.49	0.42
2:H:43:PHE:CG	2:H:152:LEU:HD12	2.54	0.42
1:C:140:ASN:OD1	1:C:141:GLN:HG3	2.19	0.42
1:C:62:GLU:OE1	1:C:63:LYS:HG3	2.19	0.42
2:D:73:LYS:HA	2:D:73:LYS:HD3	1.87	0.42
1:E:342:THR:HG23	1:E:403:LEU:HD12	2.01	0.42
2:F:73:LYS:HA	2:F:73:LYS:HZ1	1.85	0.42
1:G:235:ASN:HA	1:G:236:ASN:HA	1.79	0.42
1:G:281:TYR:CD2	1:G:321:ALA:HB3	2.54	0.42
2:B:32:TYR:CD2	2:B:32:TYR:N	2.87	0.42
1:C:116:GLY:C	1:G:115:MET:HG3	2.44	0.42
1:E:164:MET:HG3	2:F:125:SER:OG	2.20	0.42
2:F:40:ASN:HA	2:F:41:PRO:HD3	1.83	0.42
1:G:61:ASP:C	1:G:63:LYS:N	2.77	0.42
1:G:298:TYR:O	1:G:307:CYS:CA	2.67	0.42
1:C:369:CYS:SG	1:C:376:LYS:C	3.02	0.42
2:F:28:VAL:HG12	2:F:29:ALA:O	2.19	0.42
1:G:341:GLU:CD	4:G:3401:NAG:H82	2.45	0.42
1:G:373:ASP:N	1:G:374:PRO:CD	2.83	0.42
1:A:348:TRP:CD1	1:A:396:THR:HG22	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:373:ASP:HB3	1:E:376:LYS:HG3	2.01	0.42
1:G:138:ARG:HD3	1:G:141:GLN:HB2	2.00	0.42
2:H:131:ARG:HB2	2:H:134:ARG:HD3	2.01	0.42
1:A:360:ILE:HA	1:A:416:VAL:O	2.19	0.42
1:E:35:ASP:CG	1:E:38:SER:HB3	2.44	0.42
1:A:340:ASN:OD1	1:A:340:ASN:C	2.63	0.42
2:D:95:LYS:HD3	2:D:95:LYS:HA	1.66	0.42
1:E:207:THR:HG21	1:E:253:TRP:CD1	2.55	0.42
1:E:312:GLY:O	1:E:327:ARG:NE	2.51	0.42
1:G:294:PRO:CB	1:G:322:SER:O	2.61	0.42
1:G:385:HIS:O	1:G:401:THR:OG1	2.34	0.42
1:A:254:LEU:HD13	1:E:226:LEU:HD12	2.02	0.41
1:A:282:LYS:HE3	1:A:287:ASP:O	2.19	0.41
1:C:117:THR:CA	1:G:115:MET:SD	3.03	0.41
1:C:226:LEU:CD1	1:G:254:LEU:HD13	2.50	0.41
2:F:87:TYR:CE1	2:F:153:LYS:HB2	2.54	0.41
1:G:61:ASP:C	1:G:63:LYS:H	2.28	0.41
1:A:326:THR:HG21	1:A:357:ARG:HE	1.85	0.41
2:B:146:ASN:HD22	2:B:148:ARG:NH2	2.19	0.41
2:B:159:ARG:HG2	2:B:159:ARG:HH11	1.85	0.41
2:H:65:TYR:HE2	2:H:74:THR:OG1	2.03	0.41
1:A:59:ILE:C	1:A:60:MET:HE2	2.45	0.41
1:A:354:THR:HG23	1:A:356:GLY:CA	2.47	0.41
1:A:512:HIS:CE1	1:A:527:PRO:HG3	2.55	0.41
1:A:236:ASN:OD1	1:A:236:ASN:N	2.53	0.41
1:C:341:GLU:O	1:C:436:THR:HG22	2.18	0.41
2:F:45:ARG:CZ	2:F:45:ARG:HB2	2.51	0.41
1:G:471:ILE:HA	1:G:517:THR:HG22	2.02	0.41
1:G:335:LEU:HD11	1:G:346:LEU:CG	2.50	0.41
1:A:357:ARG:HH12	1:A:418:GLY:HA3	1.85	0.41
1:C:102:LYS:HA	1:C:167:ASN:O	2.20	0.41
1:C:403:LEU:HB2	1:C:409:TYR:OH	2.19	0.41
1:C:414:TRP:CH2	1:C:426:PRO:HA	2.55	0.41
1:E:129:SER:HB2	1:E:138:ARG:HH22	1.85	0.41
1:E:514:ARG:HD2	1:E:524:PHE:CZ	2.56	0.41
2:B:31:ARG:HH11	2:B:31:ARG:HD3	1.75	0.41
2:B:77:TYR:HB3	2:B:142:ALA:HA	2.02	0.41
1:E:385:HIS:HA	1:E:386:TYR:CB	2.19	0.41
1:G:306:SER:HA	1:G:321:ALA:CB	2.50	0.41
1:A:96:ARG:HE	1:A:96:ARG:HB2	1.56	0.41
1:E:56:GLU:HA	1:E:69:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:328:PRO:HB3	1:E:420:SER:HB2	2.03	0.41
1:G:237:SER:HB3	1:G:273:CYS:SG	2.61	0.41
2:H:31:ARG:HG2	2:H:57:TYR:HB2	2.03	0.41
2:H:149:ARG:O	2:H:150:SER:HB3	2.21	0.41
2:H:162:ASN:O	2:H:165:MET:HG2	2.21	0.41
1:A:357:ARG:HH12	1:A:418:GLY:H	1.69	0.41
1:C:282:LYS:HE3	1:C:287:ASP:O	2.21	0.41
2:H:40:ASN:HA	2:H:41:PRO:HD2	1.84	0.41
2:H:74:THR:O	2:H:76:ARG:NH1	2.54	0.41
2:H:82:VAL:HG12	2:H:96:GLY:HA3	2.02	0.41
1:C:118:CYS:HB2	1:G:115:MET:HE1	1.99	0.41
1:C:436:THR:HG22	1:C:437:ASN:N	2.34	0.41
1:E:320:ALA:O	1:E:322:SER:N	2.54	0.41
1:E:362:TYR:HA	1:E:414:TRP:O	2.20	0.41
1:G:106:ARG:HD2	1:G:154:PHE:CZ	2.56	0.41
2:H:119:GLN:HE22	2:H:122:THR:HG22	1.78	0.41
1:A:61:ASP:OD2	1:A:67:ILE:CD1	2.68	0.40
2:B:106:HIS:O	2:B:107:SER:C	2.64	0.40
2:D:31:ARG:HD3	2:D:59:ASP:OD2	2.22	0.40
2:D:54:ILE:HD12	2:D:132:PRO:HG3	2.01	0.40
2:D:104:ARG:HH22	2:D:108:PRO:HD3	1.86	0.40
1:G:59:ILE:O	1:G:67:ILE:N	2.49	0.40
1:C:455:TYR:CE2	1:C:540:ILE:HD12	2.56	0.40
1:G:386:TYR:CZ	1:G:390:GLN:HG3	2.55	0.40
2:H:78:VAL:HG22	2:H:101:GLU:HG2	2.02	0.40
1:C:296:HIS:CB	1:C:325:CYS:HB2	2.50	0.40
2:F:104:ARG:HB3	2:F:107:SER:HB3	2.03	0.40
2:H:49:HIS:HA	2:H:155:LYS:O	2.21	0.40
2:B:32:TYR:CD2	2:B:52:VAL:HG12	2.57	0.40
1:C:270:SER:HG	1:C:271:GLY:N	2.16	0.40
1:E:59:ILE:HD12	1:E:69:THR:HG21	2.04	0.40
2:F:154:LEU:HD12	2:F:154:LEU:HA	1.83	0.40
1:G:254:LEU:HA	1:G:254:LEU:HD23	1.79	0.40
1:G:438:GLN:HB3	1:G:468:ASN:O	2.21	0.40
2:D:40:ASN:HA	2:D:41:PRO:HD3	1.92	0.40
2:D:120:LEU:HD23	2:D:120:LEU:HA	1.89	0.40
1:E:471:ILE:HA	1:E:517:THR:HG22	2.03	0.40
1:G:91:ARG:NE	1:G:178:LYS:O	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:539:ILE:O	1:G:266:HIS:NE2[2_464]	1.99	0.21

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	514/518 (99%)	473 (92%)	38 (7%)	3 (1%)	21	50
1	C	514/518 (99%)	475 (92%)	35 (7%)	4 (1%)	16	44
1	E	514/518 (99%)	481 (94%)	29 (6%)	4 (1%)	16	44
1	G	514/518 (99%)	479 (93%)	30 (6%)	5 (1%)	12	38
2	B	139/141 (99%)	120 (86%)	17 (12%)	2 (1%)	9	31
2	D	138/141 (98%)	122 (88%)	14 (10%)	2 (1%)	9	31
2	F	136/141 (96%)	122 (90%)	13 (10%)	1 (1%)	18	47
2	H	136/141 (96%)	121 (89%)	10 (7%)	5 (4%)	2	13
All	All	2605/2636 (99%)	2393 (92%)	186 (7%)	26 (1%)	12	38

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	373	ASP
1	G	62	GLU
1	G	164	MET
1	G	165	LYS
2	B	103	ASN
1	E	41	GLY
2	H	145	ASP
1	A	390	GLN
2	B	88	SER
1	E	377	CYS
1	E	419	VAL
2	H	164	CYS

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Mol	Chain	Res	Type
1	A	419	VAL
2	D	47	ASP
2	D	146	ASN
1	E	405	ALA
2	H	39	SER
2	H	150	SER
1	A	375	SER
1	C	41	GLY
1	C	382	SER
2	F	90	CYS
1	G	334	ASN
2	H	108	PRO
1	G	419	VAL
1	C	419	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	447/447 (100%)	411 (92%)	36 (8%)	11	33
1	C	447/447 (100%)	405 (91%)	42 (9%)	8	28
1	E	447/447 (100%)	413 (92%)	34 (8%)	12	35
1	G	447/447 (100%)	417 (93%)	30 (7%)	15	39
2	B	127/127 (100%)	112 (88%)	15 (12%)	5	19
2	D	127/127 (100%)	112 (88%)	15 (12%)	5	19
2	F	127/127 (100%)	113 (89%)	14 (11%)	6	21
2	H	127/127 (100%)	113 (89%)	14 (11%)	6	21
All	All	2296/2296 (100%)	2096 (91%)	200 (9%)	9	30

All (200) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	GLU

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Mol	Chain	Res	Type
1	A	67	ILE
1	A	76	MET
1	A	90	THR
1	A	105	LEU
1	A	107	ASP
1	A	119	LYS
1	A	120	GLU
1	A	143	VAL
1	A	179	LYS
1	A	192	ILE
1	A	206	LEU
1	A	236	ASN
1	A	278	ILE
1	A	317	ASP
1	A	327	ARG
1	A	336	ILE
1	A	340	ASN
1	A	346	LEU
1	A	357	ARG
1	A	360	ILE
1	A	369	CYS
1	A	380	CYS
1	A	385	HIS
1	A	387	THR
1	A	395	THR
1	A	396	THR
1	A	403	LEU
1	A	404	LEU
1	A	413	ILE
1	A	416	VAL
1	A	436	THR
1	A	483	GLN
1	A	489	ARG
1	A	506	LEU
1	A	514	ARG
2	B	31	ARG
2	B	38	SER
2	B	42	ARG
2	B	54	ILE
2	B	58	LEU
2	B	71	GLU
2	B	74	THR

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Mol	Chain	Res	Type
2	B	79	LEU
2	B	104	ARG
2	B	112	LEU
2	B	122	THR
2	B	125	SER
2	B	126	LEU
2	B	141	SER
2	B	165	MET
1	C	43	LEU
1	C	62	GLU
1	C	67	ILE
1	C	68	ARG
1	C	107	ASP
1	C	119	LYS
1	C	120	GLU
1	C	128	GLU
1	C	139	GLU
1	C	143	VAL
1	C	192	ILE
1	C	206	LEU
1	C	232	SER
1	C	236	ASN
1	C	239	GLU
1	C	270	SER
1	C	278	ILE
1	C	300	VAL
1	C	317	ASP
1	C	318	ASN
1	C	327	ARG
1	C	336	ILE
1	C	338	ASN
1	C	339	VAL
1	C	357	ARG
1	C	360	ILE
1	C	366	CYS
1	C	367	LYS
1	C	369	CYS
1	C	373	ASP
1	C	378	ARG
1	C	380	CYS
1	C	384	VAL
1	C	387	THR

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Mol	Chain	Res	Type
1	C	393	LEU
1	C	395	THR
1	C	402	ASP
1	C	416	VAL
1	C	444	ILE
1	C	489	ARG
1	C	506	LEU
1	C	514	ARG
2	D	28	VAL
2	D	42	ARG
2	D	54	ILE
2	D	79	LEU
2	D	91	ASP
2	D	112	LEU
2	D	122	THR
2	D	125	SER
2	D	126	LEU
2	D	134	ARG
2	D	149	ARG
2	D	155	LYS
2	D	161	THR
2	D	163	SER
2	D	165	MET
1	E	43	LEU
1	E	46	ILE
1	E	51	GLU
1	E	97	VAL
1	E	107	ASP
1	E	115	MET
1	E	119	LYS
1	E	120	GLU
1	E	139	GLU
1	E	143	VAL
1	E	187	ASP
1	E	192	ILE
1	E	206	LEU
1	E	236	ASN
1	E	257	ILE
1	E	278	ILE
1	E	311	ARG
1	E	315	ARG
1	E	317	ASP

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Mol	Chain	Res	Type
1	E	318	ASN
1	E	340	ASN
1	E	357	ARG
1	E	360	ILE
1	E	369	CYS
1	E	385	HIS
1	E	387	THR
1	E	395	THR
1	E	396	THR
1	E	436	THR
1	E	465	ASP
1	E	483	GLN
1	E	489	ARG
1	E	506	LEU
1	E	514	ARG
2	F	45	ARG
2	F	54	ILE
2	F	73	LYS
2	F	79	LEU
2	F	85	ASP
2	F	93	THR
2	F	103	ASN
2	F	122	THR
2	F	125	SER
2	F	129	GLU
2	F	151	CYS
2	F	159	ARG
2	F	162	ASN
2	F	163	SER
1	G	69	THR
1	G	90	THR
1	G	107	ASP
1	G	115	MET
1	G	120	GLU
1	G	143	VAL
1	G	183	LEU
1	G	192	ILE
1	G	206	LEU
1	G	236	ASN
1	G	278	ILE
1	G	307	CYS
1	G	317	ASP

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Mol	Chain	Res	Type
1	G	327	ARG
1	G	334	ASN
1	G	346	LEU
1	G	357	ARG
1	G	360	ILE
1	G	373	ASP
1	G	376	LYS
1	G	385	HIS
1	G	387	THR
1	G	393	LEU
1	G	395	THR
1	G	416	VAL
1	G	438	GLN
1	G	483	GLN
1	G	489	ARG
1	G	506	LEU
1	G	514	ARG
2	H	38	SER
2	H	44	GLN
2	H	54	ILE
2	H	72	ASP
2	H	73	LYS
2	H	76	ARG
2	H	79	LEU
2	H	91	ASP
2	H	93	THR
2	H	104	ARG
2	H	125	SER
2	H	143	ILE
2	H	152	LEU
2	H	159	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	A	141	GLN
1	A	385	HIS
1	A	406	HIS
2	B	55	ASN
2	B	83	ASN
2	B	109	ASN

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Mol	Chain	Res	Type
2	B	146	ASN
1	C	123	ASN
1	C	141	GLN
1	C	263	ASN
1	C	389	GLN
2	D	55	ASN
2	D	106	HIS
1	E	391	ASN
1	E	438	GLN
2	F	44	GLN
2	F	109	ASN
1	G	71	GLN
1	G	141	GLN
1	G	345	ASN
2	H	64	HIS
2	H	119	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	I	1	1,3	14,14,15	0.82	1 (7%)	17,19,21	2.60	2 (11%)
3	NAG	I	2	3	14,14,15	0.50	0	17,19,21	1.06	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	J	1	3,2	14,14,15	0.45	0	17,19,21	2.60	6 (35%)
3	NAG	J	2	3	14,14,15	0.60	0	17,19,21	1.55	3 (17%)
3	NAG	K	1	1,3	14,14,15	0.55	0	17,19,21	0.93	0
3	NAG	K	2	3	14,14,15	0.54	0	17,19,21	1.97	3 (17%)
3	NAG	L	1	3,2	14,14,15	0.91	1 (7%)	17,19,21	1.77	4 (23%)
3	NAG	L	2	3	14,14,15	0.56	0	17,19,21	1.60	5 (29%)
3	NAG	M	1	1,3	14,14,15	0.62	0	17,19,21	2.88	8 (47%)
3	NAG	M	2	3	14,14,15	0.64	0	17,19,21	1.86	5 (29%)
3	NAG	N	1	3,2	14,14,15	0.52	0	17,19,21	1.93	5 (29%)
3	NAG	N	2	3	14,14,15	0.49	0	17,19,21	1.12	2 (11%)
3	NAG	O	1	1,3	14,14,15	0.44	0	17,19,21	1.62	3 (17%)
3	NAG	O	2	3	14,14,15	0.52	0	17,19,21	1.41	2 (11%)
3	NAG	P	1	3,2	14,14,15	1.04	1 (7%)	17,19,21	1.87	5 (29%)
3	NAG	P	2	3	14,14,15	0.63	0	17,19,21	0.92	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
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3,2	-	3/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	NAG	K	1	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	5/6/23/26	0/1/1/1
3	NAG	L	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	NAG	M	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	M	2	3	-	5/6/23/26	0/1/1/1
3	NAG	N	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	NAG	O	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	O	2	3	-	2/6/23/26	0/1/1/1
3	NAG	P	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	P	2	3	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1	NAG	O5-C1	-2.77	1.39	1.43
3	P	1	NAG	O7-C7	2.53	1.28	1.23
3	I	1	NAG	C1-C2	2.51	1.55	1.52

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1	NAG	C1-O5-C5	9.73	125.22	112.19
3	M	1	NAG	C2-N2-C7	7.30	132.68	122.90
3	M	1	NAG	O5-C1-C2	5.69	120.09	111.29
3	J	1	NAG	C2-N2-C7	5.66	130.48	122.90
3	M	2	NAG	C2-N2-C7	5.18	129.84	122.90
3	J	1	NAG	C1-C2-N2	4.93	118.21	110.43
3	K	2	NAG	C2-N2-C7	4.63	129.11	122.90
3	P	1	NAG	C1-O5-C5	-4.47	106.19	112.19
3	N	1	NAG	C2-N2-C7	4.45	128.86	122.90
3	O	1	NAG	C1-O5-C5	4.44	118.13	112.19
3	J	1	NAG	O5-C1-C2	-4.40	104.49	111.29
3	L	1	NAG	C2-N2-C7	-4.35	117.06	122.90
3	K	2	NAG	C1-O5-C5	4.05	117.62	112.19
3	O	2	NAG	C1-O5-C5	3.82	117.31	112.19
3	P	1	NAG	C2-N2-C7	-3.78	117.84	122.90
3	M	1	NAG	C8-C7-N2	3.59	122.07	116.12
3	N	1	NAG	C1-C2-N2	3.49	115.93	110.43
3	J	1	NAG	C3-C4-C5	-3.46	103.96	110.23
3	J	1	NAG	O5-C5-C6	3.43	114.34	107.66
3	K	2	NAG	C8-C7-N2	3.37	121.71	116.12
3	M	2	NAG	C8-C7-N2	3.37	121.71	116.12
3	N	1	NAG	O5-C5-C6	3.35	114.18	107.66
3	L	1	NAG	C3-C4-C5	-3.35	104.16	110.23
3	J	2	NAG	C3-C4-C5	-3.25	104.34	110.23
3	L	2	NAG	O3-C3-C2	3.00	115.64	109.40
3	M	1	NAG	O7-C7-C8	-2.97	116.76	122.05
3	O	1	NAG	O5-C1-C2	2.96	115.87	111.29
3	M	1	NAG	C4-C3-C2	2.94	115.33	111.02
3	L	2	NAG	O5-C1-C2	-2.92	106.78	111.29
3	P	1	NAG	O7-C7-N2	2.81	126.95	121.98
3	I	1	NAG	O4-C4-C5	2.75	116.10	109.32
3	J	1	NAG	O7-C7-N2	2.74	126.82	121.98
3	M	1	NAG	C1-O5-C5	2.67	115.76	112.19
3	P	1	NAG	C8-C7-N2	-2.57	111.86	116.12
3	M	1	NAG	C3-C4-C5	2.57	114.89	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2	NAG	O7-C7-C8	-2.55	117.52	122.05
3	L	1	NAG	C1-O5-C5	-2.52	108.81	112.19
3	N	1	NAG	C3-C4-C5	-2.48	105.73	110.23
3	I	2	NAG	C1-O5-C5	2.43	115.44	112.19
3	N	2	NAG	C1-O5-C5	2.43	115.44	112.19
3	N	1	NAG	O7-C7-N2	2.41	126.25	121.98
3	M	2	NAG	C1-O5-C5	2.38	115.37	112.19
3	L	1	NAG	O5-C1-C2	-2.31	107.72	111.29
3	P	1	NAG	O5-C5-C6	2.31	112.16	107.66
3	L	2	NAG	C1-C2-N2	-2.31	106.80	110.43
3	L	2	NAG	O7-C7-N2	2.29	126.03	121.98
3	N	2	NAG	C4-C3-C2	2.22	114.27	111.02
3	O	2	NAG	C2-N2-C7	2.22	125.87	122.90
3	O	1	NAG	O4-C4-C5	2.20	114.75	109.32
3	M	2	NAG	C1-C2-N2	2.14	113.81	110.43
3	M	1	NAG	C1-C2-N2	2.14	113.80	110.43
3	L	2	NAG	O7-C7-C8	-2.13	118.25	122.05
3	J	2	NAG	C1-C2-N2	-2.04	107.22	110.43
3	J	2	NAG	O5-C1-C2	-2.02	108.17	111.29

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	K	1	NAG	C1

All (24) torsion outliers are listed below:

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

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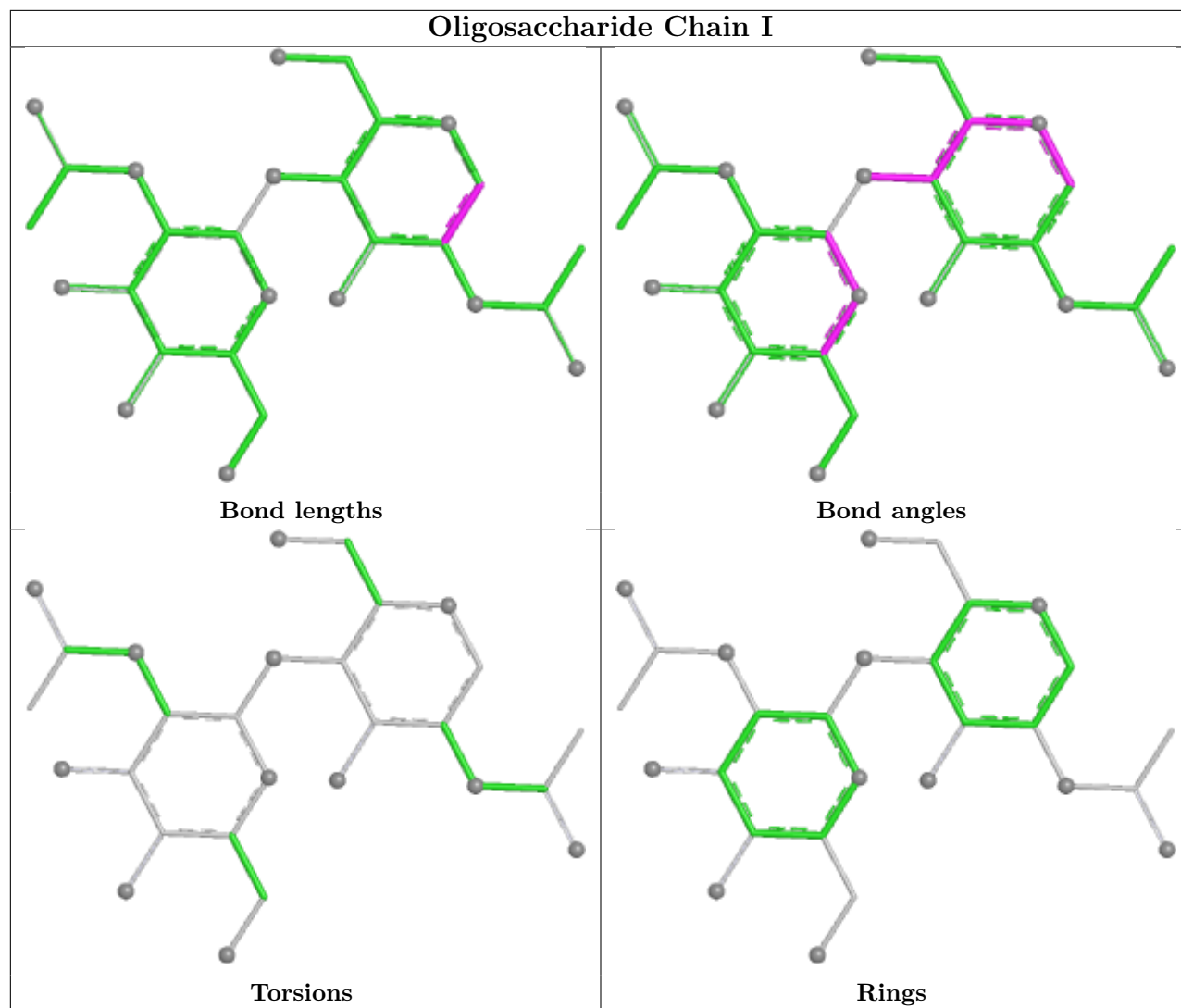
Mol	Chain	Res	Type	Atoms
3	M	2	NAG	O7-C7-N2-C2
3	J	1	NAG	O5-C5-C6-O6
3	O	1	NAG	O5-C5-C6-O6
3	O	1	NAG	C4-C5-C6-O6
3	J	1	NAG	C3-C2-N2-C7
3	M	2	NAG	C3-C2-N2-C7
3	O	2	NAG	C3-C2-N2-C7
3	M	2	NAG	O5-C5-C6-O6
3	M	2	NAG	C1-C2-N2-C7
3	O	2	NAG	C1-C2-N2-C7

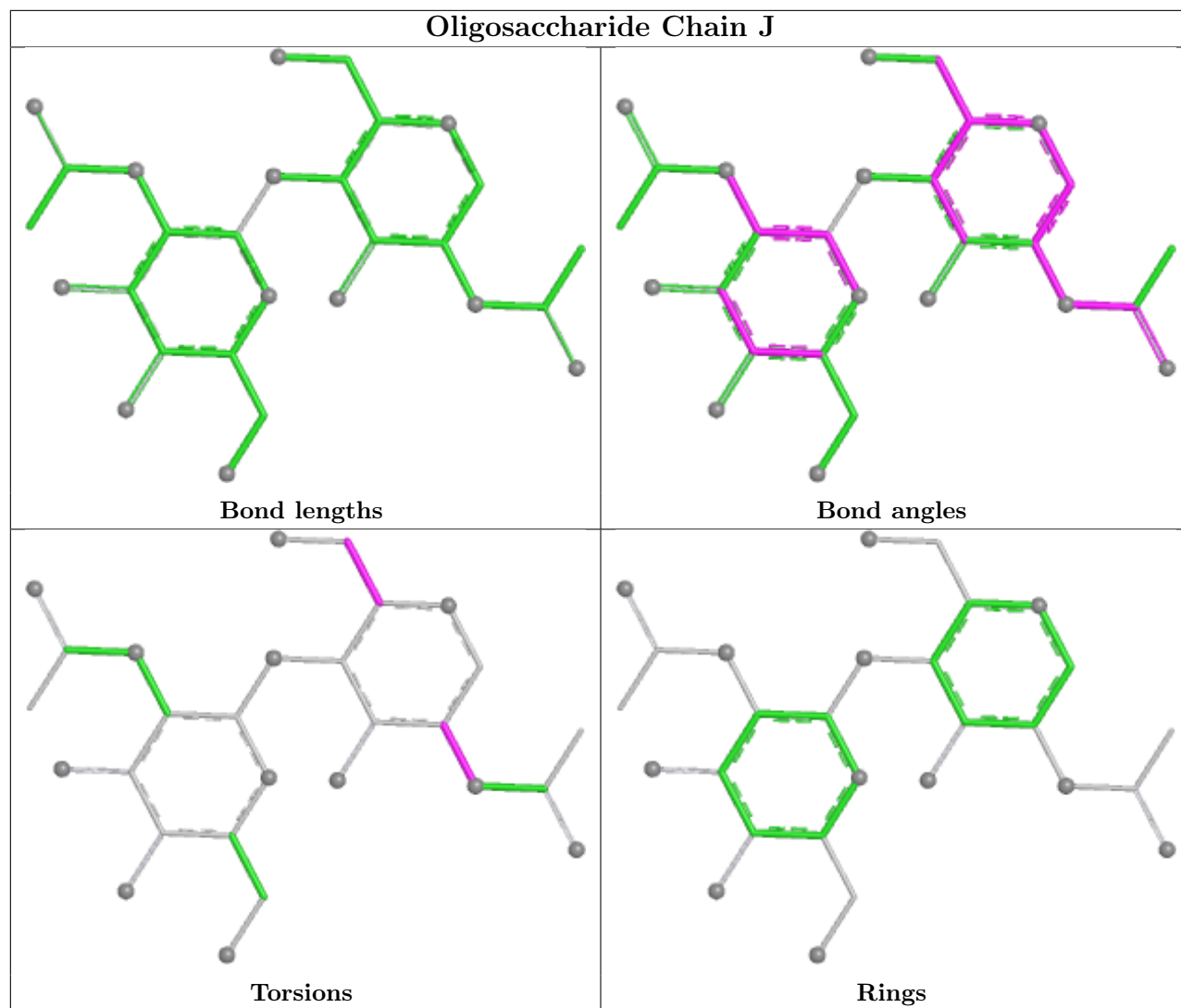
There are no ring outliers.

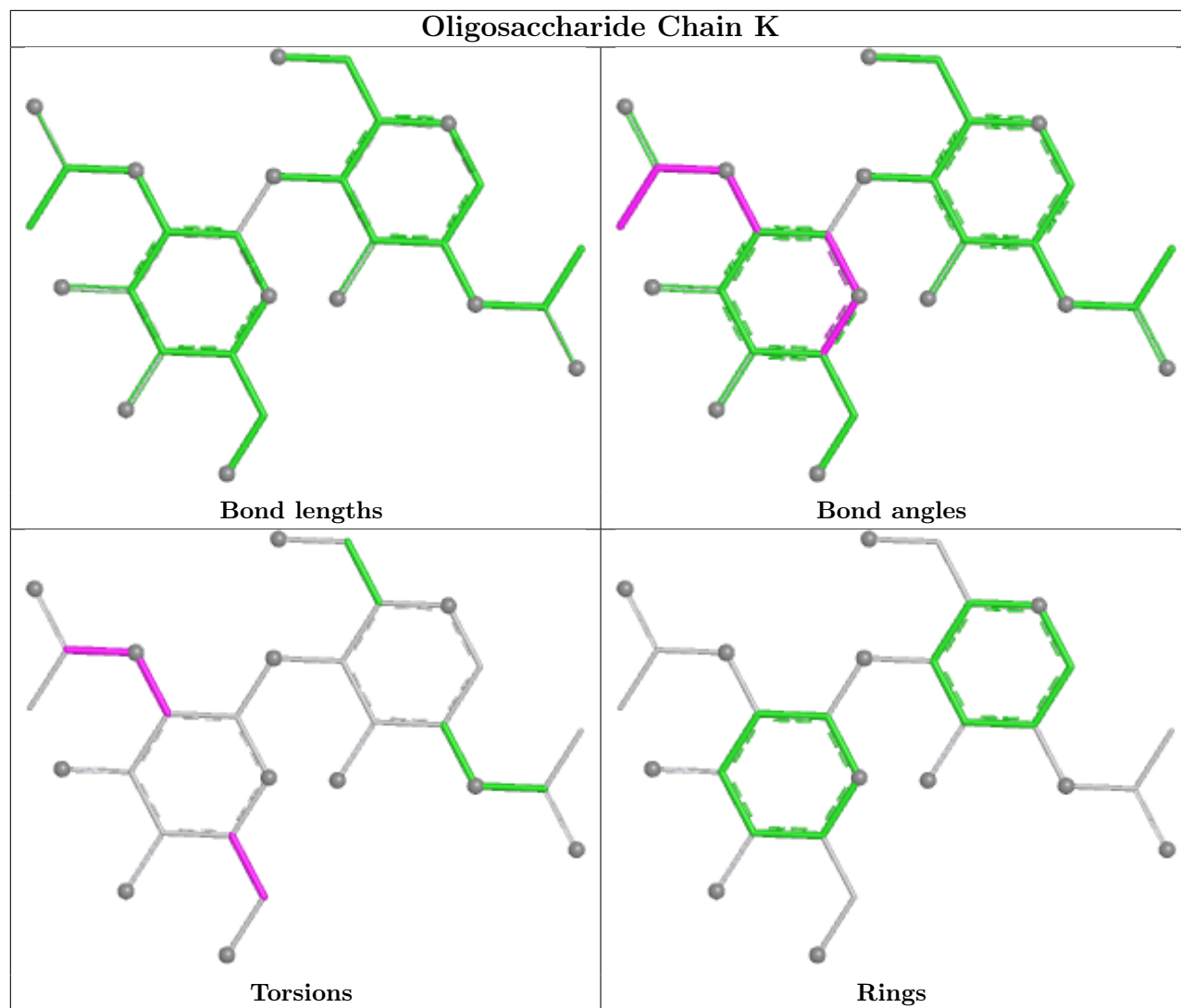
6 monomers are involved in 9 short contacts:

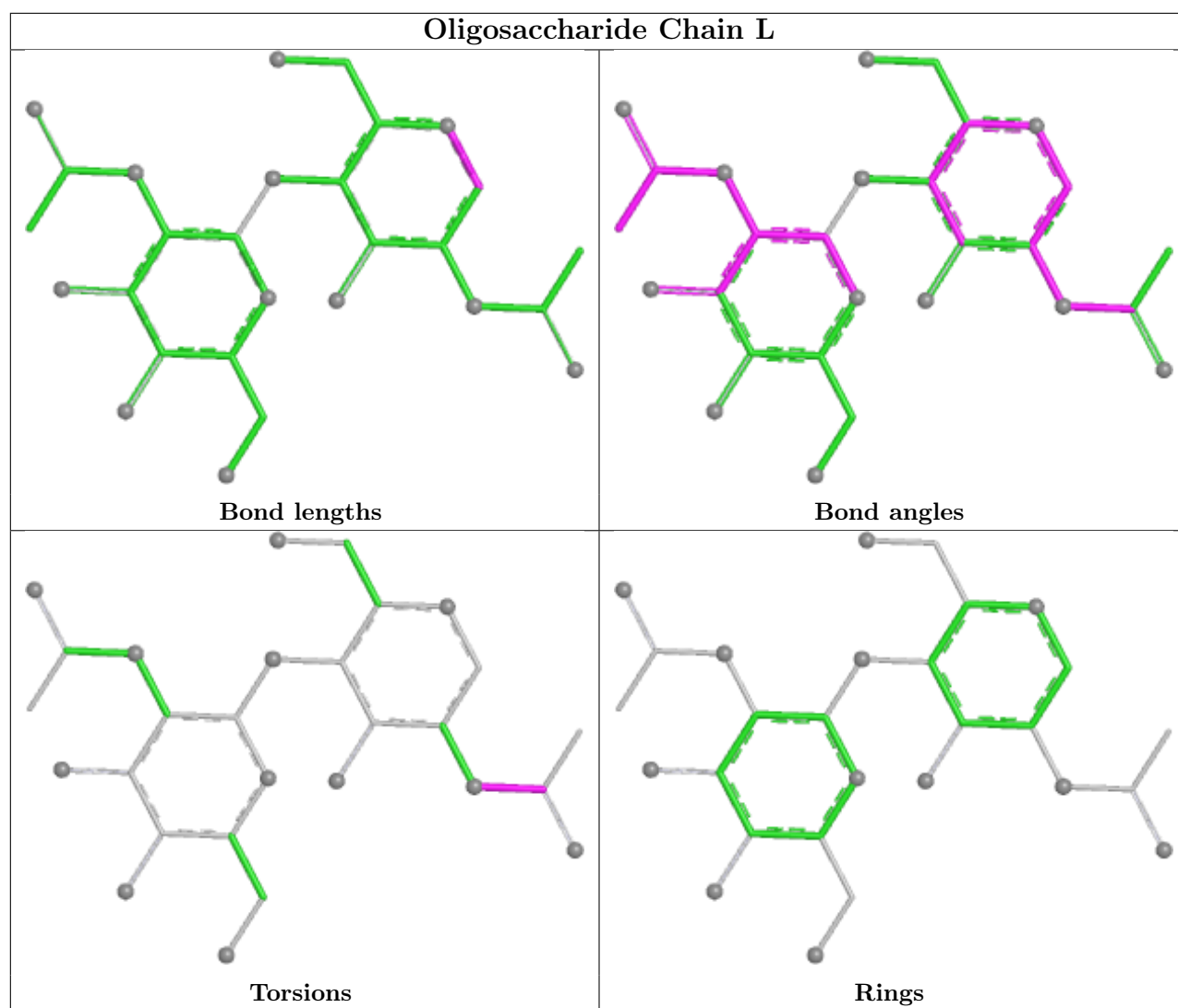
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	1	NAG	1	0
3	M	2	NAG	1	0
3	P	1	NAG	3	0
3	M	1	NAG	2	0
3	J	1	NAG	1	0
3	O	1	NAG	1	0

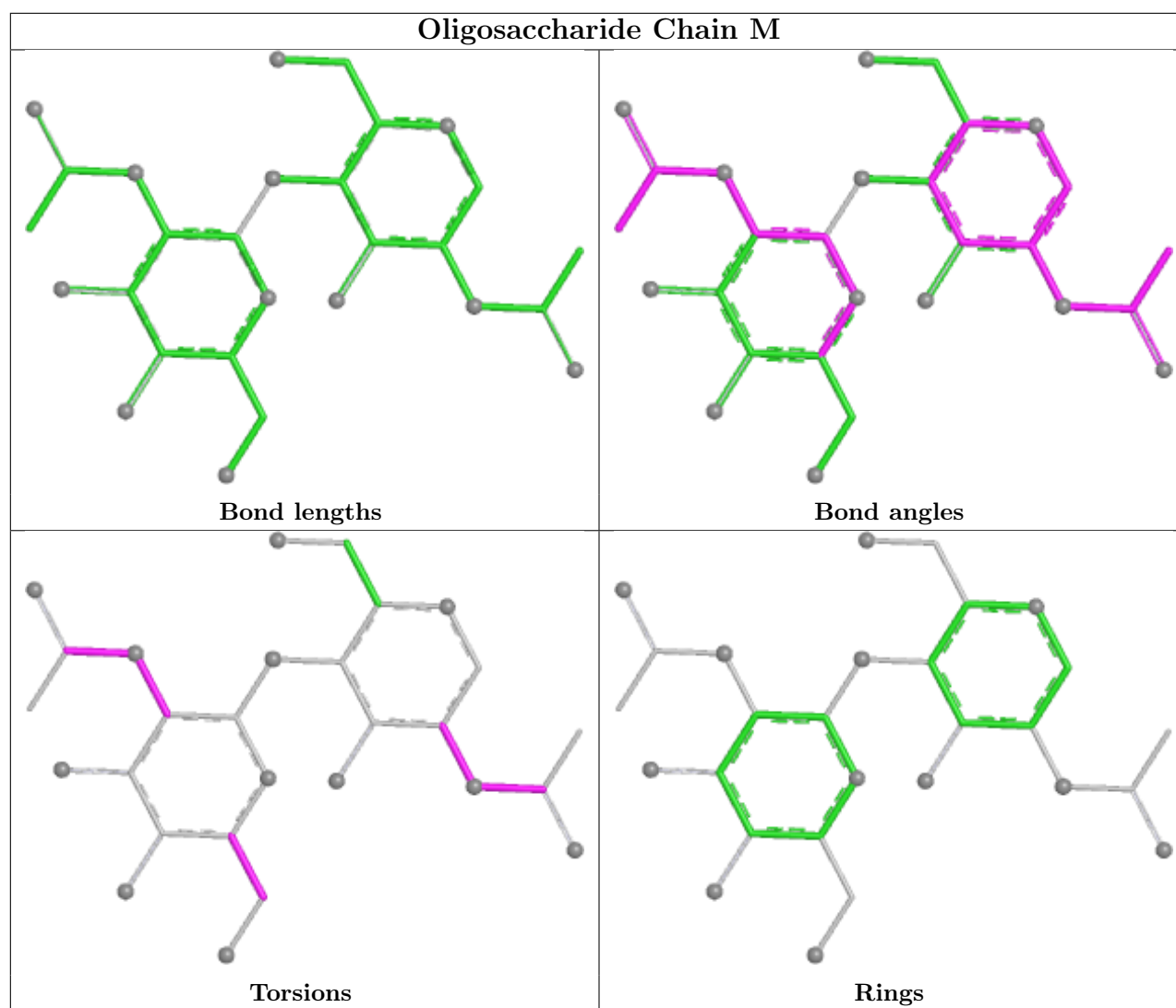
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

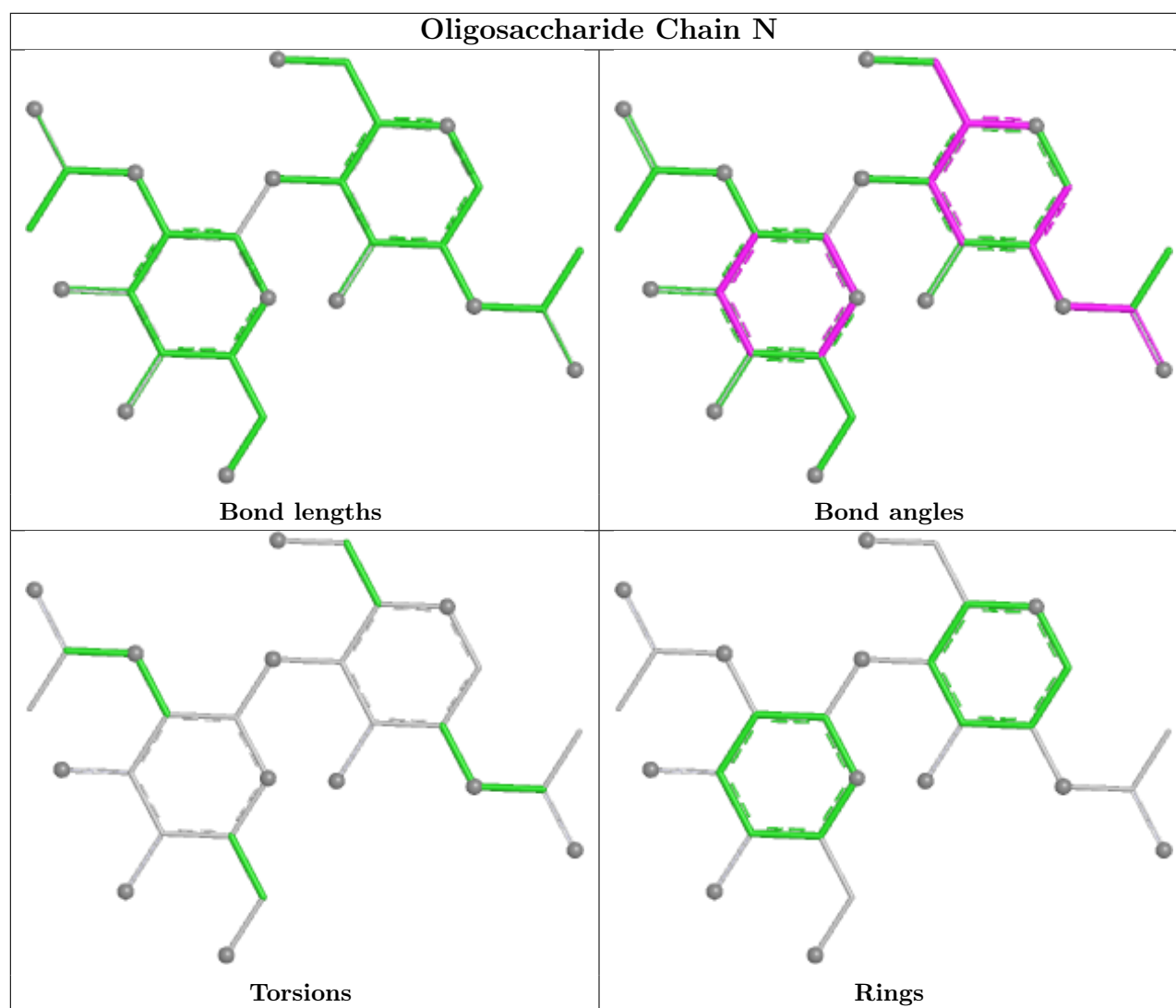


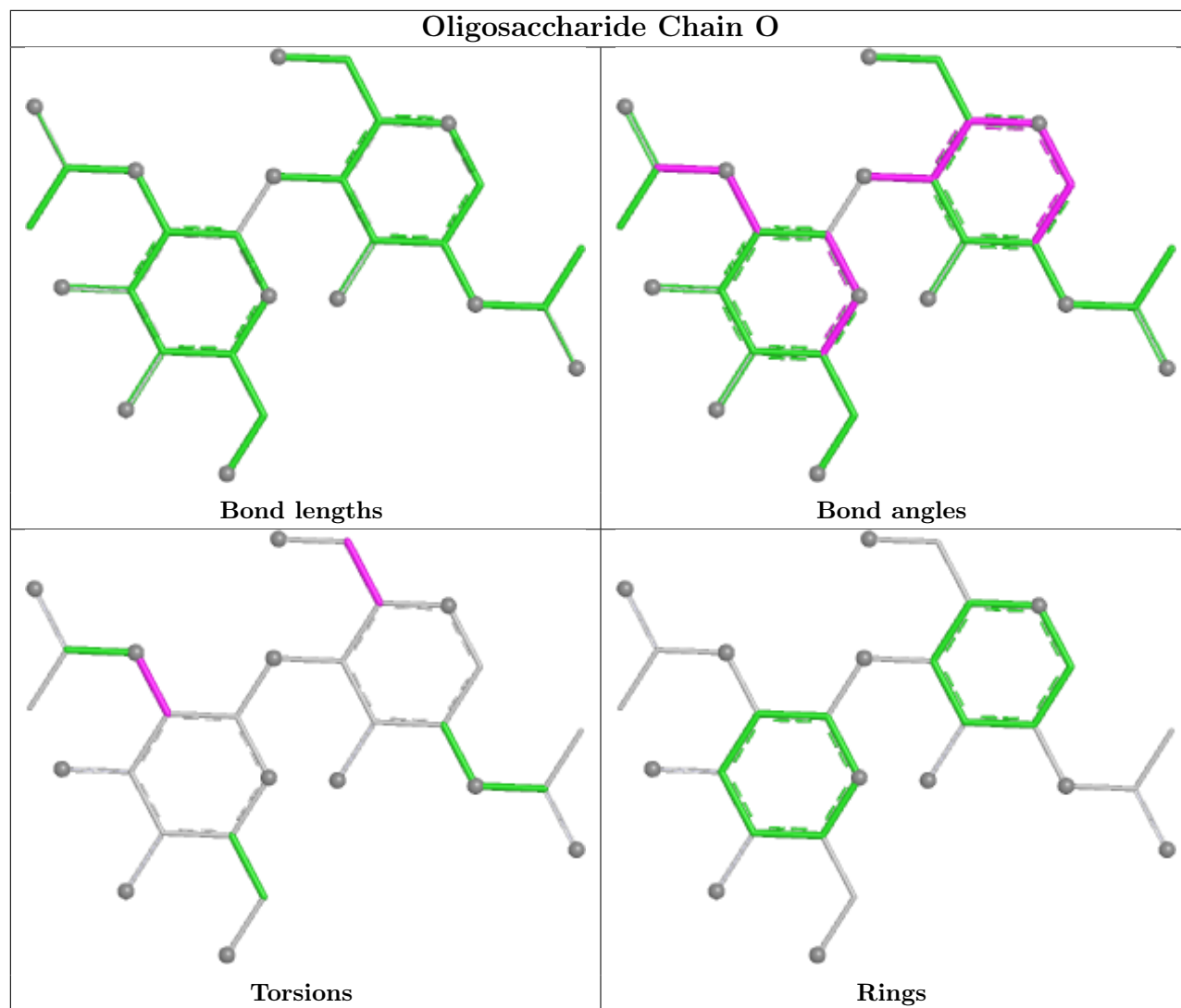


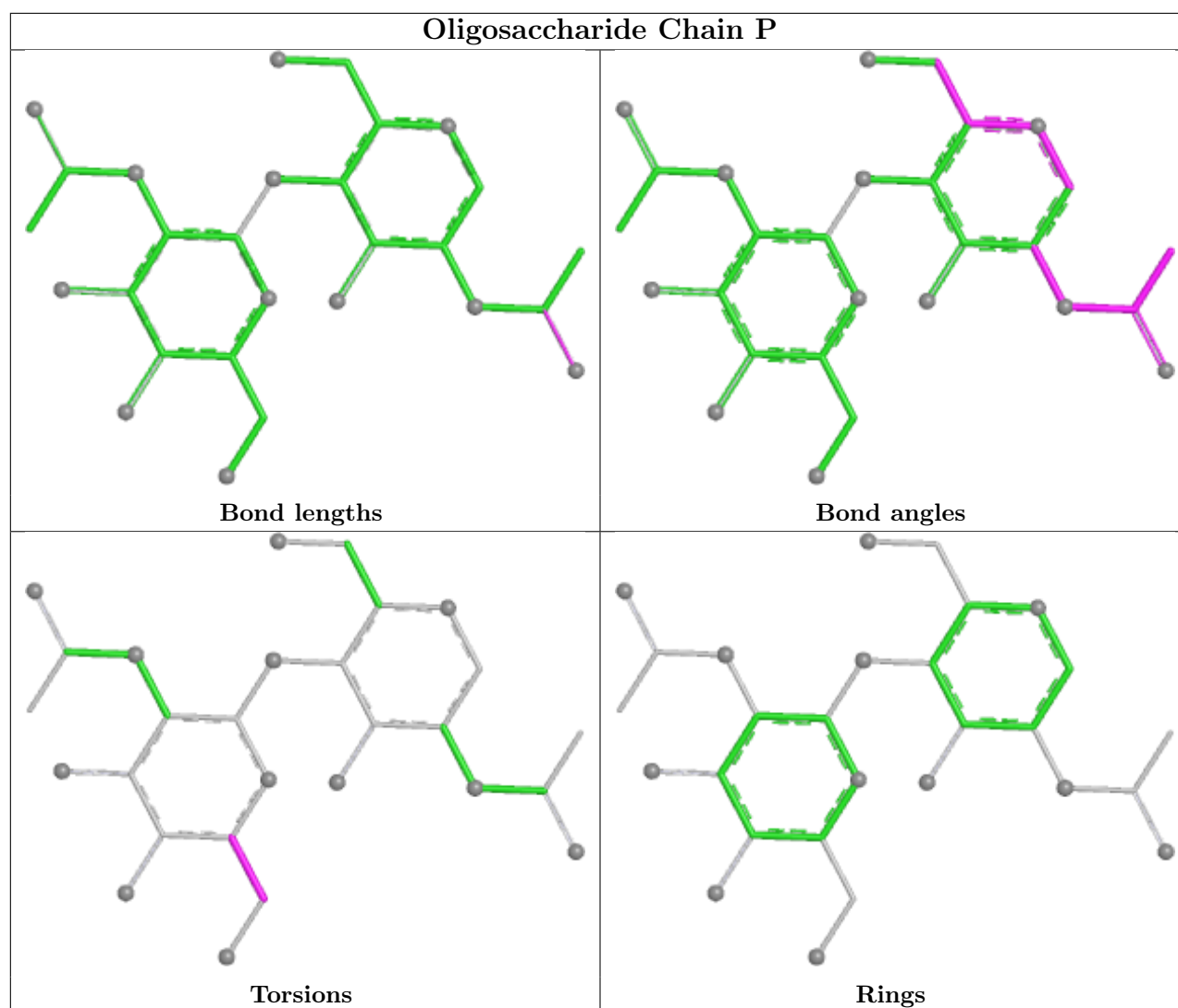












5.6 Ligand geometry [i](#)

3 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	A	3401	1	14,14,15	0.50	0	17,19,21	1.50	3 (17%)
4	NAG	G	3401	1	14,14,15	0.56	0	17,19,21	1.93	1 (5%)
4	NAG	E	3401	1	14,14,15	0.51	0	17,19,21	2.03	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
4	NAG	A	3401	1	-	4/6/23/26	0/1/1/1
4	NAG	G	3401	1	-	0/6/23/26	0/1/1/1
4	NAG	E	3401	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	3401	NAG	C1-O5-C5	7.58	122.35	112.19
4	G	3401	NAG	C1-O5-C5	6.79	121.29	112.19
4	A	3401	NAG	O5-C1-C2	-3.60	105.73	111.29
4	A	3401	NAG	C1-O5-C5	3.44	116.80	112.19
4	A	3401	NAG	O5-C5-C6	2.19	111.93	107.66
4	E	3401	NAG	O5-C1-C2	2.00	114.39	111.29

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	3401	NAG	O5-C5-C6-O6
4	E	3401	NAG	C4-C5-C6-O6
4	A	3401	NAG	C8-C7-N2-C2
4	A	3401	NAG	O7-C7-N2-C2
4	A	3401	NAG	C4-C5-C6-O6
4	A	3401	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	3401	NAG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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, 95th 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 ²)	Q<0.9
1	A	516/518 (99%)	0.84	69 (13%) 7 3	63, 154, 346, 442	0
1	C	516/518 (99%)	0.26	34 (6%) 24 12	59, 111, 216, 263	0
1	E	516/518 (99%)	0.43	36 (6%) 22 11	65, 161, 327, 484	0
1	G	516/518 (99%)	0.67	53 (10%) 12 6	74, 168, 265, 356	0
2	B	141/141 (100%)	-0.20	1 (0%) 84 68	52, 94, 187, 261	0
2	D	140/141 (99%)	-0.17	1 (0%) 84 68	55, 91, 177, 216	0
2	F	138/141 (97%)	-0.14	0 100 100	66, 112, 200, 262	0
2	H	138/141 (97%)	0.04	3 (2%) 62 41	82, 124, 238, 270	0
All	All	2621/2636 (99%)	0.41	197 (7%) 20 10	52, 135, 274, 484	0

All (197) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	155	THR	6.9
1	E	153	SER	6.8
1	A	153	SER	6.7
1	G	66	PRO	6.5
1	G	61	ASP	6.3
1	E	155	THR	6.2
1	C	154	PHE	6.2
1	A	154	PHE	6.1
1	G	155	THR	5.7
1	A	539	ILE	5.7
1	E	127	TYR	5.6
1	A	127	TYR	5.5
1	E	66	PRO	5.5
1	C	153	SER	5.4
1	G	157	VAL	5.4
1	G	159	ILE	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	418	GLY	5.1
1	G	321	ALA	5.1
1	A	61	ASP	4.7
1	A	157	VAL	4.7
1	E	158	ASP	4.6
1	E	159	ILE	4.6
1	A	159	ILE	4.6
1	C	539	ILE	4.5
1	A	491	VAL	4.5
1	G	127	TYR	4.5
1	C	156	GLN	4.5
1	G	153	SER	4.4
1	E	422	TYR	4.4
1	G	539	ILE	4.4
1	G	154	PHE	4.3
1	A	156	GLN	4.3
1	G	78	PRO	4.2
1	E	140	ASN	4.1
1	C	127	TYR	4.0
1	G	156	GLN	4.0
1	A	161	ASP	4.0
1	E	539	ILE	4.0
1	A	62	GLU	4.0
1	G	65	THR	4.0
1	G	68	ARG	3.9
1	E	154	PHE	3.9
1	A	158	ASP	3.9
1	A	136	PHE	3.7
1	G	115	MET	3.7
1	G	162	ARG	3.6
1	G	502	GLY	3.6
1	A	78	PRO	3.5
1	C	155	THR	3.5
1	A	152	GLU	3.4
1	E	157	VAL	3.4
1	C	65	THR	3.4
1	G	62	GLU	3.4
1	G	488	TYR	3.4
1	C	61	ASP	3.4
1	A	376	LYS	3.4
1	E	421	LYS	3.4
1	G	322	SER	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	319	ASP	3.3
1	E	152	GLU	3.3
1	G	380	CYS	3.3
1	A	433	THR	3.3
1	C	301	TRP	3.3
1	C	159	ILE	3.3
1	E	65	THR	3.3
1	A	412	GLU	3.2
1	A	312	GLY	3.2
1	G	116	GLY	3.2
1	A	255	VAL	3.1
1	G	140	ASN	3.1
1	G	114	VAL	3.1
1	E	156	GLN	3.1
1	G	475	GLU	3.1
1	G	366	CYS	3.1
1	E	142	PHE	3.0
1	A	476	VAL	3.0
1	E	540	ILE	3.0
1	C	540	ILE	3.0
1	C	64	ASN	3.0
1	C	255	VAL	2.9
1	G	312	GLY	2.9
1	C	373	ASP	2.9
1	A	300	VAL	2.9
1	C	135	ARG	2.9
1	E	43	LEU	2.9
1	G	254	LEU	2.9
1	C	449	ALA	2.9
1	E	374	PRO	2.9
1	E	314	PHE	2.9
1	C	158	ASP	2.8
1	E	542	ASP	2.8
1	A	65	THR	2.8
1	C	42	GLU	2.8
1	G	60	MET	2.8
1	E	62	GLU	2.8
1	A	449	ALA	2.8
1	A	342	THR	2.8
1	G	142	PHE	2.8
1	A	160	GLY	2.8
1	A	434	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	G	158	ASP	2.7
1	C	378	ARG	2.7
1	E	114	VAL	2.7
1	E	162	ARG	2.7
1	A	365	VAL	2.7
1	G	300	VAL	2.7
1	C	152	GLU	2.7
1	A	478	TYR	2.7
1	A	64	ASN	2.7
1	C	141	GLN	2.6
1	G	164	MET	2.6
1	A	296	HIS	2.6
1	C	66	PRO	2.6
1	E	60	MET	2.6
1	A	435	THR	2.6
1	A	524	PHE	2.6
1	A	318	ASN	2.6
1	C	136	PHE	2.6
1	A	495	ALA	2.6
1	G	436	THR	2.6
1	A	475	GLU	2.5
1	A	343	SER	2.5
1	A	138	ARG	2.5
1	A	140	ASN	2.5
1	A	137	ILE	2.5
1	G	59	ILE	2.5
1	A	404	LEU	2.5
1	A	116	GLY	2.5
1	C	162	ARG	2.5
1	A	494	ALA	2.5
1	A	455	TYR	2.5
1	E	501	LYS	2.5
1	A	87	ASP	2.5
2	H	33	ALA	2.4
1	C	376	LYS	2.4
1	A	540	ILE	2.4
1	A	472	LEU	2.4
1	E	278	ILE	2.4
1	A	135	ARG	2.4
1	G	343	SER	2.4
1	G	484	ASN	2.4
1	G	339	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	474	TYR	2.3
1	C	318	ASN	2.3
1	C	254	LEU	2.3
1	G	182	TYR	2.3
1	C	157	VAL	2.3
1	A	493	THR	2.3
2	H	115	SER	2.3
1	A	66	PRO	2.3
2	D	165	MET	2.3
1	A	309	CYS	2.3
1	G	486	ARG	2.3
1	A	459	LEU	2.2
1	G	301	TRP	2.2
1	E	61	ASP	2.2
1	G	152	GLU	2.2
1	E	78	PRO	2.2
1	G	308	THR	2.2
1	C	138	ARG	2.2
2	B	146	ASN	2.2
1	G	540	ILE	2.2
1	E	139	GLU	2.2
1	A	509	TYR	2.2
1	A	77	GLU	2.2
1	A	405	ALA	2.2
1	E	412	GLU	2.2
1	E	307	CYS	2.2
1	A	162	ARG	2.1
1	G	29	ASN	2.1
1	E	373	ASP	2.1
1	E	462	LEU	2.1
1	A	42	GLU	2.1
1	G	511	PHE	2.1
1	C	325	CYS	2.1
1	A	378	ARG	2.1
1	G	485	GLU	2.1
2	H	28	VAL	2.1
1	A	542	ASP	2.1
1	G	67	ILE	2.1
1	G	319	ASP	2.1
1	C	62	GLU	2.1
1	E	511	PHE	2.1
1	A	301	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	409	TYR	2.1
1	C	380	CYS	2.1
1	G	479	TYR	2.1
1	A	457	VAL	2.0
1	E	255	VAL	2.0
1	G	296	HIS	2.0
1	A	498	THR	2.0
1	A	518	ALA	2.0
1	G	401	THR	2.0
1	G	365	VAL	2.0
1	C	278	ILE	2.0
1	A	295	PRO	2.0
1	A	327	ARG	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, 95th 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.

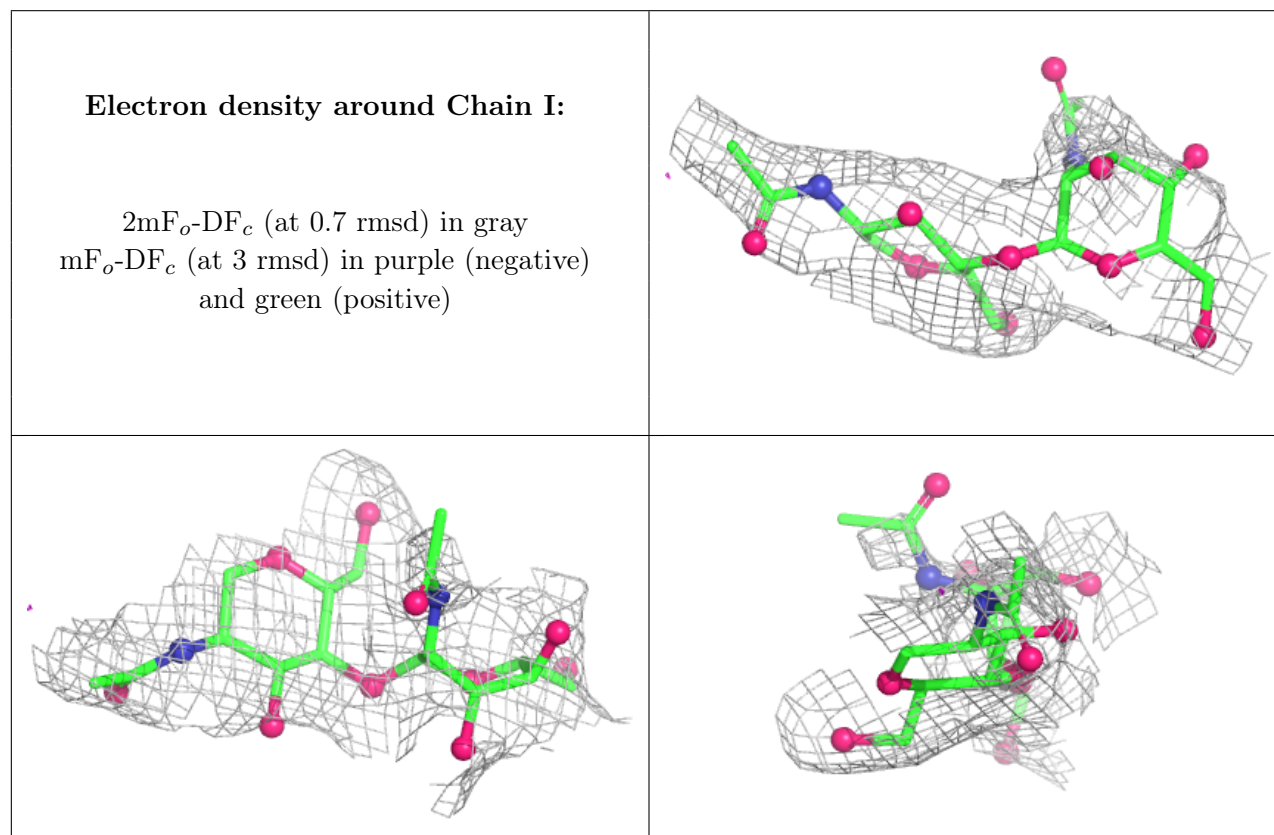
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	M	2	14/15	0.42	0.12	203,226,238,248	0
3	NAG	I	2	14/15	0.45	0.12	267,281,301,301	0
3	NAG	K	2	14/15	0.54	0.13	162,181,188,207	0
3	NAG	O	1	14/15	0.54	0.10	194,202,215,218	0
3	NAG	M	1	14/15	0.67	0.10	197,221,234,235	0
3	NAG	P	2	14/15	0.70	0.11	114,124,156,161	0
3	NAG	I	1	14/15	0.71	0.09	215,228,236,249	0
3	NAG	O	2	14/15	0.72	0.09	186,213,229,232	0
3	NAG	N	2	14/15	0.81	0.09	126,136,149,161	0
3	NAG	J	2	14/15	0.83	0.10	94,101,126,127	0
3	NAG	L	2	14/15	0.86	0.09	96,100,112,113	0
3	NAG	P	1	14/15	0.90	0.08	92,105,139,142	0
3	NAG	K	1	14/15	0.91	0.08	112,127,154,169	0
3	NAG	L	1	14/15	0.92	0.09	79,85,98,117	0
3	NAG	N	1	14/15	0.95	0.07	97,105,116,122	0

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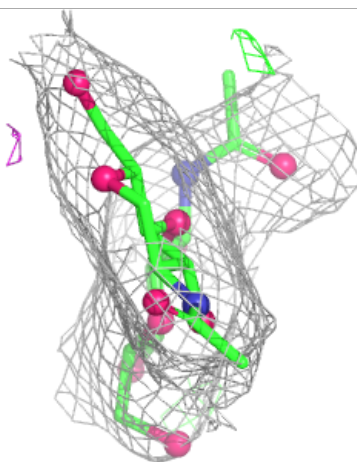
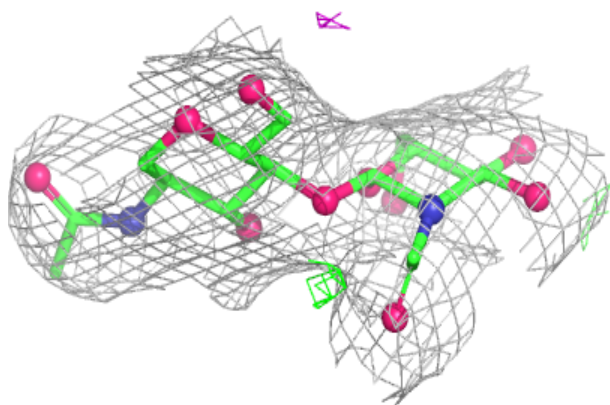
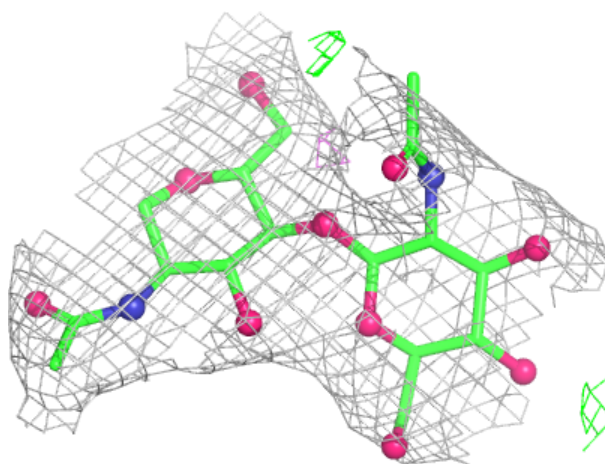
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	J	1	14/15	0.97	0.06	76,86,96,100	0

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.



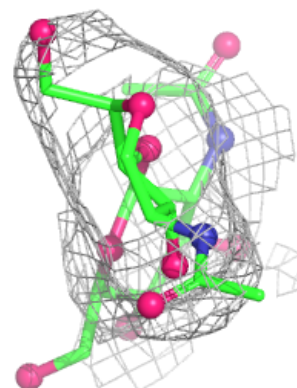
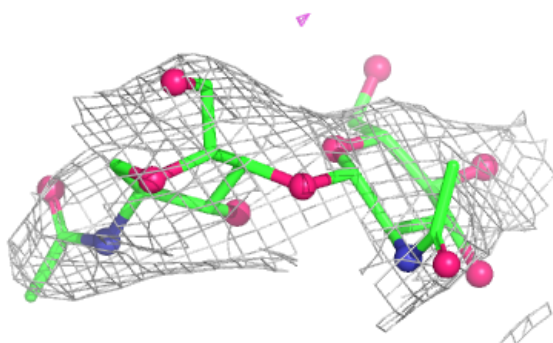
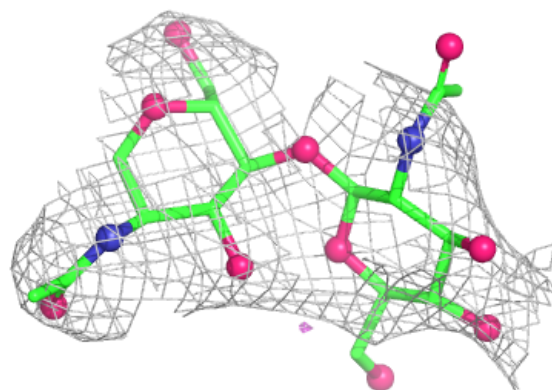
Electron density around Chain J:

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

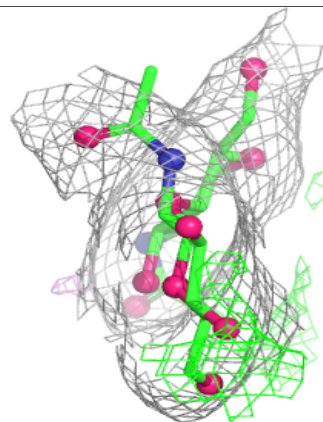
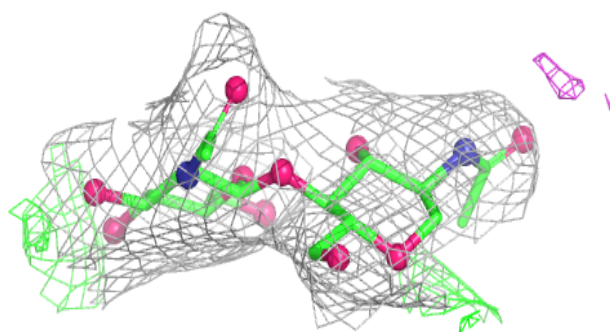
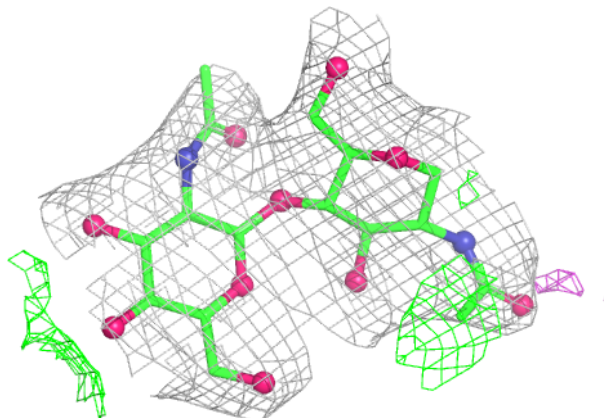


Electron density around Chain K:

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

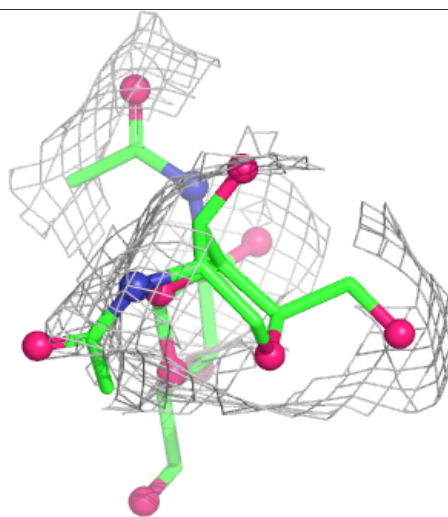
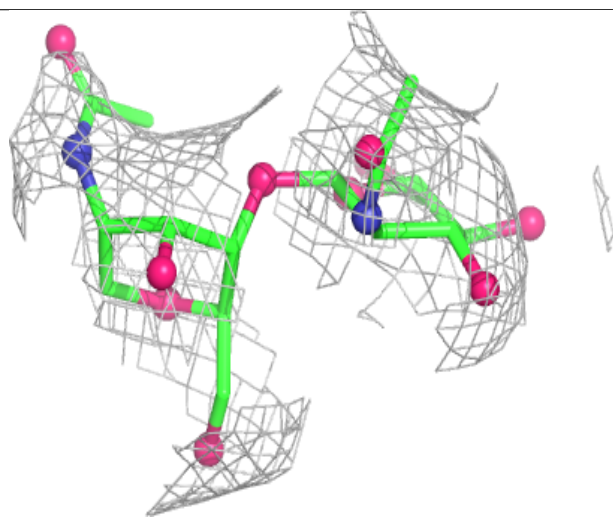
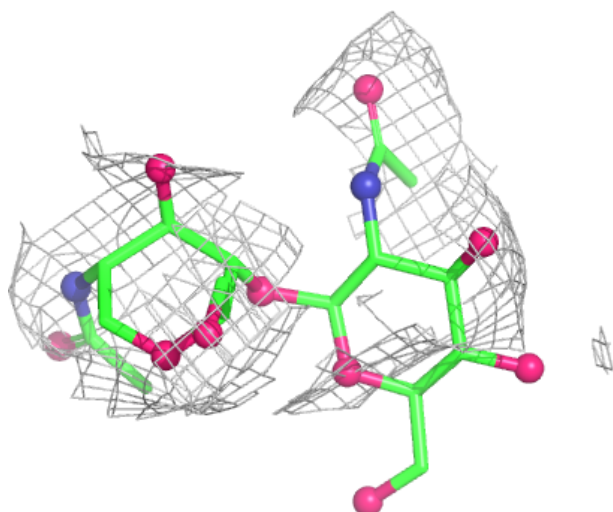
**Electron density around Chain L:**

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



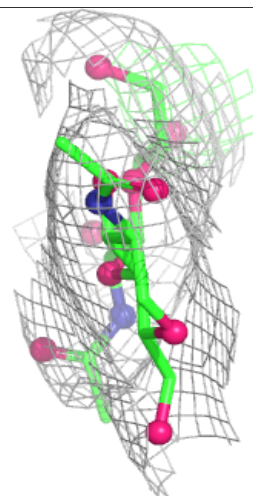
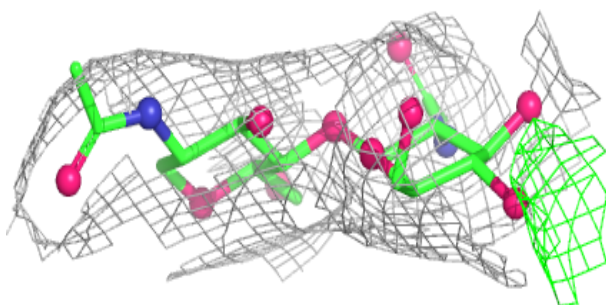
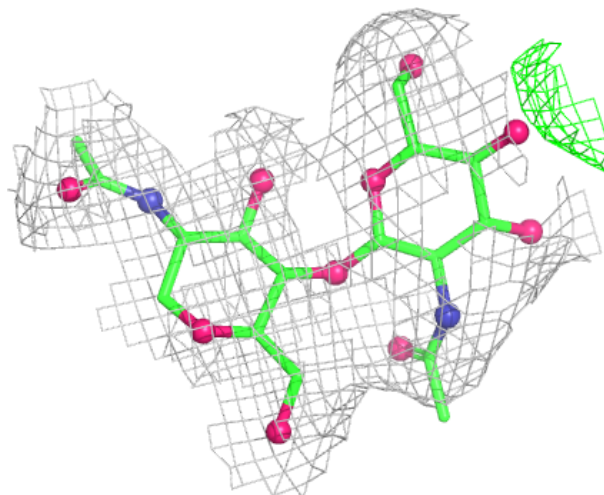
Electron density around Chain M:

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



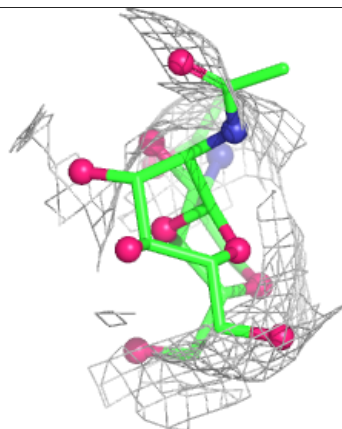
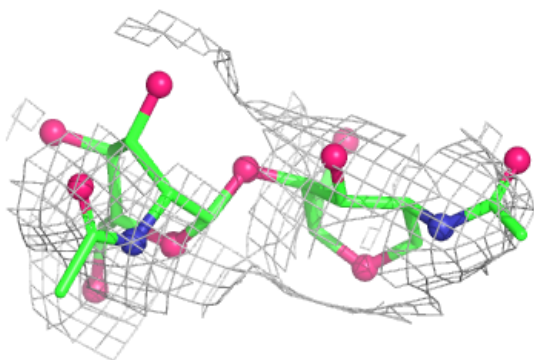
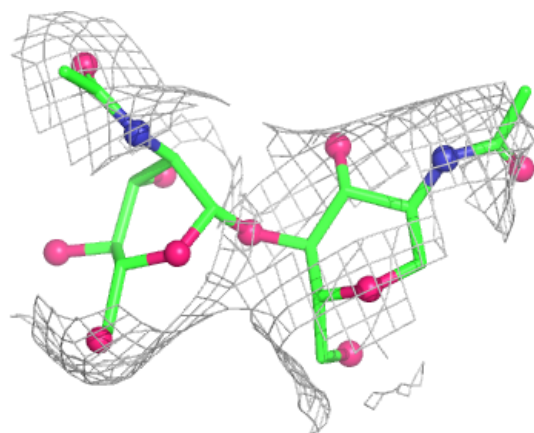
Electron density around Chain N:

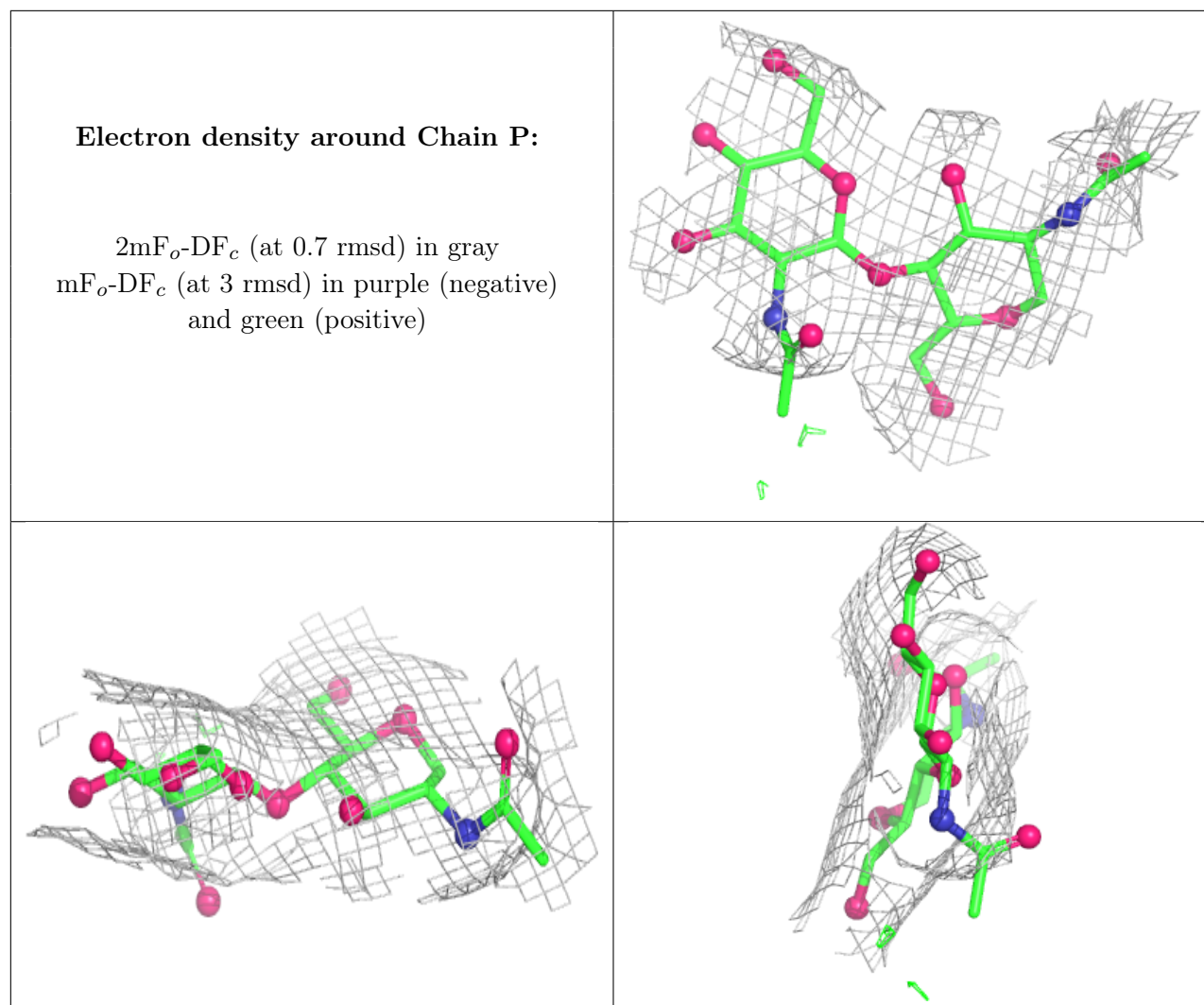
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain O:

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





6.4 Ligands [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, 95th 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($\text{\AA}^2$)	Q<0.9
4	NAG	E	3401	14/15	0.34	0.12	207,252,264,265	0
4	NAG	A	3401	14/15	0.48	0.20	195,227,234,236	0
4	NAG	G	3401	14/15	0.52	0.13	210,231,255,273	0

6.5 Other polymers [i](#)

There are no such residues in this entry.