



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 09:42 AM UTC

PDB ID : 4HG4 / pdb_00004hg4
Title : Crystal structure of Fab 2G1 in complex with a H2N2 influenza virus hemagglutinin
Authors : Xu, R.; Wilson, I.A.
Deposited on : 2012-10-06
Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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:

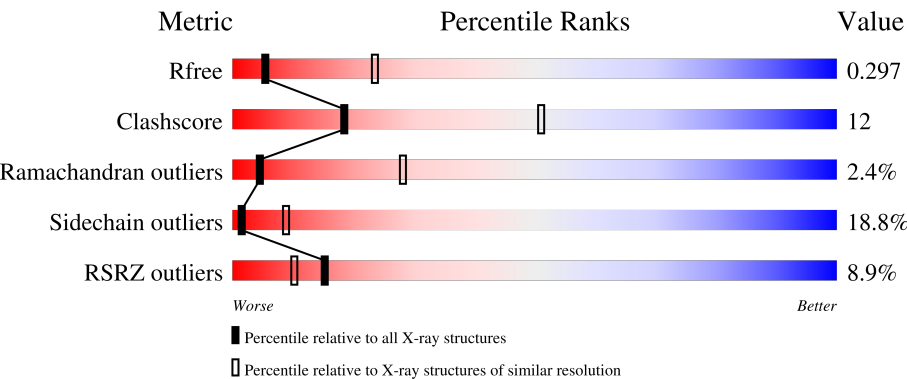
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	327	2% 62%30%6%
1	B	327	4% 58%32%6%
1	C	327	5% 58%33%7%
1	D	327	2% 63%30%5%
1	E	327	5% 59%34%5%

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Mol	Chain	Length	Quality of chain
1	F	327	
1	G	327	
1	H	327	
1	I	327	
2	a	174	
2	b	174	
2	c	174	
2	d	174	
2	e	174	
2	f	174	
2	g	174	
2	h	174	
2	i	174	
3	J	223	
3	L	223	
3	N	223	
3	P	223	
3	R	223	
3	T	223	
3	V	223	
3	X	223	
3	Z	223	
4	K	214	
4	M	214	
4	O	214	

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Mol	Chain	Length	Quality of chain
4	Q	214	
4	S	214	
4	U	214	
4	W	214	
4	Y	214	
4	z	214	
5	j	2	
5	k	2	
5	m	2	
5	n	2	
5	o	2	
5	q	2	
5	r	2	
5	s	2	
5	t	2	
6	l	3	
6	p	3	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 58742 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2531	1593	438	485	15			
1	B	319	Total	C	N	O	S	0	0	0
			2503	1577	433	478	15			
1	C	324	Total	C	N	O	S	0	0	0
			2539	1599	439	486	15			
1	D	324	Total	C	N	O	S	0	0	0
			2539	1599	439	486	15			
1	E	323	Total	C	N	O	S	0	0	0
			2531	1593	438	485	15			
1	F	324	Total	C	N	O	S	0	0	0
			2539	1599	439	486	15			
1	G	324	Total	C	N	O	S	0	0	0
			2539	1599	439	486	15			
1	H	325	Total	C	N	O	S	0	0	0
			2548	1604	440	489	15			
1	I	324	Total	C	N	O	S	0	0	0
			2539	1599	439	486	15			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	PRO	-	expression tag	UNP Q67085
B	9	PRO	-	expression tag	UNP Q67085
C	9	PRO	-	expression tag	UNP Q67085
D	9	PRO	-	expression tag	UNP Q67085
E	9	PRO	-	expression tag	UNP Q67085
F	9	PRO	-	expression tag	UNP Q67085
G	9	PRO	-	expression tag	UNP Q67085
H	9	PRO	-	expression tag	UNP Q67085
I	9	PRO	-	expression tag	UNP Q67085

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	a	171	Total	C	N	O	S	0	0	0
			1387	866	236	276	9			
2	b	167	Total	C	N	O	S	0	0	0
			1345	836	229	271	9			
2	c	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			
2	d	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			
2	e	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			
2	f	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			
2	g	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			
2	h	167	Total	C	N	O	S	0	0	0
			1355	845	231	270	9			
2	i	172	Total	C	N	O	S	0	0	0
			1396	871	237	279	9			

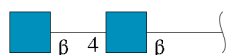
- Molecule 3 is a protein called Fab 2G1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	J	115	Total	C	N	O	S	0	0	0
			871	555	142	171	3			
3	L	212	Total	C	N	O	S	0	0	0
			1578	1004	258	311	5			
3	N	223	Total	C	N	O	S	0	0	0
			1648	1043	271	328	6			
3	P	161	Total	C	N	O	S	0	0	0
			1207	770	195	239	3			
3	R	214	Total	C	N	O	S	0	0	0
			1589	1010	260	314	5			
3	T	213	Total	C	N	O	S	0	0	0
			1580	1005	259	311	5			
3	V	117	Total	C	N	O	S	0	0	0
			883	564	144	172	3			
3	X	164	Total	C	N	O	S	0	0	0
			1232	785	201	242	4			
3	Z	167	Total	C	N	O	S	0	0	0
			1262	807	205	246	4			

- Molecule 4 is a protein called Fab 2G1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	K	106	Total	C	N	O	S	0	0	0
			826	518	140	166	2			
4	M	214	Total	C	N	O	S	0	0	0
			1661	1037	282	337	5			
4	O	214	Total	C	N	O	S	0	0	0
			1661	1037	282	337	5			
4	Q	157	Total	C	N	O	S	0	0	0
			1217	760	206	248	3			
4	S	211	Total	C	N	O	S	0	0	0
			1642	1027	279	332	4			
4	U	211	Total	C	N	O	S	0	0	0
			1642	1027	279	332	4			
4	W	105	Total	C	N	O	S	0	0	0
			818	512	139	165	2			
4	Y	109	Total	C	N	O	S	0	0	0
			853	534	147	170	2			
4	z	119	Total	C	N	O	S	0	0	0
			915	568	155	190	2			

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



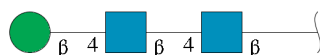
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	j	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	k	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	m	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	n	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	o	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	q	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	r	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	s	2	Total	C	N	O	0	0	0
			28	16	2	10			

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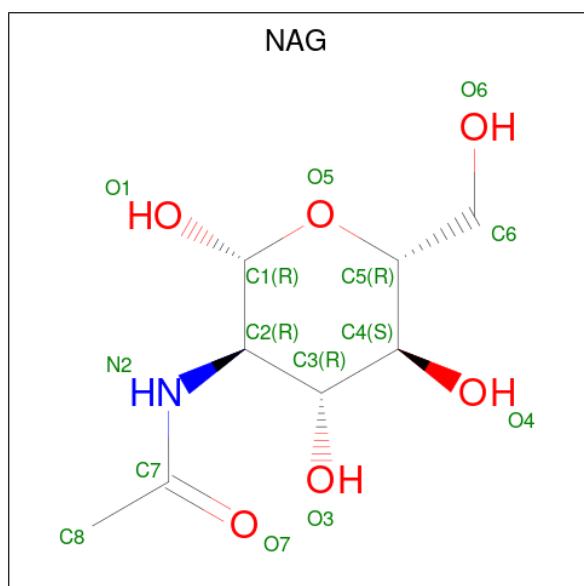
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	t	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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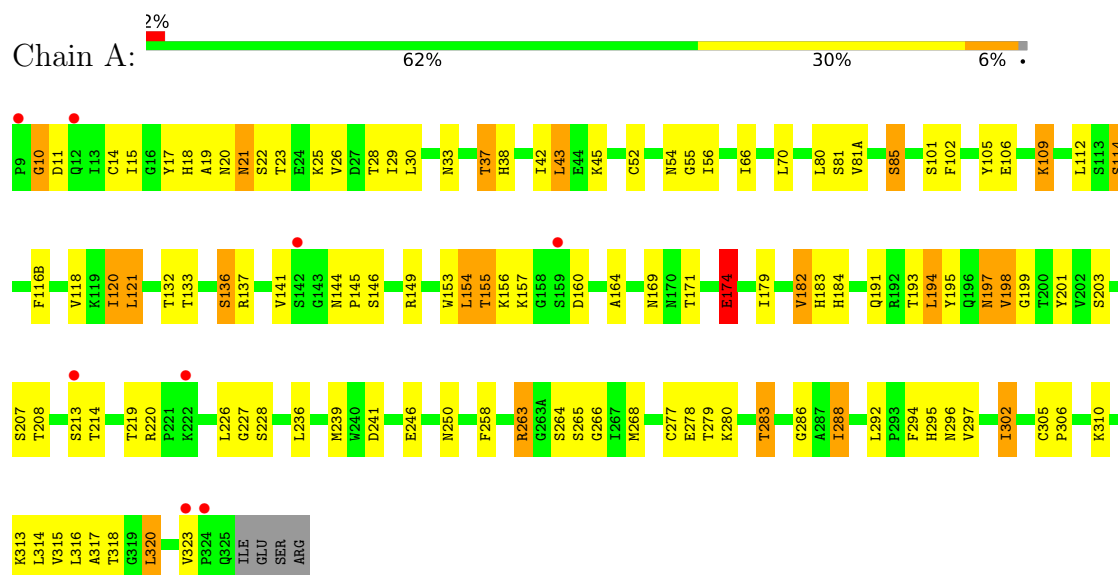
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	F	1	Total	C	N	O	0	0
			14	8	1	5		

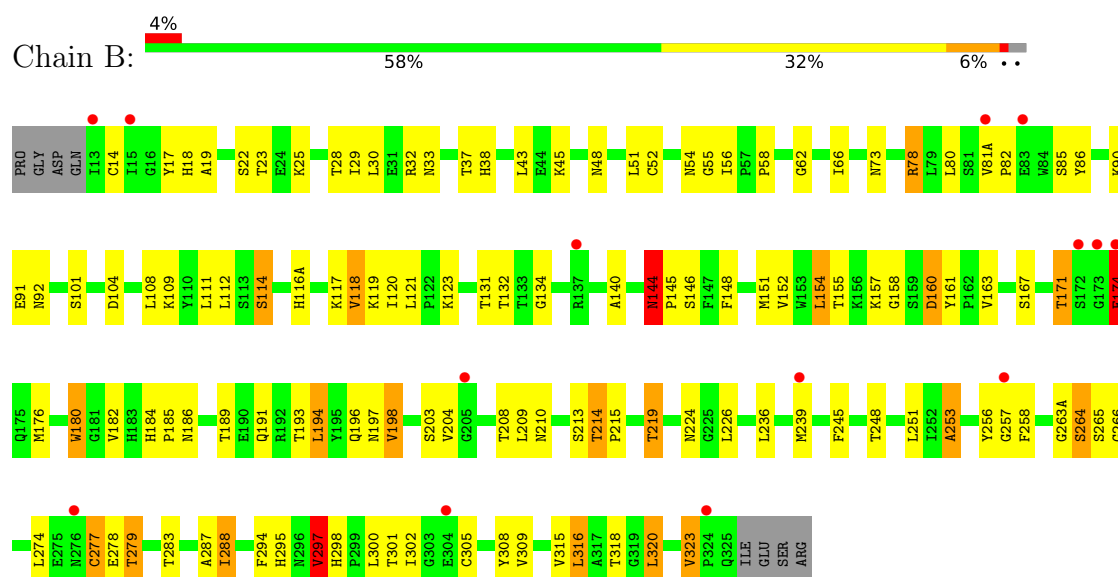
3 Residue-property plots [i](#)

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.

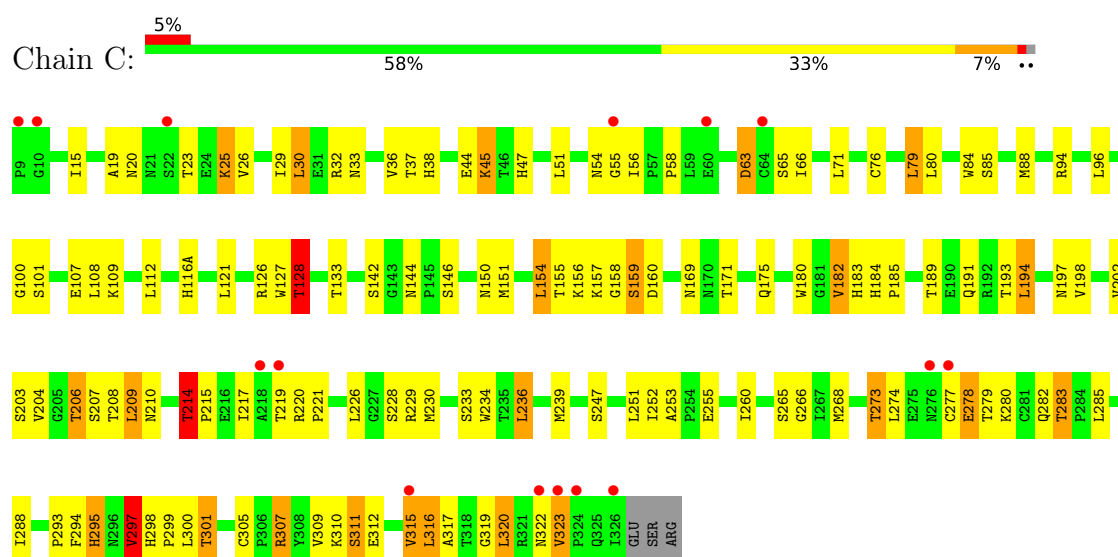
• Molecule 1: Hemagglutinin HA1



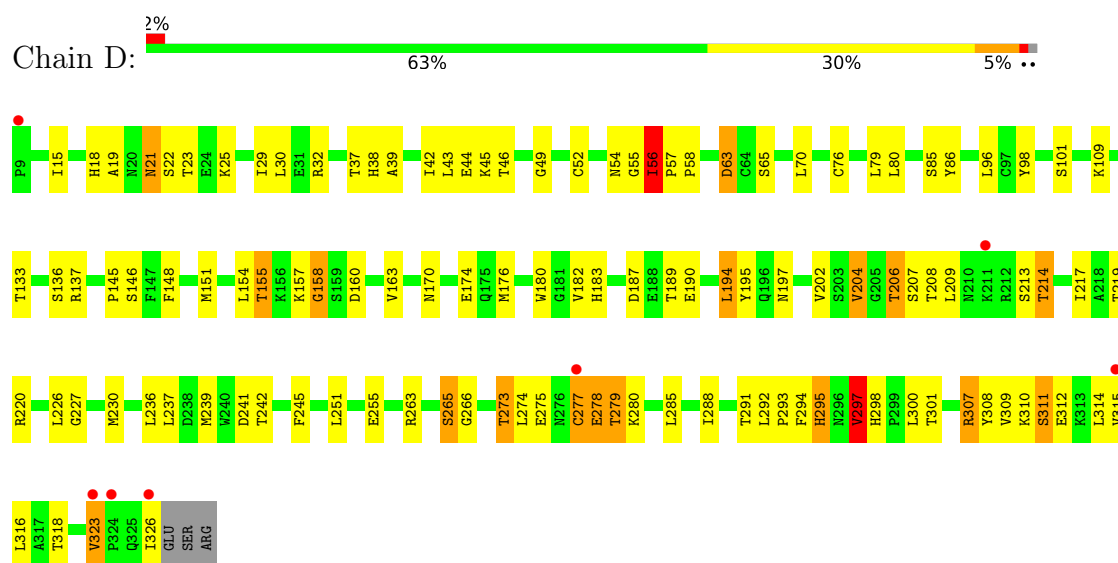
• Molecule 1: Hemagglutinin HA1



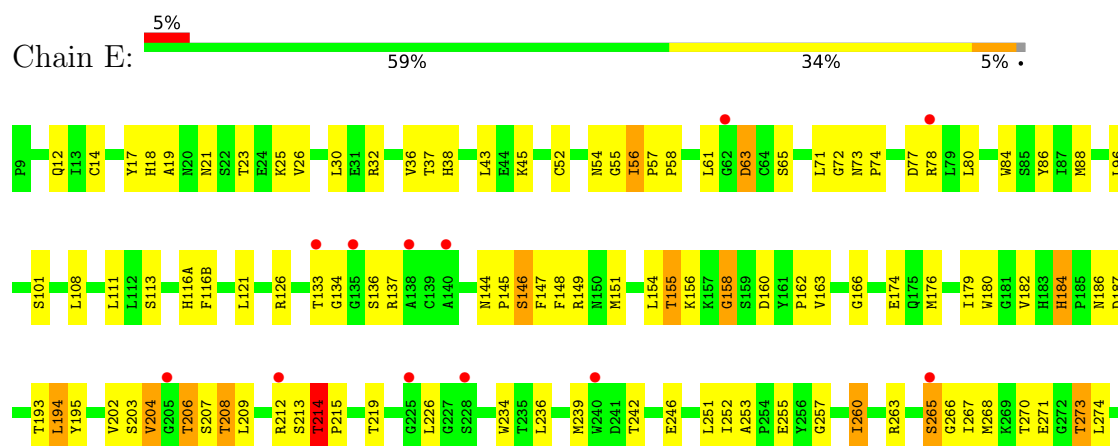
• Molecule 1: Hemagglutinin HA1

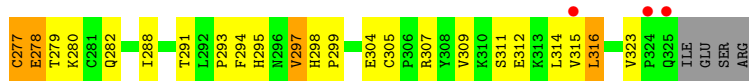


• Molecule 1: Hemagglutinin HA1

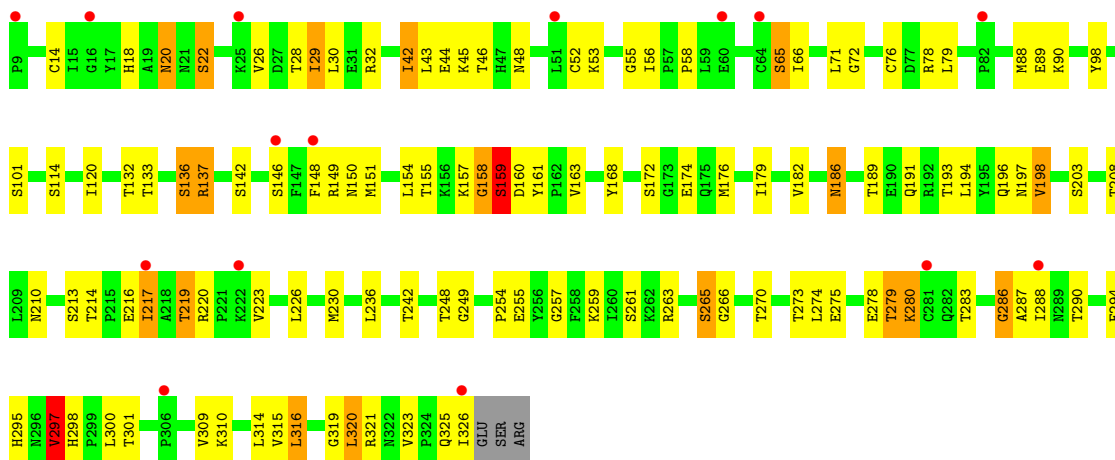


• Molecule 1: Hemagglutinin HA1

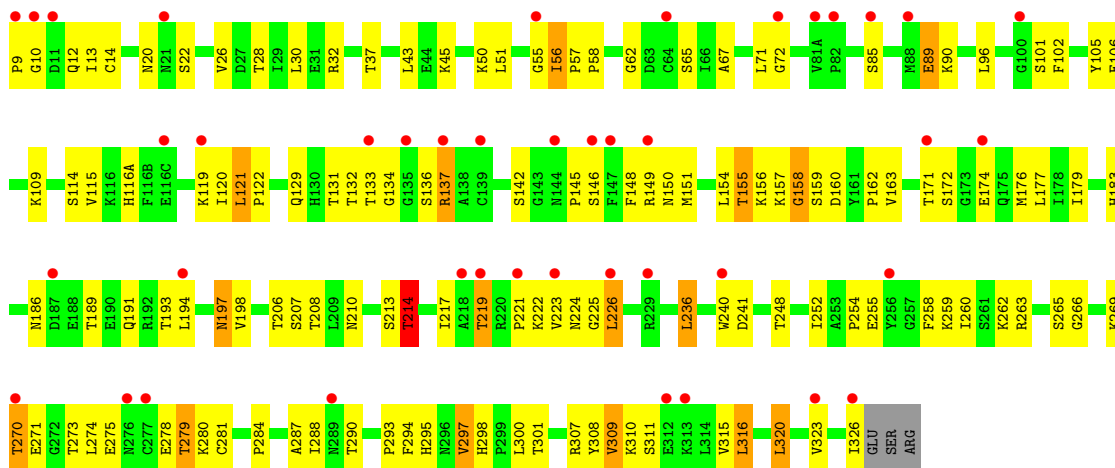




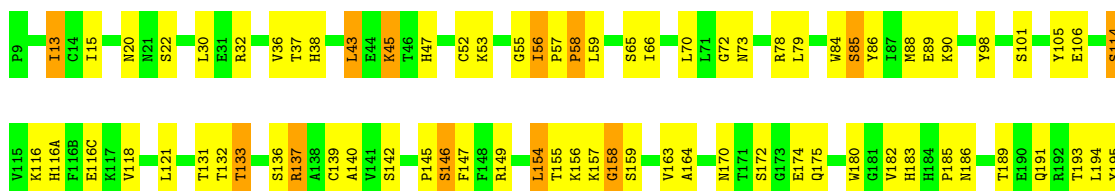
• Molecule 1: Hemagglutinin HA1

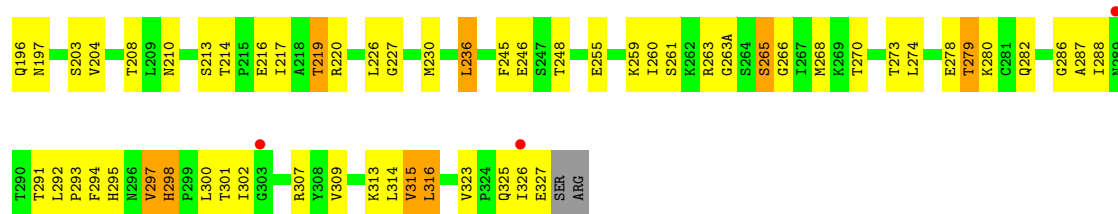


• Molecule 1: Hemagglutinin HA1

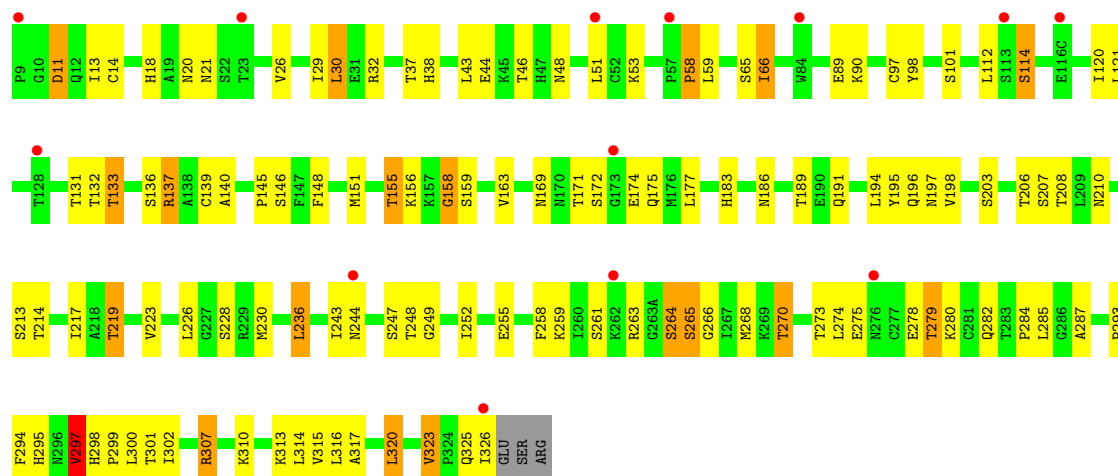


• Molecule 1: Hemagglutinin HA1

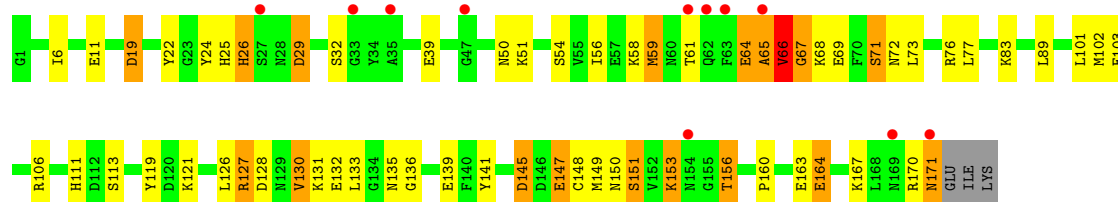




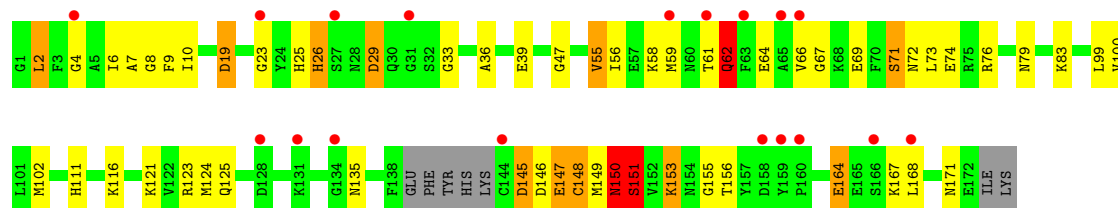
• Molecule 1: Hemagglutinin HA1



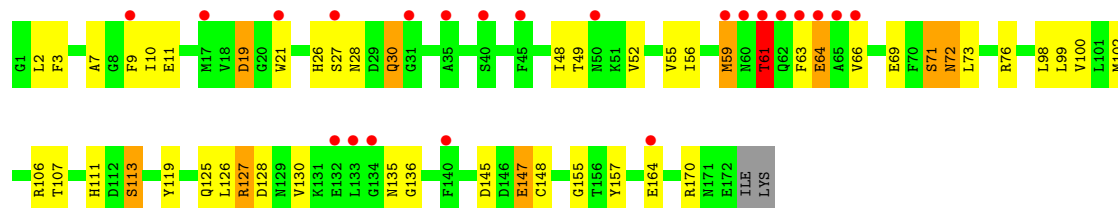
• Molecule 2: Hemagglutinin HA2



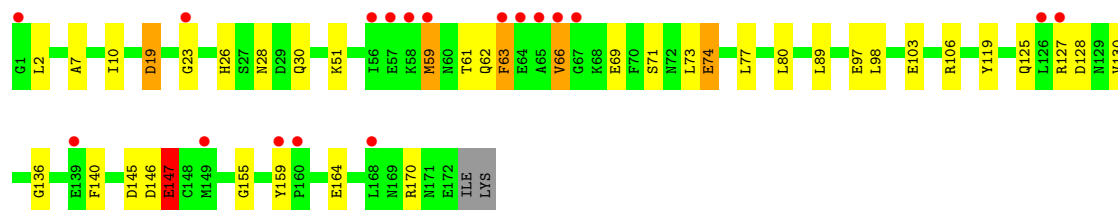
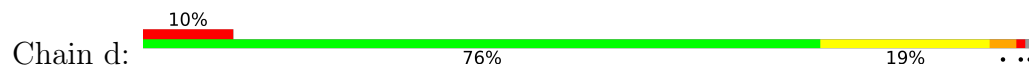
• Molecule 2: Hemagglutinin HA2



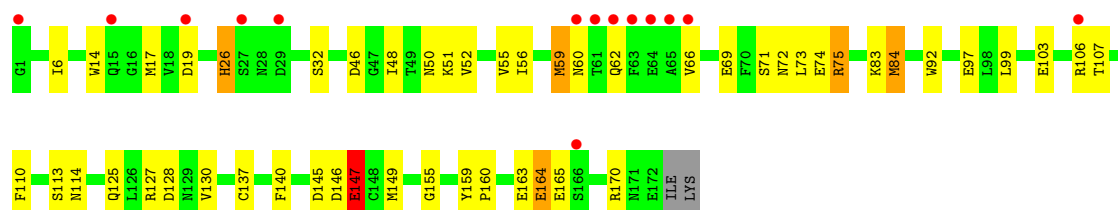
• Molecule 2: Hemagglutinin HA2



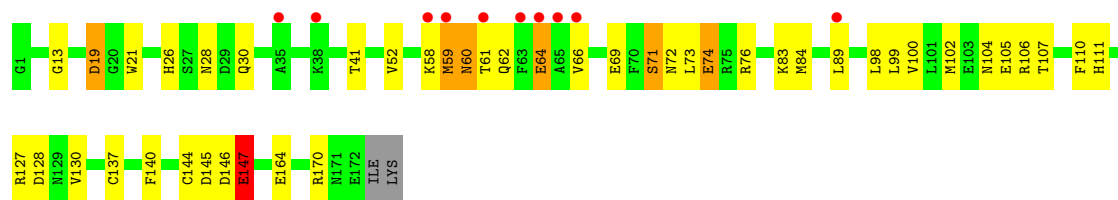
• Molecule 2: Hemagglutinin HA2



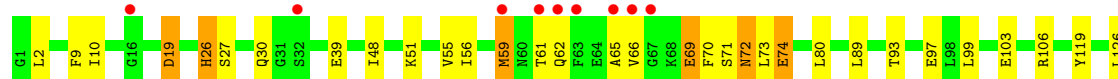
• Molecule 2: Hemagglutinin HA2

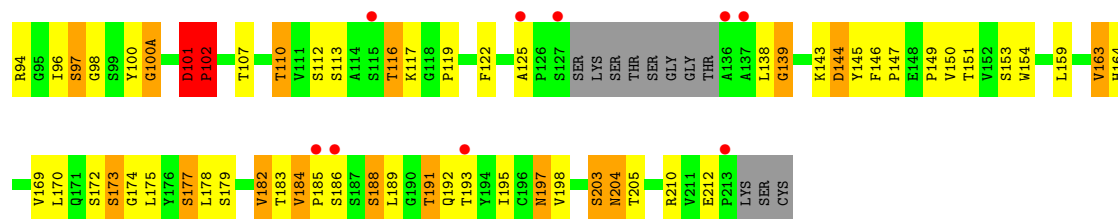


• Molecule 2: Hemagglutinin HA2

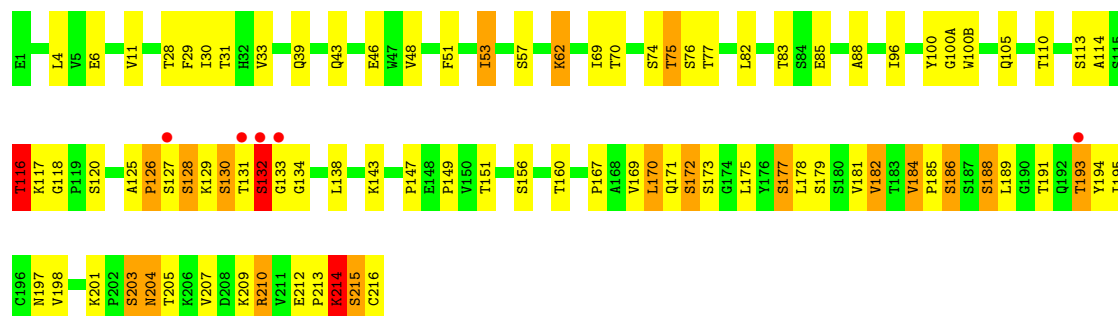


• Molecule 2: Hemagglutinin HA2

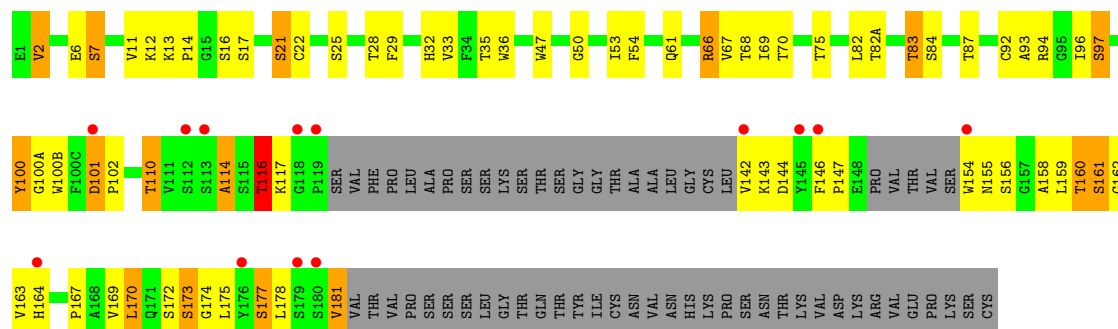




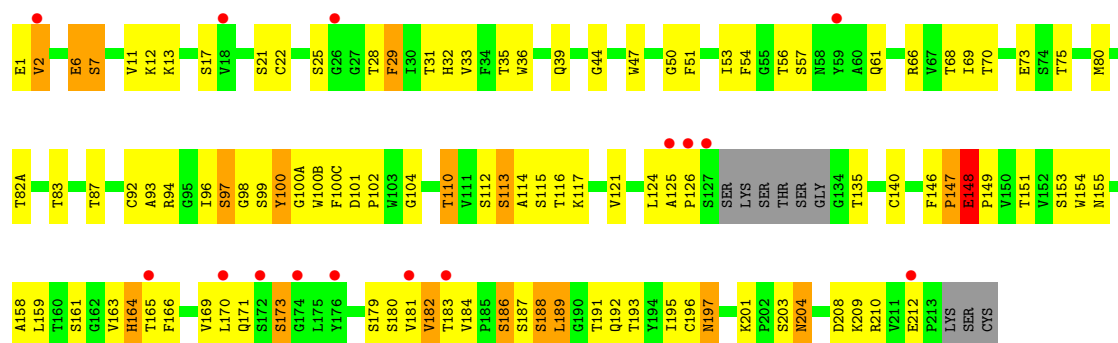
• Molecule 3: Fab 2G1 heavy chain



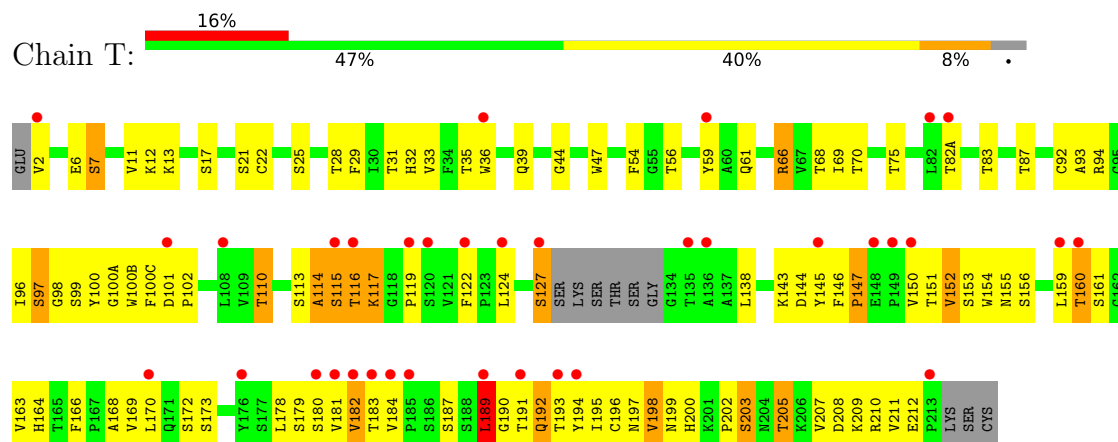
• Molecule 3: Fab 2G1 heavy chain



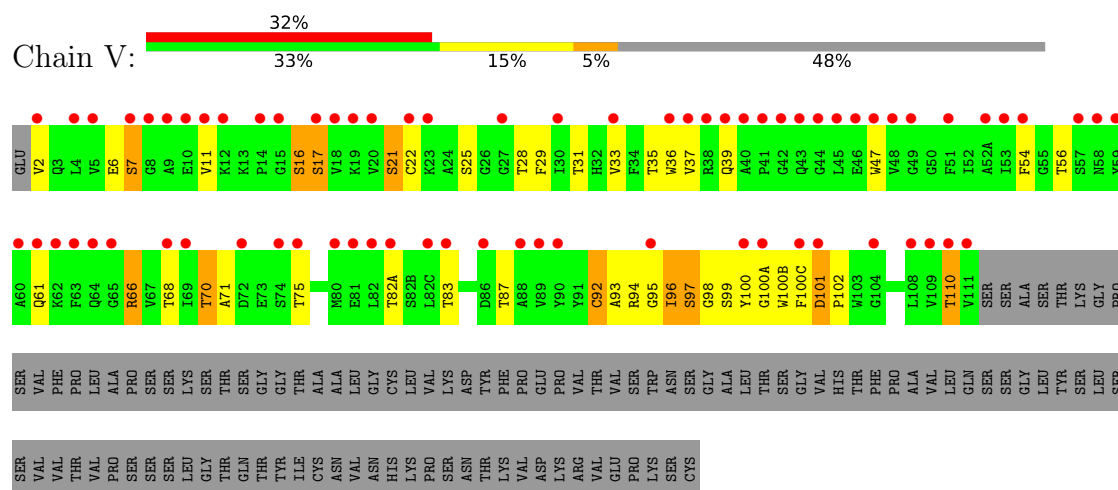
• Molecule 3: Fab 2G1 heavy chain



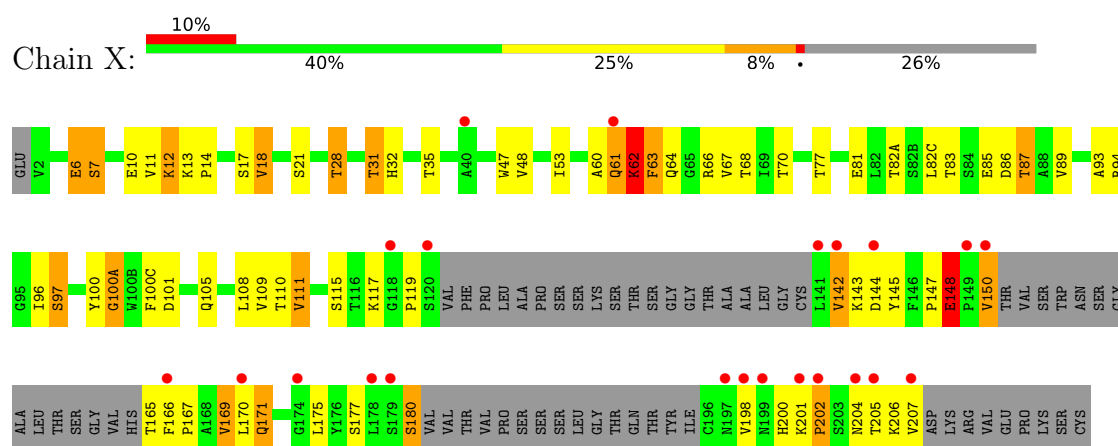
- Molecule 3: Fab 2G1 heavy chain



- Molecule 3: Fab 2G1 heavy chain

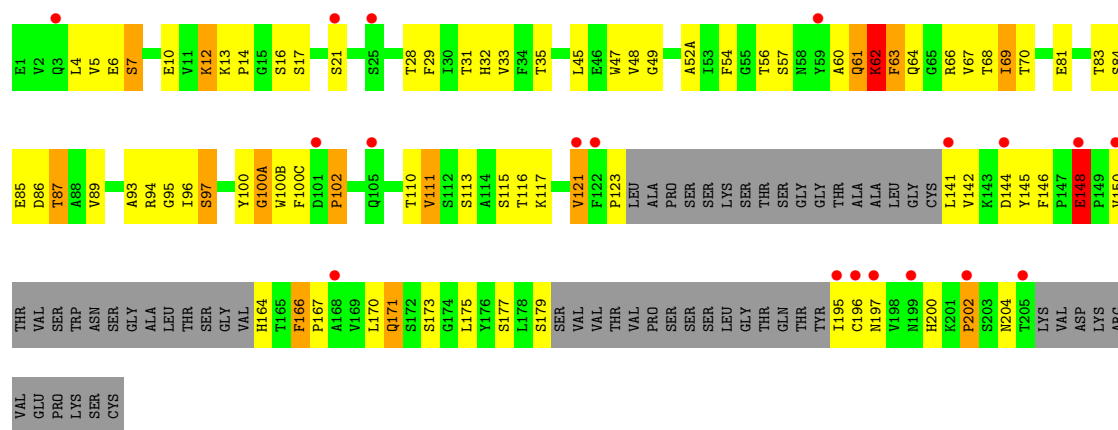


- Molecule 3: Fab 2G1 heavy chain

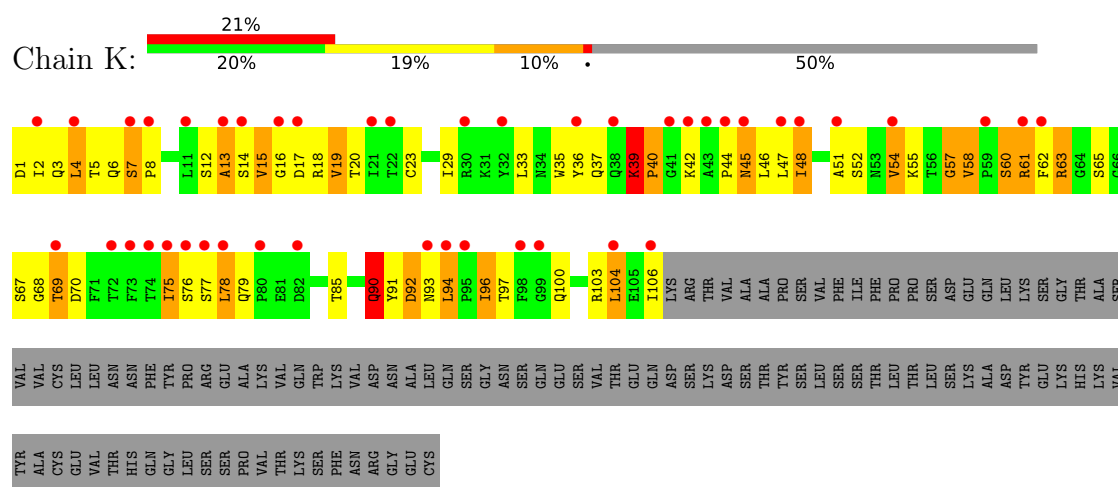


- Molecule 3: Fab 2G1 heavy chain

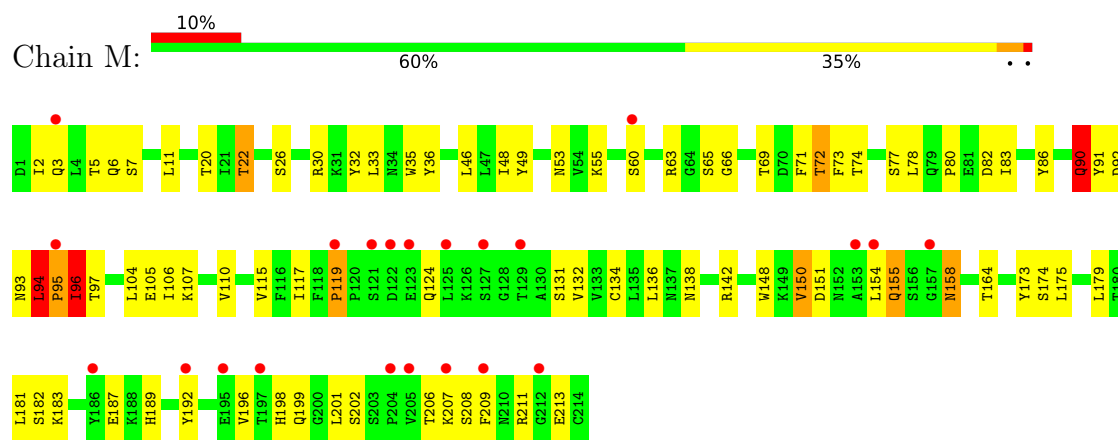




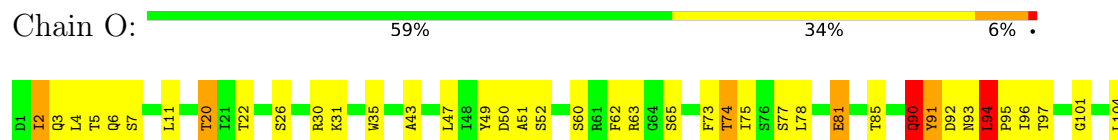
• Molecule 4: Fab 2G1 light chain

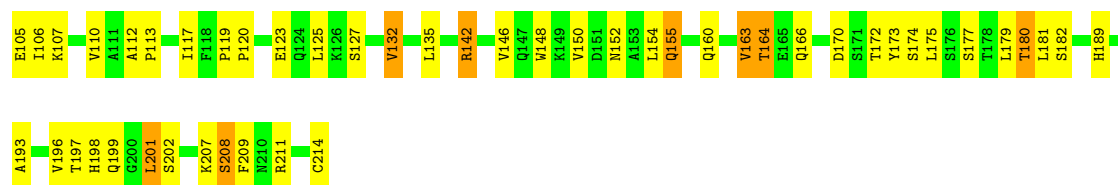


• Molecule 4: Fab 2G1 light chain

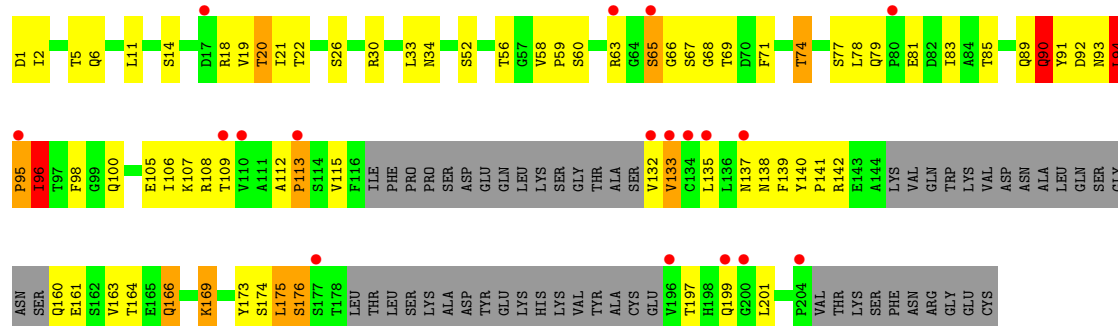
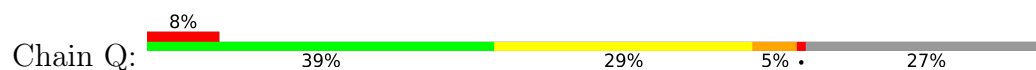


• Molecule 4: Fab 2G1 light chain

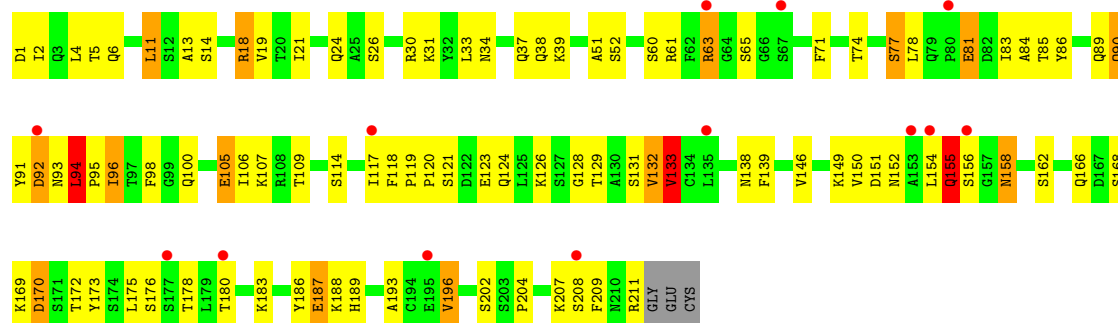




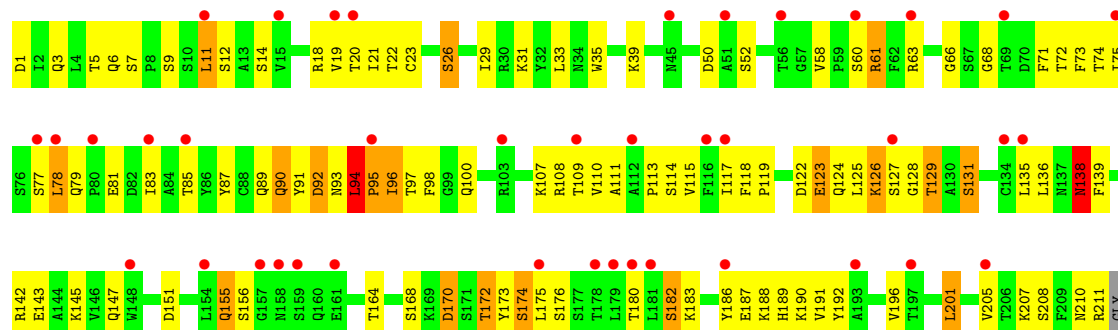
• Molecule 4: Fab 2G1 light chain



• Molecule 4: Fab 2G1 light chain



• Molecule 4: Fab 2G1 light chain

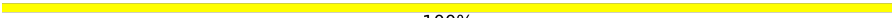


- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:  50% 50%

MAG1
MAG2

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

Chain k:  100%

MAG1
MAG2

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

Chain m:  50% 50%

MAG1
MAG2

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

Chain n:  50% 50%

MAG1
MAG2

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

Chain o:  100%

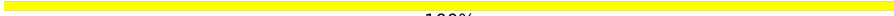
MAG1
MAG2

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

Chain q:  50% 50%

MAG1
MAG2

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

Chain r:  100%

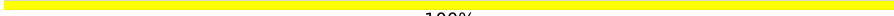
NAG1
NAG2

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

Chain s:  50% 50%

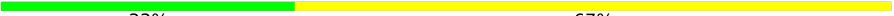
NAG1
NAG2

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

Chain t:  100%

NAG1
NAG2

- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:  33% 67%

NAG1
NAG2
BMA3

- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain p:  100%

NAG1
NAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	126.84Å 133.14Å 812.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.13 – 3.20 48.13 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.2 (48.13-3.20) 90.0 (48.13-3.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.22 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.7.2_869	Depositor
R, R_{free}	0.249 , 0.302 0.243 , 0.297	Depositor DCC
R_{free} test set	10355 reflections (4.35%)	wwPDB-VP
Wilson B-factor (Å ²)	55.3	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	58742	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.94% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, 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	0.61	0/2591	1.02	9/3517 (0.3%)
1	B	0.61	0/2562	1.09	13/3478 (0.4%)
1	C	0.64	0/2599	1.10	15/3528 (0.4%)
1	D	0.54	0/2599	0.97	6/3528 (0.2%)
1	E	0.60	0/2591	1.04	14/3517 (0.4%)
1	F	0.56	0/2599	0.98	7/3528 (0.2%)
1	G	0.51	0/2599	0.99	10/3528 (0.3%)
1	H	0.60	0/2608	1.03	12/3540 (0.3%)
1	I	0.57	0/2599	0.99	5/3528 (0.1%)
2	a	0.54	0/1415	0.99	3/1900 (0.2%)
2	b	0.54	0/1369	1.02	5/1837 (0.3%)
2	c	0.55	0/1424	0.95	5/1912 (0.3%)
2	d	0.55	0/1424	0.90	3/1912 (0.2%)
2	e	0.66	1/1424 (0.1%)	0.90	2/1912 (0.1%)
2	f	0.54	0/1424	0.93	2/1912 (0.1%)
2	g	0.54	0/1424	0.95	3/1912 (0.2%)
2	h	0.67	0/1381	0.93	2/1852 (0.1%)
2	i	0.68	0/1424	0.97	3/1912 (0.2%)
3	J	0.61	0/893	1.07	8/1213 (0.7%)
3	L	0.73	0/1618	1.13	13/2209 (0.6%)
3	N	0.79	0/1689	1.22	13/2304 (0.6%)
3	P	0.52	0/1237	0.95	7/1682 (0.4%)
3	R	0.56	0/1629	0.97	4/2224 (0.2%)
3	T	0.52	0/1620	0.95	4/2212 (0.2%)
3	V	0.54	0/905	0.96	3/1231 (0.2%)
3	X	0.62	0/1261	1.04	3/1713 (0.2%)
3	Z	0.51	0/1294	0.97	5/1760 (0.3%)
4	K	0.63	0/843	1.14	6/1146 (0.5%)
4	M	0.71	0/1695	1.12	5/2302 (0.2%)
4	O	0.85	0/1695	1.20	10/2302 (0.4%)
4	Q	0.53	0/1239	1.05	5/1682 (0.3%)
4	S	0.56	0/1676	1.03	6/2277 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	U	0.53	0/1676	0.97	8/2277 (0.4%)
4	W	0.58	0/835	0.97	4/1135 (0.4%)
4	Y	0.66	0/870	1.14	5/1181 (0.4%)
4	z	0.50	0/930	0.93	2/1261 (0.2%)
All	All	0.60	1/59661 (0.0%)	1.02	230/80864 (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	A	0	1
1	G	0	1
2	b	0	2
2	f	0	1
2	i	0	2
3	J	0	2
3	L	0	2
3	N	0	3
3	R	0	1
3	X	0	1
3	Z	0	1
4	K	0	4
4	M	0	2
4	O	0	1
4	Q	0	2
4	S	0	1
4	U	0	1
4	W	0	1
4	Y	0	1
4	z	0	1
All	All	0	31

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	e	26	HIS	CE1-NE2	9.05	1.41	1.32

All (230) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	62	GLN	N-CA-C	15.92	121.84	108.78
1	B	144	ASN	CA-C-N	11.98	132.12	119.90
1	B	144	ASN	C-N-CA	11.98	132.12	119.90
4	K	58	VAL	N-CA-C	10.94	120.03	107.77
4	Q	133	VAL	N-CA-C	10.77	117.73	106.21
4	M	94	LEU	CA-C-N	-10.27	107.00	119.84
4	M	94	LEU	C-N-CA	-10.27	107.00	119.84
4	Q	94	LEU	CA-C-N	-10.24	107.04	119.84
4	Q	94	LEU	C-N-CA	-10.24	107.04	119.84
4	Y	94	LEU	CA-C-N	-10.13	107.18	119.84
4	Y	94	LEU	C-N-CA	-10.13	107.18	119.84
3	L	101	ASP	N-CA-C	9.41	122.31	108.76
1	G	10	GLY	N-CA-C	9.13	125.15	112.37
4	U	126	LYS	N-CA-C	-8.92	101.95	112.92
1	A	121	LEU	CA-C-N	8.82	128.89	119.90
1	A	121	LEU	C-N-CA	8.82	128.89	119.90
3	V	101	ASP	CA-C-N	-8.79	109.44	120.51
3	V	101	ASP	C-N-CA	-8.79	109.44	120.51
1	C	214	THR	CA-C-N	8.75	128.68	119.85
1	C	214	THR	C-N-CA	8.75	128.68	119.85
3	N	127	SER	N-CA-C	8.70	122.92	110.14
4	S	94	LEU	CA-C-N	-8.18	109.62	119.84
4	S	94	LEU	C-N-CA	-8.18	109.62	119.84
2	i	62	GLN	N-CA-C	7.97	123.00	110.32
1	C	85	SER	N-CA-C	-7.82	103.70	113.55
4	W	94	LEU	CA-C-N	-7.78	110.11	119.84
4	W	94	LEU	C-N-CA	-7.78	110.11	119.84
4	Y	58	VAL	CA-C-N	7.71	127.75	119.89
4	Y	58	VAL	C-N-CA	7.71	127.75	119.89
2	b	62	GLN	CA-C-O	7.57	122.33	117.94
1	C	121	LEU	CA-C-N	7.53	127.52	119.76
1	C	121	LEU	C-N-CA	7.53	127.52	119.76
1	E	214	THR	CA-C-N	7.53	128.54	120.11
1	E	214	THR	C-N-CA	7.53	128.54	120.11
2	f	60	ASN	N-CA-C	7.42	123.20	107.70
4	O	94	LEU	CA-C-N	-7.37	110.62	119.84
4	O	94	LEU	C-N-CA	-7.37	110.62	119.84
1	D	214	THR	CA-C-N	7.29	127.29	119.78
1	D	214	THR	C-N-CA	7.29	127.29	119.78
1	C	184	HIS	CA-C-N	7.25	128.23	120.11
1	C	184	HIS	C-N-CA	7.25	128.23	120.11
3	N	133	GLY	N-CA-C	-7.12	105.66	114.92
4	U	94	LEU	CA-C-N	-7.11	110.95	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	94	LEU	C-N-CA	-7.11	110.95	119.84
1	H	298	HIS	CA-C-N	7.10	127.09	119.28
1	H	298	HIS	C-N-CA	7.10	127.09	119.28
3	N	125	ALA	CA-C-N	7.04	126.97	120.21
3	N	125	ALA	C-N-CA	7.04	126.97	120.21
1	F	56	ILE	N-CA-C	7.02	114.67	108.63
3	J	85	GLU	N-CA-C	-7.00	105.08	112.93
1	G	56	ILE	N-CA-C	6.97	114.80	107.76
3	N	48	VAL	CB-CA-C	-6.96	103.59	111.80
2	a	135	ASN	N-CA-C	-6.94	104.43	113.17
3	L	102	PRO	N-CA-C	-6.89	98.28	112.47
2	b	62	GLN	CB-CA-C	-6.85	107.20	117.07
4	K	57	GLY	N-CA-C	-6.82	97.01	113.18
3	N	113	SER	N-CA-C	-6.81	104.96	113.20
1	C	305	CYS	CA-C-N	6.79	126.73	120.21
1	C	305	CYS	C-N-CA	6.79	126.73	120.21
3	Z	148	GLU	CA-C-N	-6.71	111.46	119.84
3	Z	148	GLU	C-N-CA	-6.71	111.46	119.84
3	Z	166	PHE	N-CA-C	6.67	115.81	108.14
3	T	29	PHE	N-CA-C	6.65	118.52	111.28
1	H	73	ASN	CA-C-N	6.61	126.55	119.28
1	H	73	ASN	C-N-CA	6.61	126.55	119.28
3	L	69	ILE	N-CA-C	6.59	117.12	107.37
3	J	55	GLY	N-CA-C	-6.56	106.64	115.36
1	A	288	ILE	N-CA-C	6.52	118.19	107.24
1	E	305	CYS	CA-C-N	6.50	126.45	120.21
1	E	305	CYS	C-N-CA	6.50	126.45	120.21
3	L	139	GLY	N-CA-C	6.50	119.33	110.69
3	T	114	ALA	N-CA-C	6.46	118.90	110.43
3	X	198	VAL	N-CA-C	6.46	118.12	108.23
1	B	161	TYR	CA-C-N	6.43	126.40	120.03
1	B	161	TYR	C-N-CA	6.43	126.40	120.03
4	O	43	ALA	CA-C-N	-6.42	112.92	120.11
4	O	43	ALA	C-N-CA	-6.42	112.92	120.11
2	b	151	SER	N-CA-C	-6.41	105.35	113.43
1	H	56	ILE	CA-C-N	6.41	126.98	120.38
1	H	56	ILE	C-N-CA	6.41	126.98	120.38
3	R	69	ILE	N-CA-C	6.41	117.09	107.80
1	C	220	ARG	N-CA-C	6.39	113.76	108.07
4	U	155	GLN	N-CA-C	6.32	119.95	109.96
2	g	2	LEU	N-CA-C	-6.31	106.12	113.88
1	G	20	ASN	N-CA-C	6.31	116.57	108.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	188	SER	N-CA-C	-6.30	104.83	114.16
1	G	214	THR	CA-C-N	6.25	127.65	119.84
1	G	214	THR	C-N-CA	6.25	127.65	119.84
1	E	184	HIS	CA-C-N	6.23	126.75	120.14
1	E	184	HIS	C-N-CA	6.23	126.75	120.14
1	I	255	GLU	N-CA-C	-6.21	105.83	113.41
1	H	255	GLU	N-CA-C	-6.21	105.83	113.41
2	a	65	ALA	N-CA-C	-6.19	105.37	113.17
3	L	43	GLN	CB-CA-C	-6.17	106.68	114.40
1	A	85	SER	N-CA-C	-6.17	106.29	113.88
3	J	49	GLY	N-CA-C	6.17	120.31	111.12
4	Q	139	PHE	N-CA-C	6.17	116.42	108.34
3	L	174	GLY	N-CA-C	-6.09	106.84	115.30
2	h	2	LEU	N-CA-C	-6.07	106.42	113.88
1	I	297	VAL	CB-CA-C	-6.05	104.11	112.04
4	M	119	PRO	O-C-N	6.04	123.99	121.15
1	C	19	ALA	N-CA-C	-6.01	99.59	108.79
1	G	22	SER	N-CA-C	5.99	118.28	110.43
1	E	144	ASN	CA-C-N	5.98	125.92	119.76
1	E	144	ASN	C-N-CA	5.98	125.92	119.76
3	P	29	PHE	N-CA-C	5.97	118.56	111.33
1	H	121	LEU	CA-C-N	5.97	125.90	119.76
1	H	121	LEU	C-N-CA	5.97	125.90	119.76
3	R	2	VAL	N-CA-C	5.96	116.40	107.51
1	F	255	GLU	N-CA-C	-5.93	106.18	113.41
4	z	94	LEU	CA-C-N	-5.92	112.44	119.84
4	z	94	LEU	C-N-CA	-5.92	112.44	119.84
3	P	101	ASP	CA-C-N	-5.89	113.09	120.51
3	P	101	ASP	C-N-CA	-5.89	113.09	120.51
3	T	192	GLN	N-CA-C	5.88	119.67	110.32
1	A	11	ASP	N-CA-C	-5.87	102.36	110.35
2	a	11	GLU	N-CA-C	5.86	118.42	111.33
3	J	13	LYS	CA-C-N	5.85	127.15	119.84
3	J	13	LYS	C-N-CA	5.85	127.15	119.84
4	K	69	THR	N-CA-C	-5.84	106.19	113.38
3	N	182	VAL	CB-CA-C	-5.83	101.52	110.50
3	N	116	THR	N-CA-C	5.80	118.61	108.52
3	P	162	GLY	N-CA-C	-5.79	107.03	114.85
3	R	188	SER	N-CA-C	-5.78	107.22	114.56
1	I	323	VAL	N-CA-C	5.78	114.24	107.77
2	d	66	VAL	N-CA-C	5.77	118.16	108.81
1	E	267	ILE	CB-CA-C	-5.73	103.91	110.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	140	ALA	N-CA-C	5.72	117.39	109.15
4	O	90	GLN	CA-C-N	-5.72	117.00	123.13
4	O	90	GLN	C-N-CA	-5.72	117.00	123.13
1	F	223	VAL	CB-CA-C	-5.72	103.71	111.15
3	J	10	GLU	N-CA-C	5.70	117.76	108.63
4	K	60	SER	N-CA-C	-5.69	106.34	113.28
2	b	135	ASN	N-CA-C	-5.68	106.01	113.17
3	V	29	PHE	N-CA-C	5.68	118.24	111.71
2	g	65	ALA	N-CA-C	5.66	119.50	107.67
2	c	127	ARG	CB-CA-C	-5.65	110.07	116.63
1	F	136	SER	N-CA-C	5.64	115.73	108.34
1	E	121	LEU	CA-C-N	5.61	125.89	119.83
1	E	121	LEU	C-N-CA	5.61	125.89	119.83
3	Z	69	ILE	N-CA-C	5.60	115.95	108.11
4	W	58	VAL	CA-C-N	5.60	126.84	119.84
4	W	58	VAL	C-N-CA	5.60	126.84	119.84
4	S	196	VAL	N-CA-C	5.60	115.65	107.37
1	E	255	GLU	N-CA-C	-5.59	106.58	113.41
2	d	23	GLY	N-CA-C	5.57	118.37	110.74
2	e	60	ASN	N-CA-C	-5.56	106.33	114.39
3	L	102	PRO	CA-C-N	-5.55	114.61	122.94
3	L	102	PRO	C-N-CA	-5.55	114.61	122.94
2	g	39	GLU	N-CA-C	5.55	117.00	111.07
4	K	15	VAL	N-CA-C	5.53	116.83	109.37
1	B	73	ASN	CA-C-N	5.53	126.75	119.84
1	B	73	ASN	C-N-CA	5.53	126.75	119.84
2	d	2	LEU	N-CA-C	-5.52	106.91	113.97
1	D	85	SER	N-CA-C	-5.52	106.91	113.97
1	B	92	ASN	CA-C-N	5.51	125.83	119.93
1	B	92	ASN	C-N-CA	5.51	125.83	119.93
1	B	140	ALA	N-CA-C	5.51	117.85	110.35
2	c	2	LEU	N-CA-C	-5.51	106.91	113.97
3	P	2	VAL	N-CA-C	5.50	115.24	106.88
2	e	75	ARG	N-CA-C	-5.47	106.10	112.89
3	P	114	ALA	N-CA-C	5.46	117.78	110.35
2	h	29	ASP	N-CA-C	5.44	117.97	111.71
2	c	135	ASN	N-CA-C	-5.43	106.39	114.64
1	G	85	SER	N-CA-C	-5.41	106.61	113.43
1	B	253	ALA	CA-C-N	5.40	125.82	119.99
1	B	253	ALA	C-N-CA	5.40	125.82	119.99
3	L	125	ALA	CA-C-N	5.40	125.30	119.85
3	L	125	ALA	C-N-CA	5.40	125.30	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	95	PRO	N-CA-C	-5.39	101.37	112.47
1	A	184	HIS	CA-C-N	5.38	125.38	120.21
1	A	184	HIS	C-N-CA	5.38	125.38	120.21
2	c	64	GLU	N-CA-C	5.37	118.28	110.17
2	i	94	TYR	N-CA-C	-5.35	105.14	110.97
1	B	180	TRP	N-CA-C	5.32	117.35	109.69
1	B	288	ILE	N-CA-C	5.32	116.17	107.24
4	S	172	THR	N-CA-C	5.32	117.57	108.90
4	U	58	VAL	CA-C-N	5.32	125.31	119.89
4	U	58	VAL	C-N-CA	5.32	125.31	119.89
3	Z	45	LEU	N-CA-C	5.32	117.41	108.96
2	i	148	CYS	N-CA-C	-5.28	105.60	111.36
4	O	180	THR	N-CA-C	5.27	117.11	108.52
1	D	255	GLU	N-CA-C	-5.26	107.52	114.31
1	H	85	SER	N-CA-C	-5.26	106.92	113.55
4	Y	81	GLU	N-CA-C	-5.26	106.91	113.38
3	J	105	GLN	N-CA-C	-5.23	105.27	110.97
3	P	69	ILE	N-CA-C	5.23	115.38	107.75
1	D	56	ILE	N-CA-C	5.22	113.62	107.77
1	C	255	GLU	N-CA-C	-5.22	107.04	113.41
4	S	133	VAL	N-CA-C	5.22	113.88	106.53
1	C	220	ARG	CB-CA-C	-5.21	104.40	110.76
1	A	305	CYS	CA-C-N	5.21	125.42	120.31
1	A	305	CYS	C-N-CA	5.21	125.42	120.31
3	N	29	PHE	N-CA-C	5.21	116.64	111.07
4	O	196	VAL	N-CA-C	5.21	115.59	107.99
3	L	27	GLY	N-CA-C	-5.20	100.85	110.73
3	R	29	PHE	N-CA-C	5.20	118.41	111.75
4	O	2	ILE	CB-CA-C	-5.19	103.87	110.98
4	S	155	GLN	N-CA-C	5.19	118.46	110.42
1	C	315	VAL	N-CA-C	5.19	113.84	106.53
1	G	121	LEU	CA-C-N	5.18	125.12	119.78
1	G	121	LEU	C-N-CA	5.18	125.12	119.78
1	D	52	CYS	N-CA-C	5.17	117.05	109.24
1	I	223	VAL	CB-CA-C	-5.16	104.71	110.96
4	M	155	GLN	N-CA-C	5.16	117.86	109.86
3	J	62	LYS	N-CA-C	-5.16	107.28	113.21
1	F	20	ASN	N-CA-C	5.16	114.95	108.45
3	T	166	PHE	N-CA-C	5.15	117.19	110.08
4	O	2	ILE	N-CA-C	5.15	115.51	107.99
1	G	255	GLU	N-CA-C	-5.14	107.13	113.41
1	E	52	CYS	N-CA-C	5.09	117.15	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	160	ASP	N-CA-C	5.09	117.85	109.76
3	N	118	GLY	CA-C-N	5.09	124.99	119.85
3	N	118	GLY	C-N-CA	5.09	124.99	119.85
3	L	184	VAL	CA-C-N	5.08	126.48	120.23
3	L	184	VAL	C-N-CA	5.08	126.48	120.23
1	F	280	LYS	N-CA-C	-5.08	107.02	114.39
3	X	201	LYS	CA-C-N	-5.07	113.50	119.84
3	X	201	LYS	C-N-CA	-5.07	113.50	119.84
2	c	11	GLU	N-CA-C	5.06	116.88	111.36
1	C	220	ARG	NE-CZ-NH2	5.05	123.75	119.20
1	F	286	GLY	N-CA-C	5.05	117.66	110.74
1	H	315	VAL	N-CA-C	5.03	115.21	108.17
3	N	160	THR	N-CA-C	-5.03	107.53	113.97
2	f	61	THR	N-CA-C	5.01	121.48	110.80
1	I	140	ALA	N-CA-C	5.01	116.48	108.41
4	Q	137	ASN	N-CA-C	5.01	117.69	110.28
4	K	17	ASP	N-CA-C	5.01	116.40	110.19
4	U	39	LYS	CA-C-N	5.00	125.23	119.83
4	U	39	LYS	C-N-CA	5.00	125.23	119.83

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	GLY	Peptide
1	G	9	PRO	Peptide
3	J	30	ILE	Peptide
3	J	64	GLN	Peptide
4	K	39	LYS	Peptide
4	K	52	SER	Peptide
4	K	57	GLY	Peptide
4	K	90	GLN	Peptide
3	L	101	ASP	Peptide
3	L	203	SER	Peptide
4	M	90	GLN	Peptide
4	M	94	LEU	Peptide
3	N	114	ALA	Peptide
3	N	126	PRO	Peptide
3	N	203	SER	Peptide
4	O	94	LEU	Peptide
4	Q	90	GLN	Peptide
4	Q	94	LEU	Peptide

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Mol	Chain	Res	Type	Group
3	R	148	GLU	Peptide
4	S	94	LEU	Peptide
4	U	94	LEU	Peptide
4	W	94	LEU	Peptide
3	X	148	GLU	Peptide
4	Y	94	LEU	Peptide
3	Z	148	GLU	Peptide
2	b	61	THR	Peptide
2	b	62	GLN	Peptide
2	f	60	ASN	Peptide
2	i	61	THR	Peptide
2	i	62	GLN	Peptide
4	z	94	LEU	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	2531	0	2485	64	0
1	B	2503	0	2463	69	0
1	C	2539	0	2497	74	0
1	D	2539	0	2499	62	0
1	E	2531	0	2487	65	0
1	F	2539	0	2496	62	0
1	G	2539	0	2499	64	0
1	H	2548	0	2502	72	0
1	I	2539	0	2499	70	0
2	a	1387	0	1293	44	0
2	b	1345	0	1254	38	0
2	c	1396	0	1299	30	0
2	d	1396	0	1299	29	0
2	e	1396	0	1299	31	0
2	f	1396	0	1299	31	0
2	g	1396	0	1299	28	0
2	h	1355	0	1263	29	0
2	i	1396	0	1299	39	0
3	J	871	0	832	35	0
3	L	1578	0	1539	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	1648	0	1610	41	0
3	P	1207	0	1157	42	0
3	R	1589	0	1549	56	0
3	T	1580	0	1540	52	0
3	V	883	0	848	25	0
3	X	1232	0	1192	41	0
3	Z	1262	0	1217	40	0
4	K	826	0	804	24	0
4	M	1661	0	1616	40	0
4	O	1661	0	1615	38	0
4	Q	1217	0	1180	31	0
4	S	1642	0	1602	51	0
4	U	1642	0	1602	51	0
4	W	818	0	793	27	0
4	Y	853	0	837	24	0
4	z	915	0	884	21	0
5	j	28	0	25	0	0
5	k	28	0	25	0	0
5	m	28	0	25	0	0
5	n	28	0	25	0	0
5	o	28	0	25	0	0
5	q	28	0	25	0	0
5	r	28	0	25	0	0
5	s	28	0	25	0	0
5	t	28	0	25	0	0
6	l	39	0	34	0	0
6	p	39	0	34	0	0
7	A	14	0	13	0	0
7	C	14	0	13	0	0
7	E	14	0	13	0	0
7	F	14	0	13	0	0
All	All	58742	0	56793	1382	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 12.

All (1382) 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:D:307:ARG:HH12	2:d:62:GLN:HB2	1.24	1.00
3:N:171:GLN:HE21	3:N:177:SER:HB3	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:143:LYS:HA	3:L:177:SER:HB2	1.48	0.96
1:G:137:ARG:HG3	1:G:145:PRO:HG3	1.53	0.91
4:K:35:TRP:HB2	4:K:48:ILE:HG23	1.53	0.88
4:O:90:GLN:NE2	4:O:91:TYR:O	2.07	0.86
2:d:98:LEU:HD21	2:f:99:LEU:HD13	1.56	0.85
3:P:7:SER:HB3	3:P:21:SER:H	1.41	0.84
3:N:171:GLN:NE2	3:N:177:SER:HB3	1.94	0.83
1:H:288:ILE:HD11	1:H:297:VAL:HG21	1.61	0.81
1:B:288:ILE:HD11	1:B:297:VAL:HG21	1.62	0.81
1:D:265:SER:OG	1:D:266:GLY:N	2.12	0.80
3:Z:87:THR:HG22	3:Z:110:THR:HA	1.62	0.80
1:D:194:LEU:HD13	3:P:53:ILE:HD13	1.64	0.80
2:e:55:VAL:HG22	2:e:99:LEU:HD21	1.62	0.80
1:C:288:ILE:HD11	1:C:297:VAL:HG21	1.62	0.79
2:b:26:HIS:HB2	2:b:149:MET:HE3	1.63	0.79
3:R:87:THR:HG23	3:R:110:THR:HA	1.64	0.79
3:P:87:THR:HG23	3:P:110:THR:HA	1.65	0.79
3:Z:171:GLN:NE2	3:Z:175:LEU:O	2.17	0.78
3:R:96:ILE:HG22	3:R:100(A):GLY:HA3	1.65	0.78
1:F:298:HIS:HE1	1:F:300:LEU:HD12	1.49	0.76
4:M:189:HIS:O	4:M:211:ARG:NH1	2.18	0.76
1:D:137:ARG:HG3	1:D:145:PRO:HG3	1.67	0.76
3:R:7:SER:HB3	3:R:21:SER:H	1.51	0.76
4:W:1:ASP:HA	4:W:95:PRO:HG3	1.68	0.76
1:F:174:GLU:OE2	1:F:263:ARG:NH2	2.19	0.76
4:M:164:THR:HG22	4:M:174:SER:H	1.51	0.75
3:P:154:TRP:CD1	3:P:155:ASN:H	2.03	0.75
3:T:124:LEU:HD22	4:U:118:PHE:HB3	1.69	0.75
4:M:90:GLN:NE2	4:M:91:TYR:O	2.20	0.75
4:U:201:LEU:HD13	4:U:205:VAL:HG23	1.68	0.75
3:Z:12:LYS:NZ	3:Z:17:SER:O	2.19	0.75
1:D:37:THR:O	1:D:38:HIS:ND1	2.20	0.75
1:I:268:MET:HG2	1:I:270:THR:HG22	1.68	0.75
3:X:166:PHE:HD1	3:X:167:PRO:HD2	1.52	0.75
1:A:295:HIS:HD2	1:A:297:VAL:H	1.34	0.74
3:N:210:ARG:NH1	3:N:212:GLU:OE2	2.20	0.74
4:U:3:GLN:N	4:U:26:SER:OG	2.21	0.74
2:b:55:VAL:HG22	2:b:99:LEU:HD21	1.68	0.73
1:A:66:ILE:HD12	1:A:112:LEU:HD12	1.70	0.73
3:X:87:THR:HG22	3:X:110:THR:HA	1.69	0.73
3:R:193:THR:OG1	3:R:210:ARG:NH1	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:36:TRP:CZ3	3:V:92:CYS:HB2	2.24	0.72
1:B:48:ASN:HD21	1:B:287:ALA:HB3	1.53	0.72
1:E:265:SER:OG	1:E:266:GLY:N	2.20	0.72
1:D:76:CYS:HB3	1:D:79:LEU:HD12	1.71	0.72
2:h:130:VAL:HG12	2:h:140:PHE:HA	1.70	0.72
3:T:154:TRP:HD1	3:T:159:LEU:HD23	1.53	0.72
1:H:137:ARG:HG3	1:H:145:PRO:HG3	1.70	0.72
3:Z:166:PHE:HD1	3:Z:167:PRO:HD2	1.52	0.72
3:P:154:TRP:N	3:P:159:LEU:O	2.22	0.71
1:C:63:ASP:OD1	1:C:94:ARG:NH2	2.23	0.71
1:C:76:CYS:HB3	1:C:79:LEU:HD12	1.71	0.71
1:I:265:SER:OG	1:I:266:GLY:N	2.20	0.71
3:L:159:LEU:HD21	3:L:182:VAL:HG11	1.72	0.71
2:e:130:VAL:HG12	2:e:140:PHE:HA	1.71	0.71
4:S:150:VAL:HG12	4:S:155:GLN:HE22	1.56	0.71
1:H:172:SER:HB2	1:H:259:LYS:HD2	1.71	0.71
1:B:14:CYS:HB2	2:b:25:HIS:HB3	1.73	0.70
1:E:55:GLY:N	1:E:278:GLU:OE2	2.24	0.70
3:N:209:LYS:NZ	4:O:123:GLU:OE1	2.21	0.70
4:Y:6:GLN:O	4:Y:100:GLN:NE2	2.25	0.70
1:H:43:LEU:HD23	1:H:45:LYS:HE3	1.74	0.70
1:I:295:HIS:CD2	1:I:297:VAL:HG23	2.27	0.70
4:Q:90:GLN:NE2	4:Q:91:TYR:O	2.24	0.70
1:I:293:PRO:HG3	2:i:56:ILE:HG22	1.74	0.70
1:I:295:HIS:HD2	1:I:297:VAL:HG23	1.57	0.69
1:G:221:PRO:HG3	1:I:244:ASN:HD22	1.56	0.69
1:D:63:ASP:OD2	1:D:63:ASP:N	2.25	0.69
3:X:96:ILE:HG22	3:X:100(A):GLY:HA3	1.73	0.69
1:I:98:TYR:CD2	1:I:230:MET:HG3	2.28	0.69
1:C:265:SER:OG	1:C:266:GLY:N	2.25	0.69
2:i:145:ASP:O	2:i:147:GLU:N	2.24	0.69
4:S:189:HIS:O	4:S:211:ARG:NH1	2.25	0.69
3:X:171:GLN:NE2	3:X:175:LEU:O	2.25	0.69
3:T:154:TRP:CD1	3:T:159:LEU:HD23	2.27	0.69
1:H:131:THR:OG1	1:H:156:LYS:O	2.09	0.69
3:R:197:ASN:ND2	3:R:208:ASP:OD2	2.26	0.69
3:V:22:CYS:HB2	3:V:36:TRP:CH2	2.27	0.69
4:K:93:ASN:OD1	4:K:94:LEU:N	2.26	0.68
3:N:185:PRO:O	3:N:188:SER:OG	2.11	0.68
3:R:186:SER:HA	3:R:189:LEU:HB2	1.75	0.68
4:S:170:ASP:N	4:S:170:ASP:OD1	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:PHE:HZ	2:a:59:MET:HE2	1.58	0.68
3:R:66:ARG:NH1	3:R:82(A):THR:O	2.25	0.68
1:F:288:ILE:HD11	1:F:297:VAL:HG21	1.74	0.68
1:C:209:LEU:HD12	1:C:210:ASN:H	1.58	0.68
4:O:189:HIS:O	4:O:211:ARG:NH1	2.25	0.68
4:Q:6:GLN:O	4:Q:100:GLN:NE2	2.26	0.68
1:H:265:SER:OG	1:H:266:GLY:N	2.24	0.68
4:U:33:LEU:HD22	4:U:71:PHE:CD2	2.29	0.68
3:L:4:LEU:HD22	3:L:102:PRO:HG2	1.73	0.68
1:E:158:GLY:H	3:R:97:SER:HB2	1.58	0.68
1:C:37:THR:O	1:C:38:HIS:ND1	2.25	0.68
3:P:96:ILE:HG22	3:P:100(A):GLY:HA3	1.75	0.68
2:f:130:VAL:HG12	2:f:140:PHE:HA	1.74	0.67
3:Z:94:ARG:HB3	3:Z:102:PRO:HD2	1.75	0.67
2:d:19:ASP:OD1	2:d:19:ASP:N	2.26	0.67
2:f:128:ASP:O	2:f:170:ARG:NH1	2.26	0.67
3:J:97:SER:O	3:J:99:SER:N	2.27	0.67
4:S:6:GLN:O	4:S:100:GLN:NE2	2.25	0.67
4:K:15:VAL:HG13	4:K:78:LEU:HB3	1.77	0.67
1:H:133:THR:O	1:H:133:THR:OG1	2.11	0.67
1:A:288:ILE:HD11	1:A:297:VAL:HG21	1.76	0.67
3:R:97:SER:HG	3:R:99:SER:H	1.41	0.67
3:V:97:SER:OG	3:V:98:GLY:N	2.27	0.67
3:T:66:ARG:NH1	3:T:82(A):THR:O	2.28	0.67
1:D:157:LYS:NZ	4:Q:92:ASP:HA	2.10	0.66
2:g:130:VAL:HG12	2:g:140:PHE:HA	1.76	0.66
2:h:21:TRP:HB2	2:h:41:THR:HG23	1.77	0.66
1:A:37:THR:C	1:A:38:HIS:HD1	2.03	0.66
1:B:81(A):VAL:O	1:B:116(A):HIS:NE2	2.25	0.66
1:D:98:TYR:CD2	1:D:230:MET:HG3	2.31	0.66
2:f:145:ASP:O	2:f:147:GLU:N	2.29	0.66
1:G:221:PRO:HG3	1:I:244:ASN:ND2	2.11	0.66
3:T:7:SER:HB3	3:T:21:SER:H	1.59	0.66
4:U:108:ARG:HH11	4:U:111:ALA:HB2	1.60	0.66
1:F:148:PHE:HB2	1:F:151:MET:HB2	1.76	0.66
3:R:195:ILE:HG22	3:R:210:ARG:HB3	1.78	0.66
3:V:87:THR:HG23	3:V:110:THR:HA	1.76	0.66
2:d:128:ASP:O	2:d:170:ARG:NH1	2.28	0.66
4:M:132:VAL:HG13	4:M:179:LEU:HB3	1.76	0.65
1:E:193:THR:HG21	3:R:31:THR:HA	1.77	0.65
1:H:37:THR:O	1:H:38:HIS:ND1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:128:SER:HA	3:N:214:LYS:HD3	1.77	0.65
4:S:91:TYR:O	4:S:93:ASN:N	2.29	0.65
3:V:7:SER:HB3	3:V:21:SER:H	1.60	0.65
4:O:50:ASP:OD1	4:O:91:TYR:OH	2.11	0.65
2:c:55:VAL:HG22	2:c:99:LEU:HD21	1.78	0.65
2:g:30:GLN:HE22	2:g:145:ASP:HB2	1.62	0.65
1:E:194:LEU:HD13	3:R:53:ILE:HD13	1.79	0.65
1:H:170:ASN:OD1	1:H:172:SER:OG	2.12	0.65
4:S:166:GLN:HB2	4:S:173:TYR:CZ	2.31	0.65
3:X:101:ASP:OD2	4:Y:55:LYS:NZ	2.21	0.65
4:U:183:LYS:HE3	4:U:187:GLU:HG3	1.79	0.65
1:I:298:HIS:HE1	1:I:300:LEU:HD12	1.61	0.65
3:J:37:VAL:HG12	3:J:45:LEU:HD22	1.78	0.65
3:X:7:SER:HB3	3:X:21:SER:H	1.62	0.65
1:D:307:ARG:NH1	2:d:62:GLN:HB2	2.07	0.64
1:E:206:THR:OG1	1:E:207:SER:N	2.28	0.64
1:E:288:ILE:HD11	1:E:297:VAL:HG21	1.77	0.64
3:L:210:ARG:NH1	3:L:212:GLU:OE2	2.31	0.64
3:V:35:THR:OG1	3:V:47:TRP:NE1	2.30	0.64
1:A:201:TYR:OH	1:A:246:GLU:OE2	2.12	0.64
1:F:159:SER:HB3	3:T:100(B):TRP:HH2	1.62	0.64
4:Y:91:TYR:O	4:Y:93:ASN:N	2.29	0.64
1:H:158:GLY:HA2	3:X:96:ILE:HG23	1.79	0.64
3:T:96:ILE:HG22	3:T:100(A):GLY:HA3	1.80	0.64
1:A:120:ILE:HG13	1:A:121:LEU:HG	1.77	0.64
1:C:63:ASP:OD2	1:C:63:ASP:N	2.31	0.64
1:D:158:GLY:H	3:P:97:SER:CB	2.09	0.64
1:H:55:GLY:N	1:H:278:GLU:OE2	2.24	0.64
3:J:54:PHE:HB3	3:J:56:THR:HG23	1.80	0.64
4:W:50:ASP:OD1	4:W:91:TYR:OH	2.14	0.64
2:a:26:HIS:HB2	2:a:149:MET:HE3	1.79	0.64
2:d:106:ARG:HH12	2:e:106:ARG:HD2	1.63	0.63
4:Q:89:GLN:HB2	4:Q:98:PHE:CD1	2.34	0.63
1:B:294:PHE:HZ	2:b:59:MET:HE2	1.64	0.63
1:G:158:GLY:O	1:G:160:ASP:N	2.25	0.63
1:I:155:THR:HG21	3:Z:54:PHE:HZ	1.64	0.63
4:S:124:GLN:HE22	4:S:131:SER:HB2	1.63	0.63
1:B:316:LEU:HD23	2:b:100:VAL:HG22	1.80	0.63
3:P:161:SER:OG	4:Q:169:LYS:NZ	2.27	0.63
3:L:185:PRO:O	3:L:188:SER:OG	2.16	0.63
2:e:145:ASP:O	2:e:147:GLU:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:M:198:HIS:CG	4:M:199:GLN:H	2.16	0.63
3:N:171:GLN:HG3	3:N:175:LEU:O	1.98	0.63
2:c:30:GLN:HE22	2:c:145:ASP:HB2	1.62	0.63
1:D:273:THR:OG1	1:D:274:LEU:N	2.30	0.63
1:F:294:PHE:CZ	2:f:59:MET:HG3	2.34	0.63
2:g:51:LYS:HD3	2:g:103:GLU:HB3	1.81	0.63
4:K:44:PRO:O	4:K:45:ASN:ND2	2.28	0.63
4:S:150:VAL:H	4:S:155:GLN:NE2	1.96	0.63
3:V:66:ARG:NH1	3:V:82(A):THR:O	2.32	0.62
1:G:288:ILE:HD11	1:G:297:VAL:HG21	1.80	0.62
4:S:175:LEU:HD23	4:S:176:SER:N	2.14	0.62
1:I:13:ILE:HD13	2:i:152:VAL:HG11	1.82	0.62
1:I:137:ARG:HG3	1:I:145:PRO:HG3	1.80	0.62
3:T:143:LYS:NZ	3:T:144:ASP:OD1	2.32	0.62
1:B:295:HIS:CE1	1:B:308:TYR:HB2	2.33	0.62
1:F:295:HIS:CD2	1:F:297:VAL:HG23	2.34	0.62
3:V:100(B):TRP:HB3	4:W:34:ASN:ND2	2.15	0.62
1:E:180:TRP:CE2	1:E:204:VAL:HG21	2.34	0.62
1:C:221:PRO:O	1:C:229:ARG:NH1	2.33	0.62
2:a:133:LEU:HD11	2:a:139:GLU:HB2	1.80	0.62
3:T:156:SER:HB2	3:T:195:ILE:HD11	1.81	0.62
1:H:186:ASN:OD1	1:H:219:THR:HA	2.00	0.62
3:R:163:VAL:HG12	3:R:182:VAL:HG13	1.82	0.62
1:B:193:THR:HG21	3:L:31:THR:HG22	1.80	0.61
4:K:13:ALA:HB2	4:K:104:LEU:HB2	1.82	0.61
1:F:294:PHE:HZ	2:f:59:MET:HG3	1.65	0.61
4:Q:161:GLU:HB3	4:Q:175:LEU:HD21	1.82	0.61
1:B:305:CYS:O	2:b:62:GLN:NE2	2.29	0.61
1:F:28:THR:HG22	2:f:104:ASN:HB3	1.81	0.61
1:F:48:ASN:HD21	1:F:287:ALA:HB3	1.65	0.61
1:A:25:LYS:HD2	1:A:33:ASN:O	2.00	0.61
1:E:137:ARG:HG3	1:E:145:PRO:HG3	1.82	0.61
1:I:11:ASP:OD1	1:I:11:ASP:N	2.31	0.61
4:O:166:GLN:HB2	4:O:173:TYR:CZ	2.35	0.61
1:A:26:VAL:HG21	1:A:317:ALA:HB2	1.82	0.61
1:C:180:TRP:CE2	1:C:204:VAL:HG21	2.35	0.61
3:N:96:ILE:HG22	3:N:100(A):GLY:HA3	1.82	0.61
1:C:298:HIS:HE1	1:C:300:LEU:HD12	1.65	0.61
1:C:183:HIS:O	1:C:185:PRO:HD3	2.00	0.61
1:F:159:SER:HB3	3:T:100(B):TRP:CH2	2.36	0.61
1:I:279:THR:HG21	1:I:287:ALA:HB1	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:a:151:SER:OG	2:a:156:THR:O	2.17	0.61
1:B:37:THR:HG23	1:B:320:LEU:O	2.01	0.61
1:D:158:GLY:H	3:P:97:SER:HB3	1.65	0.61
3:J:97:SER:O	3:J:97:SER:OG	2.14	0.61
3:L:50:GLY:HA3	3:L:100:TYR:CE1	2.36	0.61
1:G:293:PRO:HG3	2:g:56:ILE:HG22	1.83	0.61
3:Z:93:ALA:HB1	3:Z:100(C):PHE:HB3	1.83	0.61
1:I:325:GLN:HB3	2:i:13:GLY:O	2.01	0.60
2:g:19:ASP:OD1	2:g:19:ASP:N	2.33	0.60
4:M:66:GLY:HA3	4:M:71:PHE:HA	1.83	0.60
3:V:54:PHE:HB3	3:V:56:THR:HG23	1.83	0.60
3:J:101:ASP:N	3:J:101:ASP:OD1	2.33	0.60
3:Z:61:GLN:O	3:Z:63:PHE:N	2.33	0.60
4:z:77:SER:O	4:z:77:SER:OG	2.18	0.60
1:C:100:GLY:HA3	1:C:230:MET:O	2.01	0.60
2:d:30:GLN:HE22	2:d:145:ASP:HB2	1.65	0.60
3:L:163:VAL:HG12	3:L:182:VAL:HG13	1.81	0.60
3:T:163:VAL:O	3:T:164:HIS:ND1	2.33	0.60
1:A:295:HIS:ND1	1:A:306:PRO:HG2	2.16	0.60
2:g:145:ASP:O	2:g:147:GLU:N	2.34	0.60
4:Y:89:GLN:HG2	4:Y:90:GLN:N	2.17	0.60
1:F:44:GLU:OE2	1:F:46:THR:OG1	2.18	0.60
1:H:53:LYS:HB2	1:H:278:GLU:HG2	1.83	0.60
4:S:146:VAL:HG22	4:S:196:VAL:HG22	1.84	0.60
1:H:282:GLN:NE2	1:H:286:GLY:O	2.35	0.60
3:N:96:ILE:H	3:N:100(A):GLY:H	1.50	0.60
2:f:21:TRP:HB2	2:f:41:THR:HG23	1.84	0.60
1:I:114:SER:O	1:I:114:SER:OG	2.13	0.59
2:e:106:ARG:HH12	2:f:106:ARG:HH11	1.50	0.59
1:G:37:THR:HG23	1:G:320:LEU:O	2.02	0.59
2:b:145:ASP:OD1	2:b:145:ASP:N	2.34	0.59
1:H:158:GLY:H	3:X:97:SER:CB	2.16	0.59
4:S:119:PRO:HB3	4:S:209:PHE:CE2	2.37	0.59
1:C:180:TRP:NE1	1:C:204:VAL:HG21	2.17	0.59
2:a:145:ASP:OD1	2:a:145:ASP:N	2.34	0.59
3:N:143:LYS:HA	3:N:177:SER:HB2	1.84	0.59
1:G:174:GLU:OE2	1:G:263:ARG:NH2	2.36	0.59
4:M:22:THR:HG23	4:M:72:THR:HG23	1.83	0.59
3:R:97:SER:OG	3:R:98:GLY:N	2.31	0.59
1:G:89:GLU:OE1	1:G:269:LYS:NZ	2.36	0.59
3:J:39:GLN:NE2	3:J:44:GLY:O	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:M:32:TYR:HD2	4:M:92:ASP:HB2	1.68	0.59
3:T:152:VAL:HG22	3:T:198:VAL:HG12	1.85	0.59
4:S:1:ASP:HA	4:S:95:PRO:HG3	1.85	0.59
1:B:265:SER:OG	1:B:266:GLY:N	2.29	0.58
1:C:206:THR:OG1	1:C:207:SER:N	2.31	0.58
1:D:294:PHE:HZ	2:d:59:MET:HE2	1.68	0.58
1:E:208:THR:O	1:E:208:THR:OG1	2.21	0.58
1:F:29:ILE:HD11	2:f:102:MET:HG2	1.85	0.58
1:F:320:LEU:HB3	2:f:111:HIS:CG	2.38	0.58
2:a:19:ASP:N	2:a:19:ASP:OD1	2.35	0.58
1:H:183:HIS:ND1	1:H:195:TYR:OH	2.36	0.58
3:N:170:LEU:O	4:O:160:GLN:NE2	2.32	0.58
4:Q:20:THR:HG22	4:Q:74:THR:HG23	1.85	0.58
2:b:145:ASP:O	2:b:147:GLU:N	2.36	0.58
2:g:69:GLU:O	2:h:76:ARG:NH1	2.36	0.58
1:H:158:GLY:H	3:X:97:SER:HB2	1.68	0.58
2:d:145:ASP:O	2:d:147:GLU:N	2.36	0.58
4:O:164:THR:HG22	4:O:174:SER:H	1.69	0.58
3:X:60:ALA:O	3:X:62:LYS:N	2.36	0.58
1:E:134:GLY:HA2	3:R:54:PHE:CE1	2.38	0.58
1:I:136:SER:OG	1:I:137:ARG:N	2.30	0.58
3:L:192:GLN:OE1	3:L:193:THR:N	2.36	0.58
3:X:61:GLN:O	3:X:63:PHE:N	2.36	0.58
4:z:32:TYR:HD2	4:z:92:ASP:HB2	1.67	0.58
1:A:198:VAL:HG12	1:A:199:GLY:H	1.68	0.58
1:B:186:ASN:OD1	1:B:219:THR:HA	2.03	0.58
1:E:108:LEU:HB2	1:E:234:TRP:CE2	2.39	0.58
1:F:265:SER:OG	1:F:266:GLY:N	2.35	0.58
2:g:55:VAL:HG22	2:g:99:LEU:HD21	1.85	0.58
3:J:100(C):PHE:H	4:K:36:TYR:HH	1.52	0.58
1:H:295:HIS:CD2	1:H:297:VAL:HG23	2.39	0.58
3:X:171:GLN:HE22	3:X:177:SER:HB2	1.67	0.58
4:Y:35:TRP:HB2	4:Y:48:ILE:HB	1.86	0.58
1:G:265:SER:OG	1:G:266:GLY:N	2.35	0.58
1:G:294:PHE:CZ	2:g:59:MET:HG3	2.39	0.58
1:C:29:ILE:HD11	2:c:102:MET:HG2	1.86	0.57
1:D:206:THR:HG23	1:D:209:LEU:HB3	1.86	0.57
2:h:126:LEU:HD13	2:h:130:VAL:HG11	1.86	0.57
1:F:55:GLY:N	1:F:278:GLU:OE2	2.34	0.57
1:F:193:THR:HG21	3:T:31:THR:HG22	1.85	0.57
3:N:96:ILE:CG2	3:N:100(A):GLY:HA3	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:VAL:HG22	1:B:245:PHE:HD1	1.67	0.57
3:P:22:CYS:HB2	3:P:36:TRP:CH2	2.40	0.57
4:W:6:GLN:O	4:W:100:GLN:NE2	2.37	0.57
2:d:51:LYS:HD3	2:d:103:GLU:HB3	1.86	0.57
1:E:88:MET:HE3	1:E:270:THR:HG21	1.86	0.57
1:E:158:GLY:H	3:R:97:SER:CB	2.17	0.57
4:Q:105:GLU:OE1	4:Q:173:TYR:OH	2.18	0.57
2:a:68:LYS:NZ	2:b:79:ASN:OD1	2.37	0.57
1:C:185:PRO:HG2	1:C:191:GLN:OE1	2.04	0.57
2:c:128:ASP:O	2:c:170:ARG:NH1	2.37	0.57
1:F:325:GLN:HB3	2:f:13:GLY:O	2.03	0.57
4:W:93:ASN:OD1	4:W:95:PRO:HD3	2.04	0.57
2:a:71:SER:HB2	2:a:73:LEU:H	1.70	0.57
2:a:126:LEU:HD13	2:a:130:VAL:HG11	1.86	0.57
1:I:37:THR:O	1:I:38:HIS:ND1	2.36	0.57
3:N:75:THR:HB	3:N:77:THR:HB	1.87	0.57
1:B:251:LEU:HD21	1:B:253:ALA:HB2	1.87	0.57
4:O:132:VAL:HG13	4:O:179:LEU:HB3	1.86	0.57
3:P:154:TRP:CD1	3:P:155:ASN:N	2.73	0.57
1:A:157:LYS:NZ	4:K:92:ASP:HA	2.19	0.57
4:M:158:ASN:OD1	4:M:158:ASN:N	2.30	0.57
4:U:172:THR:OG1	4:U:173:TYR:N	2.38	0.57
3:X:66:ARG:NH2	3:X:86:ASP:OD2	2.38	0.57
1:F:136:SER:OG	1:F:137:ARG:N	2.37	0.57
3:L:50:GLY:HA3	3:L:100:TYR:HE1	1.70	0.57
4:M:6:GLN:NE2	4:M:86:TYR:O	2.33	0.57
4:S:128:GLY:HA2	4:S:183:LYS:HD3	1.87	0.57
1:C:209:LEU:HD12	1:C:210:ASN:N	2.18	0.57
1:E:158:GLY:HA2	3:R:96:ILE:HG23	1.87	0.57
3:R:97:SER:OG	3:R:99:SER:N	2.25	0.57
3:L:101:ASP:OD2	4:M:55:LYS:NZ	2.37	0.56
3:X:12:LYS:NZ	3:X:17:SER:O	2.37	0.56
1:B:191:GLN:HG2	1:B:198:VAL:HG13	1.86	0.56
1:G:163:VAL:HG22	1:G:248:THR:HG22	1.86	0.56
3:P:116:THR:HA	3:P:146:PHE:HD2	1.70	0.56
4:S:150:VAL:HG12	4:S:155:GLN:NE2	2.20	0.56
1:D:279:THR:OG1	1:D:280:LYS:N	2.39	0.56
2:e:128:ASP:OD1	2:e:159:TYR:OH	2.12	0.56
1:F:65:SER:OG	1:F:66:ILE:N	2.38	0.56
3:L:193:THR:O	3:L:193:THR:OG1	2.19	0.56
4:U:7:SER:HG	4:U:22:THR:HG1	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:91:TYR:O	4:W:93:ASN:N	2.38	0.56
3:X:169:VAL:HG23	3:X:177:SER:HB3	1.86	0.56
1:G:134:GLY:HA2	3:V:54:PHE:CE1	2.41	0.56
1:H:279:THR:HG21	1:H:287:ALA:HB1	1.87	0.56
4:z:175:LEU:HD23	4:z:176:SER:N	2.20	0.56
1:C:189:THR:O	1:C:193:THR:HG23	2.06	0.56
1:H:216:GLU:O	1:H:220:ARG:NH2	2.39	0.56
3:N:204:ASN:ND2	3:N:204:ASN:O	2.39	0.56
4:Q:105:GLU:HB2	4:Q:166:GLN:NE2	2.20	0.56
1:G:222:LYS:HA	1:G:226:LEU:O	2.05	0.56
3:L:153:SER:OG	3:L:197:ASN:OD1	2.23	0.56
1:A:320:LEU:HB3	2:a:111:HIS:CD2	2.41	0.56
3:J:34:PHE:CD2	3:J:78:ALA:HB2	2.41	0.56
1:D:202:VAL:HG13	1:D:251:LEU:HD13	1.87	0.56
1:E:311:SER:OG	2:e:97:GLU:OE2	2.22	0.56
2:g:9:PHE:CE1	2:g:10:ILE:HG13	2.41	0.56
2:b:150:ASN:HA	2:b:153:LYS:HD3	1.88	0.56
2:f:19:ASP:OD1	2:f:19:ASP:N	2.34	0.56
2:i:145:ASP:OD1	2:i:145:ASP:N	2.39	0.56
3:P:164:HIS:HB2	3:P:181:VAL:HG22	1.87	0.56
2:a:149:MET:C	2:a:151:SER:H	2.13	0.55
1:F:158:GLY:HA2	3:T:96:ILE:HG23	1.88	0.55
1:I:174:GLU:OE2	1:I:263:ARG:NH2	2.39	0.55
3:P:36:TRP:CZ3	3:P:92:CYS:HB2	2.42	0.55
4:z:33:LEU:HD21	4:z:88:CYS:HB2	1.89	0.55
1:A:197:ASN:OD1	1:A:197:ASN:N	2.39	0.55
1:C:156:LYS:HE2	1:C:193:THR:O	2.06	0.55
1:H:43:LEU:N	1:H:292:LEU:HD13	2.21	0.55
4:Q:34:ASN:HB2	4:Q:89:GLN:OE1	2.06	0.55
3:Z:33:VAL:HB	3:Z:95:GLY:O	2.06	0.55
2:e:106:ARG:HH12	2:f:106:ARG:HD2	1.71	0.55
1:H:147:PHE:CE1	1:H:230:MET:HE1	2.42	0.55
1:I:294:PHE:HZ	2:i:59:MET:HE2	1.71	0.55
3:T:181:VAL:HG11	4:U:135:LEU:HD22	1.86	0.55
3:V:70:THR:OG1	3:V:71:ALA:N	2.37	0.55
1:A:265:SER:OG	1:A:266:GLY:N	2.40	0.55
2:c:125:GLN:HE22	2:c:155:GLY:C	2.15	0.55
1:H:72:GLY:O	1:H:149:ARG:HG2	2.06	0.55
4:O:91:TYR:O	4:O:92:ASP:HB3	2.05	0.55
4:S:188:LYS:H	4:S:211:ARG:HH12	1.53	0.55
1:D:180:TRP:CE2	1:D:204:VAL:HG21	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:307:ARG:HH22	2:d:62:GLN:HE21	1.54	0.55
1:F:191:GLN:HG2	1:F:198:VAL:HG12	1.88	0.55
1:G:179:ILE:O	1:G:254:PRO:HB3	2.06	0.55
3:J:83:THR:OG1	3:J:84:SER:N	2.34	0.55
1:D:58:PRO:HB3	1:D:86:TYR:CE2	2.42	0.55
2:e:164:GLU:OE1	2:e:165:GLU:N	2.40	0.55
2:h:55:VAL:HG22	2:h:99:LEU:HD21	1.88	0.55
3:L:188:SER:HA	3:L:191:THR:HG23	1.88	0.55
1:A:220:ARG:HD2	1:A:227:GLY:O	2.07	0.55
2:i:128:ASP:O	2:i:170:ARG:NH1	2.39	0.55
4:K:39:LYS:HB2	4:K:40:PRO:HD3	1.87	0.55
2:a:24:TYR:CD2	2:a:153:LYS:HG2	2.42	0.55
1:B:176:MET:SD	1:B:257:GLY:HA3	2.46	0.55
3:Z:60:ALA:O	3:Z:62:LYS:N	2.40	0.55
3:Z:87:THR:HG23	3:Z:111:VAL:H	1.72	0.55
1:B:148:PHE:HB2	1:B:151:MET:HB2	1.89	0.55
1:I:191:GLN:HG2	1:I:198:VAL:HG12	1.89	0.55
1:I:307:ARG:NH2	2:i:62:GLN:HA	2.22	0.55
2:i:71:SER:H	2:i:74:GLU:HG3	1.72	0.55
4:Q:105:GLU:OE1	4:Q:166:GLN:NE2	2.40	0.55
1:E:184:HIS:CE1	1:E:215:PRO:HA	2.42	0.54
3:J:33:VAL:HG13	3:J:52:ILE:HD13	1.88	0.54
1:B:55:GLY:N	1:B:278:GLU:OE2	2.37	0.54
4:O:163:VAL:HG22	4:O:175:LEU:HD12	1.89	0.54
4:S:186:TYR:O	4:S:188:LYS:N	2.40	0.54
1:F:316:LEU:HD12	2:f:52:VAL:HG12	1.89	0.54
1:G:191:GLN:HG2	1:G:198:VAL:HG12	1.89	0.54
3:R:93:ALA:HB1	3:R:100(C):PHE:HB3	1.89	0.54
3:T:168:ALA:HB2	3:T:178:LEU:HD12	1.89	0.54
1:A:183:HIS:ND1	1:A:195:TYR:OH	2.35	0.54
2:a:171:ASN:N	2:a:171:ASN:HD22	2.06	0.54
1:B:58:PRO:HB3	1:B:86:TYR:CE2	2.43	0.54
2:e:62:GLN:HG3	2:e:92:TRP:CD2	2.42	0.54
1:G:131:THR:O	1:G:155:THR:HG23	2.07	0.54
2:g:106:ARG:HH12	2:h:106:ARG:HD2	1.73	0.54
4:U:151:ASP:HA	4:U:191:VAL:HB	1.88	0.54
1:B:25:LYS:HD2	1:B:33:ASN:O	2.07	0.54
2:b:69:GLU:O	2:c:76:ARG:NH1	2.39	0.54
2:h:145:ASP:O	2:h:147:GLU:N	2.41	0.54
1:A:294:PHE:CZ	2:a:59:MET:HE2	2.41	0.54
1:G:158:GLY:HA2	3:V:96:ILE:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:98:TYR:CG	1:H:230:MET:HE3	2.42	0.54
1:C:159:SER:HB3	3:N:100(B):TRP:CH2	2.42	0.54
1:F:158:GLY:H	3:T:97:SER:CB	2.20	0.54
4:U:6:GLN:O	4:U:100:GLN:NE2	2.41	0.54
3:V:101:ASP:OD1	4:W:55:LYS:NZ	2.39	0.54
1:H:15:ILE:HD11	2:h:122:VAL:HG21	1.90	0.54
1:I:148:PHE:HB2	1:I:151:MET:HB2	1.90	0.54
1:B:323:VAL:HG11	2:b:7:ALA:HB2	1.90	0.54
1:C:279:THR:OG1	1:C:280:LYS:N	2.41	0.54
2:d:130:VAL:HG12	2:d:140:PHE:HA	1.90	0.53
1:C:278:GLU:OE1	1:C:279:THR:N	2.40	0.53
1:G:207:SER:OG	1:G:241:ASP:OD2	2.25	0.53
2:g:142:HIS:HE2	2:g:157:TYR:HH	1.54	0.53
3:R:32:HIS:ND1	3:R:94:ARG:NH1	2.57	0.53
1:H:157:LYS:NZ	4:Y:92:ASP:HA	2.24	0.53
2:i:126:LEU:HD13	2:i:130:VAL:HG11	1.90	0.53
3:L:173:SER:HB2	3:L:175:LEU:H	1.74	0.53
4:O:6:GLN:HE22	4:O:101:GLY:HA2	1.73	0.53
3:T:22:CYS:HB2	3:T:36:TRP:CH2	2.43	0.53
3:Z:166:PHE:CD1	3:Z:167:PRO:HD2	2.39	0.53
1:A:105:TYR:HE2	1:A:109:LYS:HZ2	1.55	0.53
1:E:156:LYS:HE2	1:E:193:THR:O	2.09	0.53
1:F:20:ASN:OD1	1:F:22:SER:HB3	2.08	0.53
1:G:298:HIS:HE1	1:G:300:LEU:HD12	1.74	0.53
2:h:164:GLU:OE1	2:h:165:GLU:N	2.41	0.53
3:J:31:THR:OG1	3:J:32:HIS:N	2.37	0.53
3:V:94:ARG:HB3	3:V:102:PRO:HD2	1.89	0.53
2:d:119:TYR:CE1	2:d:136:GLY:HA2	2.43	0.53
2:g:128:ASP:OD1	2:g:159:TYR:OH	2.19	0.53
1:H:316:LEU:HD23	2:h:100:VAL:HG22	1.91	0.53
3:N:181:VAL:HG21	4:O:135:LEU:CD1	2.39	0.53
1:G:279:THR:OG1	1:G:280:LYS:N	2.40	0.53
2:i:107:THR:O	2:i:110:PHE:HB3	2.09	0.53
2:i:125:GLN:HE22	2:i:155:GLY:HA2	1.74	0.53
4:U:183:LYS:CE	4:U:187:GLU:HG3	2.39	0.53
4:W:61:ARG:O	4:W:75:ILE:HA	2.08	0.53
1:C:20:ASN:N	1:C:322:ASN:OD1	2.32	0.53
1:G:119:LYS:HD3	1:G:122:PRO:HB3	1.89	0.53
1:G:284:PRO:HG2	1:G:298:HIS:CE1	2.44	0.53
1:B:119:LYS:HA	1:B:256:TYR:HD1	1.74	0.53
1:B:194:LEU:HD13	3:L:53:ILE:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:174:GLU:OE1	1:E:263:ARG:NH2	2.41	0.53
1:H:279:THR:OG1	1:H:280:LYS:N	2.42	0.53
2:i:4:GLY:O	2:i:8:GLY:HA3	2.07	0.53
3:R:13:LYS:NZ	3:R:114:ALA:O	2.42	0.53
3:R:171:GLN:NE2	3:R:173:SER:OG	2.41	0.53
3:T:97:SER:OG	3:T:98:GLY:N	2.41	0.53
3:T:114:ALA:HB3	3:T:146:PHE:CE1	2.44	0.53
1:D:206:THR:OG1	1:D:207:SER:N	2.40	0.52
3:L:96:ILE:O	3:L:100(A):GLY:N	2.42	0.52
3:N:134:GLY:O	3:N:186:SER:OG	2.25	0.52
3:X:87:THR:CG2	3:X:111:VAL:H	2.22	0.52
1:B:295:HIS:HD2	1:B:297:VAL:H	1.56	0.52
1:H:98:TYR:CD2	1:H:230:MET:HG3	2.44	0.52
1:H:295:HIS:HD2	1:H:297:VAL:H	1.56	0.52
4:S:89:GLN:HB2	4:S:98:PHE:CD1	2.44	0.52
1:E:273:THR:OG1	1:E:274:LEU:N	2.42	0.52
1:F:176:MET:SD	1:F:257:GLY:HA3	2.49	0.52
1:H:84:TRP:CZ3	1:H:116(A):HIS:HA	2.44	0.52
3:J:103:TRP:HE1	4:K:36:TYR:HE1	1.56	0.52
4:z:50:ASP:OD1	4:z:91:TYR:OH	2.22	0.52
2:e:106:ARG:NH1	2:f:106:ARG:HH11	2.06	0.52
1:I:295:HIS:HD2	1:I:297:VAL:H	1.57	0.52
1:D:194:LEU:HB3	1:D:195:TYR:CE2	2.45	0.52
1:F:72:GLY:O	1:F:149:ARG:HG2	2.10	0.52
1:F:314:LEU:HD22	2:f:100:VAL:HG21	1.90	0.52
1:C:323:VAL:HG11	2:c:7:ALA:HB2	1.90	0.52
2:a:141:TYR:CE2	2:a:170:ARG:HD3	2.45	0.52
1:G:214:THR:O	1:G:214:THR:OG1	2.26	0.52
1:H:180:TRP:CE2	1:H:204:VAL:HG21	2.45	0.52
4:M:198:HIS:CG	4:M:199:GLN:N	2.78	0.52
3:P:143:LYS:NZ	3:P:144:ASP:OD2	2.35	0.52
2:b:145:ASP:H	2:b:148:CYS:HB3	1.75	0.52
2:b:149:MET:C	2:b:151:SER:H	2.17	0.52
1:E:194:LEU:CD1	3:R:53:ILE:HD13	2.39	0.52
4:S:13:ALA:O	4:S:106:ILE:HA	2.10	0.52
2:b:29:ASP:OD2	2:b:29:ASP:N	2.41	0.52
1:I:30:LEU:HD22	2:i:105:GLU:OE2	2.10	0.52
1:A:191:GLN:HG2	1:A:198:VAL:HG13	1.91	0.52
1:D:21:ASN:OD1	1:D:21:ASN:N	2.36	0.52
1:I:307:ARG:HH22	2:i:62:GLN:HA	1.75	0.52
3:P:94:ARG:HB3	3:P:102:PRO:HD2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:129:ASN:O	2:g:141:TYR:HB2	2.10	0.51
1:I:284:PRO:HD3	1:I:300:LEU:O	2.09	0.51
3:T:119:PRO:HB3	3:T:145:TYR:HB3	1.92	0.51
3:X:35:THR:HG21	3:X:100(C):PHE:CE1	2.45	0.51
1:I:133:THR:O	1:I:133:THR:OG1	2.27	0.51
1:I:310:LYS:HG3	2:i:89:LEU:HD21	1.91	0.51
3:T:115:SER:O	3:T:117:LYS:N	2.43	0.51
3:T:155:ASN:HB2	3:T:159:LEU:HB2	1.91	0.51
1:G:120:ILE:O	1:G:121:LEU:HD23	2.10	0.51
3:Z:100(B):TRP:HB3	4:z:34:ASN:ND2	2.24	0.51
1:I:131:THR:OG1	1:I:156:LYS:O	2.23	0.51
3:J:61:GLN:C	3:J:63:PHE:H	2.17	0.51
4:O:105:GLU:HG3	4:O:106:ILE:N	2.25	0.51
4:Y:23:CYS:HB2	4:Y:35:TRP:CH2	2.45	0.51
4:Y:89:GLN:HB2	4:Y:98:PHE:CD1	2.44	0.51
3:Z:96:ILE:HG22	3:Z:100(A):GLY:HA3	1.92	0.51
4:z:91:TYR:O	4:z:93:ASN:N	2.43	0.51
1:D:157:LYS:HZ3	4:Q:92:ASP:HA	1.76	0.51
1:E:71:LEU:HD21	1:E:179:ILE:HG21	1.93	0.51
3:J:33:VAL:HB	3:J:95:GLY:C	2.35	0.51
4:M:49:TYR:O	4:M:53:ASN:HB2	2.11	0.51
3:X:119:PRO:HB2	3:X:142:VAL:HG12	1.92	0.51
2:e:51:LYS:HD3	2:e:103:GLU:HB3	1.93	0.51
3:L:66:ARG:O	3:L:82(A):THR:HG23	2.11	0.51
4:W:38:GLN:HG3	4:W:44:PRO:HG3	1.93	0.51
3:J:34:PHE:HD2	3:J:78:ALA:HB2	1.75	0.51
4:U:108:ARG:NH2	4:U:170:ASP:O	2.44	0.51
1:A:102:PHE:HZ	1:A:179:ILE:HD13	1.76	0.51
1:B:151:MET:HE1	1:B:180:TRP:HA	1.93	0.51
1:D:307:ARG:NH2	2:d:62:GLN:HE21	2.08	0.51
1:E:17:TYR:CE2	2:e:6:ILE:HA	2.46	0.51
4:M:142:ARG:HB3	4:M:173:TYR:CD2	2.46	0.51
1:B:37:THR:C	1:B:38:HIS:HD1	2.19	0.50
2:d:63:PHE:HE2	2:e:83:LYS:HZ1	1.58	0.50
1:E:294:PHE:HZ	2:e:59:MET:HE2	1.76	0.50
1:D:170:ASN:HB2	1:D:237:LEU:HD23	1.93	0.50
2:h:125:GLN:HE22	2:h:155:GLY:C	2.20	0.50
3:L:35:THR:HG22	3:L:93:ALA:O	2.11	0.50
4:Q:175:LEU:HD23	4:Q:176:SER:N	2.26	0.50
1:A:52:CYS:HB2	1:A:279:THR:HG22	1.93	0.50
2:d:128:ASP:OD1	2:d:159:TYR:OH	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:172:SER:HB2	1:I:259:LYS:HD2	1.93	0.50
4:M:115:VAL:HG21	4:M:196:VAL:HG21	1.92	0.50
3:P:32:HIS:ND1	3:P:94:ARG:NH1	2.59	0.50
4:S:33:LEU:HD22	4:S:71:PHE:CG	2.46	0.50
3:T:54:PHE:HB3	3:T:56:THR:HG23	1.94	0.50
1:G:72:GLY:O	1:G:149:ARG:HG2	2.11	0.50
3:T:193:THR:HG22	3:T:210:ARG:HH21	1.76	0.50
3:X:6:GLU:OE2	3:X:105:GLN:N	2.43	0.50
2:a:54:SER:HB2	1:B:32:ARG:HH21	1.76	0.50
1:D:55:GLY:N	1:D:278:GLU:OE2	2.45	0.50
1:D:158:GLY:O	1:D:160:ASP:N	2.39	0.50
2:e:110:PHE:O	2:e:114:ASN:ND2	2.44	0.50
2:e:125:GLN:HE22	2:e:155:GLY:C	2.19	0.50
1:G:172:SER:HB2	1:G:259:LYS:HD2	1.94	0.50
1:H:66:ILE:HB	1:H:105:TYR:OH	2.11	0.50
2:i:19:ASP:OD1	2:i:19:ASP:N	2.34	0.50
3:J:30:ILE:HG22	3:J:31:THR:H	1.77	0.50
4:Q:33:LEU:HD22	4:Q:71:PHE:CG	2.46	0.50
3:X:96:ILE:O	3:X:100(A):GLY:N	2.45	0.50
1:B:52:CYS:HB2	1:B:279:THR:HG22	1.93	0.50
1:F:14:CYS:HA	2:f:137:CYS:HA	1.94	0.50
1:I:158:GLY:H	3:Z:97:SER:CB	2.25	0.50
1:C:15:ILE:O	2:c:10:ILE:HD13	2.12	0.50
1:E:212:ARG:NH2	1:F:217:ILE:O	2.45	0.50
2:i:130:VAL:HG12	2:i:140:PHE:HA	1.94	0.50
1:I:294:PHE:CZ	2:i:59:MET:HG3	2.47	0.50
3:P:154:TRP:HD1	3:P:155:ASN:H	1.57	0.50
4:Y:35:TRP:CZ3	4:Y:88:CYS:HB3	2.47	0.50
1:A:54:ASN:OD1	1:A:280:LYS:HG3	2.11	0.50
1:H:268:MET:HE3	1:H:302:ILE:HD12	1.94	0.50
3:V:93:ALA:HB1	3:V:100(C):PHE:HB3	1.94	0.50
2:g:119:TYR:CE1	2:g:136:GLY:HA2	2.47	0.49
2:h:24:TYR:CD2	2:h:153:LYS:HG2	2.47	0.49
1:B:58:PRO:HD2	1:B:274:LEU:HD22	1.94	0.49
1:C:156:LYS:HB2	1:C:160:ASP:O	2.12	0.49
1:F:283:THR:OG1	1:F:286:GLY:N	2.42	0.49
1:G:197:ASN:OD1	1:G:197:ASN:N	2.45	0.49
1:I:155:THR:HG21	3:Z:54:PHE:CZ	2.44	0.49
3:T:138:LEU:HG	3:T:182:VAL:HG23	1.93	0.49
4:Y:39:LYS:HE2	4:Y:81:GLU:O	2.11	0.49
2:b:4:GLY:O	2:b:8:GLY:HA3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:164:ALA:O	1:H:246:GLU:HA	2.12	0.49
4:O:193:ALA:HB2	4:O:208:SER:HB2	1.95	0.49
1:C:51:LEU:HD22	1:C:88:MET:HE3	1.93	0.49
1:C:159:SER:HB3	3:N:100(B):TRP:HH2	1.77	0.49
4:K:60:SER:O	4:K:63:ARG:NH2	2.46	0.49
3:N:201:LYS:O	3:N:204:ASN:N	2.45	0.49
3:V:97:SER:OG	3:V:99:SER:N	2.36	0.49
3:Z:171:GLN:HB3	3:Z:173:SER:H	1.75	0.49
1:A:14:CYS:O	1:A:15:ILE:HD13	2.13	0.49
1:F:216:GLU:O	1:F:220:ARG:NH2	2.46	0.49
2:g:9:PHE:CD1	2:g:10:ILE:HG13	2.47	0.49
1:H:52:CYS:HB2	1:H:279:THR:HG22	1.93	0.49
3:T:32:HIS:ND1	3:T:94:ARG:NH1	2.60	0.49
4:W:23:CYS:HB2	4:W:35:TRP:CH2	2.48	0.49
1:C:55:GLY:N	1:C:278:GLU:OE2	2.45	0.49
3:R:101:ASP:HB3	3:R:102:PRO:HD3	1.95	0.49
3:J:63:PHE:HB3	3:J:67:VAL:HG12	1.95	0.49
3:P:144:ASP:HB3	3:P:175:LEU:HD13	1.93	0.49
3:R:22:CYS:HB2	3:R:36:TRP:CH2	2.47	0.49
2:a:65:ALA:C	2:a:67:GLY:H	2.20	0.49
1:C:294:PHE:HZ	2:c:59:MET:HE2	1.76	0.49
1:D:15:ILE:O	2:d:10:ILE:HD13	2.12	0.49
1:D:158:GLY:HA2	3:P:96:ILE:HG23	1.95	0.49
1:D:190:GLU:O	1:D:194:LEU:HB2	2.13	0.49
1:I:14:CYS:HA	2:i:137:CYS:HA	1.94	0.49
3:P:100(B):TRP:HB3	4:Q:34:ASN:ND2	2.28	0.49
3:V:95:GLY:HA2	3:V:100(B):TRP:O	2.13	0.49
3:Z:7:SER:HB3	3:Z:21:SER:H	1.77	0.49
1:B:158:GLY:H	3:L:97:SER:CB	2.26	0.49
1:C:316:LEU:HD12	2:c:52:VAL:HG12	1.95	0.49
1:E:108:LEU:HB2	1:E:234:TRP:CZ2	2.48	0.49
1:G:193:THR:HG21	3:V:31:THR:HA	1.94	0.49
1:I:279:THR:OG1	1:I:280:LYS:N	2.46	0.49
3:J:32:HIS:CE1	3:J:94:ARG:HH12	2.31	0.49
3:R:47:TRP:CE3	4:S:96:ILE:HB	2.48	0.49
3:R:97:SER:HG	3:R:99:SER:N	2.06	0.49
3:R:124:LEU:HB3	4:S:118:PHE:CD1	2.48	0.49
4:U:90:GLN:NE2	4:U:91:TYR:O	2.46	0.49
1:B:174:GLU:N	1:B:239:MET:SD	2.86	0.49
2:b:123:ARG:HH21	2:b:124:MET:HE3	1.78	0.49
1:F:172:SER:HB2	1:F:259:LYS:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:31:LYS:HB3	4:U:31:LYS:HE2	1.63	0.49
1:C:126:ARG:O	1:C:128:THR:HG23	2.14	0.48
1:D:187:ASP:OD1	1:D:189:THR:OG1	2.25	0.48
1:E:148:PHE:HB2	1:E:151:MET:HB2	1.94	0.48
1:E:279:THR:OG1	1:E:280:LYS:N	2.46	0.48
1:I:177:LEU:HB3	1:I:258:PHE:HB2	1.95	0.48
3:P:154:TRP:HD1	3:P:155:ASN:N	2.10	0.48
1:C:175:GLN:HB3	1:C:236:LEU:HD23	1.96	0.48
1:C:251:LEU:HD12	1:C:252:ILE:N	2.28	0.48
4:O:119:PRO:HB3	4:O:209:PHE:CE2	2.48	0.48
4:U:21:ILE:HD12	4:U:73:PHE:HD2	1.77	0.48
4:W:32:TYR:CD1	4:W:91:TYR:CE1	3.01	0.48
3:Z:87:THR:CG2	3:Z:111:VAL:H	2.26	0.48
1:C:319:GLY:HA2	2:c:21:TRP:CZ2	2.49	0.48
1:D:194:LEU:HB3	1:D:195:TYR:CD2	2.47	0.48
1:E:18:HIS:ND1	1:E:19:ALA:N	2.61	0.48
4:U:189:HIS:O	4:U:211:ARG:NH1	2.45	0.48
4:Y:1:ASP:HA	4:Y:95:PRO:HG3	1.94	0.48
1:A:155:THR:OG1	1:A:156:LYS:N	2.47	0.48
1:B:279:THR:HG21	1:B:287:ALA:HB1	1.93	0.48
1:F:193:THR:CG2	3:T:31:THR:HG22	2.44	0.48
1:G:131:THR:OG1	1:G:156:LYS:O	2.26	0.48
4:M:187:GLU:O	4:M:211:ARG:NH1	2.46	0.48
3:T:200:HIS:NE2	3:T:202:PRO:HG2	2.27	0.48
4:W:78:LEU:HD23	4:W:79:GLN:N	2.28	0.48
2:d:97:GLU:HB3	2:f:58:LYS:HE3	1.95	0.48
1:E:63:ASP:OD2	1:E:63:ASP:N	2.45	0.48
2:e:48:ILE:HD11	2:e:107:THR:HG23	1.95	0.48
1:I:294:PHE:CZ	2:i:59:MET:HE2	2.48	0.48
2:i:125:GLN:HE22	2:i:155:GLY:CA	2.26	0.48
4:K:19:VAL:HB	4:K:75:ILE:HG23	1.96	0.48
1:E:43:LEU:HB2	1:E:314:LEU:HB2	1.96	0.48
1:F:279:THR:OG1	1:F:280:LYS:N	2.46	0.48
1:G:71:LEU:O	1:G:150:ASN:ND2	2.46	0.48
1:H:88:MET:HE3	1:H:270:THR:HG21	1.96	0.48
3:N:215:SER:O	3:N:215:SER:OG	2.31	0.48
4:S:4:LEU:HA	4:S:24:GLN:O	2.13	0.48
4:z:94:LEU:HD22	4:z:96:ILE:HG12	1.95	0.48
1:B:118:VAL:O	1:B:120:ILE:HG23	2.13	0.48
2:b:19:ASP:OD1	2:b:19:ASP:N	2.46	0.48
1:F:310:LYS:HG3	2:f:89:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:f:30:GLN:HE22	2:f:145:ASP:HB2	1.77	0.48
1:I:298:HIS:CG	1:I:299:PRO:HD2	2.49	0.48
4:S:158:ASN:OD1	4:S:158:ASN:N	2.43	0.48
4:U:91:TYR:O	4:U:93:ASN:N	2.47	0.48
1:A:295:HIS:CD2	1:A:297:VAL:HG23	2.49	0.48
1:E:14:CYS:HA	2:e:137:CYS:HA	1.96	0.48
3:R:100(B):TRP:HB3	4:S:34:ASN:ND2	2.29	0.48
1:F:71:LEU:O	1:F:150:ASN:ND2	2.47	0.48
4:O:62:PHE:CE1	4:O:75:ILE:HG12	2.49	0.48
4:U:78:LEU:HD23	4:U:79:GLN:O	2.13	0.48
1:B:17:TYR:CE2	2:b:6:ILE:HA	2.49	0.48
2:c:27:SER:O	2:c:27:SER:OG	2.32	0.48
1:E:182:VAL:HG12	1:E:202:VAL:HG11	1.96	0.48
1:E:246:GLU:OE1	1:F:219:THR:HG23	2.14	0.48
2:g:71:SER:H	2:g:74:GLU:HG3	1.78	0.48
1:I:163:VAL:HG22	1:I:248:THR:HG22	1.95	0.48
3:X:166:PHE:CD1	3:X:167:PRO:HD2	2.41	0.48
1:A:55:GLY:N	1:A:278:GLU:OE2	2.44	0.47
1:C:169:ASN:O	1:C:171:THR:HG23	2.14	0.47
1:G:279:THR:HG21	1:G:287:ALA:HB1	1.95	0.47
1:H:220:ARG:HB2	1:H:227:GLY:O	2.13	0.47
3:R:112:SER:HB3	3:R:146:PHE:CZ	2.49	0.47
3:T:39:GLN:HG3	3:T:44:GLY:O	2.14	0.47
1:E:155:THR:HG21	3:R:54:PHE:HZ	1.79	0.47
3:T:101:ASP:HB3	3:T:102:PRO:HD3	1.96	0.47
1:A:207:SER:OG	1:A:241:ASP:OD2	2.23	0.47
2:a:119:TYR:CE1	2:a:136:GLY:HA2	2.50	0.47
1:C:295:HIS:C	1:C:295:HIS:CD2	2.92	0.47
1:F:157:LYS:HE2	4:U:92:ASP:HA	1.96	0.47
1:F:159:SER:H	3:T:96:ILE:HD13	1.79	0.47
1:G:102:PHE:HZ	1:G:179:ILE:HD13	1.79	0.47
3:N:51:PHE:HB2	3:N:69:ILE:HG21	1.97	0.47
3:P:163:VAL:O	3:P:164:HIS:ND1	2.47	0.47
3:X:87:THR:HG23	3:X:111:VAL:H	1.79	0.47
2:c:19:ASP:OD1	2:c:19:ASP:N	2.37	0.47
1:D:288:ILE:HD11	1:D:297:VAL:HG21	1.96	0.47
1:F:186:ASN:OD1	1:F:219:THR:HA	2.14	0.47
4:K:62:PHE:CE1	4:K:75:ILE:HD13	2.49	0.47
4:Q:89:GLN:HB2	4:Q:98:PHE:CE1	2.50	0.47
3:T:197:ASN:ND2	3:T:208:ASP:OD2	2.40	0.47
1:C:298:HIS:CE1	1:C:300:LEU:HD12	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:PRO:O	1:C:301:THR:HG23	2.14	0.47
2:c:145:ASP:OD1	2:c:145:ASP:N	2.46	0.47
1:F:279:THR:HG21	1:F:287:ALA:HB1	1.96	0.47
3:N:129:LYS:HE2	3:N:129:LYS:HB2	1.67	0.47
2:b:23:GLY:HA3	2:b:36:ALA:HA	1.96	0.47
2:c:27:SER:HB2	4:S:63:ARG:HH22	1.79	0.47
3:J:10:GLU:HB2	3:J:12:LYS:NZ	2.30	0.47
4:K:37:GLN:HB2	4:K:47:LEU:HD11	1.96	0.47
3:X:32:HIS:ND1	3:X:94:ARG:NH1	2.62	0.47
2:a:64:GLU:HB3	2:a:66:VAL:H	1.78	0.47
1:C:66:ILE:HD12	1:C:112:LEU:CD1	2.44	0.47
1:C:214:THR:HA	1:C:215:PRO:HD3	1.67	0.47
1:C:282:GLN:NE2	1:C:283:THR:O	2.41	0.47
1:C:295:HIS:HE1	1:C:301:THR:HG21	1.79	0.47
1:F:53:LYS:HB2	1:F:278:GLU:HG2	1.97	0.47
2:f:28:ASN:ND2	2:f:144:CYS:O	2.28	0.47
1:H:294:PHE:CZ	2:h:59:MET:HG3	2.49	0.47
1:I:183:HIS:HB2	1:I:252:ILE:HD11	1.97	0.47
4:M:6:GLN:HA	4:M:22:THR:O	2.15	0.47
3:N:39:GLN:C	3:N:88:ALA:HB1	2.40	0.47
4:W:33:LEU:HD22	4:W:71:PHE:CG	2.50	0.47
1:B:29:ILE:HD11	2:b:102:MET:HG2	1.97	0.47
1:D:44:GLU:HB2	1:D:292:LEU:HD12	1.97	0.47
1:E:23:THR:O	1:E:23:THR:OG1	2.31	0.47
1:G:157:LYS:NZ	4:W:92:ASP:HA	2.30	0.47
1:H:185:PRO:HG2	1:H:191:GLN:OE1	2.15	0.47
3:R:50:GLY:HA3	3:R:100:TYR:CE1	2.50	0.47
1:B:157:LYS:HE2	4:M:92:ASP:HA	1.97	0.47
1:E:21:ASN:OD1	1:E:21:ASN:N	2.48	0.47
1:I:66:ILE:HD12	1:I:112:LEU:HD12	1.96	0.47
4:M:35:TRP:CE2	4:M:73:PHE:HB2	2.49	0.47
3:R:165:THR:HG23	3:R:180:SER:HB2	1.96	0.47
4:U:124:GLN:HG2	4:U:129:THR:O	2.14	0.47
2:e:128:ASP:O	2:e:170:ARG:NH1	2.48	0.47
1:H:204:VAL:HG22	1:H:245:PHE:CD1	2.50	0.47
3:J:5:VAL:HG13	3:J:23:LYS:HG2	1.95	0.46
4:M:35:TRP:HB2	4:M:48:ILE:HB	1.97	0.46
3:N:30:ILE:HD12	3:N:53:ILE:HD12	1.96	0.46
2:a:29:ASP:OD2	2:a:29:ASP:N	2.48	0.46
1:G:129:GLN:HB3	1:G:162:PRO:HG3	1.96	0.46
1:H:114:SER:O	1:H:263:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:100(B):TRP:CE3	4:O:49:TYR:HB2	2.49	0.46
3:X:87:THR:HG23	3:X:111:VAL:HG12	1.96	0.46
3:X:171:GLN:NE2	3:X:177:SER:HB2	2.30	0.46
1:A:29:ILE:HD11	2:a:102:MET:HG2	1.98	0.46
1:F:76:CYS:HB3	1:F:79:LEU:HD12	1.96	0.46
1:H:174:GLU:OE2	1:H:263:ARG:NH2	2.48	0.46
3:L:139:GLY:HA2	3:L:154:TRP:CZ2	2.51	0.46
3:N:181:VAL:HG21	4:O:135:LEU:HD13	1.98	0.46
3:P:92:CYS:SG	3:P:93:ALA:N	2.89	0.46
3:T:160:THR:OG1	3:T:161:SER:N	2.46	0.46
4:U:131:SER:HB3	4:U:180:THR:HG22	1.96	0.46
4:U:164:THR:HG22	4:U:174:SER:H	1.80	0.46
3:X:18:VAL:HG12	3:X:82(C):LEU:HD11	1.98	0.46
3:X:87:THR:HG23	3:X:111:VAL:CG1	2.45	0.46
1:F:163:VAL:HG22	1:F:248:THR:HG22	1.96	0.46
1:G:183:HIS:HB2	1:G:252:ILE:HD11	1.97	0.46
1:G:311:SER:OG	2:g:97:GLU:OE2	2.30	0.46
1:H:85:SER:OG	1:H:86:TYR:HD2	1.99	0.46
2:h:119:TYR:CE1	2:h:136:GLY:HA2	2.51	0.46
3:Z:167:PRO:HG2	4:z:162:SER:OG	2.16	0.46
2:d:98:LEU:HD12	2:d:98:LEU:HA	1.72	0.46
2:f:107:THR:O	2:f:110:PHE:HB3	2.16	0.46
2:h:23:GLY:HA3	2:h:36:ALA:HA	1.98	0.46
1:I:26:VAL:HG21	1:I:317:ALA:HB2	1.98	0.46
1:I:169:ASN:O	1:I:171:THR:HG23	2.15	0.46
4:O:146:VAL:HG11	4:O:177:SER:CB	2.46	0.46
3:R:197:ASN:N	3:R:197:ASN:OD1	2.49	0.46
3:T:35:THR:HG21	3:T:100(C):PHE:CE1	2.51	0.46
4:z:48:ILE:CD1	4:z:54:VAL:HG22	2.45	0.46
1:C:194:LEU:HD11	3:N:53:ILE:HG12	1.96	0.46
2:c:71:SER:OG	2:c:72:ASN:N	2.47	0.46
1:F:159:SER:OG	1:F:160:ASP:N	2.47	0.46
1:F:193:THR:HG21	3:T:31:THR:HA	1.98	0.46
1:H:156:LYS:HE2	1:H:193:THR:O	2.15	0.46
2:i:125:GLN:HE22	2:i:155:GLY:C	2.23	0.46
4:M:80:PRO:HA	4:M:106:ILE:HD11	1.98	0.46
4:U:61:ARG:O	4:U:75:ILE:HA	2.15	0.46
1:C:273:THR:OG1	1:C:274:LEU:N	2.47	0.46
1:D:42:ILE:HA	1:D:292:LEU:HD22	1.98	0.46
1:E:58:PRO:HB3	1:E:86:TYR:CE2	2.51	0.46
2:e:145:ASP:OD1	2:e:145:ASP:N	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:f:71:SER:H	2:f:74:GLU:HG3	1.81	0.46
1:G:171:THR:HA	1:G:240:TRP:CZ3	2.50	0.46
2:h:124:MET:HE1	2:i:9:PHE:CG	2.51	0.46
3:L:122:PHE:CG	4:M:124:GLN:HB2	2.51	0.46
4:W:11:LEU:HD23	4:W:11:LEU:HA	1.78	0.46
3:X:28:THR:O	3:X:31:THR:OG1	2.32	0.46
4:Y:21:ILE:HD12	4:Y:73:PHE:HD2	1.81	0.46
1:B:160:ASP:HA	1:B:196:GLN:OE1	2.16	0.46
1:C:268:MET:HE1	1:C:282:GLN:HG3	1.98	0.46
1:D:323:VAL:HG11	2:d:7:ALA:HB2	1.97	0.46
1:E:61:LEU:O	1:E:78:ARG:NH2	2.48	0.46
1:F:120:ILE:HG22	1:F:168:TYR:CE1	2.51	0.46
3:J:35:THR:HG21	3:J:100(C):PHE:CD1	2.49	0.46
4:O:198:HIS:CG	4:O:199:GLN:N	2.84	0.46
4:Q:112:ALA:HA	4:Q:113:PRO:HD2	1.83	0.46
4:S:89:GLN:HB2	4:S:98:PHE:CE1	2.51	0.46
4:U:115:VAL:HG22	4:U:136:LEU:HG	1.97	0.46
4:Y:33:LEU:HD22	4:Y:71:PHE:CD2	2.51	0.46
2:d:145:ASP:OD1	2:d:145:ASP:N	2.45	0.46
1:E:56:ILE:HA	1:E:57:PRO:HD3	1.77	0.46
4:U:23:CYS:HB2	4:U:35:TRP:CH2	2.51	0.46
2:a:164:GLU:HA	2:a:167:LYS:HE2	1.98	0.46
1:H:147:PHE:HE1	1:H:230:MET:HE1	1.80	0.46
1:I:183:HIS:ND1	1:I:195:TYR:OH	2.38	0.46
3:R:7:SER:CB	3:R:21:SER:H	2.24	0.46
3:R:163:VAL:O	3:R:164:HIS:ND1	2.49	0.46
4:S:31:LYS:HE2	4:S:51:ALA:HB3	1.98	0.46
3:X:200:HIS:HB3	3:X:205:THR:OG1	2.16	0.46
4:Y:2:ILE:HD12	4:Y:90:GLN:NE2	2.31	0.46
1:B:114:SER:O	1:B:114:SER:OG	2.35	0.45
1:C:44:GLU:OE2	1:C:45:LYS:N	2.50	0.45
1:C:127:TRP:CG	1:C:154:LEU:HD11	2.51	0.45
3:R:155:ASN:HB2	3:R:159:LEU:H	1.81	0.45
4:U:50:ASP:OD1	4:U:91:TYR:OH	2.29	0.45
1:A:268:MET:HE3	1:A:302:ILE:HD11	1.99	0.45
2:b:164:GLU:HA	2:b:167:LYS:HE2	1.97	0.45
1:C:307:ARG:CZ	2:c:61:THR:HA	2.45	0.45
1:G:105:TYR:O	1:G:109:LYS:HG3	2.16	0.45
1:H:106:GLU:CD	1:H:106:GLU:H	2.24	0.45
1:I:48:ASN:HD21	1:I:287:ALA:HB3	1.80	0.45
1:I:120:ILE:O	1:I:121:LEU:HD23	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:127:SER:O	3:T:127:SER:OG	2.22	0.45
4:U:113:PRO:O	4:U:115:VAL:HG23	2.16	0.45
4:Y:90:GLN:NE2	4:Y:91:TYR:O	2.49	0.45
1:A:70:LEU:HA	1:A:70:LEU:HD23	1.67	0.45
1:G:116(A):HIS:HB3	1:G:262:LYS:H	1.81	0.45
1:I:51:LEU:HA	1:I:282:GLN:HE22	1.81	0.45
2:i:14:TRP:HE3	2:i:17:MET:HE2	1.81	0.45
4:O:20:THR:HG22	4:O:74:THR:HG23	1.99	0.45
4:Q:78:LEU:HD23	4:Q:79:GLN:N	2.30	0.45
3:V:39:GLN:HE22	4:W:38:GLN:HE22	1.64	0.45
3:X:67:VAL:HA	3:X:81:GLU:O	2.16	0.45
1:A:17:TYR:CE2	2:a:6:ILE:HA	2.52	0.45
1:B:263(A):GLY:O	1:B:265:SER:N	2.50	0.45
2:c:28:ASN:ND2	2:c:30:GLN:OE1	2.49	0.45
2:c:119:TYR:CE1	2:c:136:GLY:HA2	2.52	0.45
1:H:58:PRO:HB3	1:H:86:TYR:CE2	2.52	0.45
1:H:313:LYS:O	1:H:314:LEU:HD23	2.15	0.45
1:I:186:ASN:OD1	1:I:219:THR:HA	2.15	0.45
3:T:198:VAL:HG22	3:T:207:VAL:HB	1.97	0.45
4:z:2:ILE:HD12	4:z:90:GLN:NE2	2.32	0.45
1:E:37:THR:O	1:E:38:HIS:ND1	2.49	0.45
1:E:298:HIS:CG	1:E:299:PRO:HD2	2.51	0.45
1:F:52:CYS:HB2	1:F:279:THR:HG22	1.98	0.45
4:K:4:LEU:HG	4:K:23:CYS:SG	2.56	0.45
4:M:119:PRO:HB3	4:M:209:PHE:CE2	2.51	0.45
3:Z:121:VAL:O	3:Z:123:PRO:HD3	2.17	0.45
1:A:313:LYS:O	1:A:314:LEU:HD23	2.17	0.45
2:a:113:SER:OG	2:b:2:LEU:O	2.32	0.45
2:a:149:MET:O	2:a:151:SER:N	2.50	0.45
2:a:160:PRO:HA	2:a:163:GLU:HB2	1.99	0.45
1:I:158:GLY:HA2	3:Z:96:ILE:HG23	1.99	0.45
4:Q:65:SER:OG	4:Q:66:GLY:N	2.50	0.45
4:W:6:GLN:HE21	4:W:35:TRP:HZ3	1.65	0.45
4:W:35:TRP:CE2	4:W:73:PHE:HB2	2.52	0.45
3:X:93:ALA:HB1	3:X:100(C):PHE:HB3	1.97	0.45
3:Z:32:HIS:ND1	3:Z:94:ARG:NH1	2.65	0.45
4:z:6:GLN:HE22	4:z:87:TYR:HA	1.82	0.45
1:B:152:VAL:HG12	1:B:154:LEU:HD13	1.97	0.45
1:B:277:CYS:HB2	1:B:278:GLU:H	1.56	0.45
1:B:295:HIS:HD2	1:B:297:VAL:HG23	1.82	0.45
1:B:295:HIS:CD2	1:B:297:VAL:HG23	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:155:THR:HG21	3:P:54:PHE:HZ	1.81	0.45
1:E:294:PHE:CZ	2:e:59:MET:HG3	2.51	0.45
2:g:70:PHE:HB3	2:g:74:GLU:HB2	1.99	0.45
1:I:159:SER:N	3:Z:96:ILE:HD13	2.32	0.45
3:V:66:ARG:HH11	3:V:66:ARG:HB3	1.82	0.45
3:Z:141:LEU:HA	3:Z:179:SER:HA	1.98	0.45
4:z:23:CYS:HB2	4:z:35:TRP:CH2	2.51	0.45
1:A:156:LYS:HE2	1:A:193:THR:C	2.42	0.45
1:B:121:LEU:HD21	1:B:167:SER:O	2.17	0.45
1:E:316:LEU:HD12	2:e:52:VAL:HG12	1.99	0.45
1:I:43:LEU:HB2	1:I:314:LEU:HB2	1.99	0.45
3:J:37:VAL:CG1	3:J:45:LEU:HD22	2.46	0.45
4:M:150:VAL:HB	4:M:192:TYR:CD1	2.52	0.45
3:V:47:TRP:CE3	4:W:96:ILE:HB	2.51	0.45
4:M:189:HIS:HB2	4:M:192:TYR:OH	2.17	0.45
4:O:199:GLN:C	4:O:201:LEU:H	2.24	0.45
3:V:16:SER:HB2	3:V:17:SER:H	1.60	0.45
3:Z:145:TYR:OH	3:Z:148:GLU:HG3	2.17	0.45
1:A:320:LEU:HB3	2:a:111:HIS:CG	2.51	0.45
1:B:298:HIS:HE1	1:B:300:LEU:HD12	1.82	0.45
1:D:204:VAL:HG13	1:D:245:PHE:CE1	2.52	0.45
1:E:268:MET:HE1	1:E:282:GLN:HG3	1.99	0.45
2:g:126:LEU:HD21	2:g:152:VAL:HG22	1.99	0.45
2:g:164:GLU:OE1	2:g:165:GLU:N	2.49	0.45
1:H:47:HIS:HA	1:H:287:ALA:O	2.17	0.45
1:H:56:ILE:HA	1:H:57:PRO:HD3	1.71	0.45
3:N:6:GLU:OE1	3:N:105:GLN:N	2.50	0.45
3:N:171:GLN:O	3:N:172:SER:C	2.60	0.45
4:O:4:LEU:HD23	4:O:4:LEU:HA	1.80	0.45
4:S:2:ILE:HD12	4:S:90:GLN:NE2	2.31	0.45
3:T:122:PHE:CD1	4:U:123:GLU:HG3	2.52	0.45
3:V:96:ILE:HG22	3:V:100(A):GLY:HA3	1.98	0.45
1:A:21:ASN:OD1	1:A:21:ASN:N	2.43	0.44
2:a:127:ARG:HB3	2:a:128:ASP:H	1.60	0.44
1:B:17:TYR:CD2	2:b:6:ILE:HG12	2.52	0.44
1:D:295:HIS:C	1:D:295:HIS:CD2	2.96	0.44
4:K:35:TRP:HD1	4:K:48:ILE:HG12	1.83	0.44
4:Q:140:TYR:CE2	4:Q:141:PRO:HG3	2.52	0.44
4:S:91:TYR:HD1	4:S:92:ASP:H	1.64	0.44
4:U:186:TYR:HA	4:U:192:TYR:OH	2.17	0.44
4:z:89:GLN:HB2	4:z:98:PHE:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:LEU:HB3	2:c:111:HIS:CG	2.52	0.44
1:D:56:ILE:HA	1:D:57:PRO:HD3	1.82	0.44
2:d:61:THR:OG1	2:d:62:GLN:N	2.50	0.44
1:F:98:TYR:CD2	1:F:230:MET:HE3	2.53	0.44
3:L:80:MET:HB3	3:L:80:MET:HE3	1.73	0.44
4:S:187:GLU:HA	4:S:211:ARG:NH2	2.33	0.44
3:X:143:LYS:NZ	3:X:171:GLN:OE1	2.28	0.44
1:B:117:LYS:HD2	1:B:256:TYR:CD2	2.52	0.44
2:h:14:TRP:CE3	2:h:17:MET:HE2	2.53	0.44
3:J:94:ARG:HB3	3:J:102:PRO:HD2	1.99	0.44
3:L:43:GLN:HB3	3:L:44:GLY:H	1.45	0.44
3:N:201:LYS:O	3:N:203:SER:N	2.50	0.44
3:T:152:VAL:HG11	3:T:180:SER:OG	2.17	0.44
1:D:70:LEU:HD23	1:D:70:LEU:HA	1.80	0.44
2:f:145:ASP:OD1	2:f:145:ASP:N	2.45	0.44
1:H:20:ASN:OD1	1:H:22:SER:HB3	2.18	0.44
1:H:137:ARG:HE	1:H:137:ARG:HB2	1.38	0.44
1:I:44:GLU:OE2	1:I:46:THR:OG1	2.35	0.44
3:J:92:CYS:SG	3:J:93:ALA:N	2.90	0.44
4:O:208:SER:OG	4:O:209:PHE:N	2.48	0.44
3:P:160:THR:OG1	3:P:161:SER:N	2.51	0.44
3:R:146:PHE:HA	3:R:147:PRO:HA	1.79	0.44
4:S:166:GLN:HB2	4:S:173:TYR:CE1	2.51	0.44
1:A:106:GLU:HB3	2:a:69:GLU:O	2.17	0.44
1:C:295:HIS:CE1	1:C:301:THR:HG21	2.52	0.44
1:D:151:MET:HE1	1:D:180:TRP:HA	1.99	0.44
1:F:90:LYS:HA	1:F:270:THR:O	2.17	0.44
4:K:2:ILE:HD11	4:K:90:GLN:NE2	2.32	0.44
3:L:163:VAL:HG12	3:L:182:VAL:CG1	2.46	0.44
3:P:35:THR:HG22	3:P:93:ALA:O	2.18	0.44
4:U:12:SER:HB3	4:U:107:LYS:HG3	1.99	0.44
1:B:204:VAL:HG22	1:B:245:PHE:CD1	2.51	0.44
1:C:142:SER:C	1:C:144:ASN:H	2.25	0.44
1:D:220:ARG:HB2	1:D:227:GLY:O	2.17	0.44
1:E:270:THR:OG1	1:E:271:GLU:N	2.51	0.44
1:F:42:ILE:HG13	1:F:314:LEU:O	2.17	0.44
1:G:136:SER:OG	1:G:137:ARG:N	2.51	0.44
3:J:33:VAL:HB	3:J:95:GLY:O	2.18	0.44
3:N:184:VAL:HG21	3:N:194:TYR:CZ	2.53	0.44
4:O:47:LEU:HD23	4:O:47:LEU:HA	1.78	0.44
3:P:67:VAL:HB	3:P:82:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:59:TYR:HE1	3:T:69:ILE:HG13	1.83	0.44
4:U:129:THR:HG22	4:U:182:SER:HA	2.00	0.44
4:Y:50:ASP:O	4:Y:52:SER:N	2.46	0.44
2:b:9:PHE:CE1	2:b:10:ILE:HG13	2.52	0.44
1:I:58:PRO:HB2	1:I:59:LEU:H	1.58	0.44
3:L:30:ILE:HD12	3:L:53:ILE:HD12	1.99	0.44
3:L:47:TRP:CD2	4:M:96:ILE:HB	2.53	0.44
4:M:136:LEU:HB2	4:M:175:LEU:HB3	1.99	0.44
3:R:166:PHE:CE2	4:S:176:SER:HB2	2.53	0.44
4:S:31:LYS:HE2	4:S:31:LYS:HB3	1.64	0.44
3:X:147:PRO:HD2	3:X:202:PRO:CG	2.48	0.44
4:Y:50:ASP:OD1	4:Y:91:TYR:OH	2.32	0.44
1:A:106:GLU:CD	1:A:106:GLU:H	2.26	0.44
1:A:153:TRP:CD1	1:A:153:TRP:C	2.93	0.44
1:C:58:PRO:HD2	1:C:274:LEU:HD22	2.00	0.44
1:D:295:HIS:CD2	1:D:308:TYR:HA	2.52	0.44
1:D:311:SER:OG	2:d:97:GLU:OE2	2.36	0.44
1:G:106:GLU:CD	1:G:106:GLU:H	2.26	0.44
2:i:118:LEU:O	2:i:121:LYS:N	2.46	0.44
3:J:13:LYS:O	3:J:16:SER:OG	2.31	0.44
3:P:50:GLY:HA3	3:P:100:TYR:CE1	2.53	0.44
4:Q:108:ARG:HE	4:Q:108:ARG:HB2	1.68	0.44
4:Y:19:VAL:HG23	4:Y:75:ILE:HB	1.99	0.44
2:c:125:GLN:HG2	2:c:157:TYR:HB3	2.00	0.44
1:I:206:THR:HG22	1:I:243:ILE:HG13	2.00	0.44
2:i:26:HIS:ND1	2:i:26:HIS:C	2.76	0.44
3:L:119:PRO:HA	3:L:144:ASP:O	2.18	0.44
3:L:204:ASN:O	3:L:204:ASN:ND2	2.51	0.44
4:O:148:TRP:O	4:O:155:GLN:HB2	2.17	0.44
3:Z:67:VAL:HA	3:Z:81:GLU:O	2.18	0.44
2:a:25:HIS:HE1	2:a:32:SER:HB3	1.83	0.43
1:E:295:HIS:C	1:E:295:HIS:CD2	2.96	0.43
1:G:148:PHE:HB2	1:G:151:MET:HB2	2.00	0.43
1:H:236:LEU:HD23	1:H:236:LEU:HA	1.80	0.43
4:M:20:THR:HG22	4:M:74:THR:HG23	1.98	0.43
4:O:142:ARG:HB3	4:O:173:TYR:CD2	2.53	0.43
3:R:35:THR:HG22	3:R:93:ALA:O	2.17	0.43
3:R:155:ASN:HB3	3:R:158:ALA:HB3	2.00	0.43
4:W:4:LEU:HB2	4:W:98:PHE:O	2.18	0.43
2:a:106:ARG:HD2	2:c:106:ARG:HH12	1.83	0.43
2:b:145:ASP:C	2:b:147:GLU:N	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:HIS:HE1	1:D:300:LEU:HD12	1.83	0.43
2:g:26:HIS:HB2	2:g:149:MET:SD	2.58	0.43
1:H:298:HIS:HE1	1:H:300:LEU:HD12	1.82	0.43
1:I:97:CYS:SG	1:I:139:CYS:SG	3.16	0.43
4:O:112:ALA:HA	4:O:113:PRO:HD3	1.81	0.43
1:A:37:THR:HG1	1:A:38:HIS:CE1	2.36	0.43
3:L:83:THR:OG1	3:L:84:SER:N	2.50	0.43
3:P:47:TRP:CD2	4:Q:96:ILE:HB	2.53	0.43
3:P:66:ARG:NH1	3:P:82(A):THR:O	2.52	0.43
3:R:124:LEU:HD22	4:S:118:PHE:HB3	2.00	0.43
3:T:13:LYS:NZ	3:T:113:SER:O	2.47	0.43
3:Z:116:THR:HA	3:Z:146:PHE:HB3	2.01	0.43
3:Z:171:GLN:HE22	3:Z:177:SER:HB2	1.83	0.43
3:Z:200:HIS:NE2	3:Z:202:PRO:HG2	2.33	0.43
1:B:214:THR:HA	1:B:215:PRO:HD3	1.90	0.43
1:C:26:VAL:HG21	1:C:317:ALA:HB2	1.99	0.43
1:C:228:SER:C	1:C:229:ARG:HG2	2.42	0.43
1:G:223:VAL:O	1:G:225:GLY:N	2.52	0.43
4:K:61:ARG:H	4:K:61:ARG:HG2	1.59	0.43
3:N:130:SER:C	3:N:132:SER:H	2.26	0.43
4:z:91:TYR:HD1	4:z:92:ASP:H	1.66	0.43
1:A:164:ALA:O	1:A:246:GLU:HA	2.18	0.43
1:B:320:LEU:HB3	2:b:111:HIS:CG	2.54	0.43
2:d:63:PHE:HE2	2:e:83:LYS:NZ	2.15	0.43
1:E:77:ASP:OD2	1:E:149:ARG:NH2	2.44	0.43
1:E:176:MET:SD	1:E:257:GLY:HA3	2.59	0.43
1:H:163:VAL:HG22	1:H:248:THR:HG22	2.01	0.43
2:h:128:ASP:O	2:h:170:ARG:NH1	2.51	0.43
3:J:38:ARG:HD3	3:J:90:TYR:CE2	2.54	0.43
3:P:170:LEU:O	4:Q:160:GLN:NE2	2.51	0.43
4:S:39:LYS:HE2	4:S:81:GLU:O	2.18	0.43
4:U:29:ILE:HD11	4:U:71:PHE:HE2	1.83	0.43
4:U:111:ALA:HB3	4:U:139:PHE:HA	2.00	0.43
3:X:17:SER:HA	3:X:82(A):THR:HA	2.00	0.43
3:X:145:TYR:OH	3:X:150:VAL:HG21	2.19	0.43
1:C:182:VAL:HG12	1:C:202:VAL:HG11	2.00	0.43
2:e:84:MET:HB3	2:e:84:MET:HE2	1.69	0.43
1:G:206:THR:OG1	1:G:207:SER:N	2.50	0.43
1:G:279:THR:OG1	1:G:281:CYS:O	2.30	0.43
1:H:183:HIS:O	1:H:185:PRO:HD3	2.18	0.43
4:S:77:SER:O	4:S:77:SER:OG	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:182:SER:OG	4:U:183:LYS:N	2.52	0.43
3:X:87:THR:HA	3:X:109:VAL:O	2.19	0.43
1:A:169:ASN:O	1:A:171:THR:HG23	2.19	0.43
2:b:73:LEU:HD23	2:b:73:LEU:HA	1.85	0.43
1:C:297:VAL:HB	1:C:298:HIS:H	1.54	0.43
1:G:177:LEU:HB3	1:G:258:PHE:HB2	2.00	0.43
1:G:310:LYS:HG3	2:g:89:LEU:HD21	2.01	0.43
1:I:264:SER:OG	2:i:64:GLU:OE2	2.37	0.43
2:i:160:PRO:HA	2:i:163:GLU:HB2	1.99	0.43
3:J:31:THR:O	3:J:32:HIS:HB2	2.19	0.43
4:K:7:SER:HA	4:K:8:PRO:HA	1.78	0.43
1:A:141:VAL:HG21	1:A:149:ARG:HH22	1.83	0.43
1:B:131:THR:HG21	3:L:98:GLY:HA3	2.01	0.43
2:b:167:LYS:HE2	2:b:167:LYS:HB3	1.89	0.43
1:D:148:PHE:HB2	1:D:151:MET:HB2	2.01	0.43
1:G:56:ILE:HA	1:G:57:PRO:HD3	1.79	0.43
1:I:137:ARG:HE	1:I:137:ARG:HB2	1.59	0.43
4:M:2:ILE:HD11	4:M:93:ASN:HB2	2.00	0.43
4:M:90:GLN:H	4:M:90:GLN:HG3	1.49	0.43
3:N:75:THR:HB	3:N:77:THR:CB	2.48	0.43
4:U:33:LEU:HD22	4:U:71:PHE:CG	2.53	0.43
4:U:139:PHE:N	4:U:172:THR:OG1	2.52	0.43
1:B:163:VAL:HG22	1:B:248:THR:HG22	2.00	0.43
1:C:151:MET:HE3	1:C:253:ALA:O	2.19	0.43
1:D:207:SER:OG	1:D:241:ASP:OD1	2.36	0.43
1:E:214:THR:HA	1:E:215:PRO:HD3	1.66	0.43
1:F:53:LYS:HD3	1:F:55:GLY:O	2.19	0.43
2:g:71:SER:OG	2:g:72:ASN:N	2.50	0.43
3:R:92:CYS:O	3:R:104:GLY:N	2.49	0.43
4:U:11:LEU:HD23	4:U:11:LEU:HA	1.88	0.43
4:U:138:ASN:N	4:U:138:ASN:OD1	2.52	0.43
4:U:186:TYR:CE1	4:U:192:TYR:HE2	2.36	0.43
3:X:47:TRP:CD2	4:Y:96:ILE:HB	2.54	0.43
2:a:24:TYR:CG	2:a:153:LYS:HG2	2.54	0.43
1:B:66:ILE:HD12	1:B:112:LEU:HD12	2.00	0.43
1:E:126:ARG:HH22	1:E:166:GLY:HA2	1.83	0.43
1:F:88:MET:HE3	1:F:270:THR:HG21	2.00	0.43
3:L:87:THR:HG23	3:L:110:THR:HA	2.01	0.43
4:M:124:GLN:OE1	4:M:131:SER:HB2	2.19	0.43
4:M:198:HIS:HB3	4:M:201:LEU:HG	2.00	0.43
3:N:126:PRO:HG2	3:N:213:PRO:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:16:SER:HB2	3:P:17:SER:H	1.59	0.43
3:R:201:LYS:HA	3:R:204:ASN:HA	2.01	0.43
3:X:11:VAL:HA	3:X:110:THR:O	2.19	0.43
1:D:277:CYS:SG	1:D:278:GLU:N	2.92	0.42
2:e:26:HIS:HD2	2:e:149:MET:HG3	1.83	0.42
1:F:161:TYR:CZ	1:F:249:GLY:HA2	2.54	0.42
1:G:55:GLY:N	1:G:278:GLU:OE2	2.43	0.42
2:h:14:TRP:HE3	2:h:17:MET:HE2	1.84	0.42
2:h:51:LYS:O	2:h:55:VAL:HG23	2.19	0.42
3:J:96:ILE:HG12	3:J:97:SER:N	2.34	0.42
4:K:54:VAL:HG11	4:K:58:VAL:HG23	2.01	0.42
3:L:139:GLY:HA2	3:L:154:TRP:CH2	2.54	0.42
4:S:38:GLN:C	4:S:84:ALA:HB1	2.44	0.42
3:Z:47:TRP:CD2	4:z:96:ILE:HB	2.54	0.42
3:Z:49:GLY:HA3	3:Z:69:ILE:HD11	2.01	0.42
1:C:293:PRO:HG3	2:c:56:ILE:HG22	2.01	0.42
2:c:9:PHE:CE1	2:c:10:ILE:HG13	2.54	0.42
1:E:158:GLY:HA2	3:R:96:ILE:CG2	2.48	0.42
1:E:194:LEU:HB3	1:E:195:TYR:CD2	2.54	0.42
1:E:277:CYS:SG	1:E:278:GLU:N	2.92	0.42
1:G:62:GLY:O	1:G:90:LYS:HG3	2.19	0.42
1:I:320:LEU:HB3	2:i:111:HIS:CG	2.54	0.42
4:K:91:TYR:O	4:K:93:ASN:N	2.52	0.42
3:L:32:HIS:ND1	3:L:94:ARG:NH1	2.65	0.42
4:Q:91:TYR:O	4:Q:93:ASN:N	2.51	0.42
4:S:96:ILE:HG23	4:S:96:ILE:HD12	1.67	0.42
3:T:146:PHE:HA	3:T:147:PRO:HA	1.71	0.42
1:A:114:SER:O	1:A:263:ARG:HG3	2.19	0.42
1:A:136:SER:C	1:A:145:PRO:HB3	2.44	0.42
2:c:48:ILE:CD1	2:c:107:THR:HG23	2.50	0.42
1:D:43:LEU:HB2	1:D:314:LEU:HB2	2.02	0.42
1:G:155:THR:HG21	3:V:54:PHE:HZ	1.85	0.42
4:O:170:ASP:OD1	4:O:172:THR:HG22	2.19	0.42
4:Q:6:GLN:HA	4:Q:22:THR:O	2.19	0.42
4:Q:113:PRO:O	4:Q:115:VAL:HG23	2.19	0.42
4:W:21:ILE:HD12	4:W:73:PHE:HD2	1.84	0.42
3:Z:66:ARG:NH2	3:Z:86:ASP:OD2	2.52	0.42
2:a:145:ASP:OD2	2:a:147:GLU:HB3	2.20	0.42
1:B:297:VAL:HB	1:B:298:HIS:H	1.75	0.42
1:D:39:ALA:HA	1:D:318:THR:HG23	2.01	0.42
1:D:182:VAL:HG11	1:D:213:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:28:THR:HB	2:f:105:GLU:HB2	2.01	0.42
1:H:13:ILE:HG23	2:h:138:PHE:HD2	1.84	0.42
1:H:98:TYR:CD1	1:H:230:MET:HE3	2.54	0.42
2:h:106:ARG:HH12	2:i:106:ARG:HD2	1.82	0.42
3:J:34:PHE:O	3:J:50:GLY:HA2	2.20	0.42
3:L:46:GLU:OE2	3:L:62:LYS:HD3	2.19	0.42
4:M:183:LYS:O	4:M:187:GLU:HG2	2.19	0.42
3:N:82:LEU:HD12	3:N:82:LEU:HA	1.83	0.42
3:N:205:THR:HG22	3:N:207:VAL:HG23	2.00	0.42
4:S:193:ALA:HA	4:S:208:SER:HB2	2.01	0.42
1:A:10:GLY:HA3	2:a:139:GLU:HG2	2.00	0.42
1:E:84:TRP:CZ3	1:E:116(A):HIS:HA	2.54	0.42
1:G:115:VAL:HG13	1:G:260:ILE:HG23	2.02	0.42
2:i:30:GLN:HE22	2:i:145:ASP:HB2	1.83	0.42
3:L:72:ASP:OD2	3:L:75:THR:OG1	2.38	0.42
3:R:29:PHE:CD2	3:R:73:GLU:HG3	2.54	0.42
3:R:36:TRP:CE2	3:R:80:MET:HB2	2.54	0.42
4:S:37:GLN:HB2	4:S:86:TYR:CE1	2.54	0.42
1:A:18:HIS:ND1	1:A:19:ALA:N	2.68	0.42
1:A:37:THR:HG23	1:A:320:LEU:O	2.19	0.42
1:B:18:HIS:ND1	1:B:19:ALA:N	2.67	0.42
2:b:26:HIS:CE1	2:b:33:GLY:HA3	2.54	0.42
1:E:226:LEU:HD13	1:E:226:LEU:HA	1.87	0.42
2:e:14:TRP:CE3	2:e:17:MET:HE2	2.54	0.42
1:H:139:CYS:HB2	1:H:146:SER:O	2.20	0.42
1:H:316:LEU:HA	1:H:316:LEU:HD22	1.76	0.42
1:I:175:GLN:HB3	1:I:236:LEU:HD13	2.01	0.42
4:M:134:CYS:HB2	4:M:148:TRP:CZ2	2.54	0.42
3:P:13:LYS:NZ	3:P:114:ALA:O	2.51	0.42
4:Q:1:ASP:HA	4:Q:95:PRO:HG3	2.02	0.42
4:S:18:ARG:HE	4:S:18:ARG:HB2	1.55	0.42
4:S:139:PHE:N	4:S:173:TYR:O	2.48	0.42
4:Y:58:VAL:HA	4:Y:59:PRO:HD3	1.80	0.42
3:Z:13:LYS:HA	3:Z:14:PRO:HD3	1.91	0.42
3:Z:16:SER:HB2	3:Z:17:SER:H	1.65	0.42
2:a:126:LEU:HD13	2:a:130:VAL:HG21	2.01	0.42
2:b:76:ARG:H	2:b:76:ARG:HG3	1.69	0.42
1:E:278:GLU:OE1	1:E:279:THR:N	2.52	0.42
1:H:70:LEU:HD23	1:H:70:LEU:HA	1.90	0.42
4:O:193:ALA:CB	4:O:208:SER:HB2	2.50	0.42
4:S:89:GLN:HG2	4:S:90:GLN:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:6:GLN:HE22	4:U:87:TYR:HA	1.85	0.42
1:C:108:LEU:HB2	1:C:234:TRP:CE2	2.55	0.42
1:H:116(C):GLU:O	1:H:118:VAL:HG23	2.20	0.42
3:J:89:VAL:HG23	3:J:107:THR:H	1.84	0.42
3:N:46:GLU:OE2	3:N:62:LYS:HD3	2.19	0.42
3:P:144:ASP:HA	3:P:175:LEU:HB3	2.01	0.42
4:W:49:TYR:CE1	4:W:53:ASN:HB2	2.55	0.42
4:O:81:GLU:CD	4:O:81:GLU:H	2.28	0.42
3:R:112:SER:C	3:R:114:ALA:H	2.28	0.42
4:U:139:PHE:CE2	4:U:174:SER:HA	2.55	0.42
1:A:42:ILE:HA	1:A:292:LEU:HD22	2.02	0.42
1:B:78:ARG:H	1:B:78:ARG:HG3	1.54	0.42
1:B:171:THR:O	1:B:171:THR:OG1	2.29	0.42
1:C:84:TRP:CZ3	1:C:116(A):HIS:HA	2.55	0.42
1:E:72:GLY:O	1:E:149:ARG:HG2	2.20	0.42
3:N:39:GLN:O	3:N:88:ALA:HB1	2.19	0.42
4:O:30:ARG:HG2	4:O:31:LYS:H	1.85	0.42
4:S:105:GLU:HG3	4:S:166:GLN:HE22	1.84	0.42
4:U:66:GLY:HA3	4:U:71:PHE:CD1	2.55	0.42
4:U:89:GLN:HB2	4:U:98:PHE:CD1	2.55	0.42
4:W:104:LEU:HD23	4:W:104:LEU:HA	1.84	0.42
3:Z:29:PHE:CE2	3:Z:52(A):ALA:HB1	2.55	0.42
4:z:37:GLN:HB2	4:z:86:TYR:CE1	2.55	0.42
1:E:151:MET:HE3	1:E:253:ALA:O	2.21	0.41
1:G:316:LEU:HD22	1:G:316:LEU:HA	1.91	0.41
1:H:90:LYS:HA	1:H:270:THR:O	2.19	0.41
1:H:136:SER:OG	1:H:137:ARG:N	2.48	0.41
2:h:126:LEU:HA	2:h:157:TYR:CE2	2.55	0.41
1:I:247:SER:OG	1:I:249:GLY:O	2.38	0.41
2:i:84:MET:HE2	2:i:84:MET:HB3	1.82	0.41
4:M:36:TYR:CE1	4:M:46:LEU:HD13	2.55	0.41
3:R:124:LEU:HD23	3:R:124:LEU:HA	1.77	0.41
3:T:189:LEU:O	3:T:191:THR:N	2.53	0.41
2:a:77:LEU:HD12	2:a:77:LEU:HA	1.85	0.41
1:C:202:VAL:HA	1:C:247:SER:HB2	2.02	0.41
1:C:316:LEU:HD23	2:c:100:VAL:HG22	2.01	0.41
1:D:183:HIS:ND1	1:D:195:TYR:OH	2.48	0.41
1:E:116(B):PHE:HE1	1:E:260:ILE:HG12	1.85	0.41
1:G:102:PHE:CZ	1:G:179:ILE:HD13	2.55	0.41
2:h:145:ASP:OD1	2:h:145:ASP:N	2.53	0.41
1:I:18:HIS:HE1	1:I:20:ASN:HB3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:170:ASP:OD1	4:O:170:ASP:N	2.49	0.41
4:S:120:PRO:HD3	4:S:132:VAL:HB	2.02	0.41
1:B:184:HIS:HA	1:B:185:PRO:HD3	1.80	0.41
1:D:18:HIS:ND1	1:D:19:ALA:N	2.69	0.41
1:D:293:PRO:HG2	1:D:294:PHE:CD2	2.55	0.41
1:E:293:PRO:HG3	2:e:56:ILE:HG22	2.02	0.41
1:F:320:LEU:HD12	1:F:321:ARG:O	2.20	0.41
2:f:98:LEU:O	2:f:102:MET:HG3	2.20	0.41
1:I:53:LYS:HB2	1:I:278:GLU:HG2	2.02	0.41
3:J:84:SER:C	3:J:86:ASP:H	2.28	0.41
4:K:16:GLY:HA2	4:K:77:SER:HA	2.03	0.41
4:O:198:HIS:CG	4:O:199:GLN:H	2.38	0.41
3:P:177:SER:O	3:P:177:SER:OG	2.35	0.41
3:R:50:GLY:HA3	3:R:100:TYR:CZ	2.55	0.41
4:S:81:GLU:H	4:S:81:GLU:HG2	1.71	0.41
2:a:68:LYS:HD3	2:b:76:ARG:HB3	2.02	0.41
1:B:17:TYR:OH	2:b:10:ILE:O	2.37	0.41
1:E:251:LEU:HD12	1:E:252:ILE:N	2.35	0.41
2:h:25:HIS:ND1	2:h:33:GLY:O	2.43	0.41
1:I:313:LYS:O	1:I:314:LEU:HD23	2.20	0.41
2:i:14:TRP:CE3	2:i:17:MET:HE2	2.55	0.41
3:N:193:THR:O	3:N:193:THR:OG1	2.35	0.41
4:U:136:LEU:HD21	4:U:196:VAL:HG13	2.02	0.41
4:z:31:LYS:HB3	4:z:31:LYS:HE2	1.82	0.41
1:A:43:LEU:HD11	1:A:296:ASN:HB3	2.01	0.41
1:A:116(B):PHE:CD1	1:A:258:PHE:HB3	2.56	0.41
1:A:121:LEU:HA	1:A:121:LEU:HD23	1.72	0.41
1:A:136:SER:OG	1:A:137:ARG:N	2.53	0.41
2:a:76:ARG:HG3	1:C:107:GLU:OE2	2.20	0.41
1:C:71:LEU:C	1:C:150:ASN:HD22	2.28	0.41
1:C:157:LYS:NZ	4:O:92:ASP:HA	2.36	0.41
2:d:125:GLN:OE1	2:d:155:GLY:HA2	2.21	0.41
1:E:73:ASN:HA	1:E:74:PRO:HD3	1.89	0.41
2:h:135:ASN:OD1	2:h:137:CYS:HB2	2.21	0.41
2:i:77:LEU:HD12	2:i:77:LEU:HA	1.92	0.41
3:L:122:PHE:CD2	4:M:124:GLN:HB2	2.55	0.41
4:O:120:PRO:HG2	4:O:125:LEU:HD11	2.02	0.41
4:U:94:LEU:HD22	4:U:94:LEU:HA	1.87	0.41
3:V:96:ILE:O	3:V:100(A):GLY:N	2.52	0.41
1:D:44:GLU:OE2	1:D:46:THR:OG1	2.35	0.41
1:G:295:HIS:NE2	1:G:308:TYR:HB2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:78:ARG:HG3	1:H:79:LEU:HG	2.03	0.41
1:H:325:GLN:HB3	2:h:13:GLY:O	2.21	0.41
2:i:9:PHE:CD1	2:i:10:ILE:HG13	2.56	0.41
3:P:13:LYS:O	3:P:16:SER:OG	2.29	0.41
3:P:96:ILE:O	3:P:100(A):GLY:N	2.54	0.41
3:R:39:GLN:HG3	3:R:44:GLY:O	2.20	0.41
4:S:11:LEU:HD23	4:S:11:LEU:HA	1.69	0.41
4:W:33:LEU:HD21	4:W:88:CYS:HB2	2.03	0.41
3:Z:54:PHE:HB3	3:Z:56:THR:HG23	2.03	0.41
1:B:294:PHE:CZ	2:b:59:MET:HE2	2.49	0.41
1:C:309:VAL:C	1:C:311:SER:H	2.29	0.41
2:d:77:LEU:HD12	2:d:77:LEU:HA	1.75	0.41
2:e:46:ASP:O	2:e:50:ASN:HB2	2.21	0.41
1:F:298:HIS:ND1	1:F:300:LEU:HB2	2.36	0.41
1:G:50:LYS:C	1:G:51:LEU:HD12	2.46	0.41
1:G:176:MET:O	1:G:236:LEU:HD22	2.21	0.41
4:K:6:GLN:O	4:K:100:GLN:NE2	2.54	0.41
4:M:90:GLN:HE21	4:M:90:GLN:HB2	1.60	0.41
4:Q:56:THR:O	4:Q:56:THR:OG1	2.35	0.41
3:R:6:GLU:OE1	3:R:104:GLY:HA3	2.20	0.41
4:U:94:LEU:HD22	4:U:96:ILE:HG12	2.03	0.41
4:W:6:GLN:HG3	4:W:88:CYS:SG	2.60	0.41
2:a:131:LYS:O	2:a:133:LEU:HD12	2.21	0.41
1:C:159:SER:OG	1:C:160:ASP:N	2.54	0.41
2:c:49:THR:HA	2:c:52:VAL:HG22	2.02	0.41
2:e:160:PRO:HA	2:e:163:GLU:HB2	2.02	0.41
2:g:27:SER:O	2:g:27:SER:OG	2.31	0.41
1:I:268:MET:HE3	1:I:268:MET:HB2	1.84	0.41
4:O:35:TRP:CE2	4:O:73:PHE:HB2	2.55	0.41
3:P:47:TRP:CE3	4:Q:96:ILE:HB	2.56	0.41
3:R:54:PHE:HB3	3:R:56:THR:HG23	2.01	0.41
3:Z:100(C):PHE:H	4:z:36:TYR:HH	1.67	0.41
1:A:102:PHE:CZ	1:A:179:ILE:HD13	2.55	0.41
1:A:201:TYR:CD1	1:A:201:TYR:C	2.98	0.41
1:B:119:LYS:HA	1:B:256:TYR:CD1	2.53	0.41
1:C:293:PRO:HG2	1:C:294:PHE:CD2	2.55	0.41
2:c:3:PHE:CE1	2:c:113:SER:HB2	2.55	0.41
1:D:176:MET:HE3	1:D:176:MET:HB2	1.97	0.41
1:E:146:SER:HB3	1:E:147:PHE:H	1.74	0.41
1:E:316:LEU:CD1	2:e:52:VAL:HG12	2.51	0.41
1:F:158:GLY:O	1:F:160:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:179:ILE:O	1:F:254:PRO:HB3	2.21	0.41
1:F:319:GLY:O	2:f:111:HIS:NE2	2.54	0.41
2:f:28:ASN:ND2	2:f:145:ASP:HA	2.36	0.41
1:G:14:CYS:HA	2:g:137:CYS:HA	2.03	0.41
2:h:102:MET:O	2:h:104:ASN:N	2.53	0.41
1:I:51:LEU:HA	1:I:282:GLN:NE2	2.36	0.41
1:I:320:LEU:HB3	2:i:111:HIS:CD2	2.55	0.41
2:i:26:HIS:C	2:i:26:HIS:HD1	2.29	0.41
3:L:145:TYR:CE1	3:L:150:VAL:HG13	2.55	0.41
4:O:91:TYR:O	4:O:93:ASN:N	2.51	0.41
3:P:101:ASP:HB3	3:P:102:PRO:HD3	2.03	0.41
3:T:47:TRP:CD2	4:U:96:ILE:HB	2.56	0.41
3:T:93:ALA:HB1	3:T:100(C):PHE:HB3	2.02	0.41
3:T:114:ALA:HB3	3:T:146:PHE:CZ	2.56	0.41
3:T:151:THR:OG1	3:T:199:ASN:HB2	2.20	0.41
4:U:1:ASP:HA	4:U:95:PRO:HG3	2.02	0.41
4:W:31:LYS:HE2	4:W:31:LYS:HB3	1.91	0.41
3:X:165:THR:HG22	3:X:180:SER:OG	2.20	0.41
4:Y:4:LEU:HD22	4:Y:23:CYS:SG	2.61	0.41
4:Y:33:LEU:HD22	4:Y:71:PHE:CG	2.55	0.41
3:Z:35:THR:HG22	3:Z:93:ALA:O	2.21	0.41
1:A:29:ILE:HG12	2:a:101:LEU:HB3	2.03	0.41
1:C:206:THR:H	1:C:209:LEU:HB3	1.86	0.41
1:F:18:HIS:N	2:f:21:TRP:O	2.41	0.41
1:G:309:VAL:HG12	2:g:93:THR:HA	2.02	0.41
1:H:116:LYS:NZ	1:H:263(A):GLY:HA3	2.35	0.41
3:L:112:SER:OG	3:L:113:SER:N	2.54	0.41
3:N:116:THR:O	3:N:116:THR:OG1	2.31	0.41
3:P:83:THR:OG1	3:P:84:SER:N	2.53	0.41
3:R:186:SER:C	3:R:188:SER:H	2.29	0.41
4:S:133:VAL:HG13	4:S:178:THR:HG23	2.03	0.41
3:T:203:SER:OG	3:T:205:THR:OG1	2.37	0.41
3:X:13:LYS:HA	3:X:14:PRO:HD3	1.97	0.41
4:z:19:VAL:HG23	4:z:75:ILE:HB	2.02	0.41
1:A:144:ASN:OD1	1:A:144:ASN:N	2.52	0.40
1:C:206:THR:HG23	1:C:209:LEU:HB3	2.04	0.40
1:D:49:GLY:HA2	1:D:285:LEU:O	2.21	0.40
1:D:297:VAL:H	1:D:297:VAL:HG23	1.62	0.40
1:I:20:ASN:HB2	1:I:21:ASN:H	1.67	0.40
4:K:39:LYS:H	4:K:39:LYS:HG2	1.65	0.40
3:R:51:PHE:HD1	3:R:57:SER:HB3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:HIS:HE1	1:A:20:ASN:HB3	1.87	0.40
2:a:51:LYS:NZ	2:a:103:GLU:OE1	2.53	0.40
2:b:71:SER:HB2	2:b:73:LEU:H	1.86	0.40
2:b:125:GLN:NE2	2:b:155:GLY:O	2.52	0.40
2:d:71:SER:H	2:d:74:GLU:HG3	1.86	0.40
1:G:186:ASN:OD1	1:G:219:THR:HA	2.21	0.40
1:G:222:LYS:HD3	1:G:225:GLY:O	2.21	0.40
1:I:307:ARG:NH2	2:i:61:THR:O	2.55	0.40
4:M:151:ASP:OD2	4:M:189:HIS:HB3	2.21	0.40
4:Q:58:VAL:HA	4:Q:59:PRO:HD3	1.89	0.40
3:R:125:ALA:HA	3:R:126:PRO:HD3	1.90	0.40
3:T:87:THR:HG23	3:T:110:THR:HA	2.03	0.40
3:T:196:CYS:O	3:T:209:LYS:N	2.48	0.40
4:U:118:PHE:HA	4:U:119:PRO:HD3	1.95	0.40
4:Y:18:ARG:HE	4:Y:18:ARG:HB2	1.69	0.40
1:A:182:VAL:HA	1:A:250:ASN:O	2.21	0.40
1:B:81(A):VAL:HA	1:B:82:PRO:HD2	1.95	0.40
1:B:144:ASN:HA	1:B:145:PRO:HD3	1.93	0.40
1:B:320:LEU:HB3	2:b:111:HIS:CD2	2.56	0.40
2:c:126:LEU:HD13	2:c:130:VAL:HG11	2.03	0.40
1:D:174:GLU:OE1	1:D:263:ARG:NH2	2.54	0.40
1:D:310:LYS:HD2	2:d:89:LEU:HD21	2.02	0.40
2:f:59:MET:H	2:f:59:MET:HG2	1.77	0.40
1:G:207:SER:HG	1:G:241:ASP:CG	2.23	0.40
1:G:270:THR:OG1	1:G:271:GLU:N	2.55	0.40
1:I:90:LYS:HA	1:I:270:THR:O	2.21	0.40
3:J:70:THR:HB	3:J:71:ALA:H	1.67	0.40
3:L:7:SER:HB3	3:L:21:SER:OG	2.21	0.40
3:L:146:PHE:HA	3:L:147:PRO:HA	1.69	0.40
4:M:60:SER:O	4:M:63:ARG:NH1	2.53	0.40
4:M:80:PRO:C	4:M:82:ASP:H	2.29	0.40
4:S:188:LYS:HB3	4:S:189:HIS:ND1	2.37	0.40
4:U:126:LYS:HB2	4:U:126:LYS:HE3	1.89	0.40
3:Z:62:LYS:HB3	3:Z:62:LYS:HE3	1.94	0.40
1:A:154:LEU:HD12	1:A:154:LEU:HA	1.79	0.40
1:A:174:GLU:OE1	1:A:263:ARG:NH2	2.55	0.40
1:A:194:LEU:HD11	3:J:53:ILE:HG12	2.04	0.40
1:B:176:MET:HG3	1:B:258:PHE:C	2.46	0.40
1:B:209:LEU:HD12	1:B:210:ASN:H	1.85	0.40
1:B:320:LEU:H	1:B:320:LEU:HG	1.72	0.40
2:b:47:GLY:O	1:C:30:LEU:HD12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:HIS:CD2	1:C:47:HIS:H	2.40	0.40
2:c:98:LEU:HD12	2:c:98:LEU:HA	1.93	0.40
1:H:58:PRO:HB2	1:H:59:LEU:H	1.75	0.40
1:H:154:LEU:HD12	1:H:154:LEU:HA	1.90	0.40
4:K:12:SER:O	4:K:14:SER:N	2.48	0.40
3:L:16:SER:OG	3:L:17:SER:N	2.50	0.40
3:P:167:PRO:HG2	4:Q:163:VAL:O	2.21	0.40
4:W:27:GLN:O	4:W:29:ILE:HG23	2.21	0.40
3:X:35:THR:HG22	3:X:93:ALA:O	2.22	0.40
1:A:283:THR:OG1	1:A:286:GLY:N	2.54	0.40
1:A:310:LYS:HG3	2:a:89:LEU:HD21	2.04	0.40
2:a:50:ASN:HD21	1:B:32:ARG:HG2	1.87	0.40
2:a:149:MET:C	2:a:151:SER:N	2.80	0.40
1:B:62:GLY:O	1:B:90:LYS:HG3	2.21	0.40
1:C:25:LYS:HG2	1:C:33:ASN:OD1	2.21	0.40
2:d:28:ASN:HD22	2:d:145:ASP:HA	1.87	0.40
2:g:48:ILE:HD13	2:g:48:ILE:HA	1.94	0.40
1:H:175:GLN:O	1:H:260:ILE:HG13	2.22	0.40
1:H:293:PRO:HG2	1:H:294:PHE:CD2	2.56	0.40
2:h:52:VAL:O	2:h:56:ILE:HG23	2.21	0.40
3:J:12:LYS:HA	3:J:12:LYS:HD3	1.80	0.40
3:N:214:LYS:HD2	3:N:215:SER:H	1.86	0.40
4:S:123:GLU:HA	4:S:126:LYS:HG3	2.03	0.40
4:S:150:VAL:H	4:S:155:GLN:HE22	1.65	0.40
3:T:92:CYS:SG	3:T:93:ALA:N	2.94	0.40
4:Y:31:LYS:HE2	4:Y:51:ALA:HB3	2.03	0.40
4:z:18:ARG:HE	4:z:18:ARG:HB2	1.54	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	321/327 (98%)	292 (91%)	28 (9%)	1 (0%)	36	68
1	B	317/327 (97%)	283 (89%)	30 (10%)	4 (1%)	9	40
1	C	322/327 (98%)	288 (89%)	29 (9%)	5 (2%)	7	36
1	D	322/327 (98%)	293 (91%)	26 (8%)	3 (1%)	14	47
1	E	321/327 (98%)	291 (91%)	26 (8%)	4 (1%)	10	42
1	F	322/327 (98%)	288 (89%)	28 (9%)	6 (2%)	6	33
1	G	322/327 (98%)	285 (88%)	32 (10%)	5 (2%)	7	36
1	H	323/327 (99%)	286 (88%)	34 (10%)	3 (1%)	14	47
1	I	322/327 (98%)	287 (89%)	32 (10%)	3 (1%)	14	47
2	a	169/174 (97%)	143 (85%)	20 (12%)	6 (4%)	2	19
2	b	163/174 (94%)	135 (83%)	24 (15%)	4 (2%)	4	27
2	c	170/174 (98%)	147 (86%)	19 (11%)	4 (2%)	4	28
2	d	170/174 (98%)	147 (86%)	21 (12%)	2 (1%)	10	42
2	e	170/174 (98%)	154 (91%)	14 (8%)	2 (1%)	10	42
2	f	170/174 (98%)	144 (85%)	22 (13%)	4 (2%)	4	28
2	g	170/174 (98%)	148 (87%)	20 (12%)	2 (1%)	10	42
2	h	163/174 (94%)	143 (88%)	15 (9%)	5 (3%)	3	22
2	i	170/174 (98%)	144 (85%)	21 (12%)	5 (3%)	3	24
3	J	113/223 (51%)	80 (71%)	26 (23%)	7 (6%)	1	9
3	L	208/223 (93%)	186 (89%)	13 (6%)	9 (4%)	2	16
3	N	221/223 (99%)	200 (90%)	14 (6%)	7 (3%)	3	21
3	P	155/223 (70%)	134 (86%)	12 (8%)	9 (6%)	1	10
3	R	210/223 (94%)	185 (88%)	18 (9%)	7 (3%)	3	21
3	T	209/223 (94%)	184 (88%)	19 (9%)	6 (3%)	3	24
3	V	115/223 (52%)	106 (92%)	8 (7%)	1 (1%)	14	47
3	X	156/223 (70%)	129 (83%)	19 (12%)	8 (5%)	1	13
3	Z	159/223 (71%)	133 (84%)	16 (10%)	10 (6%)	1	8
4	K	104/214 (49%)	77 (74%)	17 (16%)	10 (10%)	0	3
4	M	212/214 (99%)	191 (90%)	18 (8%)	3 (1%)	9	39
4	O	212/214 (99%)	190 (90%)	18 (8%)	4 (2%)	6	33
4	Q	149/214 (70%)	125 (84%)	20 (13%)	4 (3%)	4	25
4	S	209/214 (98%)	182 (87%)	20 (10%)	7 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	U	209/214 (98%)	177 (85%)	25 (12%)	7 (3%)	3	21
4	W	103/214 (48%)	89 (86%)	10 (10%)	4 (4%)	2	18
4	Y	107/214 (50%)	94 (88%)	9 (8%)	4 (4%)	2	18
4	z	113/214 (53%)	97 (86%)	11 (10%)	5 (4%)	2	15
All	All	7371/8442 (87%)	6457 (88%)	734 (10%)	180 (2%)	4	28

All (180) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a	66	VAL
1	B	264	SER
2	c	61	THR
2	e	146	ASP
2	f	62	GLN
2	f	64	GLU
2	f	146	ASP
2	g	146	ASP
2	h	147	GLU
2	i	146	ASP
3	J	98	GLY
4	K	13	ALA
4	K	51	ALA
3	L	102	PRO
3	L	204	ASN
4	M	96	ILE
3	N	204	ASN
4	O	51	ALA
3	P	147	PRO
3	R	148	GLU
3	R	203	SER
3	R	204	ASN
3	T	116	THR
3	T	189	LEU
3	T	203	SER
3	X	148	GLU
3	Z	62	LYS
2	a	67	GLY
2	a	147	GLU
2	a	150	ASN
1	B	134	GLY
1	B	174	GLU

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Mol	Chain	Res	Type
2	b	67	GLY
2	b	146	ASP
2	b	147	GLU
2	c	147	GLU
1	D	297	VAL
2	d	146	ASP
2	d	147	GLU
2	e	147	GLU
1	F	58	PRO
1	F	158	GLY
1	G	159	SER
2	g	147	GLU
1	H	58	PRO
2	h	146	ASP
1	I	58	PRO
2	i	64	GLU
4	K	3	GLN
4	K	68	GLY
3	L	16	SER
3	L	116	THR
3	L	188	SER
4	M	95	PRO
4	O	96	ILE
4	O	152	ASN
3	P	100	TYR
3	P	116	THR
3	P	173	SER
3	R	100	TYR
4	S	138	ASN
4	S	187	GLU
3	T	100	TYR
3	T	190	GLY
4	U	96	ILE
4	U	128	GLY
4	U	143	GLU
3	X	61	GLN
3	X	62	LYS
3	X	63	PHE
4	Y	51	ALA
3	Z	61	GLN
1	A	174	GLU
2	b	150	ASN

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Mol	Chain	Res	Type
1	C	297	VAL
1	E	186	ASN
1	F	159	SER
1	F	196	GLN
2	f	147	GLU
1	G	58	PRO
1	G	67	ALA
2	h	103	GLU
1	I	196	GLN
2	i	7	ALA
2	i	147	GLU
3	J	79	TYR
3	L	144	ASP
3	L	203	SER
4	M	138	ASN
3	N	100	TYR
4	O	95	PRO
3	P	97	SER
3	R	113	SER
4	S	92	ASP
4	S	204	PRO
4	U	92	ASP
4	U	138	ASN
4	W	92	ASP
3	X	100	TYR
3	X	144	ASP
3	Z	63	PHE
4	z	92	ASP
2	a	127	ARG
1	C	128	THR
2	c	63	PHE
1	E	297	VAL
1	F	186	ASN
3	J	16	SER
3	J	32	HIS
3	J	83	THR
3	J	100	TYR
4	K	76	SER
4	K	92	ASP
3	N	172	SER
3	P	158	ALA
4	S	121	SER

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Mol	Chain	Res	Type
3	V	100	TYR
4	W	84	ALA
4	Y	92	ASP
3	Z	100	TYR
3	Z	144	ASP
3	Z	196	CYS
4	z	96	ILE
2	c	30	GLN
1	D	96	LEU
1	H	196	GLN
2	h	102	MET
2	i	5	ALA
4	K	67	SER
3	L	149	PRO
3	N	132	SER
3	N	214	LYS
4	Q	68	GLY
4	Q	96	ILE
4	S	114	SER
3	T	147	PRO
4	W	96	ILE
3	Z	148	GLU
4	z	51	ALA
2	a	132	GLU
1	C	310	LYS
1	E	162	PRO
1	G	224	ASN
1	I	158	GLY
4	K	40	PRO
3	L	100(A)	GLY
3	P	172	SER
3	R	149	PRO
4	S	96	ILE
4	Y	96	ILE
3	Z	100(A)	GLY
3	Z	202	PRO
1	D	158	GLY
1	F	297	VAL
1	H	158	GLY
2	h	91	VAL
3	J	41	PRO
3	P	174	GLY

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Mol	Chain	Res	Type
3	X	202	PRO
1	B	297	VAL
1	C	158	GLY
1	G	158	GLY
4	K	94	LEU
4	Q	95	PRO
1	E	158	GLY
4	K	96	ILE
3	N	149	PRO
3	P	14	PRO
4	U	95	PRO
4	W	68	GLY
3	X	100(A)	GLY
4	Y	68	GLY
4	z	68	GLY
4	z	95	PRO
4	Q	113	PRO
4	U	68	GLY
1	C	217	ILE
3	Z	102	PRO
3	R	147	PRO
3	N	147	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	285/289 (99%)	236 (83%)	49 (17%)	2	10
1	B	282/289 (98%)	227 (80%)	55 (20%)	1	8
1	C	286/289 (99%)	235 (82%)	51 (18%)	2	10
1	D	286/289 (99%)	235 (82%)	51 (18%)	2	10
1	E	285/289 (99%)	237 (83%)	48 (17%)	2	11
1	F	286/289 (99%)	235 (82%)	51 (18%)	2	10
1	G	286/289 (99%)	240 (84%)	46 (16%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	287/289 (99%)	241 (84%)	46 (16%)	2	13
1	I	286/289 (99%)	240 (84%)	46 (16%)	2	13
2	a	148/151 (98%)	125 (84%)	23 (16%)	2	14
2	b	144/151 (95%)	119 (83%)	25 (17%)	2	10
2	c	149/151 (99%)	134 (90%)	15 (10%)	7	30
2	d	149/151 (99%)	137 (92%)	12 (8%)	11	39
2	e	149/151 (99%)	134 (90%)	15 (10%)	7	30
2	f	149/151 (99%)	133 (89%)	16 (11%)	6	27
2	g	149/151 (99%)	135 (91%)	14 (9%)	8	33
2	h	145/151 (96%)	128 (88%)	17 (12%)	5	23
2	i	149/151 (99%)	133 (89%)	16 (11%)	6	27
3	J	91/185 (49%)	66 (72%)	25 (28%)	0	2
3	L	176/185 (95%)	135 (77%)	41 (23%)	1	5
3	N	185/185 (100%)	139 (75%)	46 (25%)	0	3
3	P	130/185 (70%)	102 (78%)	28 (22%)	1	6
3	R	177/185 (96%)	130 (73%)	47 (27%)	0	3
3	T	176/185 (95%)	134 (76%)	42 (24%)	1	4
3	V	93/185 (50%)	72 (77%)	21 (23%)	1	5
3	X	136/185 (74%)	103 (76%)	33 (24%)	1	4
3	Z	139/185 (75%)	106 (76%)	33 (24%)	1	4
4	K	93/190 (49%)	62 (67%)	31 (33%)	0	1
4	M	190/190 (100%)	156 (82%)	34 (18%)	2	9
4	O	190/190 (100%)	148 (78%)	42 (22%)	1	5
4	Q	140/190 (74%)	99 (71%)	41 (29%)	0	1
4	S	188/190 (99%)	146 (78%)	42 (22%)	1	5
4	U	188/190 (99%)	137 (73%)	51 (27%)	0	2
4	W	92/190 (48%)	71 (77%)	21 (23%)	1	5
4	Y	96/190 (50%)	72 (75%)	24 (25%)	0	3
4	z	105/190 (55%)	81 (77%)	24 (23%)	1	5
All	All	6485/7335 (88%)	5263 (81%)	1222 (19%)	1	9

All (1222) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	22	SER
1	A	23	THR
1	A	28	THR
1	A	30	LEU
1	A	37	THR
1	A	43	LEU
1	A	45	LYS
1	A	56	ILE
1	A	80	LEU
1	A	81	SER
1	A	81(A)	VAL
1	A	85	SER
1	A	101	SER
1	A	109	LYS
1	A	114	SER
1	A	118	VAL
1	A	120	ILE
1	A	132	THR
1	A	133	THR
1	A	136	SER
1	A	146	SER
1	A	154	LEU
1	A	155	THR
1	A	160	ASP
1	A	174	GLU
1	A	182	VAL
1	A	194	LEU
1	A	197	ASN
1	A	198	VAL
1	A	203	SER
1	A	208	THR
1	A	213	SER
1	A	214	THR
1	A	219	THR
1	A	226	LEU
1	A	228	SER
1	A	236	LEU
1	A	239	MET
1	A	263	ARG
1	A	264	SER
1	A	277	CYS
1	A	283	THR

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Mol	Chain	Res	Type
1	A	302	ILE
1	A	315	VAL
1	A	316	LEU
1	A	318	THR
1	A	320	LEU
1	A	323	VAL
2	a	19	ASP
2	a	22	TYR
2	a	26	HIS
2	a	29	ASP
2	a	39	GLU
2	a	56	ILE
2	a	58	LYS
2	a	59	MET
2	a	61	THR
2	a	64	GLU
2	a	66	VAL
2	a	71	SER
2	a	72	ASN
2	a	83	LYS
2	a	121	LYS
2	a	130	VAL
2	a	145	ASP
2	a	148	CYS
2	a	151	SER
2	a	153	LYS
2	a	156	THR
2	a	164	GLU
2	a	171	ASN
1	B	22	SER
1	B	23	THR
1	B	28	THR
1	B	30	LEU
1	B	43	LEU
1	B	45	LYS
1	B	51	LEU
1	B	54	ASN
1	B	56	ILE
1	B	78	ARG
1	B	80	LEU
1	B	85	SER
1	B	91	GLU

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Mol	Chain	Res	Type
1	B	101	SER
1	B	104	ASP
1	B	108	LEU
1	B	109	LYS
1	B	111	LEU
1	B	114	SER
1	B	118	VAL
1	B	123	LYS
1	B	132	THR
1	B	144	ASN
1	B	146	SER
1	B	154	LEU
1	B	155	THR
1	B	160	ASP
1	B	171	THR
1	B	174	GLU
1	B	182	VAL
1	B	189	THR
1	B	194	LEU
1	B	197	ASN
1	B	198	VAL
1	B	203	SER
1	B	208	THR
1	B	213	SER
1	B	214	THR
1	B	219	THR
1	B	224	ASN
1	B	226	LEU
1	B	236	LEU
1	B	264	SER
1	B	277	CYS
1	B	279	THR
1	B	283	THR
1	B	297	VAL
1	B	301	THR
1	B	302	ILE
1	B	309	VAL
1	B	315	VAL
1	B	316	LEU
1	B	318	THR
1	B	320	LEU
1	B	323	VAL

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Mol	Chain	Res	Type
2	b	2	LEU
2	b	19	ASP
2	b	26	HIS
2	b	29	ASP
2	b	39	GLU
2	b	55	VAL
2	b	56	ILE
2	b	58	LYS
2	b	64	GLU
2	b	66	VAL
2	b	71	SER
2	b	72	ASN
2	b	74	GLU
2	b	83	LYS
2	b	116	LYS
2	b	121	LYS
2	b	145	ASP
2	b	148	CYS
2	b	150	ASN
2	b	151	SER
2	b	153	LYS
2	b	156	THR
2	b	164	GLU
2	b	168	LEU
2	b	171	ASN
1	C	23	THR
1	C	25	LYS
1	C	30	LEU
1	C	32	ARG
1	C	36	VAL
1	C	45	LYS
1	C	54	ASN
1	C	56	ILE
1	C	63	ASP
1	C	65	SER
1	C	79	LEU
1	C	80	LEU
1	C	96	LEU
1	C	101	SER
1	C	109	LYS
1	C	128	THR
1	C	133	THR

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Mol	Chain	Res	Type
1	C	146	SER
1	C	154	LEU
1	C	155	THR
1	C	159	SER
1	C	182	VAL
1	C	194	LEU
1	C	197	ASN
1	C	198	VAL
1	C	203	SER
1	C	206	THR
1	C	208	THR
1	C	209	LEU
1	C	214	THR
1	C	219	THR
1	C	226	LEU
1	C	233	SER
1	C	236	LEU
1	C	239	MET
1	C	260	ILE
1	C	273	THR
1	C	277	CYS
1	C	278	GLU
1	C	283	THR
1	C	285	LEU
1	C	295	HIS
1	C	297	VAL
1	C	301	THR
1	C	307	ARG
1	C	311	SER
1	C	312	GLU
1	C	315	VAL
1	C	316	LEU
1	C	320	LEU
1	C	323	VAL
2	c	19	ASP
2	c	26	HIS
2	c	59	MET
2	c	61	THR
2	c	64	GLU
2	c	66	VAL
2	c	69	GLU
2	c	71	SER

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Mol	Chain	Res	Type
2	c	72	ASN
2	c	73	LEU
2	c	113	SER
2	c	127	ARG
2	c	147	GLU
2	c	148	CYS
2	c	164	GLU
1	D	21	ASN
1	D	22	SER
1	D	23	THR
1	D	25	LYS
1	D	29	ILE
1	D	30	LEU
1	D	32	ARG
1	D	45	LYS
1	D	54	ASN
1	D	56	ILE
1	D	63	ASP
1	D	65	SER
1	D	80	LEU
1	D	101	SER
1	D	109	LYS
1	D	133	THR
1	D	136	SER
1	D	146	SER
1	D	154	LEU
1	D	155	THR
1	D	163	VAL
1	D	194	LEU
1	D	197	ASN
1	D	204	VAL
1	D	206	THR
1	D	208	THR
1	D	214	THR
1	D	217	ILE
1	D	219	THR
1	D	226	LEU
1	D	236	LEU
1	D	239	MET
1	D	242	THR
1	D	265	SER
1	D	273	THR

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Mol	Chain	Res	Type
1	D	275	GLU
1	D	277	CYS
1	D	278	GLU
1	D	279	THR
1	D	291	THR
1	D	295	HIS
1	D	297	VAL
1	D	301	THR
1	D	307	ARG
1	D	309	VAL
1	D	311	SER
1	D	312	GLU
1	D	315	VAL
1	D	316	LEU
1	D	323	VAL
1	D	326	ILE
2	d	19	ASP
2	d	26	HIS
2	d	59	MET
2	d	63	PHE
2	d	66	VAL
2	d	69	GLU
2	d	73	LEU
2	d	74	GLU
2	d	80	LEU
2	d	127	ARG
2	d	147	GLU
2	d	164	GLU
1	E	12	GLN
1	E	25	LYS
1	E	26	VAL
1	E	30	LEU
1	E	32	ARG
1	E	36	VAL
1	E	45	LYS
1	E	54	ASN
1	E	56	ILE
1	E	63	ASP
1	E	65	SER
1	E	80	LEU
1	E	96	LEU
1	E	101	SER

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Mol	Chain	Res	Type
1	E	111	LEU
1	E	113	SER
1	E	133	THR
1	E	136	SER
1	E	146	SER
1	E	154	LEU
1	E	155	THR
1	E	163	VAL
1	E	187	ASP
1	E	194	LEU
1	E	203	SER
1	E	204	VAL
1	E	206	THR
1	E	208	THR
1	E	209	LEU
1	E	213	SER
1	E	214	THR
1	E	219	THR
1	E	236	LEU
1	E	239	MET
1	E	242	THR
1	E	260	ILE
1	E	265	SER
1	E	273	THR
1	E	277	CYS
1	E	278	GLU
1	E	291	THR
1	E	304	GLU
1	E	307	ARG
1	E	309	VAL
1	E	312	GLU
1	E	315	VAL
1	E	316	LEU
1	E	323	VAL
2	e	19	ASP
2	e	32	SER
2	e	59	MET
2	e	66	VAL
2	e	69	GLU
2	e	71	SER
2	e	72	ASN
2	e	73	LEU

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Mol	Chain	Res	Type
2	e	74	GLU
2	e	75	ARG
2	e	84	MET
2	e	113	SER
2	e	127	ARG
2	e	147	GLU
2	e	164	GLU
1	F	22	SER
1	F	26	VAL
1	F	29	ILE
1	F	30	LEU
1	F	32	ARG
1	F	42	ILE
1	F	43	LEU
1	F	45	LYS
1	F	65	SER
1	F	78	ARG
1	F	89	GLU
1	F	101	SER
1	F	114	SER
1	F	132	THR
1	F	133	THR
1	F	137	ARG
1	F	142	SER
1	F	146	SER
1	F	154	LEU
1	F	155	THR
1	F	159	SER
1	F	182	VAL
1	F	189	THR
1	F	194	LEU
1	F	197	ASN
1	F	198	VAL
1	F	203	SER
1	F	208	THR
1	F	210	ASN
1	F	213	SER
1	F	214	THR
1	F	217	ILE
1	F	219	THR
1	F	226	LEU
1	F	236	LEU

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Mol	Chain	Res	Type
1	F	242	THR
1	F	261	SER
1	F	265	SER
1	F	273	THR
1	F	274	LEU
1	F	275	GLU
1	F	279	THR
1	F	290	THR
1	F	297	VAL
1	F	301	THR
1	F	309	VAL
1	F	315	VAL
1	F	316	LEU
1	F	320	LEU
1	F	323	VAL
1	F	326	ILE
2	f	19	ASP
2	f	26	HIS
2	f	59	MET
2	f	64	GLU
2	f	66	VAL
2	f	69	GLU
2	f	71	SER
2	f	72	ASN
2	f	73	LEU
2	f	74	GLU
2	f	76	ARG
2	f	83	LYS
2	f	84	MET
2	f	127	ARG
2	f	147	GLU
2	f	164	GLU
1	G	12	GLN
1	G	13	ILE
1	G	26	VAL
1	G	28	THR
1	G	30	LEU
1	G	32	ARG
1	G	43	LEU
1	G	45	LYS
1	G	65	SER
1	G	89	GLU

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Mol	Chain	Res	Type
1	G	96	LEU
1	G	101	SER
1	G	114	SER
1	G	132	THR
1	G	133	THR
1	G	137	ARG
1	G	142	SER
1	G	146	SER
1	G	154	LEU
1	G	155	THR
1	G	189	THR
1	G	194	LEU
1	G	197	ASN
1	G	208	THR
1	G	210	ASN
1	G	213	SER
1	G	214	THR
1	G	217	ILE
1	G	219	THR
1	G	226	LEU
1	G	236	LEU
1	G	270	THR
1	G	273	THR
1	G	274	LEU
1	G	275	GLU
1	G	279	THR
1	G	290	THR
1	G	297	VAL
1	G	301	THR
1	G	307	ARG
1	G	309	VAL
1	G	315	VAL
1	G	316	LEU
1	G	320	LEU
1	G	323	VAL
1	G	326	ILE
2	g	19	ASP
2	g	26	HIS
2	g	59	MET
2	g	61	THR
2	g	62	GLN
2	g	66	VAL

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Mol	Chain	Res	Type
2	g	69	GLU
2	g	72	ASN
2	g	73	LEU
2	g	74	GLU
2	g	80	LEU
2	g	147	GLU
2	g	148	CYS
2	g	164	GLU
1	H	13	ILE
1	H	30	LEU
1	H	32	ARG
1	H	36	VAL
1	H	43	LEU
1	H	45	LYS
1	H	65	SER
1	H	89	GLU
1	H	101	SER
1	H	114	SER
1	H	132	THR
1	H	133	THR
1	H	137	ARG
1	H	142	SER
1	H	146	SER
1	H	154	LEU
1	H	155	THR
1	H	159	SER
1	H	182	VAL
1	H	189	THR
1	H	194	LEU
1	H	197	ASN
1	H	203	SER
1	H	208	THR
1	H	210	ASN
1	H	213	SER
1	H	214	THR
1	H	217	ILE
1	H	219	THR
1	H	226	LEU
1	H	236	LEU
1	H	261	SER
1	H	265	SER
1	H	273	THR

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Mol	Chain	Res	Type
1	H	274	LEU
1	H	279	THR
1	H	291	THR
1	H	297	VAL
1	H	301	THR
1	H	307	ARG
1	H	309	VAL
1	H	315	VAL
1	H	316	LEU
1	H	323	VAL
1	H	326	ILE
1	H	327	GLU
2	h	19	ASP
2	h	21	TRP
2	h	26	HIS
2	h	32	SER
2	h	43	LYS
2	h	49	THR
2	h	59	MET
2	h	66	VAL
2	h	69	GLU
2	h	72	ASN
2	h	73	LEU
2	h	74	GLU
2	h	113	SER
2	h	116	LYS
2	h	127	ARG
2	h	151	SER
2	h	164	GLU
1	I	11	ASP
1	I	29	ILE
1	I	30	LEU
1	I	32	ARG
1	I	65	SER
1	I	66	ILE
1	I	89	GLU
1	I	101	SER
1	I	114	SER
1	I	132	THR
1	I	133	THR
1	I	137	ARG
1	I	146	SER

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Mol	Chain	Res	Type
1	I	155	THR
1	I	189	THR
1	I	194	LEU
1	I	197	ASN
1	I	203	SER
1	I	207	SER
1	I	208	THR
1	I	210	ASN
1	I	213	SER
1	I	214	THR
1	I	217	ILE
1	I	219	THR
1	I	226	LEU
1	I	228	SER
1	I	236	LEU
1	I	261	SER
1	I	264	SER
1	I	265	SER
1	I	270	THR
1	I	273	THR
1	I	274	LEU
1	I	275	GLU
1	I	279	THR
1	I	285	LEU
1	I	297	VAL
1	I	301	THR
1	I	302	ILE
1	I	307	ARG
1	I	315	VAL
1	I	316	LEU
1	I	320	LEU
1	I	323	VAL
1	I	326	ILE
2	i	19	ASP
2	i	26	HIS
2	i	27	SER
2	i	43	LYS
2	i	56	ILE
2	i	59	MET
2	i	64	GLU
2	i	66	VAL
2	i	69	GLU

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Mol	Chain	Res	Type
2	i	73	LEU
2	i	74	GLU
2	i	80	LEU
2	i	116	LYS
2	i	127	ARG
2	i	147	GLU
2	i	164	GLU
3	J	2	VAL
3	J	3	GLN
3	J	4	LEU
3	J	5	VAL
3	J	6	GLU
3	J	10	GLU
3	J	11	VAL
3	J	12	LYS
3	J	19	LYS
3	J	21	SER
3	J	36	TRP
3	J	38	ARG
3	J	48	VAL
3	J	53	ILE
3	J	57	SER
3	J	70	THR
3	J	72	ASP
3	J	74	SER
3	J	79	TYR
3	J	80	MET
3	J	85	GLU
3	J	87	THR
3	J	96	ILE
3	J	97	SER
3	J	101	ASP
4	K	1	ASP
4	K	4	LEU
4	K	5	THR
4	K	7	SER
4	K	18	ARG
4	K	19	VAL
4	K	20	THR
4	K	29	ILE
4	K	33	LEU
4	K	39	LYS

Continued on next page...

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Mol	Chain	Res	Type
4	K	42	LYS
4	K	45	ASN
4	K	46	LEU
4	K	48	ILE
4	K	54	VAL
4	K	55	LYS
4	K	61	ARG
4	K	63	ARG
4	K	65	SER
4	K	69	THR
4	K	70	ASP
4	K	75	ILE
4	K	78	LEU
4	K	79	GLN
4	K	85	THR
4	K	90	GLN
4	K	96	ILE
4	K	97	THR
4	K	103	ARG
4	K	104	LEU
4	K	106	ILE
3	L	3	GLN
3	L	4	LEU
3	L	5	VAL
3	L	11	VAL
3	L	17	SER
3	L	28	THR
3	L	33	VAL
3	L	43	GLN
3	L	53	ILE
3	L	57	SER
3	L	74	SER
3	L	75	THR
3	L	76	SER
3	L	83	THR
3	L	85	GLU
3	L	97	SER
3	L	107	THR
3	L	110	THR
3	L	116	THR
3	L	117	LYS
3	L	138	LEU

Continued on next page...

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Mol	Chain	Res	Type
3	L	151	THR
3	L	163	VAL
3	L	164	HIS
3	L	169	VAL
3	L	170	LEU
3	L	172	SER
3	L	173	SER
3	L	177	SER
3	L	178	LEU
3	L	179	SER
3	L	182	VAL
3	L	183	THR
3	L	184	VAL
3	L	186	SER
3	L	189	LEU
3	L	191	THR
3	L	195	ILE
3	L	197	ASN
3	L	198	VAL
3	L	205	THR
4	M	3	GLN
4	M	5	THR
4	M	7	SER
4	M	11	LEU
4	M	22	THR
4	M	26	SER
4	M	30	ARG
4	M	33	LEU
4	M	65	SER
4	M	69	THR
4	M	72	THR
4	M	77	SER
4	M	78	LEU
4	M	83	ILE
4	M	90	GLN
4	M	94	LEU
4	M	96	ILE
4	M	97	THR
4	M	104	LEU
4	M	105	GLU
4	M	107	LYS
4	M	110	VAL

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Mol	Chain	Res	Type
4	M	117	ILE
4	M	150	VAL
4	M	154	LEU
4	M	155	GLN
4	M	158	ASN
4	M	181	LEU
4	M	182	SER
4	M	202	SER
4	M	206	THR
4	M	207	LYS
4	M	208	SER
4	M	213	GLU
3	N	4	LEU
3	N	11	VAL
3	N	28	THR
3	N	31	THR
3	N	33	VAL
3	N	43	GLN
3	N	53	ILE
3	N	57	SER
3	N	62	LYS
3	N	70	THR
3	N	74	SER
3	N	75	THR
3	N	76	SER
3	N	83	THR
3	N	85	GLU
3	N	110	THR
3	N	116	THR
3	N	117	LYS
3	N	120	SER
3	N	128	SER
3	N	130	SER
3	N	131	THR
3	N	132	SER
3	N	138	LEU
3	N	151	THR
3	N	156	SER
3	N	167	PRO
3	N	169	VAL
3	N	170	LEU
3	N	173	SER

Continued on next page...

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Mol	Chain	Res	Type
3	N	177	SER
3	N	178	LEU
3	N	179	SER
3	N	182	VAL
3	N	184	VAL
3	N	186	SER
3	N	189	LEU
3	N	191	THR
3	N	193	THR
3	N	195	ILE
3	N	197	ASN
3	N	198	VAL
3	N	210	ARG
3	N	214	LYS
3	N	215	SER
3	N	216	CYS
4	O	2	ILE
4	O	3	GLN
4	O	5	THR
4	O	7	SER
4	O	11	LEU
4	O	20	THR
4	O	22	THR
4	O	26	SER
4	O	52	SER
4	O	60	SER
4	O	63	ARG
4	O	65	SER
4	O	74	THR
4	O	77	SER
4	O	78	LEU
4	O	81	GLU
4	O	85	THR
4	O	90	GLN
4	O	91	TYR
4	O	94	LEU
4	O	97	THR
4	O	104	LEU
4	O	107	LYS
4	O	110	VAL
4	O	117	ILE
4	O	127	SER

Continued on next page...

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Mol	Chain	Res	Type
4	O	132	VAL
4	O	142	ARG
4	O	150	VAL
4	O	154	LEU
4	O	155	GLN
4	O	163	VAL
4	O	164	THR
4	O	180	THR
4	O	181	LEU
4	O	182	SER
4	O	197	THR
4	O	201	LEU
4	O	202	SER
4	O	207	LYS
4	O	208	SER
4	O	214	CYS
3	P	2	VAL
3	P	6	GLU
3	P	7	SER
3	P	11	VAL
3	P	12	LYS
3	P	21	SER
3	P	25	SER
3	P	28	THR
3	P	33	VAL
3	P	61	GLN
3	P	66	ARG
3	P	68	THR
3	P	70	THR
3	P	75	THR
3	P	83	THR
3	P	110	THR
3	P	116	THR
3	P	117	LYS
3	P	142	VAL
3	P	156	SER
3	P	160	THR
3	P	161	SER
3	P	169	VAL
3	P	170	LEU
3	P	173	SER
3	P	177	SER

Continued on next page...

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Mol	Chain	Res	Type
3	P	178	LEU
3	P	181	VAL
4	Q	2	ILE
4	Q	5	THR
4	Q	11	LEU
4	Q	14	SER
4	Q	18	ARG
4	Q	19	VAL
4	Q	20	THR
4	Q	21	ILE
4	Q	26	SER
4	Q	30	ARG
4	Q	52	SER
4	Q	60	SER
4	Q	63	ARG
4	Q	65	SER
4	Q	67	SER
4	Q	69	THR
4	Q	74	THR
4	Q	77	SER
4	Q	81	GLU
4	Q	83	ILE
4	Q	85	THR
4	Q	90	GLN
4	Q	94	LEU
4	Q	96	ILE
4	Q	106	ILE
4	Q	107	LYS
4	Q	109	THR
4	Q	132	VAL
4	Q	133	VAL
4	Q	135	LEU
4	Q	138	ASN
4	Q	142	ARG
4	Q	164	THR
4	Q	166	GLN
4	Q	169	LYS
4	Q	174	SER
4	Q	175	LEU
4	Q	176	SER
4	Q	197	THR
4	Q	199	GLN

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Mol	Chain	Res	Type
4	Q	201	LEU
3	R	1	GLU
3	R	2	VAL
3	R	6	GLU
3	R	7	SER
3	R	11	VAL
3	R	12	LYS
3	R	17	SER
3	R	25	SER
3	R	28	THR
3	R	33	VAL
3	R	61	GLN
3	R	68	THR
3	R	70	THR
3	R	75	THR
3	R	83	THR
3	R	97	SER
3	R	110	THR
3	R	113	SER
3	R	115	SER
3	R	116	THR
3	R	117	LYS
3	R	121	VAL
3	R	135	THR
3	R	140	CYS
3	R	148	GLU
3	R	151	THR
3	R	153	SER
3	R	154	TRP
3	R	161	SER
3	R	164	HIS
3	R	169	VAL
3	R	170	LEU
3	R	173	SER
3	R	179	SER
3	R	181	VAL
3	R	182	VAL
3	R	183	THR
3	R	184	VAL
3	R	186	SER
3	R	187	SER
3	R	189	LEU

Continued on next page...

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Mol	Chain	Res	Type
3	R	191	THR
3	R	192	GLN
3	R	196	CYS
3	R	197	ASN
3	R	209	LYS
3	R	212	GLU
4	S	5	THR
4	S	11	LEU
4	S	14	SER
4	S	18	ARG
4	S	19	VAL
4	S	21	ILE
4	S	26	SER
4	S	30	ARG
4	S	52	SER
4	S	60	SER
4	S	61	ARG
4	S	63	ARG
4	S	65	SER
4	S	74	THR
4	S	77	SER
4	S	78	LEU
4	S	81	GLU
4	S	83	ILE
4	S	85	THR
4	S	90	GLN
4	S	94	LEU
4	S	105	GLU
4	S	107	LYS
4	S	109	THR
4	S	117	ILE
4	S	129	THR
4	S	132	VAL
4	S	133	VAL
4	S	149	LYS
4	S	151	ASP
4	S	152	ASN
4	S	154	LEU
4	S	155	GLN
4	S	156	SER
4	S	158	ASN
4	S	162	SER

Continued on next page...

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Mol	Chain	Res	Type
4	S	168	SER
4	S	169	LYS
4	S	170	ASP
4	S	180	THR
4	S	202	SER
4	S	207	LYS
3	T	2	VAL
3	T	6	GLU
3	T	7	SER
3	T	11	VAL
3	T	12	LYS
3	T	17	SER
3	T	25	SER
3	T	28	THR
3	T	33	VAL
3	T	61	GLN
3	T	66	ARG
3	T	68	THR
3	T	70	THR
3	T	75	THR
3	T	83	THR
3	T	97	SER
3	T	99	SER
3	T	110	THR
3	T	115	SER
3	T	116	THR
3	T	117	LYS
3	T	127	SER
3	T	150	VAL
3	T	152	VAL
3	T	153	SER
3	T	160	THR
3	T	169	VAL
3	T	170	LEU
3	T	172	SER
3	T	173	SER
3	T	179	SER
3	T	182	VAL
3	T	183	THR
3	T	184	VAL
3	T	187	SER
3	T	189	LEU

Continued on next page...

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Mol	Chain	Res	Type
3	T	192	GLN
3	T	194	TYR
3	T	198	VAL
3	T	205	THR
3	T	211	VAL
3	T	212	GLU
4	U	5	THR
4	U	9	SER
4	U	11	LEU
4	U	14	SER
4	U	18	ARG
4	U	19	VAL
4	U	20	THR
4	U	26	SER
4	U	52	SER
4	U	60	SER
4	U	61	ARG
4	U	63	ARG
4	U	72	THR
4	U	74	THR
4	U	77	SER
4	U	78	LEU
4	U	81	GLU
4	U	83	ILE
4	U	85	THR
4	U	90	GLN
4	U	94	LEU
4	U	97	THR
4	U	109	THR
4	U	110	VAL
4	U	114	SER
4	U	117	ILE
4	U	122	ASP
4	U	123	GLU
4	U	125	LEU
4	U	127	SER
4	U	129	THR
4	U	131	SER
4	U	138	ASN
4	U	142	ARG
4	U	145	LYS
4	U	147	GLN

Continued on next page...

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Mol	Chain	Res	Type
4	U	155	GLN
4	U	156	SER
4	U	168	SER
4	U	170	ASP
4	U	172	THR
4	U	174	SER
4	U	175	LEU
4	U	176	SER
4	U	182	SER
4	U	188	LYS
4	U	190	LYS
4	U	201	LEU
4	U	207	LYS
4	U	208	SER
4	U	210	ASN
3	V	2	VAL
3	V	6	GLU
3	V	7	SER
3	V	11	VAL
3	V	16	SER
3	V	17	SER
3	V	21	SER
3	V	25	SER
3	V	28	THR
3	V	33	VAL
3	V	37	VAL
3	V	61	GLN
3	V	66	ARG
3	V	68	THR
3	V	70	THR
3	V	75	THR
3	V	83	THR
3	V	92	CYS
3	V	96	ILE
3	V	97	SER
3	V	110	THR
4	W	5	THR
4	W	9	SER
4	W	11	LEU
4	W	14	SER
4	W	18	ARG
4	W	19	VAL

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Mol	Chain	Res	Type
4	W	20	THR
4	W	26	SER
4	W	30	ARG
4	W	52	SER
4	W	60	SER
4	W	61	ARG
4	W	63	ARG
4	W	67	SER
4	W	74	THR
4	W	77	SER
4	W	78	LEU
4	W	81	GLU
4	W	85	THR
4	W	90	GLN
4	W	94	LEU
3	X	6	GLU
3	X	7	SER
3	X	10	GLU
3	X	12	LYS
3	X	18	VAL
3	X	28	THR
3	X	31	THR
3	X	48	VAL
3	X	53	ILE
3	X	62	LYS
3	X	64	GLN
3	X	68	THR
3	X	70	THR
3	X	77	THR
3	X	83	THR
3	X	85	GLU
3	X	87	THR
3	X	89	VAL
3	X	97	SER
3	X	108	LEU
3	X	111	VAL
3	X	115	SER
3	X	117	LYS
3	X	142	VAL
3	X	148	GLU
3	X	150	VAL
3	X	169	VAL

Continued on next page...

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Mol	Chain	Res	Type
3	X	170	LEU
3	X	171	GLN
3	X	180	SER
3	X	204	ASN
3	X	206	LYS
3	X	207	VAL
4	Y	5	THR
4	Y	6	GLN
4	Y	9	SER
4	Y	11	LEU
4	Y	14	SER
4	Y	18	ARG
4	Y	19	VAL
4	Y	26	SER
4	Y	30	ARG
4	Y	52	SER
4	Y	60	SER
4	Y	61	ARG
4	Y	63	ARG
4	Y	65	SER
4	Y	74	THR
4	Y	77	SER
4	Y	78	LEU
4	Y	81	GLU
4	Y	83	ILE
4	Y	89	GLN
4	Y	90	GLN
4	Y	94	LEU
4	Y	105	GLU
4	Y	108	ARG
3	Z	4	LEU
3	Z	5	VAL
3	Z	6	GLU
3	Z	7	SER
3	Z	10	GLU
3	Z	12	LYS
3	Z	28	THR
3	Z	31	THR
3	Z	48	VAL
3	Z	57	SER
3	Z	62	LYS
3	Z	64	GLN

Continued on next page...

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Mol	Chain	Res	Type
3	Z	68	THR
3	Z	70	THR
3	Z	83	THR
3	Z	84	SER
3	Z	85	GLU
3	Z	87	THR
3	Z	89	VAL
3	Z	97	SER
3	Z	111	VAL
3	Z	113	SER
3	Z	115	SER
3	Z	117	LYS
3	Z	121	VAL
3	Z	142	VAL
3	Z	150	VAL
3	Z	164	HIS
3	Z	170	LEU
3	Z	171	GLN
3	Z	195	ILE
3	Z	197	ASN
3	Z	204	ASN
4	z	5	THR
4	z	11	LEU
4	z	14	SER
4	z	18	ARG
4	z	19	VAL
4	z	21	ILE
4	z	26	SER
4	z	60	SER
4	z	61	ARG
4	z	63	ARG
4	z	65	SER
4	z	67	SER
4	z	69	THR
4	z	74	THR
4	z	77	SER
4	z	78	LEU
4	z	81	GLU
4	z	83	ILE
4	z	85	THR
4	z	90	GLN
4	z	94	LEU

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Mol	Chain	Res	Type
4	z	156	SER
4	z	158	ASN
4	z	176	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	224	ASN
1	A	295	HIS
2	a	25	HIS
2	a	125	GLN
2	a	171	ASN
1	B	295	HIS
2	b	26	HIS
2	b	171	ASN
1	C	47	HIS
1	C	298	HIS
1	C	325	GLN
2	c	171	ASN
1	D	54	ASN
1	D	197	ASN
1	D	282	GLN
1	D	295	HIS
1	E	33	ASN
1	E	47	HIS
1	E	129	GLN
1	E	295	HIS
2	e	26	HIS
2	e	171	ASN
1	F	92	ASN
1	F	298	HIS
2	f	79	ASN
2	f	81	ASN
2	g	62	GLN
2	g	171	ASN
1	H	92	ASN
1	H	129	GLN
1	H	295	HIS
1	H	298	HIS
2	h	30	GLN
1	I	244	ASN
1	I	295	HIS

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Mol	Chain	Res	Type
2	i	79	ASN
2	i	125	GLN
2	i	171	ASN
4	K	34	ASN
4	K	90	GLN
3	L	43	GLN
3	L	58	ASN
3	L	64	GLN
3	L	204	ASN
4	M	27	GLN
3	N	39	GLN
3	N	171	GLN
4	O	38	GLN
4	O	90	GLN
4	O	155	GLN
3	P	171	GLN
4	Q	3	GLN
4	Q	90	GLN
4	Q	138	ASN
3	R	39	GLN
3	R	171	GLN
3	R	192	GLN
3	R	199	ASN
4	S	24	GLN
4	S	38	GLN
4	S	155	GLN
4	S	210	ASN
3	T	39	GLN
3	T	43	GLN
4	U	37	GLN
4	U	38	GLN
3	V	39	GLN
4	W	6	GLN
4	W	38	GLN
3	X	58	ASN
3	X	199	ASN
4	Y	37	GLN
4	Y	90	GLN
3	Z	39	GLN
3	Z	58	ASN
4	z	38	GLN
4	z	90	GLN

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 ⓘ

24 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	$\# Z > 2$
5	NAG	j	1	5,1	14,14,15	0.54	0	17,19,21	1.24	2 (11%)
5	NAG	j	2	5	14,14,15	0.61	0	17,19,21	0.82	0
5	NAG	k	1	5,1	14,14,15	0.52	0	17,19,21	1.07	1 (5%)
5	NAG	k	2	5	14,14,15	0.54	0	17,19,21	0.93	1 (5%)
6	NAG	l	1	6,1	14,14,15	0.60	0	17,19,21	1.72	3 (17%)
6	NAG	l	2	6	14,14,15	0.52	0	17,19,21	0.98	0
6	BMA	l	3	6	11,11,12	0.55	0	15,15,17	1.12	1 (6%)
5	NAG	m	1	5,1	14,14,15	0.48	0	17,19,21	1.09	2 (11%)
5	NAG	m	2	5	14,14,15	0.57	0	17,19,21	0.65	0
5	NAG	n	1	5,1	14,14,15	0.62	0	17,19,21	1.52	3 (17%)
5	NAG	n	2	5	14,14,15	0.58	0	17,19,21	0.96	0
5	NAG	o	1	5,1	14,14,15	0.62	0	17,19,21	1.68	3 (17%)
5	NAG	o	2	5	14,14,15	0.41	0	17,19,21	1.18	1 (5%)
6	NAG	p	1	6,1	14,14,15	0.62	0	17,19,21	1.06	1 (5%)
6	NAG	p	2	6	14,14,15	0.53	0	17,19,21	0.94	1 (5%)
6	BMA	p	3	6	11,11,12	0.65	0	15,15,17	1.05	2 (13%)
5	NAG	q	1	5,1	14,14,15	0.50	0	17,19,21	1.02	1 (5%)
5	NAG	q	2	5	14,14,15	0.56	0	17,19,21	0.83	0
5	NAG	r	1	5,1	14,14,15	0.49	0	17,19,21	1.39	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	r	2	5	14,14,15	0.52	0	17,19,21	0.77	1 (5%)
5	NAG	s	1	5,1	14,14,15	0.48	0	17,19,21	1.29	1 (5%)
5	NAG	s	2	5	14,14,15	0.51	0	17,19,21	0.64	0
5	NAG	t	1	5,1	14,14,15	0.46	0	17,19,21	1.03	1 (5%)
5	NAG	t	2	5	14,14,15	0.48	0	17,19,21	1.19	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
5	NAG	j	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	j	2	5	-	4/6/23/26	0/1/1/1
5	NAG	k	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	k	2	5	-	2/6/23/26	0/1/1/1
6	NAG	l	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	l	2	6	-	2/6/23/26	0/1/1/1
6	BMA	l	3	6	-	2/2/19/22	0/1/1/1
5	NAG	m	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	m	2	5	-	2/6/23/26	0/1/1/1
5	NAG	n	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	n	2	5	-	4/6/23/26	0/1/1/1
5	NAG	o	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	o	2	5	-	2/6/23/26	0/1/1/1
6	NAG	p	1	6,1	-	4/6/23/26	0/1/1/1
6	NAG	p	2	6	-	2/6/23/26	0/1/1/1
6	BMA	p	3	6	-	2/2/19/22	0/1/1/1
5	NAG	q	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	q	2	5	-	0/6/23/26	0/1/1/1
5	NAG	r	1	5,1	-	5/6/23/26	0/1/1/1
5	NAG	r	2	5	-	2/6/23/26	0/1/1/1
5	NAG	s	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	s	2	5	-	2/6/23/26	0/1/1/1
5	NAG	t	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	t	2	5	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	l	1	NAG	C2-N2-C7	-5.22	115.90	122.90
5	o	1	NAG	C2-N2-C7	-5.03	116.16	122.90
5	n	1	NAG	C2-N2-C7	4.00	128.27	122.90
5	r	1	NAG	C3-C4-C5	3.67	116.89	110.23
5	j	1	NAG	C1-O5-C5	3.29	116.59	112.19
6	l	3	BMA	O5-C5-C6	3.28	114.05	107.66
5	o	2	NAG	C1-O5-C5	3.12	116.37	112.19
6	p	2	NAG	C2-N2-C7	-2.85	119.08	122.90
5	k	1	NAG	C1-O5-C5	2.79	115.92	112.19
6	p	1	NAG	C2-N2-C7	-2.77	119.19	122.90
5	t	1	NAG	O5-C1-C2	-2.74	107.05	111.29
6	l	1	NAG	O5-C1-C2	-2.61	107.25	111.29
5	t	2	NAG	C1-O5-C5	2.49	115.52	112.19
5	m	1	NAG	O5-C5-C6	2.47	112.46	107.66
6	p	3	BMA	C1-C2-C3	2.44	113.20	109.64
5	n	1	NAG	O7-C7-C8	-2.40	117.78	122.05
5	s	1	NAG	O5-C5-C6	2.38	112.29	107.66
6	l	1	NAG	C3-C4-C5	2.35	114.49	110.23
6	p	3	BMA	C1-O5-C5	2.25	115.21	112.19
5	t	2	NAG	O5-C5-C6	2.21	111.97	107.66
5	m	1	NAG	C4-C3-C2	-2.21	107.78	111.02
5	r	2	NAG	C2-N2-C7	-2.16	120.01	122.90
5	o	1	NAG	O5-C1-C2	-2.15	107.96	111.29
5	k	2	NAG	C1-O5-C5	2.14	115.06	112.19
5	q	1	NAG	O5-C5-C6	2.13	111.81	107.66
5	o	1	NAG	O7-C7-N2	-2.09	118.29	121.98
5	j	1	NAG	C2-N2-C7	-2.08	120.11	122.90
5	n	1	NAG	C1-O5-C5	2.06	114.95	112.19

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	k	1	NAG	C8-C7-N2-C2
5	k	1	NAG	O7-C7-N2-C2
5	o	1	NAG	C8-C7-N2-C2
5	o	1	NAG	O7-C7-N2-C2
5	q	1	NAG	C8-C7-N2-C2
5	q	1	NAG	O7-C7-N2-C2
5	r	1	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
5	r	1	NAG	O7-C7-N2-C2
5	s	2	NAG	C8-C7-N2-C2
5	s	2	NAG	O7-C7-N2-C2
5	t	1	NAG	C8-C7-N2-C2
5	t	1	NAG	O7-C7-N2-C2
6	l	1	NAG	C8-C7-N2-C2
6	l	1	NAG	O7-C7-N2-C2
6	p	1	NAG	C8-C7-N2-C2
6	p	1	NAG	O7-C7-N2-C2
5	m	1	NAG	O5-C5-C6-O6
6	p	3	BMA	O5-C5-C6-O6
5	n	2	NAG	O5-C5-C6-O6
5	r	1	NAG	O5-C5-C6-O6
5	m	2	NAG	O5-C5-C6-O6
6	l	3	BMA	O5-C5-C6-O6
5	m	1	NAG	C4-C5-C6-O6
5	n	2	NAG	C4-C5-C6-O6
5	r	1	NAG	C4-C5-C6-O6
6	l	3	BMA	C4-C5-C6-O6
6	p	3	BMA	C4-C5-C6-O6
5	j	2	NAG	O5-C5-C6-O6
5	t	2	NAG	O5-C5-C6-O6
5	m	2	NAG	C4-C5-C6-O6
5	j	1	NAG	C8-C7-N2-C2
5	r	2	NAG	C8-C7-N2-C2
5	r	2	NAG	O7-C7-N2-C2
6	p	2	NAG	C8-C7-N2-C2
6	p	2	NAG	O7-C7-N2-C2
6	p	1	NAG	C4-C5-C6-O6
5	j	2	NAG	C4-C5-C6-O6
5	j	2	NAG	C8-C7-N2-C2
5	n	2	NAG	C8-C7-N2-C2
5	j	1	NAG	O7-C7-N2-C2
5	j	2	NAG	O7-C7-N2-C2
5	n	2	NAG	O7-C7-N2-C2
6	l	2	NAG	C8-C7-N2-C2
6	p	1	NAG	O5-C5-C6-O6
5	t	2	NAG	C4-C5-C6-O6
6	l	2	NAG	O7-C7-N2-C2
5	o	2	NAG	C8-C7-N2-C2
5	k	2	NAG	O5-C5-C6-O6
5	k	2	NAG	C4-C5-C6-O6

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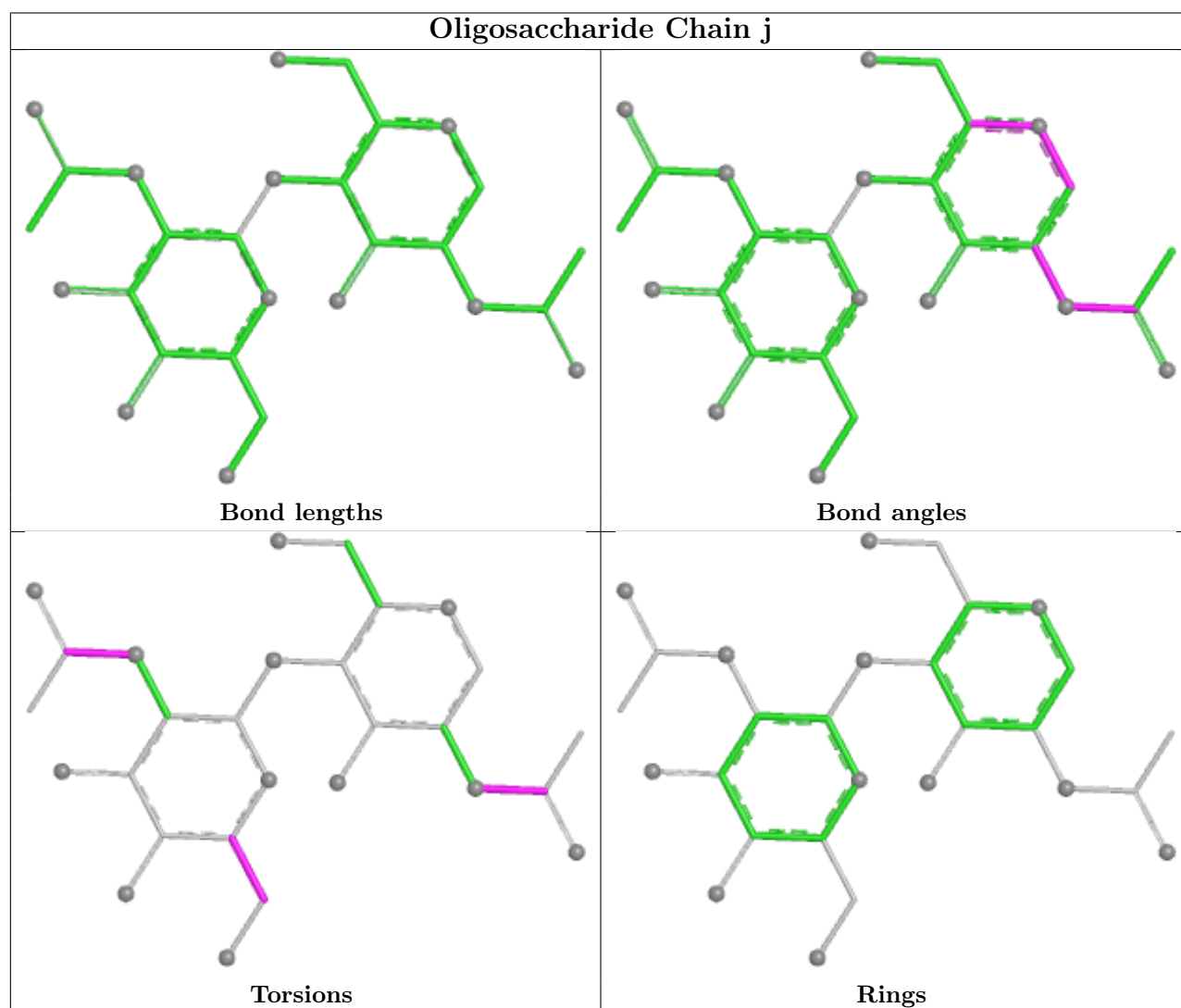
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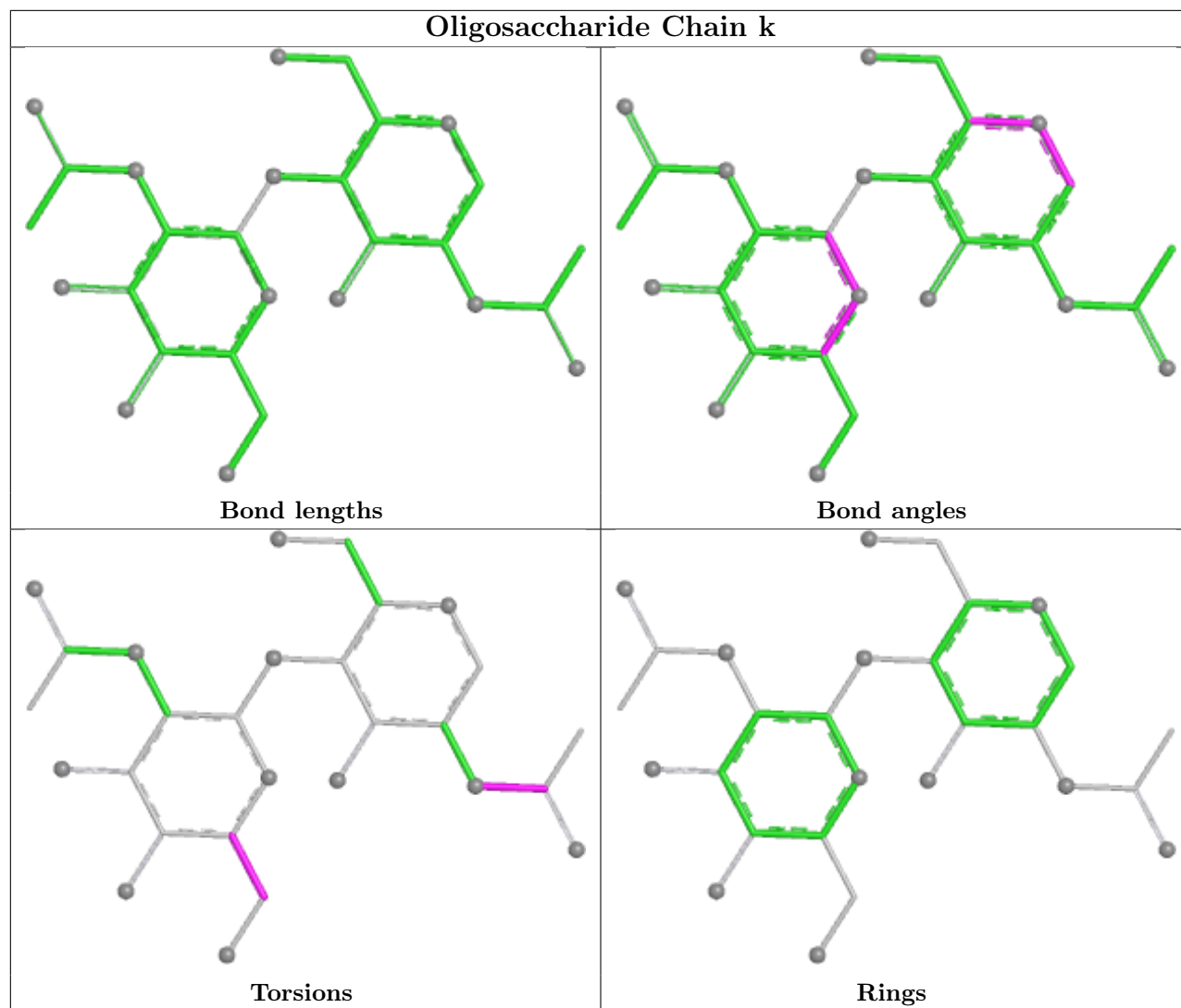
Mol	Chain	Res	Type	Atoms
5	n	1	NAG	C4-C5-C6-O6
5	o	2	NAG	O7-C7-N2-C2
5	t	2	NAG	C8-C7-N2-C2
5	t	2	NAG	O7-C7-N2-C2
5	n	1	NAG	O5-C5-C6-O6
5	r	1	NAG	C3-C2-N2-C7

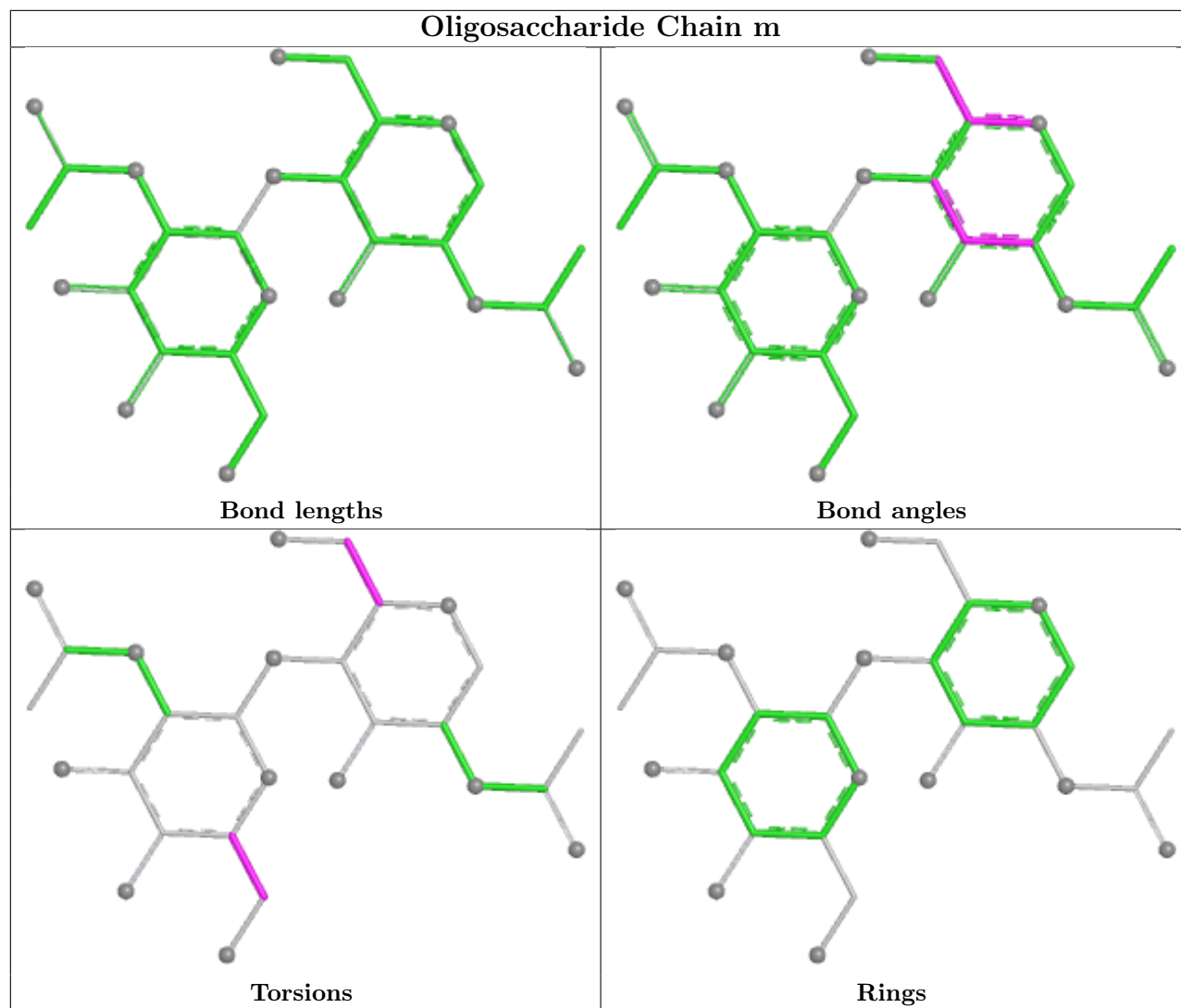
There are no ring outliers.

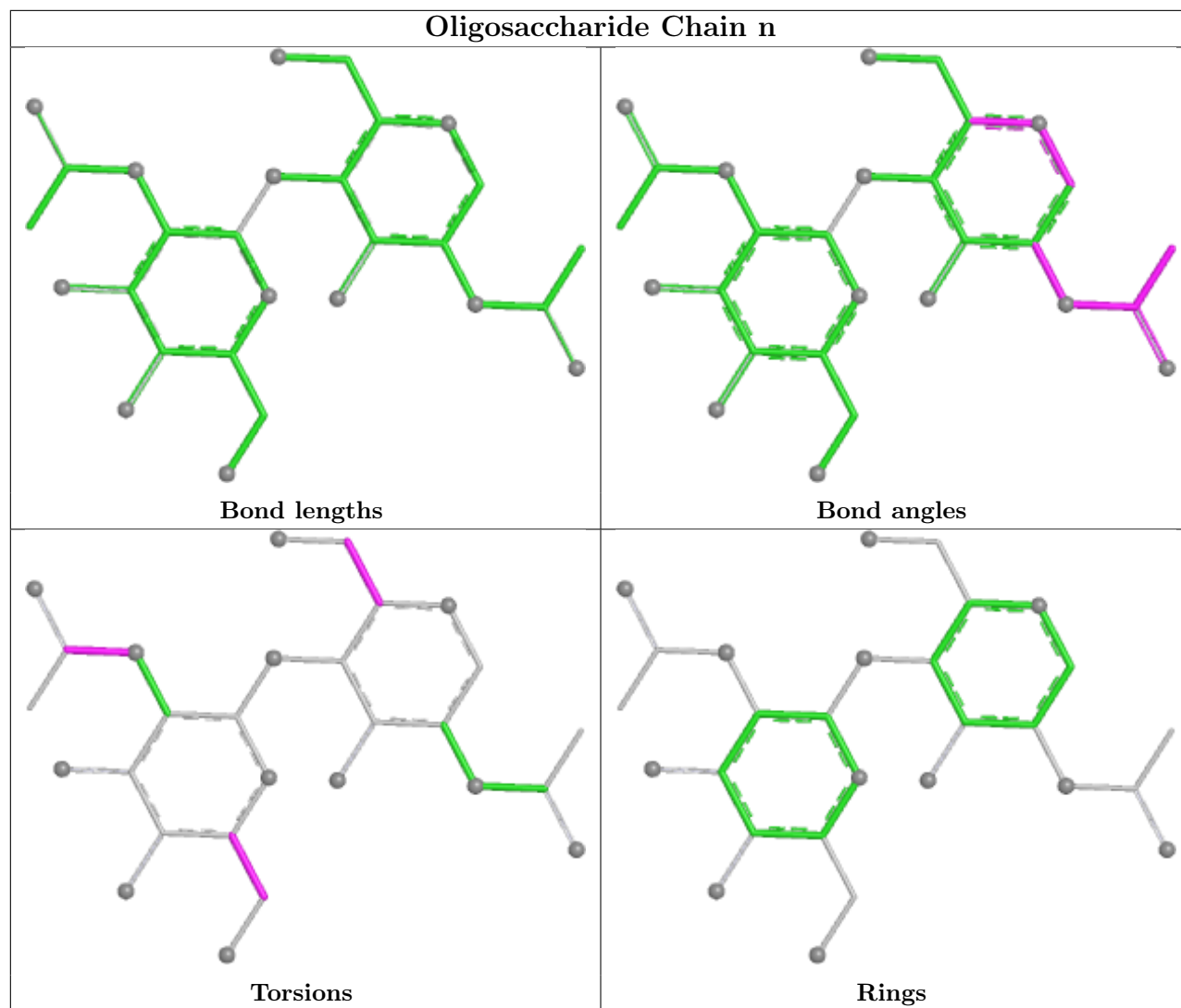
No monomer is involved in short contacts.

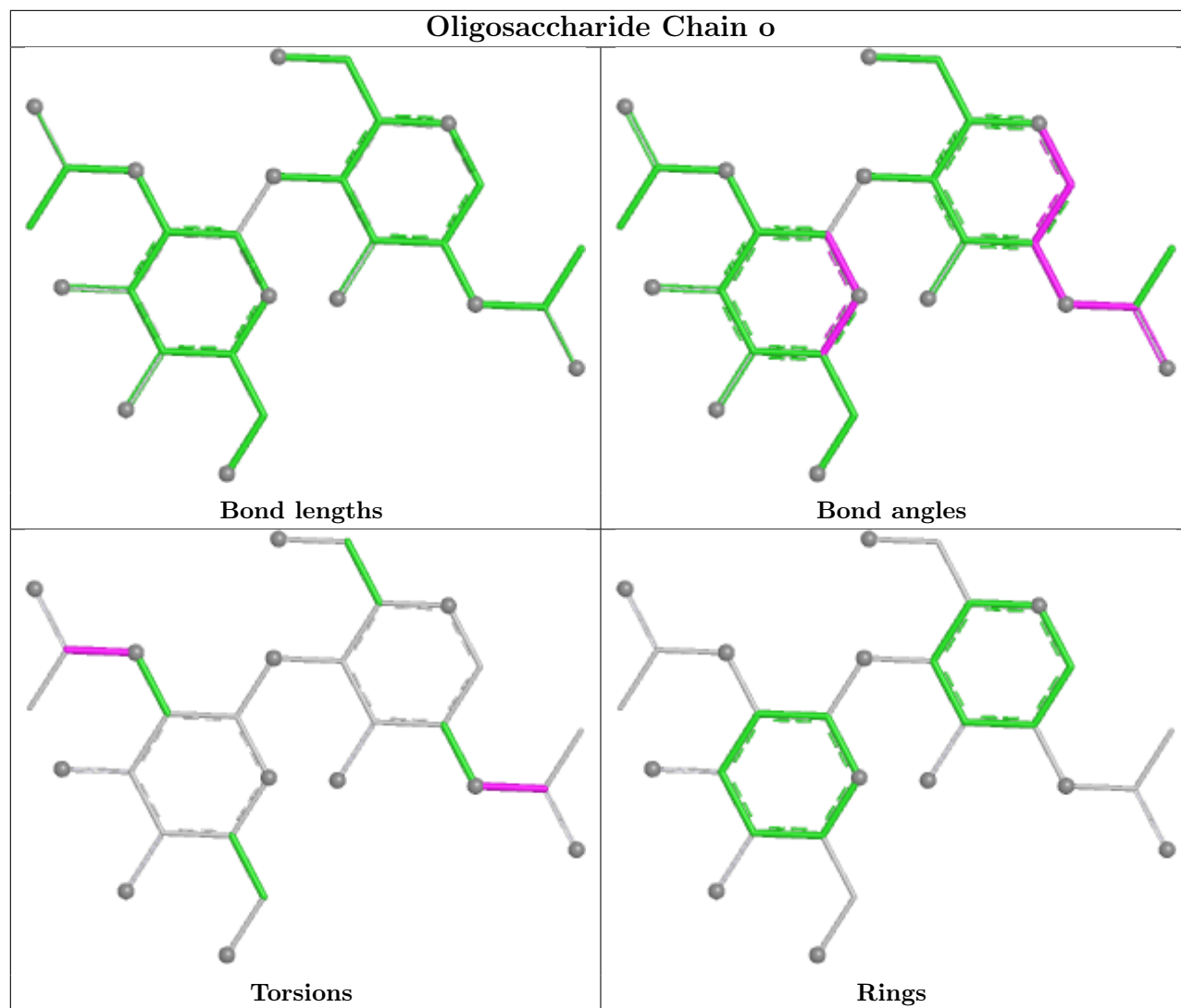
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

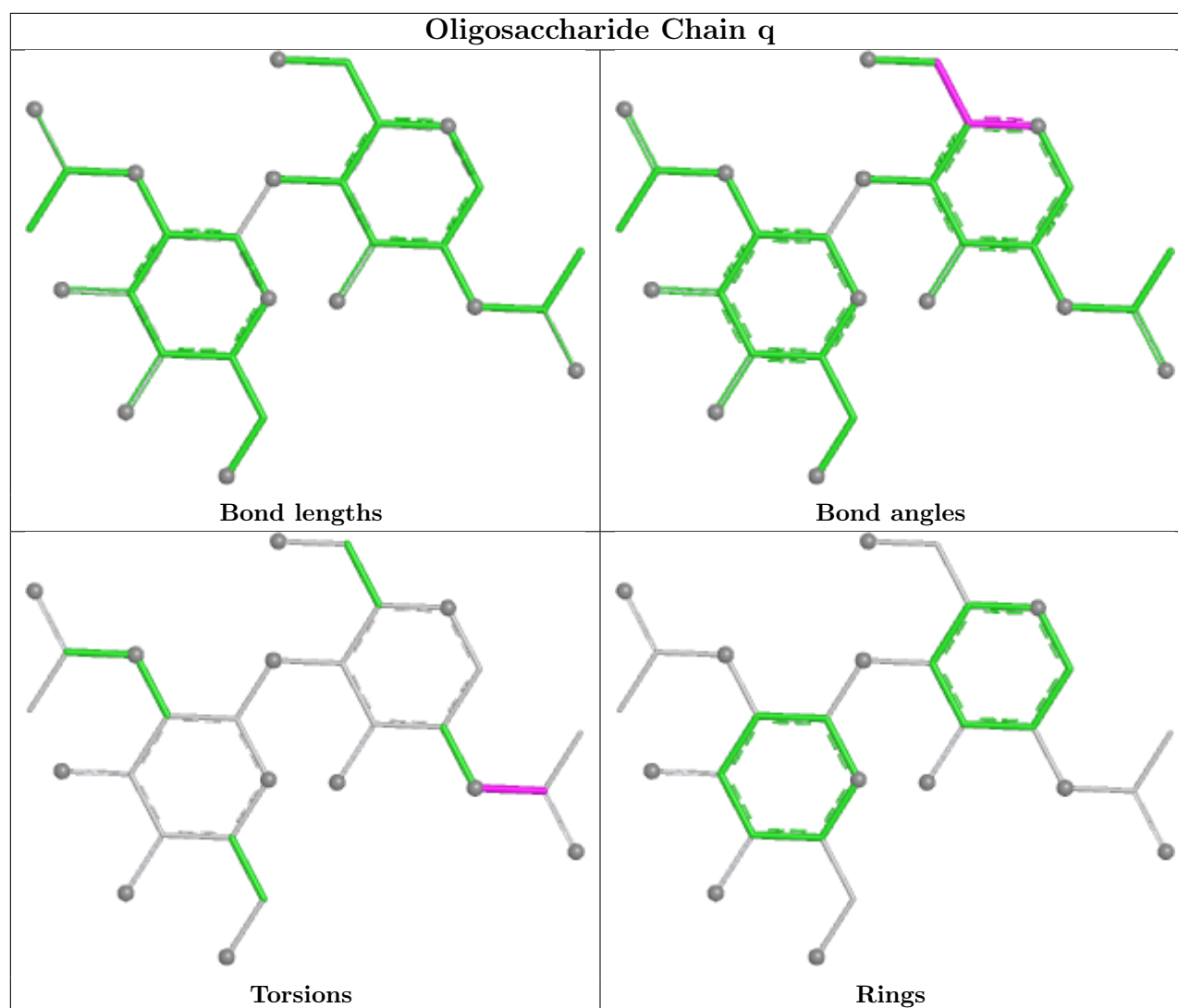


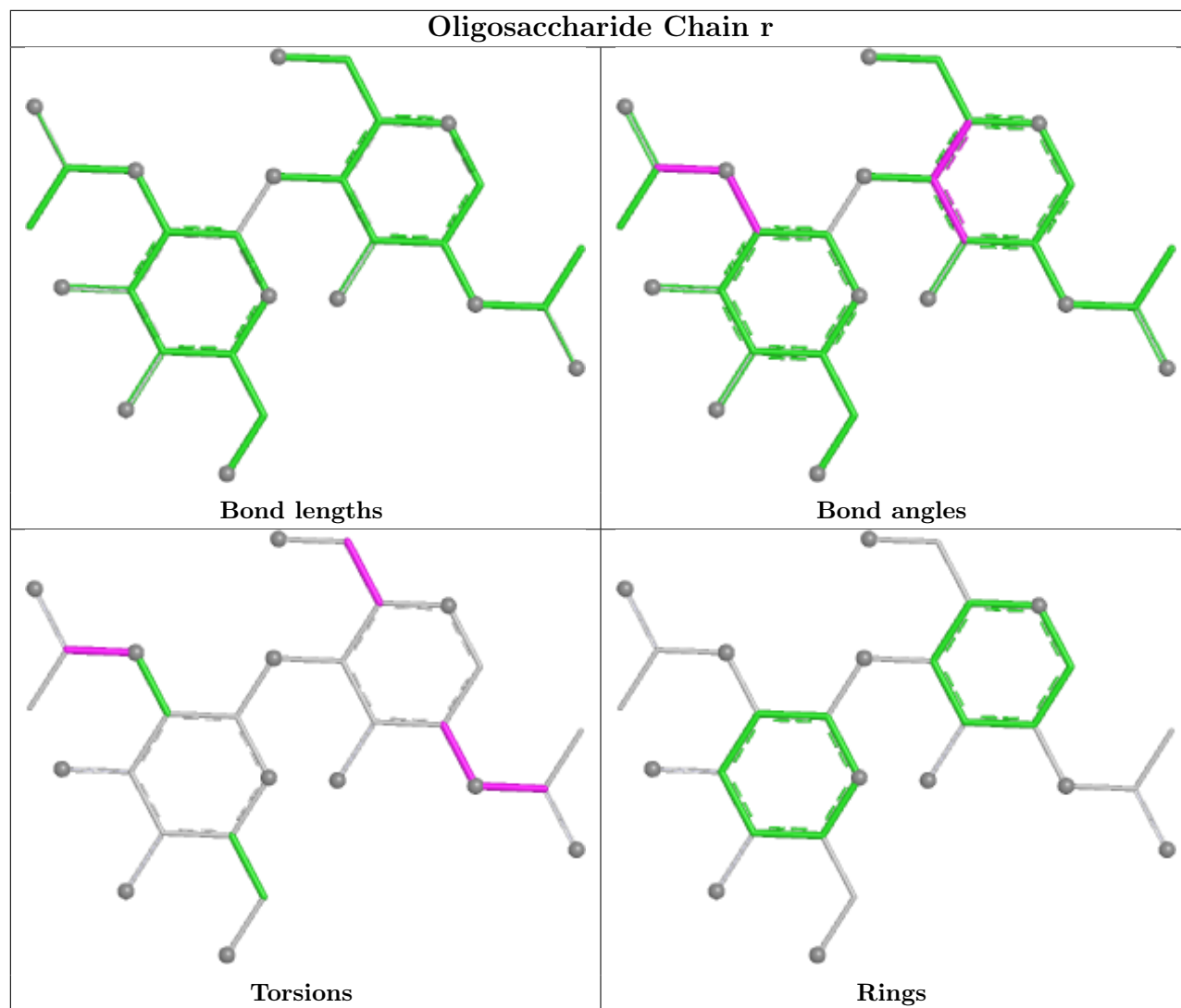


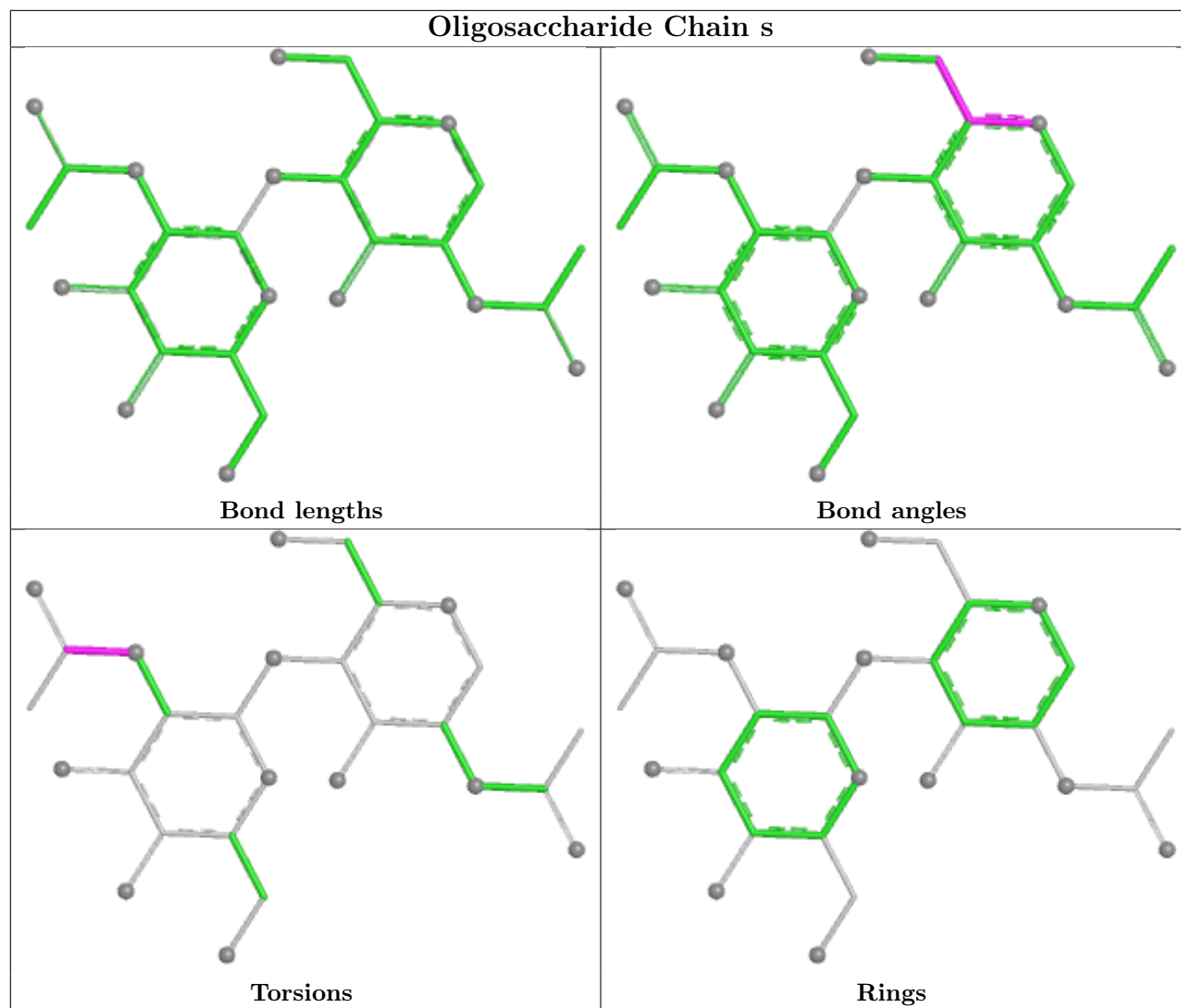


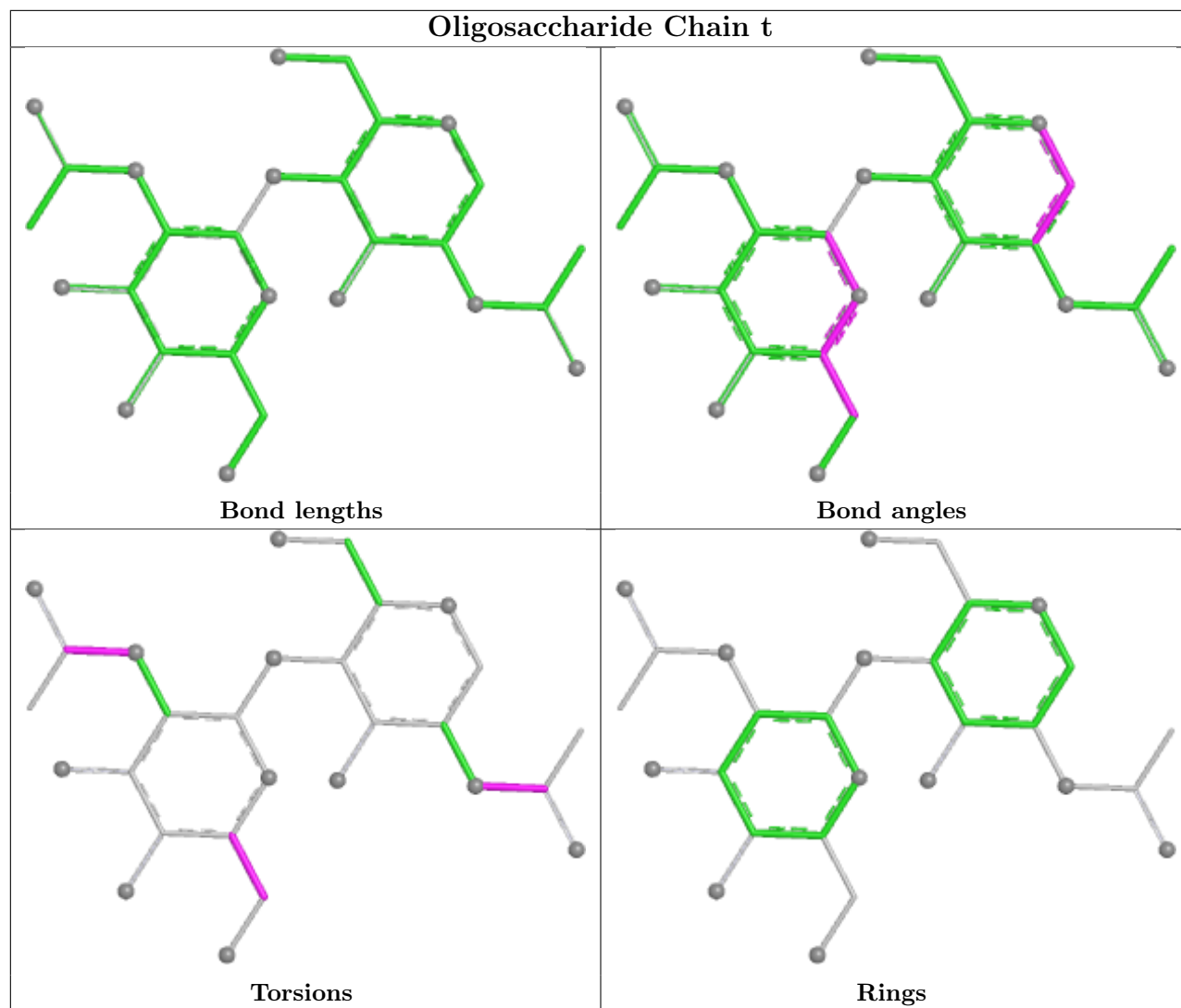


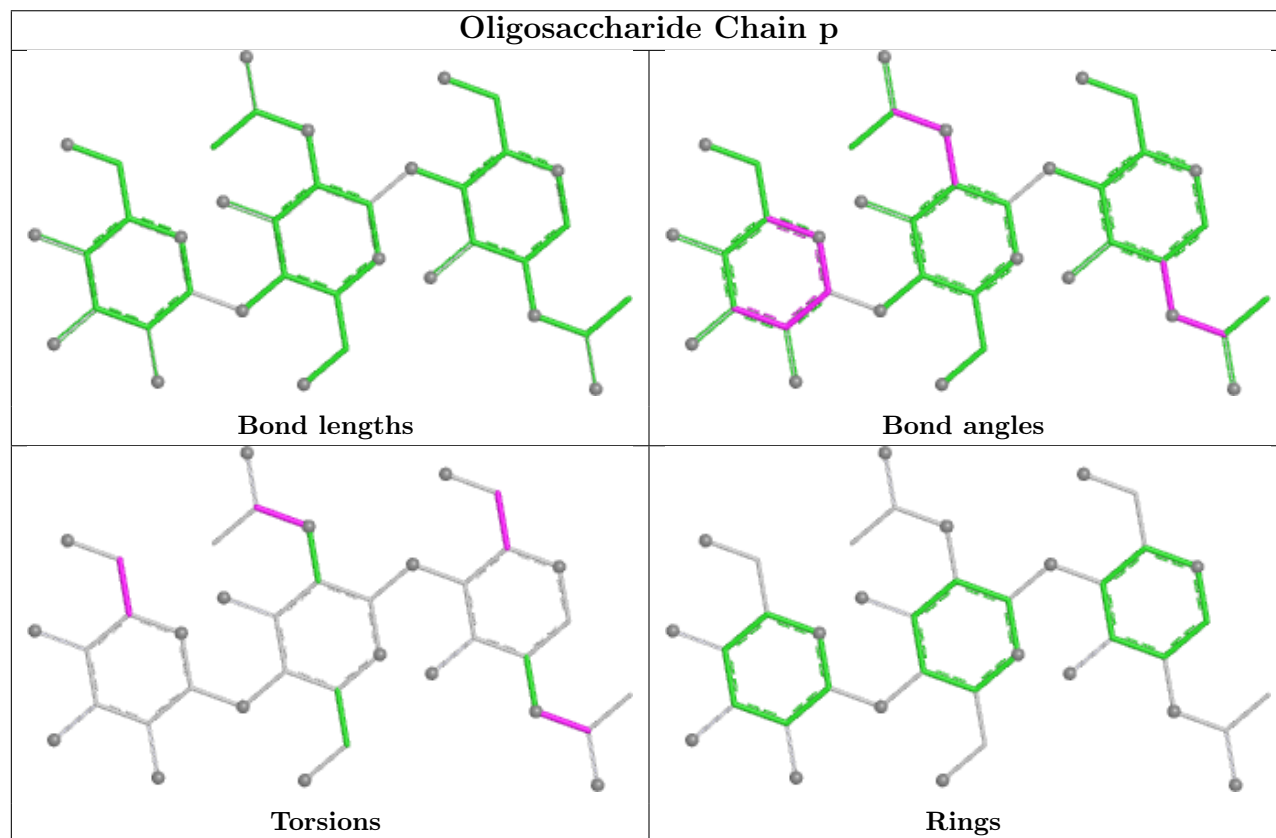
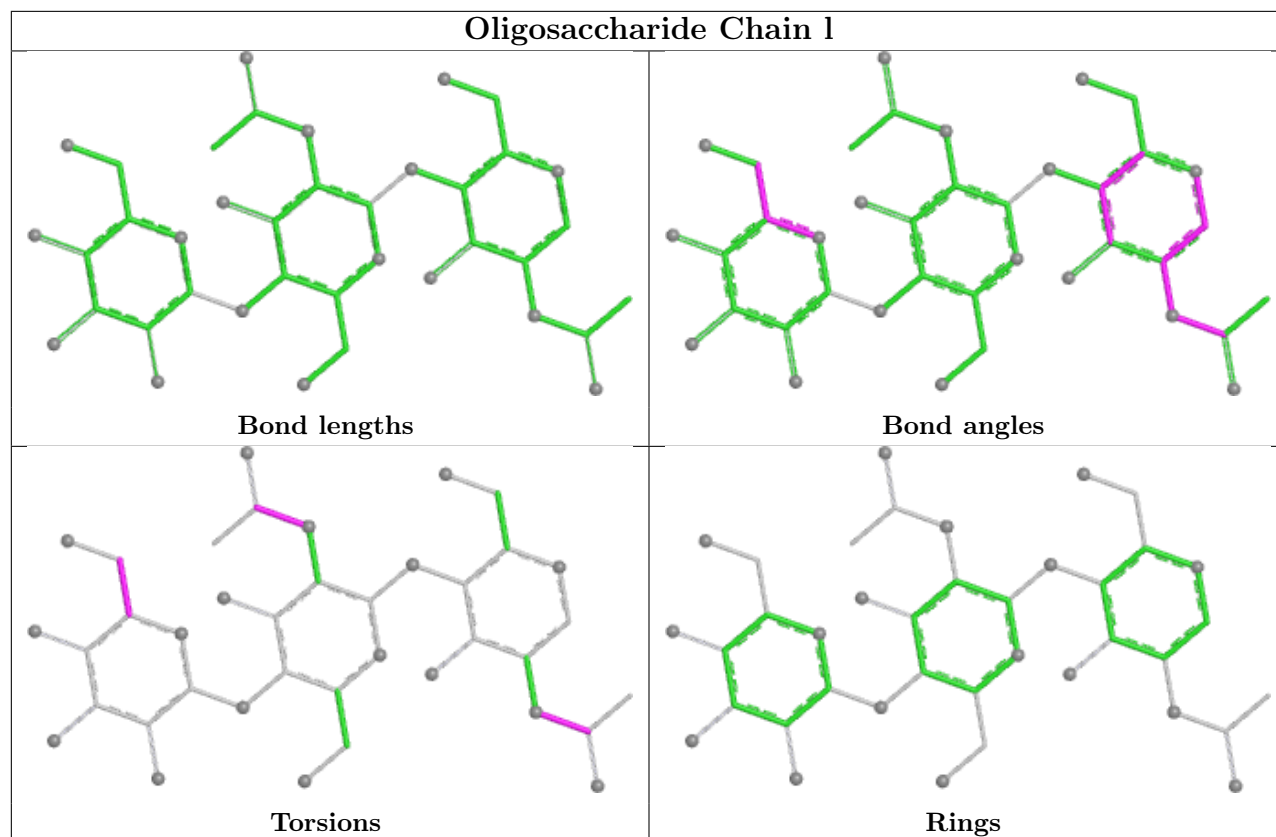












5.6 Ligand geometry

4 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$
7	NAG	A	403	1	14,14,15	0.49	0	17,19,21	1.31	1 (5%)
7	NAG	F	403	1	14,14,15	0.37	0	17,19,21	1.17	1 (5%)
7	NAG	E	401	1	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
7	NAG	C	404	1	14,14,15	1.78	2 (14%)	17,19,21	2.66	4 (23%)

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
7	NAG	A	403	1	-	2/6/23/26	0/1/1/1
7	NAG	F	403	1	-	2/6/23/26	0/1/1/1
7	NAG	E	401	1	-	2/6/23/26	0/1/1/1
7	NAG	C	404	1	-	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)
7	C	404	NAG	C1-C2	4.18	1.58	1.52
7	C	404	NAG	O5-C5	3.84	1.50	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	404	NAG	C1-O5-C5	9.78	125.29	112.19
7	A	403	NAG	C1-O5-C5	3.68	117.12	112.19
7	F	403	NAG	C1-O5-C5	3.35	116.67	112.19
7	E	401	NAG	C1-O5-C5	2.97	116.16	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	404	NAG	C1-C2-N2	-2.35	106.72	110.43
7	E	401	NAG	C2-N2-C7	-2.31	119.81	122.90
7	C	404	NAG	O5-C1-C2	2.27	114.81	111.29
7	C	404	NAG	C4-C3-C2	-2.26	107.71	111.02
7	E	401	NAG	O5-C1-C2	-2.07	108.09	111.29

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	403	NAG	O7-C7-N2-C2
7	A	403	NAG	C8-C7-N2-C2
7	C	404	NAG	O5-C5-C6-O6
7	C	404	NAG	C8-C7-N2-C2
7	F	403	NAG	C8-C7-N2-C2
7	C	404	NAG	O7-C7-N2-C2
7	E	401	NAG	C8-C7-N2-C2
7	F	403	NAG	O7-C7-N2-C2
7	E	401	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	323/327 (98%)	0.14	8 (2%) 58 39	20, 53, 91, 130	0
1	B	319/327 (97%)	0.50	14 (4%) 39 24	25, 60, 101, 142	0
1	C	324/327 (99%)	0.39	15 (4%) 37 23	21, 58, 98, 133	0
1	D	324/327 (99%)	0.31	7 (2%) 62 42	38, 66, 99, 168	0
1	E	323/327 (98%)	0.52	15 (4%) 37 23	45, 68, 97, 125	0
1	F	324/327 (99%)	0.61	15 (4%) 37 23	45, 76, 107, 138	0
1	G	324/327 (99%)	0.97	42 (12%) 7 6	46, 82, 124, 162	0
1	H	325/327 (99%)	0.06	3 (0%) 81 64	31, 53, 82, 122	0
1	I	324/327 (99%)	0.62	13 (4%) 42 26	42, 75, 107, 127	0
2	a	171/174 (98%)	0.56	11 (6%) 25 16	25, 75, 130, 168	0
2	b	167/174 (95%)	0.81	18 (10%) 11 7	24, 79, 138, 179	0
2	c	172/174 (98%)	0.82	22 (12%) 7 6	30, 79, 134, 176	0
2	d	172/174 (98%)	0.94	18 (10%) 11 8	43, 91, 149, 196	0
2	e	172/174 (98%)	0.59	14 (8%) 18 11	38, 69, 123, 176	0
2	f	172/174 (98%)	0.52	10 (5%) 29 18	46, 74, 125, 195	0
2	g	172/174 (98%)	0.85	21 (12%) 8 6	43, 81, 145, 169	0
2	h	167/174 (95%)	0.13	6 (3%) 46 28	35, 49, 85, 134	0
2	i	172/174 (98%)	0.40	11 (6%) 25 16	33, 55, 122, 187	0
3	J	115/223 (51%)	1.27	25 (21%) 2 2	46, 94, 132, 166	0
3	L	212/223 (95%)	-0.06	9 (4%) 40 25	20, 38, 99, 134	0
3	N	223/223 (100%)	-0.15	5 (2%) 62 42	14, 28, 73, 129	0
3	P	161/223 (72%)	0.82	13 (8%) 18 11	52, 90, 147, 172	0
3	R	214/223 (95%)	0.78	15 (7%) 22 14	45, 83, 114, 128	0
3	T	213/223 (95%)	1.19	35 (16%) 4 3	62, 107, 153, 233	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
3	V	117/223 (52%)	2.43	72 (61%) 0 0	66, 122, 174, 221	0
3	X	164/223 (73%)	0.68	22 (13%) 7 6	35, 67, 110, 147	0
3	Z	167/223 (74%)	0.91	19 (11%) 10 7	59, 95, 128, 180	0
4	K	106/214 (49%)	1.90	44 (41%) 0 1	63, 111, 145, 173	0
4	M	214/214 (100%)	0.37	22 (10%) 12 8	19, 42, 96, 150	0
4	O	214/214 (100%)	-0.30	0 100 100	16, 30, 52, 70	0
4	Q	157/214 (73%)	0.99	18 (11%) 9 7	49, 90, 134, 161	0
4	S	211/214 (98%)	0.85	13 (6%) 26 17	52, 77, 123, 185	0
4	U	211/214 (98%)	1.24	40 (18%) 3 2	66, 104, 140, 162	0
4	W	105/214 (49%)	1.53	34 (32%) 1 1	57, 88, 125, 148	0
4	Y	109/214 (50%)	0.04	0 100 100	36, 51, 76, 98	0
4	z	119/214 (55%)	1.26	16 (13%) 7 6	61, 98, 140, 161	0
All	All	7479/8442 (88%)	0.62	665 (8%) 15 10	14, 70, 129, 233	0

All (665) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	K	106	ILE	7.5
2	i	66	VAL	7.4
3	V	48	VAL	6.8
2	c	66	VAL	6.8
2	c	65	ALA	6.3
2	b	63	PHE	5.8
3	Z	122	PHE	5.6
1	G	326	ILE	5.6
3	T	184	VAL	5.6
1	C	9	PRO	5.5
3	V	11	VAL	5.3
2	e	65	ALA	5.3
1	B	205	GLY	5.2
2	b	61	THR	5.2
3	X	174	GLY	5.2
4	S	154	LEU	5.1
4	K	41	GLY	5.1
2	e	66	VAL	5.0
1	B	81(A)	VAL	5.0
2	b	65	ALA	5.0
3	T	180	SER	5.0

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Mol	Chain	Res	Type	RSRZ
4	z	83	ILE	4.9
4	K	45	ASN	4.9
2	d	65	ALA	4.9
3	T	136	ALA	4.8
2	g	62	GLN	4.8
4	U	134	CYS	4.7
4	Q	134	CYS	4.7
4	Q	80	PRO	4.7
2	e	61	THR	4.7
3	T	183	THR	4.7
4	U	180	THR	4.6
4	M	125	LEU	4.6
3	X	199	ASN	4.5
4	W	80	PRO	4.5
2	f	65	ALA	4.5
2	i	65	ALA	4.5
4	U	179	LEU	4.5
2	e	63	PHE	4.4
1	C	10	GLY	4.4
3	V	20	VAL	4.4
2	f	59	MET	4.4
1	G	135	GLY	4.4
2	i	63	PHE	4.3
2	g	63	PHE	4.3
4	U	45	ASN	4.3
2	d	63	PHE	4.3
2	g	168	LEU	4.3
3	J	34	PHE	4.2
3	V	101	ASP	4.2
3	V	41	PRO	4.2
2	e	62	GLN	4.2
1	I	9	PRO	4.2
3	V	8	GLY	4.2
2	d	66	VAL	4.2
4	Q	113	PRO	4.2
3	Z	121	VAL	4.1
3	R	127	SER	4.1
3	N	131	THR	4.1
4	K	47	LEU	4.1
4	U	178	THR	4.1
3	V	40	ALA	4.1
3	V	7	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	D	326	ILE	4.0
3	N	193	THR	4.0
2	a	65	ALA	4.0
4	K	11	LEU	4.0
1	C	326	ILE	4.0
1	G	82	PRO	4.0
4	K	95	PRO	3.9
4	W	95	PRO	3.9
2	c	134	GLY	3.9
4	Q	196	VAL	3.9
3	Z	150	VAL	3.9
4	W	87	TYR	3.9
1	G	9	PRO	3.9
3	T	185	PRO	3.9
3	V	47	TRP	3.9
3	L	127	SER	3.9
2	c	61	THR	3.8
3	V	42	GLY	3.8
2	c	63	PHE	3.8
3	V	14	PRO	3.8
3	V	108	LEU	3.8
3	J	11	VAL	3.8
3	V	81	GLU	3.8
3	X	142	VAL	3.7
3	V	109	VAL	3.7
3	V	36	TRP	3.7
4	S	208	SER	3.7
1	F	25	LYS	3.7
4	U	63	ARG	3.7
3	T	127	SER	3.7
3	V	63	PHE	3.7
4	K	8	PRO	3.6
2	h	66	VAL	3.6
3	V	57	SER	3.6
3	Z	25	SER	3.6
3	X	204	ASN	3.6
4	Q	135	LEU	3.6
3	X	179	SER	3.6
4	W	97	THR	3.6
1	I	57	PRO	3.5
3	V	82(A)	THR	3.5
3	R	181	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
2	g	159	TYR	3.5
3	J	104	GLY	3.5
3	V	18	VAL	3.5
2	d	1	GLY	3.5
2	g	66	VAL	3.5
3	J	101	ASP	3.5
2	b	160	PRO	3.5
3	V	58	ASN	3.5
4	K	54	VAL	3.5
2	b	27	SER	3.5
4	S	135	LEU	3.4
3	J	90	TYR	3.4
3	V	100	TYR	3.4
4	U	158	ASN	3.4
2	f	66	VAL	3.4
3	J	65	GLY	3.4
3	X	197	ASN	3.4
1	G	323	VAL	3.4
3	J	2	VAL	3.4
3	V	45	LEU	3.4
3	V	39	GLN	3.4
4	K	22	THR	3.4
4	M	119	PRO	3.4
4	U	95	PRO	3.4
3	Z	199	ASN	3.3
4	Q	65	SER	3.3
3	J	95	GLY	3.3
1	C	277	CYS	3.3
2	b	158	ASP	3.3
3	V	53	ILE	3.3
2	g	127	ARG	3.3
1	A	142	SER	3.3
2	c	35	ALA	3.3
3	V	69	ILE	3.3
2	e	29	ASP	3.3
3	T	160	THR	3.3
4	K	72	THR	3.3
1	E	325	GLN	3.2
3	V	51	PHE	3.2
3	V	37	VAL	3.2
3	R	125	ALA	3.2
1	B	173	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
4	U	135	LEU	3.2
1	G	11	ASP	3.2
3	V	80	MET	3.2
4	K	36	TYR	3.2
1	A	159	SER	3.2
4	Q	177	SER	3.2
4	U	159	SER	3.2
3	J	105	GLN	3.2
1	C	323	VAL	3.2
3	V	61	GLN	3.2
4	S	67	SER	3.2
3	N	133	GLY	3.1
2	i	164	GLU	3.1
4	U	161	GLU	3.1
3	J	64	GLN	3.1
2	i	67	GLY	3.1
3	X	178	LEU	3.1
4	Q	110	VAL	3.1
2	b	159	TYR	3.1
3	T	145	TYR	3.1
4	S	153	ALA	3.1
3	L	115	SER	3.1
3	P	179	SER	3.1
1	G	144	ASN	3.1
1	B	174	GLU	3.1
1	A	9	PRO	3.1
4	K	42	LYS	3.1
3	R	59	TYR	3.1
4	U	75	ILE	3.1
2	i	61	THR	3.1
4	W	90	GLN	3.0
2	b	23	GLY	3.0
3	V	17	SER	3.0
4	U	80	PRO	3.0
2	b	168	LEU	3.0
4	K	78	LEU	3.0
2	d	67	GLY	3.0
3	J	87	THR	3.0
2	f	63	PHE	3.0
1	D	9	PRO	3.0
2	b	144	CYS	3.0
3	V	5	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	304	GLU	3.0
4	W	44	PRO	3.0
4	U	181	LEU	3.0
1	G	137	ARG	3.0
3	V	10	GLU	3.0
4	K	32	TYR	3.0
3	T	101	ASP	3.0
3	V	43	GLN	3.0
2	g	59	MET	3.0
3	T	189	LEU	2.9
1	F	60	GLU	2.9
3	V	12	LYS	2.9
1	G	270	THR	2.9
1	A	324	PRO	2.9
2	c	64	GLU	2.9
4	K	80	PRO	2.9
3	J	33	VAL	2.9
3	V	104	GLY	2.9
2	i	59	MET	2.9
4	W	46	LEU	2.9
1	E	133	THR	2.9
1	F	281	CYS	2.9
3	Z	197	ASN	2.9
4	U	20	THR	2.9
3	T	148	GLU	2.9
4	W	40	PRO	2.9
4	z	19	VAL	2.9
4	W	8	PRO	2.9
1	G	55	GLY	2.9
3	X	144	ASP	2.9
2	d	160	PRO	2.9
3	V	110	THR	2.9
4	K	44	PRO	2.9
4	M	95	PRO	2.9
4	Q	109	THR	2.9
4	K	38	GLN	2.8
3	X	205	THR	2.8
4	M	197	THR	2.8
3	X	150	VAL	2.8
1	G	10	GLY	2.8
3	Z	59	TYR	2.8
4	U	11	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
3	T	120	SER	2.8
4	Q	199	GLN	2.8
2	d	56	ILE	2.8
2	d	168	LEU	2.8
3	V	54	PHE	2.8
3	X	118	GLY	2.8
3	P	112	SER	2.8
1	I	116(C)	GLU	2.8
2	e	64	GLU	2.8
2	f	64	GLU	2.8
4	M	154	LEU	2.8
1	E	138	ALA	2.8
2	c	62	GLN	2.8
3	X	40	ALA	2.8
1	G	81(A)	VAL	2.8
3	R	183	THR	2.8
4	K	82	ASP	2.8
4	W	2	ILE	2.8
4	z	62	PHE	2.8
3	V	49	GLY	2.8
4	U	157	GLY	2.8
1	I	244	ASN	2.8
3	T	176	TYR	2.8
4	Q	204	PRO	2.8
3	V	82(C)	LEU	2.8
2	a	63	PHE	2.7
2	a	171	ASN	2.7
1	G	256	TYR	2.7
2	g	65	ALA	2.7
3	V	89	VAL	2.7
2	c	133	LEU	2.7
3	V	4	LEU	2.7
1	F	148	PHE	2.7
3	V	30	ILE	2.7
4	U	60	SER	2.7
2	f	61	THR	2.7
4	M	129	THR	2.7
4	U	197	THR	2.7
2	h	146	ASP	2.7
2	c	60	ASN	2.7
3	V	88	ALA	2.7
1	A	323	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
3	V	100(C)	PHE	2.7
4	M	195	GLU	2.7
1	C	219	THR	2.7
2	e	166	SER	2.7
1	G	240	TRP	2.7
3	V	19	LYS	2.7
3	V	62	LYS	2.7
4	W	1	ASP	2.7
3	V	111	VAL	2.7
4	K	59	PRO	2.7
1	G	147	PHE	2.7
1	I	326	ILE	2.7
4	K	98	PHE	2.7
3	V	15	GLY	2.7
3	X	201	LYS	2.7
2	b	66	VAL	2.7
3	V	2	VAL	2.7
1	B	324	PRO	2.7
3	V	64	GLN	2.7
2	d	59	MET	2.7
4	Q	63	ARG	2.7
4	W	7	SER	2.7
3	Z	202	PRO	2.6
1	G	149	ARG	2.6
1	G	174	GLU	2.6
3	V	82	LEU	2.6
4	M	121	SER	2.6
4	S	177	SER	2.6
1	C	324	PRO	2.6
2	c	9	PHE	2.6
1	B	83	GLU	2.6
2	i	172	GLU	2.6
3	V	46	GLU	2.6
3	V	75	THR	2.6
4	U	85	THR	2.6
4	z	47	LEU	2.6
3	X	120	SER	2.6
3	Z	21	SER	2.6
4	M	127	SER	2.6
3	Z	195	ILE	2.6
3	P	119	PRO	2.6
3	T	213	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
4	U	116	PHE	2.6
1	E	240	TRP	2.6
3	J	103	TRP	2.6
4	S	63	ARG	2.6
3	V	59	TYR	2.6
4	W	67	SER	2.6
2	c	17	MET	2.6
3	T	149	PRO	2.6
4	W	38	GLN	2.6
4	K	94	LEU	2.6
4	W	11	LEU	2.6
1	I	23	THR	2.6
4	K	43	ALA	2.6
4	U	51	ALA	2.6
4	W	13	ALA	2.6
1	E	228	SER	2.6
3	R	126	PRO	2.6
2	g	128	ASP	2.6
1	C	60	GLU	2.6
4	W	105	GLU	2.6
4	K	51	ALA	2.6
1	G	171	THR	2.6
4	K	62	PHE	2.5
4	W	36	TYR	2.5
3	L	213	PRO	2.5
1	G	146	SER	2.5
4	S	156	SER	2.5
4	M	3	GLN	2.5
1	G	223	VAL	2.5
3	T	150	VAL	2.5
3	V	86	ASP	2.5
2	h	172	GLU	2.5
1	G	219	THR	2.5
3	T	116	THR	2.5
3	T	135	THR	2.5
3	T	119	PRO	2.5
1	G	139	CYS	2.5
3	T	181	VAL	2.5
1	C	322	ASN	2.5
1	B	13	ILE	2.5
3	V	68	THR	2.5
1	D	211	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
3	Z	196	CYS	2.5
3	P	180	SER	2.5
3	L	136	ALA	2.5
2	e	60	ASN	2.5
4	Q	137	ASN	2.5
1	I	128	THR	2.5
1	E	324	PRO	2.5
4	W	94	LEU	2.5
2	a	33	GLY	2.5
2	e	1	GLY	2.5
1	D	315	VAL	2.5
3	X	207	VAL	2.5
3	Z	105	GLN	2.5
4	K	7	SER	2.5
3	L	193	THR	2.5
3	R	165	THR	2.5
4	W	18	ARG	2.5
1	G	221	PRO	2.5
4	M	192	TYR	2.5
1	A	213	SER	2.4
3	R	172	SER	2.4
1	G	229	ARG	2.4
3	V	38	ARG	2.4
3	J	107	THR	2.4
3	R	176	TYR	2.4
3	V	65	GLY	2.4
1	F	146	SER	2.4
1	G	277	CYS	2.4
3	V	74	SER	2.4
4	U	103	ARG	2.4
1	G	194	LEU	2.4
2	i	60	ASN	2.4
3	V	90	TYR	2.4
4	M	157	GLY	2.4
4	Q	132	VAL	2.4
4	Q	133	VAL	2.4
4	z	36	TYR	2.4
1	F	288	ILE	2.4
3	J	40	ALA	2.4
4	W	3	GLN	2.4
1	F	222	LYS	2.4
2	h	106	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
3	R	212	GLU	2.4
3	Z	148	GLU	2.4
3	P	113	SER	2.4
3	J	36	TRP	2.4
3	P	154	TRP	2.4
1	F	82	PRO	2.4
4	K	93	ASN	2.4
2	e	19	ASP	2.4
4	Q	17	ASP	2.4
2	d	159	TYR	2.4
1	C	218	ALA	2.4
1	E	140	ALA	2.4
2	f	58	LYS	2.4
2	c	132	GLU	2.4
3	T	115	SER	2.4
4	z	80	PRO	2.4
3	Z	144	ASP	2.4
3	V	60	ALA	2.4
4	U	83	ILE	2.4
4	W	89	GLN	2.4
3	T	82	LEU	2.4
1	B	172	SER	2.4
3	L	186	SER	2.4
4	K	76	SER	2.4
3	V	22	CYS	2.4
3	Z	205	THR	2.3
4	K	74	THR	2.3
4	U	69	THR	2.3
4	W	69	THR	2.3
4	z	69	THR	2.3
3	V	23	LYS	2.3
4	K	21	ILE	2.3
4	W	45	ASN	2.3
3	P	176	TYR	2.3
4	W	96	ILE	2.3
4	z	103	ARG	2.3
3	J	85	GLU	2.3
4	M	123	GLU	2.3
1	E	315	VAL	2.3
3	N	132	SER	2.3
4	U	77	SER	2.3
2	a	61	THR	2.3

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Mol	Chain	Res	Type	RSRZ
2	g	61	THR	2.3
2	h	1	GLY	2.3
3	T	82(A)	THR	2.3
4	K	48	ILE	2.3
4	K	75	ILE	2.3
4	z	93	ASN	2.3
2	c	164	GLU	2.3
2	b	131	LYS	2.3
2	f	38	LYS	2.3
4	M	204	PRO	2.3
1	I	173	GLY	2.3
3	V	100(A)	GLY	2.3
3	V	9	ALA	2.3
4	U	56	THR	2.3
4	z	22	THR	2.3
1	D	277	CYS	2.3
1	G	276	ASN	2.3
3	X	170	LEU	2.3
4	M	122	ASP	2.3
4	S	80	PRO	2.3
2	b	134	GLY	2.3
1	B	239	MET	2.3
3	V	83	THR	2.3
3	X	141	LEU	2.3
3	T	59	TYR	2.3
1	F	64	CYS	2.3
2	c	140	PHE	2.3
3	P	146	PHE	2.3
1	I	276	ASN	2.3
3	R	2	VAL	2.3
4	M	205	VAL	2.3
1	F	9	PRO	2.3
1	F	326	ILE	2.3
2	d	23	GLY	2.3
3	P	118	GLY	2.3
3	V	95	GLY	2.3
2	c	21	TRP	2.3
4	U	175	LEU	2.3
1	I	113	SER	2.3
2	b	166	SER	2.3
3	J	79	TYR	2.3
3	P	145	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
3	T	194	TYR	2.3
1	G	21	ASN	2.3
1	G	313	LYS	2.3
2	d	58	LYS	2.3
4	K	61	ARG	2.3
3	J	67	VAL	2.3
4	U	15	VAL	2.3
4	U	205	VAL	2.3
1	E	205	GLY	2.2
2	a	35	ALA	2.2
2	a	47	GLY	2.2
3	Z	168	ALA	2.2
4	M	153	ALA	2.2
4	U	112	ALA	2.2
4	W	43	ALA	2.2
3	T	108	LEU	2.2
3	T	159	LEU	2.2
2	g	156	THR	2.2
2	g	32	SER	2.2
4	U	127	SER	2.2
4	W	9	SER	2.2
2	g	144	CYS	2.2
2	g	158	ASP	2.2
1	C	55	GLY	2.2
1	D	324	PRO	2.2
1	G	218	ALA	2.2
2	c	31	GLY	2.2
3	V	27	GLY	2.2
4	W	101	GLY	2.2
2	c	27	SER	2.2
2	e	27	SER	2.2
3	N	127	SER	2.2
4	K	77	SER	2.2
3	Z	3	GLN	2.2
1	G	289	ASN	2.2
2	c	50	ASN	2.2
1	G	64	CYS	2.2
2	d	64	GLU	2.2
2	b	4	GLY	2.2
2	b	31	GLY	2.2
2	f	89	LEU	2.2
3	J	41	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
4	K	104	LEU	2.2
4	z	95	PRO	2.2
1	B	137	ARG	2.2
3	T	2	VAL	2.2
2	i	40	SER	2.2
4	z	156	SER	2.2
1	H	289	ASN	2.2
2	a	154	ASN	2.2
2	d	57	GLU	2.2
2	g	150	ASN	2.2
2	i	105	GLU	2.2
3	T	124	LEU	2.2
4	Q	95	PRO	2.2
3	J	31	THR	2.2
4	K	69	THR	2.2
2	c	40	SER	2.2
2	g	166	SER	2.2
3	X	61	GLN	2.2
4	W	12	SER	2.2
1	G	88	MET	2.2
3	L	125	ALA	2.2
4	K	13	ALA	2.2
1	B	257	GLY	2.2
1	G	72	GLY	2.2
1	G	100	GLY	2.2
3	R	174	GLY	2.2
3	X	202	PRO	2.2
4	K	16	GLY	2.2
1	C	64	CYS	2.2
4	M	209	PHE	2.2
1	I	84	TRP	2.2
1	D	323	VAL	2.1
3	R	18	VAL	2.1
3	V	33	VAL	2.1
4	U	19	VAL	2.1
3	T	170	LEU	2.1
2	b	59	MET	2.1
4	M	207	LYS	2.1
4	W	84	ALA	2.1
1	E	212	ARG	2.1
3	R	26	GLY	2.1
4	M	212	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	a	169	ASN	2.1
1	C	315	VAL	2.1
1	G	133	THR	2.1
3	T	191	THR	2.1
4	U	109	THR	2.1
1	H	326	ILE	2.1
4	z	75	ILE	2.1
2	d	126	LEU	2.1
2	d	149	MET	2.1
2	e	15	GLN	2.1
3	V	52(A)	ALA	2.1
1	F	16	GLY	2.1
2	a	27	SER	2.1
4	z	10	SER	2.1
3	P	142	VAL	2.1
3	T	36	TRP	2.1
3	T	182	VAL	2.1
1	G	226	LEU	2.1
3	J	28	THR	2.1
3	R	170	LEU	2.1
3	T	193	THR	2.1
4	K	2	ILE	2.1
4	S	117	ILE	2.1
4	S	180	THR	2.1
4	U	154	LEU	2.1
2	c	59	MET	2.1
2	d	127	ARG	2.1
2	e	106	ARG	2.1
1	A	12	GLN	2.1
4	U	193	ALA	2.1
1	E	225	GLY	2.1
1	C	22	SER	2.1
3	J	100(C)	PHE	2.1
4	K	14	SER	2.1
4	K	73	PHE	2.1
4	W	26	SER	2.1
3	X	198	VAL	2.1
1	G	119	LYS	2.1
1	I	51	LEU	2.1
2	b	128	ASP	2.1
3	P	101	ASP	2.1
4	S	92	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
4	z	20	THR	2.1
3	L	137	ALA	2.1
2	a	62	GLN	2.1
1	E	62	GLY	2.1
1	E	135	GLY	2.1
1	H	303	GLY	2.1
2	g	16	GLY	2.1
4	K	99	GLY	2.1
4	z	57	GLY	2.1
1	F	306	PRO	2.1
4	S	195	GLU	2.1
1	E	265	SER	2.1
4	M	60	SER	2.1
2	g	130	VAL	2.1
1	C	276	ASN	2.1
1	F	217	ILE	2.1
2	h	168	LEU	2.1
3	J	30	ILE	2.1
4	U	148	TRP	2.1
1	G	187	ASP	2.1
2	f	35	ALA	2.1
3	J	61	GLN	2.1
2	d	139	GLU	2.1
1	I	262	LYS	2.0
1	G	85	SER	2.0
1	B	276	ASN	2.0
3	Z	141	LEU	2.0
4	W	83	ILE	2.0
3	V	72	ASP	2.0
4	M	186	TYR	2.0
4	W	17	ASP	2.0
4	W	91	TYR	2.0
2	c	45	PHE	2.0
2	g	67	GLY	2.0
3	T	122	PHE	2.0
3	V	44	GLY	2.0
4	Q	200	GLY	2.0
3	X	149	PRO	2.0
1	A	222	LYS	2.0
1	G	312	GLU	2.0
1	F	51	LEU	2.0
4	K	4	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
4	K	30	ARG	2.0
4	U	78	LEU	2.0
3	P	164	HIS	2.0
2	g	162	TYR	2.0
4	U	186	TYR	2.0
3	Z	101	ASP	2.0
4	K	17	ASP	2.0
3	X	166	PHE	2.0
3	L	185	PRO	2.0
1	G	116(C)	GLU	2.0
2	g	164	GLU	2.0
1	E	78	ARG	2.0
1	B	15	ILE	2.0
4	U	117	ILE	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.

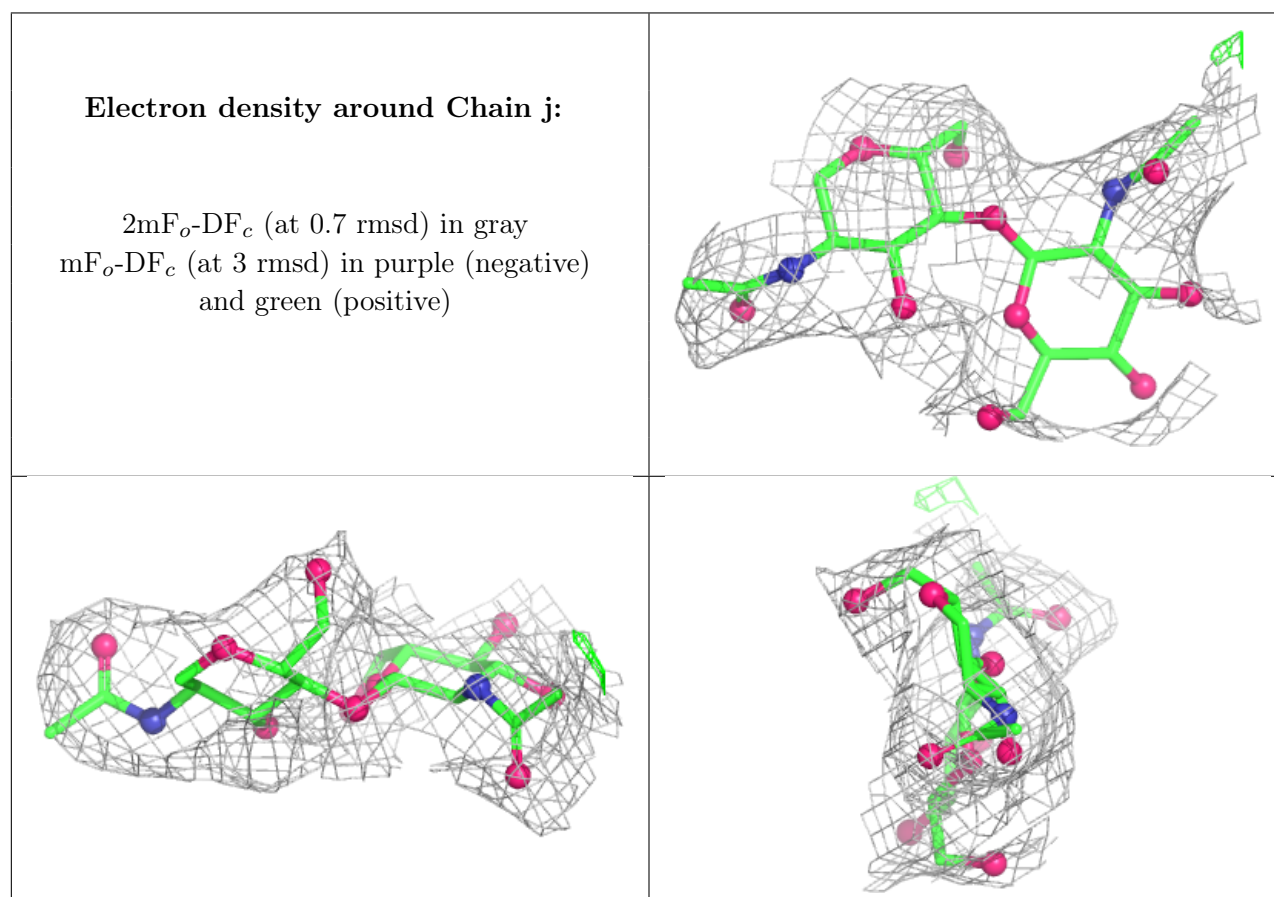
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	j	1	14/15	-	-	72,88,97,98	0
5	NAG	j	2	14/15	-	-	90,107,119,121	0
5	NAG	k	1	14/15	-	-	63,92,107,114	0
5	NAG	k	2	14/15	-	-	125,133,136,140	0
5	NAG	m	1	14/15	-	-	61,84,89,97	0
5	NAG	m	2	14/15	-	-	85,111,119,120	0
5	NAG	n	1	14/15	-	-	60,86,97,102	0
5	NAG	n	2	14/15	-	-	101,113,121,122	0
5	NAG	o	1	14/15	-	-	60,82,88,96	0
5	NAG	o	2	14/15	-	-	97,113,122,124	0
5	NAG	q	1	14/15	-	-	50,75,92,93	0
5	NAG	q	2	14/15	-	-	98,107,122,125	0
5	NAG	r	1	14/15	-	-	61,80,90,101	0
5	NAG	r	2	14/15	-	-	94,108,128,135	0

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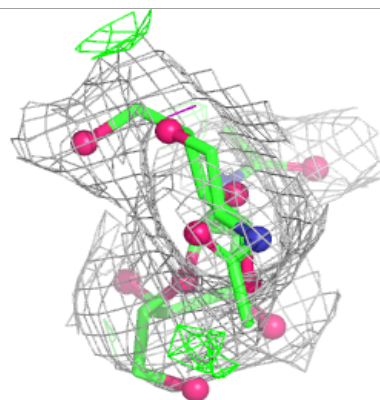
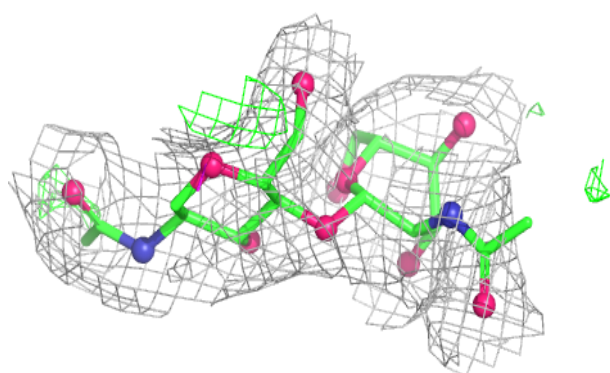
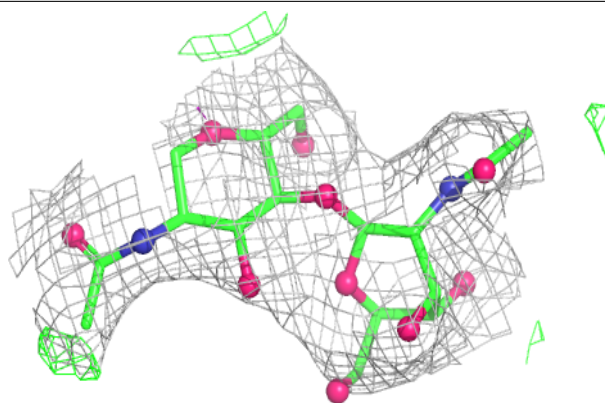
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	s	1	14/15	-	-	88,112,125,131	0
5	NAG	s	2	14/15	-	-	148,157,164,167	0
5	NAG	t	1	14/15	-	-	68,81,87,88	0
5	NAG	t	2	14/15	-	-	82,103,118,122	0
6	NAG	l	1	14/15	-	-	56,81,94,108	0
6	NAG	l	2	14/15	-	-	88,117,138,139	0
6	BMA	l	3	11/12	-	-	109,140,145,148	0
6	NAG	p	1	14/15	-	-	84,97,101,102	0
6	NAG	p	2	14/15	-	-	93,112,127,132	0
6	BMA	p	3	11/12	-	-	117,121,132,137	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.



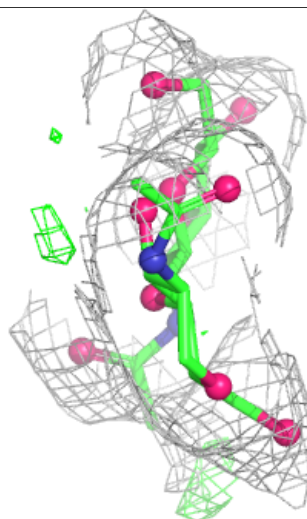
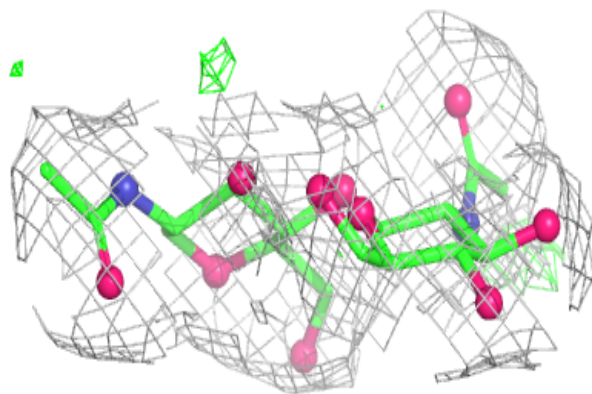
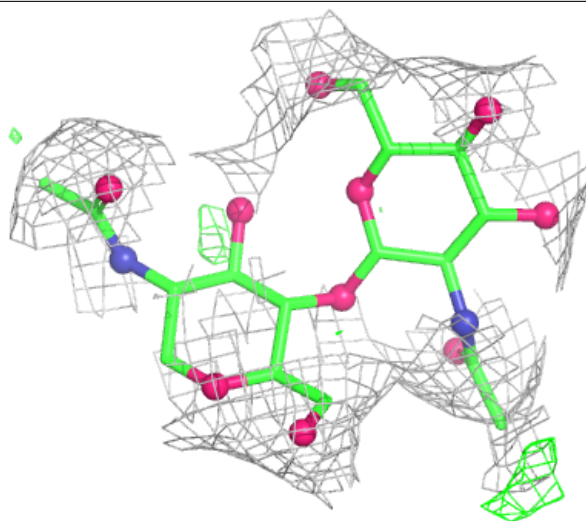
Electron density around Chain k:

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



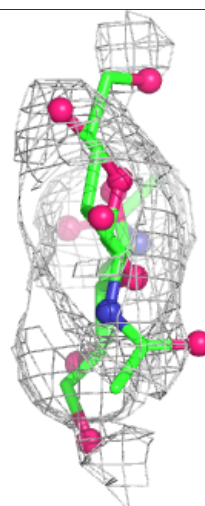
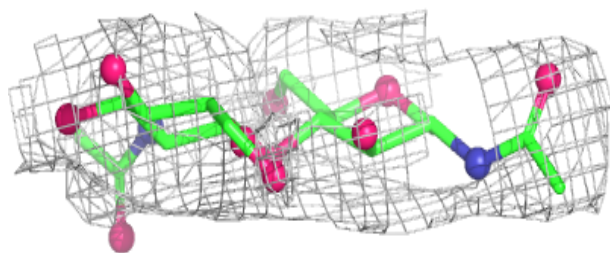
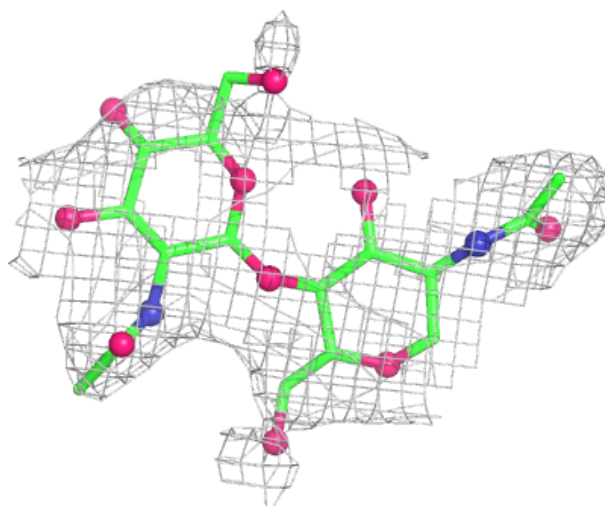
Electron density around Chain m:

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



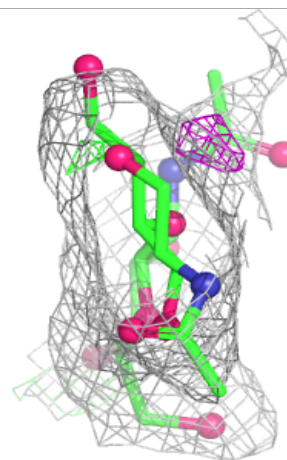
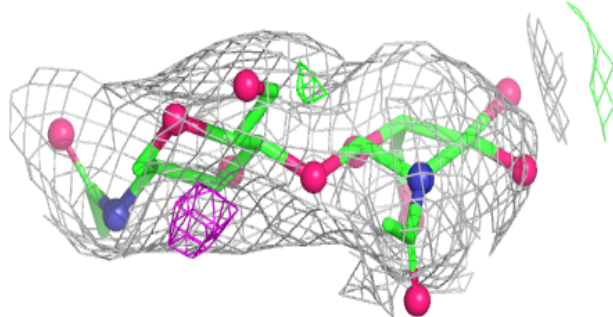
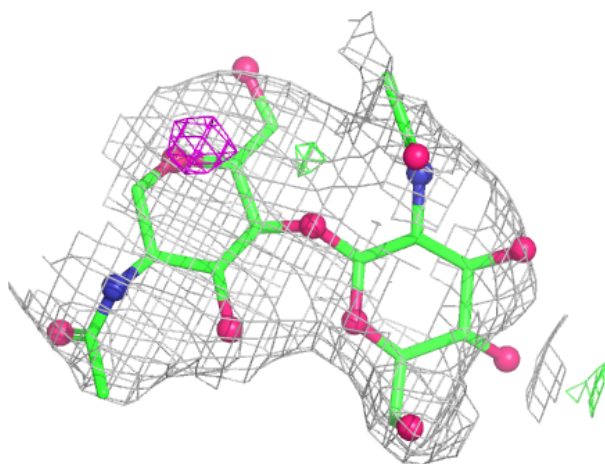
Electron density around Chain n:

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



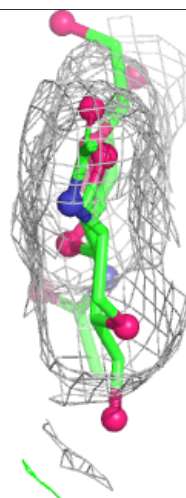
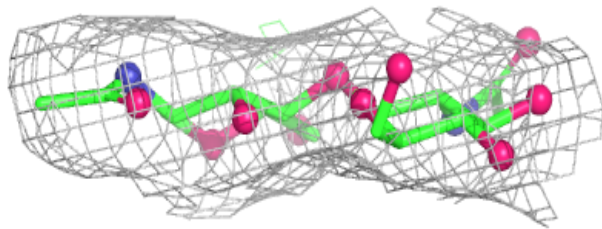
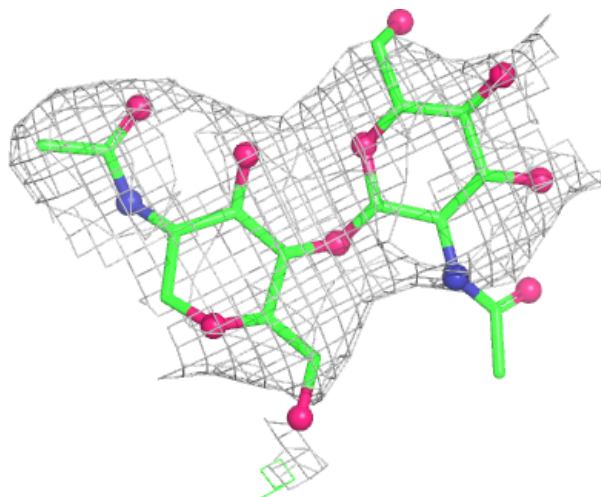
Electron density around Chain o:

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



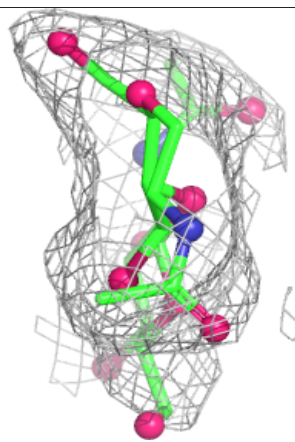
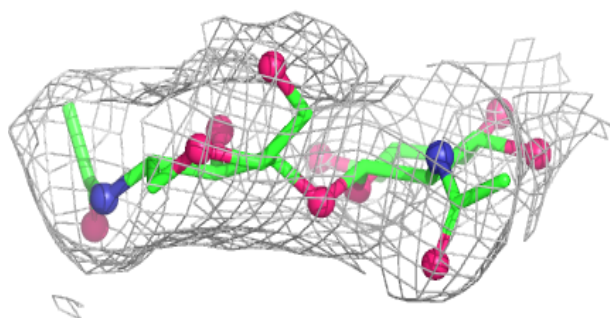
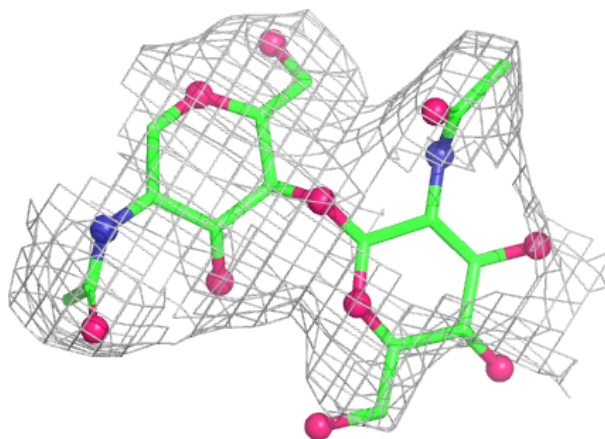
Electron density around Chain q:

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



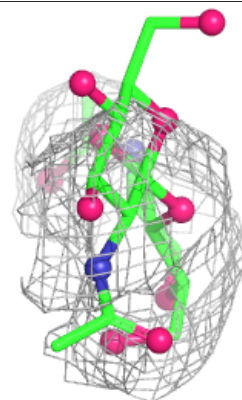
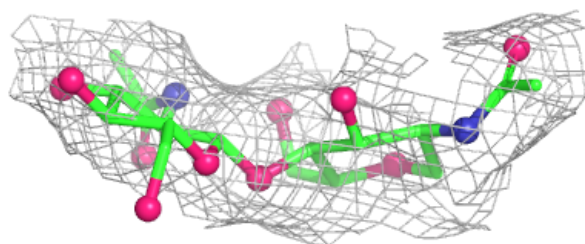
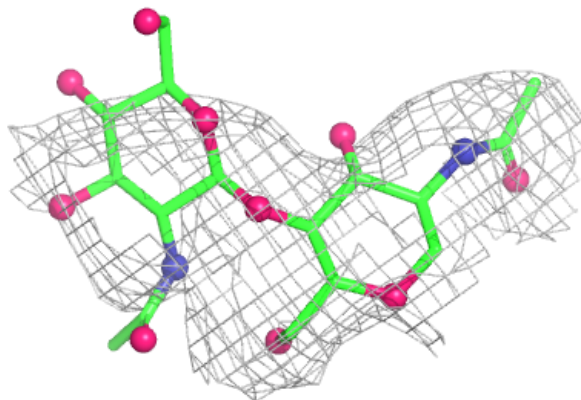
Electron density around Chain r:

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



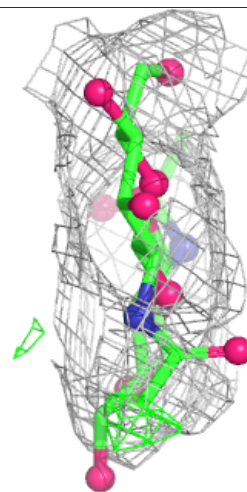
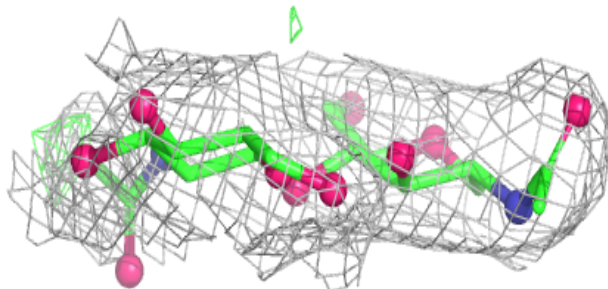
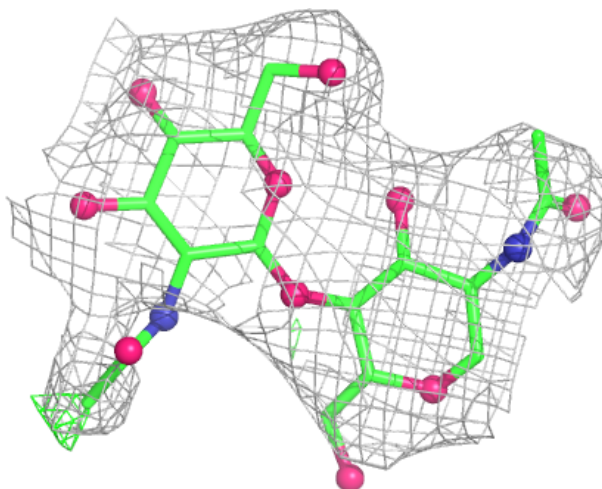
Electron density around Chain s:

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



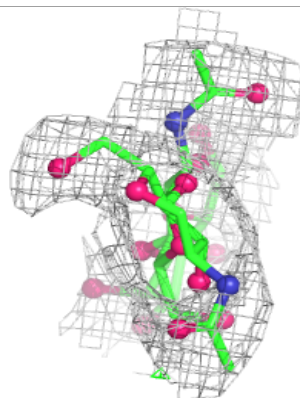
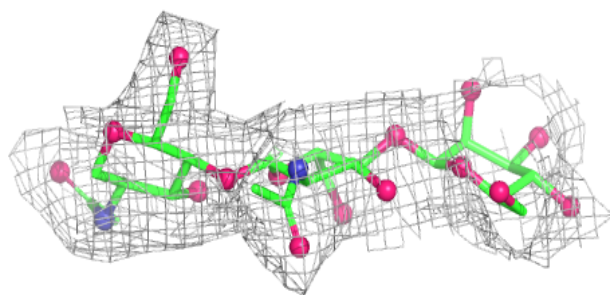
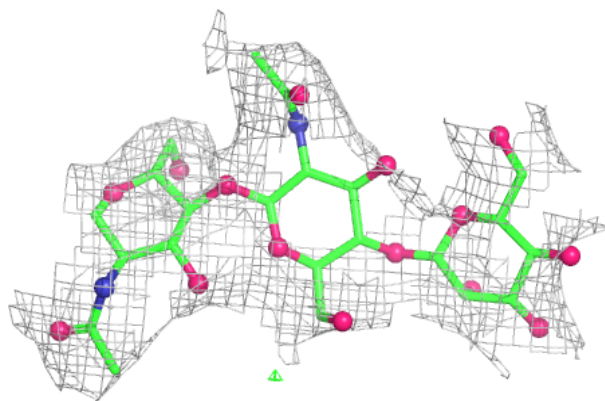
Electron density around Chain t:

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

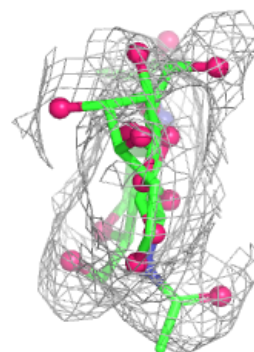
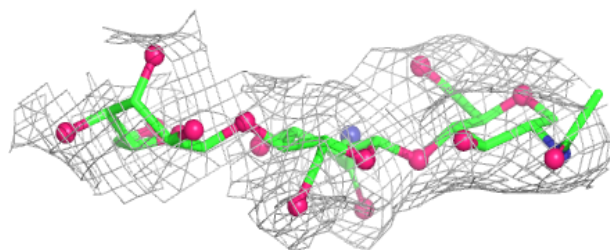
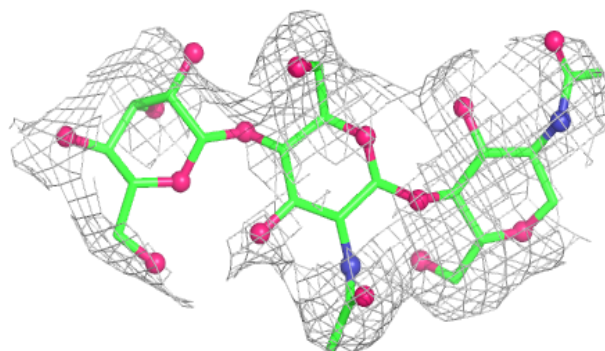


Electron density around Chain l:

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

**Electron density around Chain p:**

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
7	NAG	C	404	14/15	0.64	0.17	116,126,129,130	0
7	NAG	A	403	14/15	0.68	0.12	75,97,108,109	0
7	NAG	E	401	14/15	0.74	0.14	80,99,105,113	0
7	NAG	F	403	14/15	0.79	0.11	68,81,94,96	0

6.5 Other polymers [i](#)

There are no such residues in this entry.