



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 02:23 AM UTC

PDB ID : 3HS0 / pdb_00003hs0
Title : Cobra Venom Factor (CVF) in complex with human factor B
Authors : Janssen, B.J.C.; Gomes, L.; Koning, R.I.; Svergun, D.I.; Koster, A.J.;
Fritzinger, D.C.; Vogel, C.-W.; Gros, P.
Deposited on : 2009-06-10
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

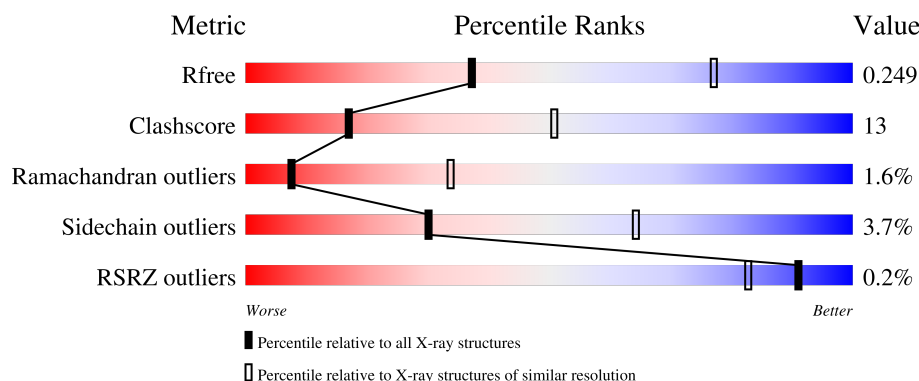
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



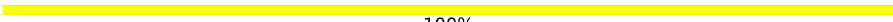
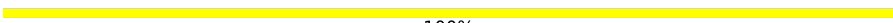
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	627	
1	F	627	
2	B	252	
2	G	252	
3	C	379	

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Mol	Chain	Length	Quality of chain
3	H	379	 75% 18% • •
4	D	741	 66% 25% • • 6%
4	I	741	 65% 26% • 5%
5	E	2	 100%
5	J	2	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 30435 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 Cobra venom factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	0	0
			4794	3069	804	906	15			
1	F	617	Total	C	N	O	S	0	0	0
			4826	3085	811	915	15			

- Molecule 2 is a protein called Cobra venom factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	233	Total	C	N	O	S	0	0	0
			1856	1194	311	346	5			
2	G	233	Total	C	N	O	S	0	0	0
			1856	1194	311	346	5			

- Molecule 3 is a protein called Cobra venom factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	359	Total	C	N	O	S	0	0	0
			2900	1831	484	566	19			
3	H	366	Total	C	N	O	S	0	0	0
			2957	1864	496	578	19			

- Molecule 4 is a protein called Complement factor B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	699	Total	C	N	O	S	0	0	0
			5513	3474	954	1052	33			
4	I	704	Total	C	N	O	S	0	0	0
			5567	3506	972	1056	33			

There are 8 discrepancies between the modelled and reference sequences:

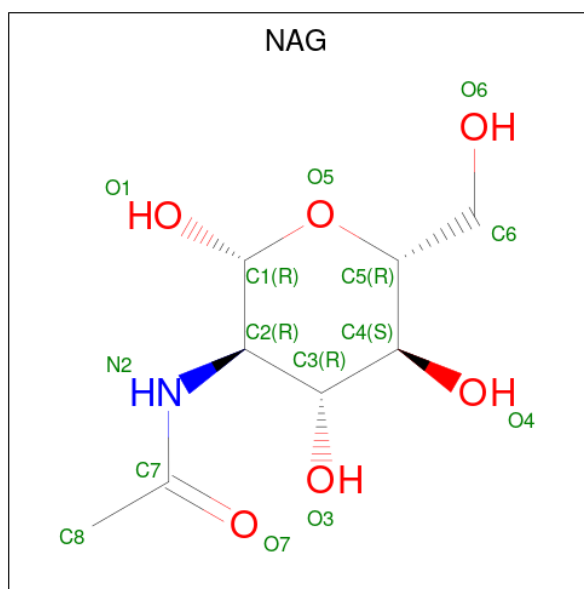
Chain	Residue	Modelled	Actual	Comment	Reference
D	254	GLY	ASP	engineered mutation	UNP P00751
D	260	ASP	ASN	engineered mutation	UNP P00751
D	740	ALA	-	insertion	UNP P00751
D	741	ALA	-	insertion	UNP P00751
I	254	GLY	ASP	engineered mutation	UNP P00751
I	260	ASP	ASN	engineered mutation	UNP P00751
I	740	ALA	-	insertion	UNP P00751
I	741	ALA	-	insertion	UNP P00751

- 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	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O 14 8 1 5	0	0
6	C	1	Total C N O 14 8 1 5	0	0
6	D	1	Total C N O 14 8 1 5	0	0
6	D	1	Total C N O 14 8 1 5	0	0
6	F	1	Total C N O 14 8 1 5	0	0
6	H	1	Total C N O 14 8 1 5	0	0
6	I	1	Total C N O 14 8 1 5	0	0

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Mg 1 1	0	0
7	D	1	Total Mg 1 1	0	0
7	F	1	Total Mg 1 1	0	0
7	I	1	Total Mg 1 1	0	0

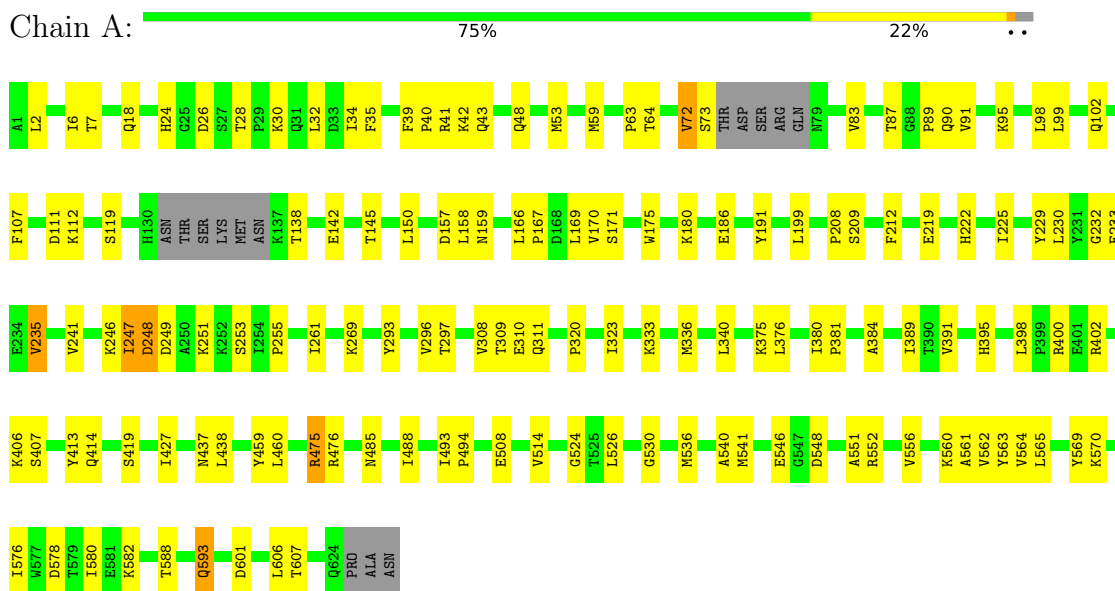
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	2	Total O 2 2	0	0
8	C	1	Total O 1 1	0	0
8	D	1	Total O 1 1	0	0
8	F	2	Total O 2 2	0	0
8	H	1	Total O 1 1	0	0
8	I	1	Total O 1 1	0	0

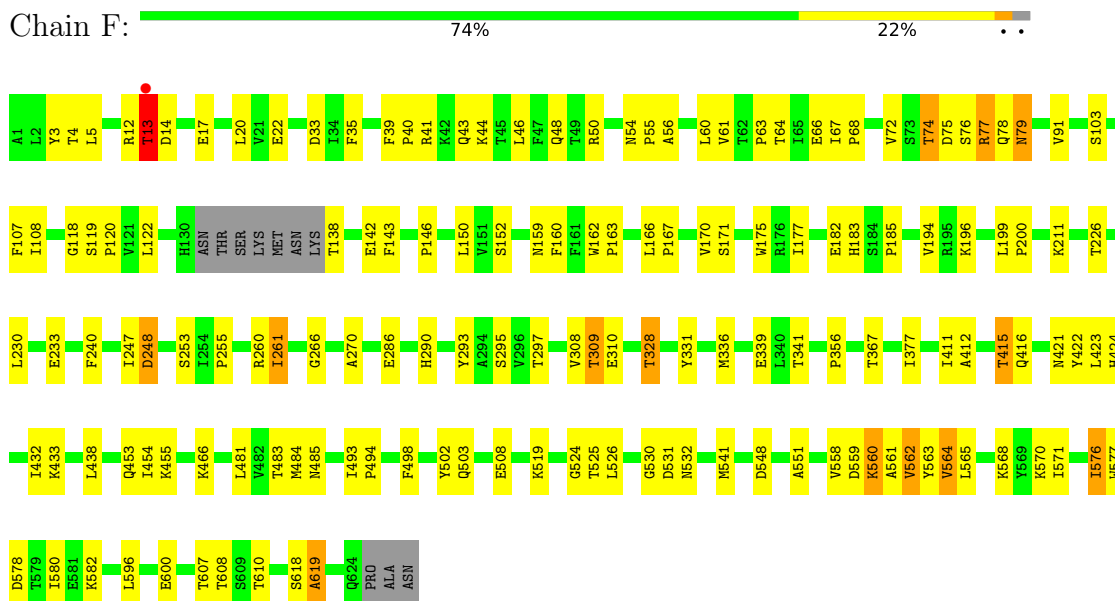
3 Residue-property plots

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

• Molecule 1: Cobra venom factor

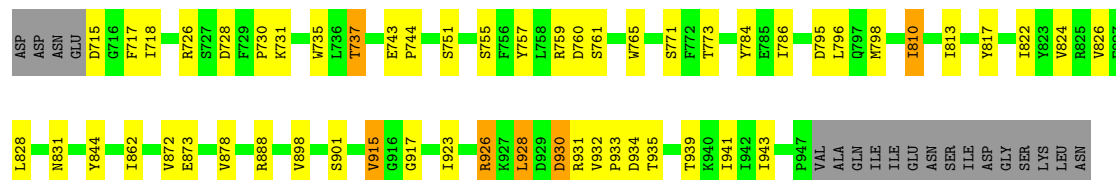


• Molecule 1: Cobra venom factor



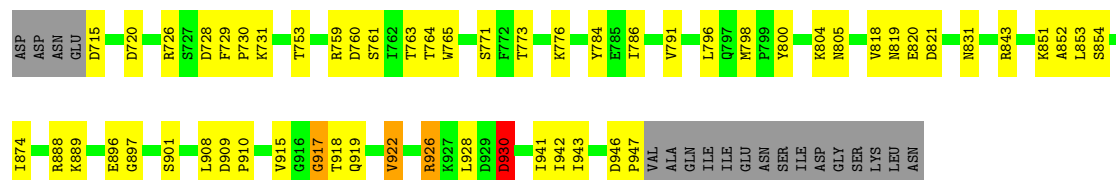
- Molecule 2: Cobra venom factor

Chain B: 



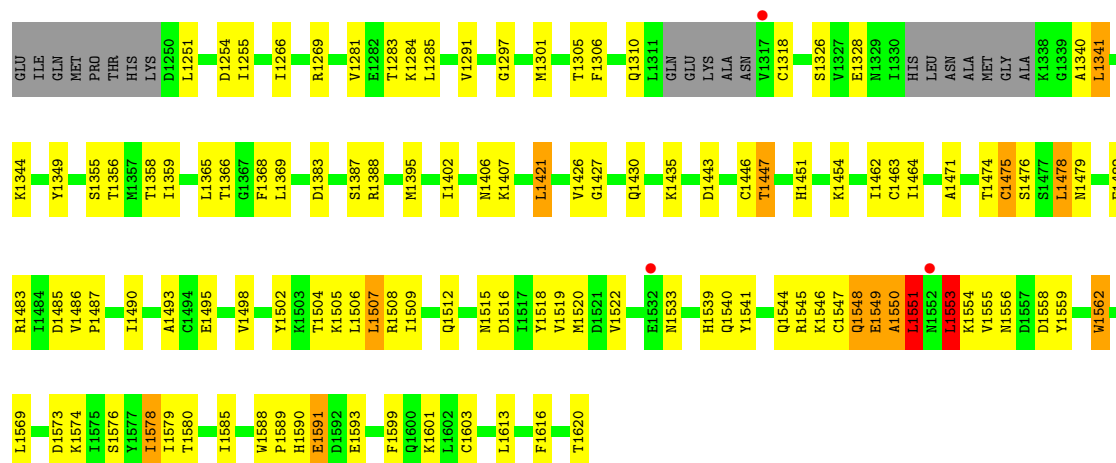
- Molecule 2: Cobra venom factor

Chain G: 



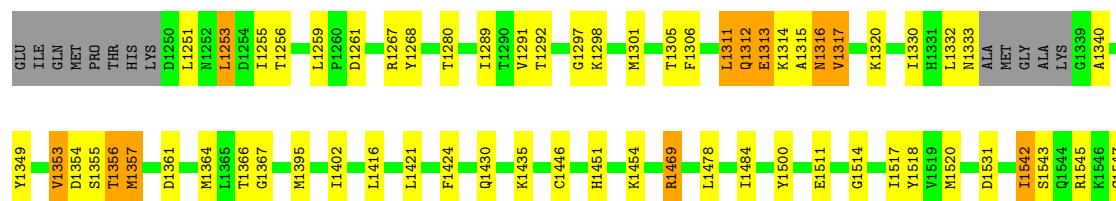
- Molecule 3: Cobra venom factor

Chain C: 



- Molecule 3: Cobra venom factor

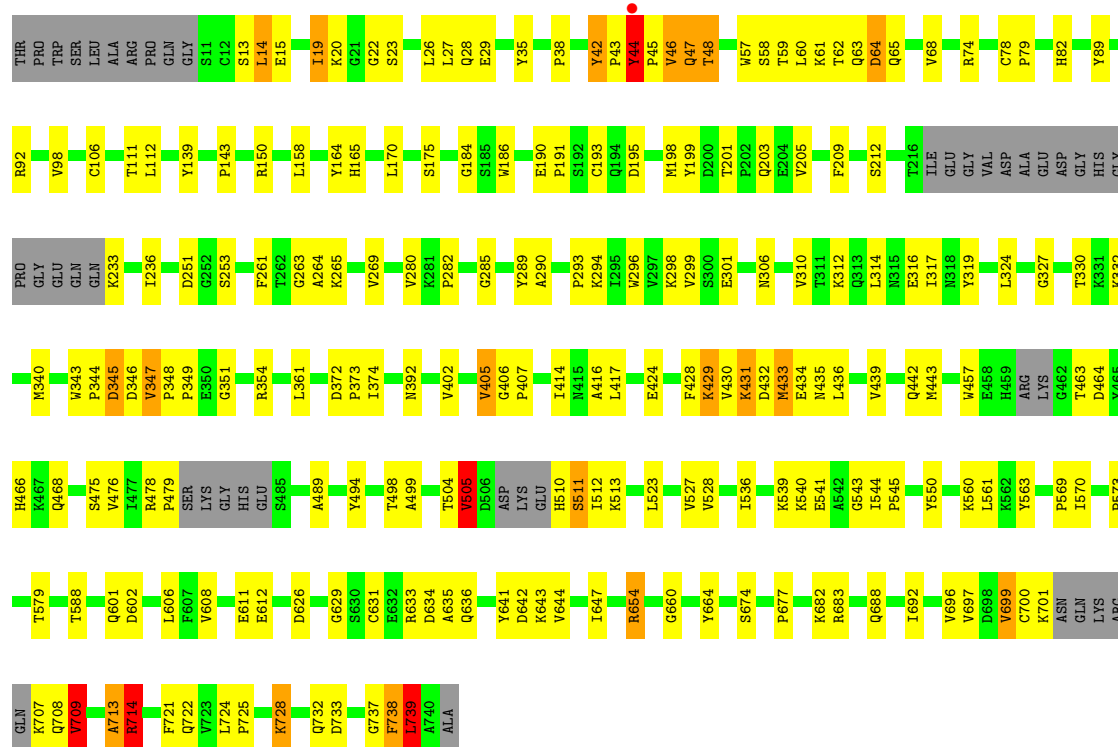
Chain H: 





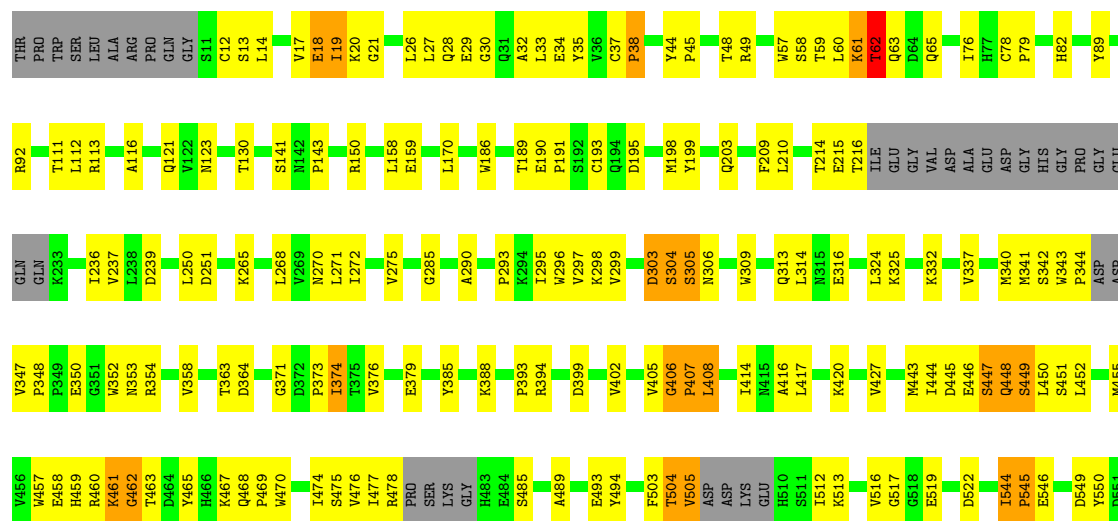
• Molecule 4: Complement factor B

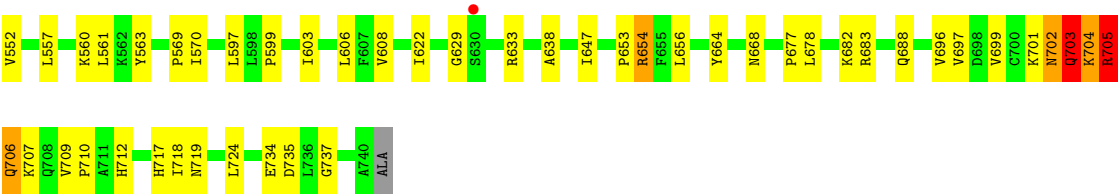
Chain D: 66% 25% 6%



• Molecule 4: Complement factor B

Chain I: 65% 26% 5%





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

Chain E: 100%



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

Chain J: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.03Å 136.97Å 283.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.88 – 3.00 34.88 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (34.88-3.00) 85.2 (34.88-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 3.00Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.189 , 0.243 (Not available) , 0.249	Depositor DCC
R_{free} test set	2093 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	72.0	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	30435	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% 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: MG, 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	0.33	0/4902	0.76	5/6668 (0.1%)
1	F	0.34	0/4935	0.77	3/6715 (0.0%)
2	B	0.34	0/1894	0.79	2/2570 (0.1%)
2	G	0.36	0/1894	0.81	6/2570 (0.2%)
3	C	0.32	0/2950	0.76	4/3989 (0.1%)
3	H	0.32	0/3009	0.73	1/4071 (0.0%)
4	D	0.34	1/5636 (0.0%)	0.83	18/7629 (0.2%)
4	I	0.33	0/5691	0.77	5/7699 (0.1%)
All	All	0.33	1/30911 (0.0%)	0.78	44/41911 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	1	0
3	C	0	1
All	All	1	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	739	LEU	CA-C	6.26	1.55	1.52

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1553	LEU	N-CA-C	10.92	127.12	109.76
4	D	64	ASP	N-CA-C	-10.08	101.00	113.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	44	TYR	CA-C-N	-9.17	111.33	120.31
4	D	44	TYR	C-N-CA	-9.17	111.33	120.31
4	D	42	TYR	CA-C-N	8.07	128.09	119.78
4	D	42	TYR	C-N-CA	8.07	128.09	119.78
1	F	13	THR	CA-C-N	7.92	135.96	121.70
1	F	13	THR	C-N-CA	7.92	135.96	121.70
4	D	433	MET	N-CA-C	-7.66	102.86	112.90
4	D	434	GLU	N-CA-C	-7.28	103.35	111.28
1	F	13	THR	N-CA-C	6.31	124.24	110.80
1	A	380	ILE	N-CA-C	6.19	114.63	107.89
2	G	915	VAL	N-CA-C	6.17	116.34	110.42
4	D	392	ASN	CA-C-N	6.16	125.78	119.56
4	D	392	ASN	C-N-CA	6.16	125.78	119.56
4	D	347	VAL	CA-C-N	6.02	126.58	120.38
4	D	347	VAL	C-N-CA	6.02	126.58	120.38
3	C	1533	ASN	CA-C-N	5.86	126.37	120.04
3	C	1533	ASN	C-N-CA	5.86	126.37	120.04
2	G	930	ASP	N-CA-C	-5.80	106.21	113.28
4	D	44	TYR	CA-CB-CG	-5.74	103.57	113.90
1	A	119	SER	CA-C-N	5.68	125.44	119.76
1	A	119	SER	C-N-CA	5.68	125.44	119.76
3	C	1551	LEU	N-CA-C	-5.66	99.16	108.49
4	I	544	ILE	CA-C-N	5.66	126.91	119.84
4	I	544	ILE	C-N-CA	5.66	126.91	119.84
4	I	406	GLY	CA-C-N	5.63	126.88	119.84
4	I	406	GLY	C-N-CA	5.63	126.88	119.84
1	A	232	GLY	N-CA-C	5.60	119.57	113.58
2	G	831	ASN	CA-C-N	5.59	125.26	119.56
2	G	831	ASN	C-N-CA	5.59	125.26	119.56
2	B	831	ASN	CA-C-N	5.55	125.90	119.47
2	B	831	ASN	C-N-CA	5.55	125.90	119.47
4	D	405	VAL	N-CA-C	5.50	115.64	110.30
2	G	917	GLY	N-CA-C	5.49	126.18	113.18
4	I	303	ASP	N-CA-C	5.32	118.11	111.24
4	D	46	VAL	N-CA-C	5.30	120.36	109.34
4	D	184	GLY	N-CA-C	-5.27	107.41	115.00
4	D	468	GLN	CA-C-N	5.21	125.01	119.28
4	D	468	GLN	C-N-CA	5.21	125.01	119.28
2	G	854	SER	N-CA-C	5.20	117.24	110.43
4	D	739	LEU	N-CA-C	5.18	116.39	108.30
3	H	1542	ILE	N-CA-C	5.12	115.34	108.17
1	A	248	ASP	N-CA-C	-5.09	106.16	112.93

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	13	THR	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	1551	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4794	0	4801	96	0
1	F	4826	0	4826	121	0
2	B	1856	0	1900	46	0
2	G	1856	0	1900	41	0
3	C	2900	0	2851	108	0
3	H	2957	0	2900	70	0
4	D	5513	0	5376	161	0
4	I	5567	0	5446	172	0
5	E	28	0	25	0	0
5	J	28	0	25	0	0
6	A	14	0	13	2	0
6	C	14	0	13	0	0
6	D	28	0	26	0	0
6	F	14	0	13	0	0
6	H	14	0	13	0	0
6	I	14	0	13	0	0
7	A	1	0	0	0	0
7	D	1	0	0	0	0
7	F	1	0	0	0	0
7	I	1	0	0	0	0
8	A	2	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
8	F	2	0	0	0	0
8	H	1	0	0	0	0
8	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	30435	0	30141	770	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 13.

All (770) 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)
3:H:1469:ARG:HG2	3:H:1469:ARG:HH11	1.10	1.12
4:D:714:ARG:HG2	4:D:714:ARG:HH11	1.17	1.07
4:I:705:ARG:HB3	4:I:707:LYS:HG2	1.37	1.04
4:D:699:VAL:HG23	4:D:707:LYS:HD2	1.42	1.01
1:F:13:THR:HG23	1:F:14:ASP:CB	1.89	1.01
3:C:1553:LEU:HG	3:C:1559:TYR:CE1	1.96	1.01
4:I:61:LYS:HD3	4:I:65:GLN:HG3	1.44	0.99
3:H:1251:LEU:HD12	3:H:1297:GLY:HA3	1.45	0.99
1:A:18:GLN:HG2	1:A:64:THR:HG22	1.46	0.97
1:F:13:THR:HG23	1:F:14:ASP:HB2	0.99	0.97
1:F:13:THR:CG2	1:F:14:ASP:HB2	1.94	0.97
3:C:1435:LYS:HG2	3:C:1447:THR:HG23	1.45	0.95
2:B:943:ILE:HD11	3:C:1301:MET:HE3	1.49	0.94
3:C:1549:GLU:C	3:C:1551:LEU:H	1.74	0.92
4:I:448:GLN:HG2	4:I:449:SER:N	1.83	0.92
1:F:526:LEU:HD22	2:G:771:SER:HB3	1.48	0.92
4:D:47:GLN:HE21	4:D:47:GLN:H	0.97	0.91
2:G:763:THR:HG22	2:G:764:THR:H	1.34	0.90
3:C:1474:THR:HG22	3:C:1475:CYS:H	1.35	0.89
2:G:763:THR:HG22	2:G:764:THR:N	1.86	0.88
2:G:852:ALA:O	2:G:853:LEU:HB2	1.73	0.88
1:A:475:ARG:HG2	1:A:475:ARG:HH11	1.38	0.87
4:D:489:ALA:HB2	4:D:677:PRO:HG3	1.54	0.87
1:F:20:LEU:HD11	1:F:60:LEU:HD11	1.59	0.85
4:D:373:PRO:HB2	4:D:417:LEU:HD21	1.58	0.85
4:I:475:SER:HB2	4:I:513:LYS:HE3	1.59	0.85
4:D:707:LYS:O	4:D:707:LYS:HD3	1.75	0.85
4:D:44:TYR:HB3	4:D:45:PRO:HD3	1.58	0.84
3:C:1508:ARG:NH1	3:C:1519:VAL:HG11	1.94	0.83
3:C:1369:LEU:HB2	3:C:1395:MET:HE2	1.62	0.81
3:C:1251:LEU:HD13	3:C:1297:GLY:HA3	1.61	0.81
4:I:447:SER:O	4:I:448:GLN:HB3	1.81	0.80
1:F:41:ARG:HH11	1:F:43:GLN:HG3	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:62:THR:HG23	4:D:68:VAL:HG21	1.61	0.80
4:D:299:VAL:HG13	4:D:340:MET:HE2	1.63	0.79
1:A:247:ILE:HG22	1:A:248:ASP:N	1.97	0.79
4:I:407:PRO:O	4:I:408:LEU:HB2	1.83	0.78
4:I:209:PHE:CD2	4:I:443:MET:HE1	2.17	0.78
4:D:170:LEU:HD23	4:D:193:CYS:HB3	1.65	0.77
4:I:705:ARG:HG2	4:I:707:LYS:HE2	1.64	0.77
4:I:14:LEU:HD11	4:I:26:LEU:HD11	1.66	0.77
4:D:550:TYR:CZ	4:D:654:ARG:HD3	2.20	0.77
4:I:489:ALA:HB2	4:I:677:PRO:HG3	1.67	0.77
2:G:763:THR:CG2	2:G:764:THR:H	1.98	0.76
3:H:1291:VAL:HG21	3:H:1301:MET:HE1	1.67	0.76
1:A:253:SER:O	1:A:255:PRO:HD3	1.85	0.76
4:I:209:PHE:HD2	4:I:443:MET:HE1	1.52	0.75
4:I:705:ARG:H	4:I:705:ARG:HD2	1.50	0.75
4:I:706:GLN:N	4:I:707:LYS:HA	2.02	0.74
3:C:1553:LEU:CD1	3:C:1554:LYS:H	2.00	0.73
3:H:1469:ARG:HG2	3:H:1469:ARG:NH1	1.89	0.73
4:I:449:SER:O	4:I:451:SER:N	2.22	0.73
2:G:909:ASP:H	2:G:919:GLN:NE2	1.86	0.73
4:I:199:TYR:OH	4:I:407:PRO:HG3	1.89	0.73
4:I:734:GLU:O	4:I:735:ASP:HB2	1.86	0.73
2:B:796:LEU:HD21	2:B:798:MET:HE3	1.69	0.73
1:F:578:ASP:O	1:F:582:LYS:HG2	1.89	0.73
4:D:527:VAL:HG22	4:D:528:VAL:H	1.53	0.72
4:I:446:GLU:O	4:I:448:GLN:N	2.22	0.72
3:C:1395:MET:HE3	3:C:1421:LEU:HB2	1.71	0.71
1:A:247:ILE:HG22	1:A:248:ASP:H	1.56	0.71
1:A:551:ALA:HA	2:B:773:THR:HG22	1.72	0.71
4:D:47:GLN:H	4:D:47:GLN:NE2	1.81	0.71
3:H:1395:MET:HE2	3:H:1421:LEU:HB2	1.71	0.71
3:H:1511:GLU:HB3	3:H:1545:ARG:NH2	2.05	0.71
4:D:47:GLN:HE21	4:D:47:GLN:N	1.80	0.71
3:H:1312:GLN:O	3:H:1314:LYS:N	2.24	0.71
4:D:714:ARG:HG2	4:D:714:ARG:NH1	1.94	0.70
4:I:447:SER:O	4:I:448:GLN:CB	2.39	0.70
4:D:143:PRO:HG3	4:D:186:TRP:CE2	2.26	0.70
2:B:798:MET:HE1	2:B:872:VAL:HB	1.74	0.70
4:D:285:GLY:HA3	4:D:340:MET:HE1	1.71	0.70
3:H:1314:LYS:HG3	3:H:1317:VAL:CG2	2.20	0.70
1:F:541:MET:HE2	2:G:786:ILE:HD13	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:1511:GLU:HB3	3:H:1545:ARG:HH21	1.58	0.69
3:H:1469:ARG:HH11	3:H:1469:ARG:CG	1.98	0.69
1:A:41:ARG:HB3	1:A:43:GLN:HG3	1.73	0.69
4:I:701:LYS:N	4:I:702:ASN:O	2.20	0.69
4:D:38:PRO:HG3	4:D:664:TYR:CZ	2.28	0.68
4:D:263:GLY:C	4:D:433:MET:HE2	2.18	0.68
4:D:374:ILE:HD11	4:D:416:ALA:HB1	1.74	0.68
4:D:476:VAL:HG11	4:D:478:ARG:HE	1.59	0.68
4:I:705:ARG:C	4:I:707:LYS:HA	2.19	0.68
3:C:1553:LEU:HD13	3:C:1554:LYS:H	1.58	0.68
3:C:1549:GLU:C	3:C:1551:LEU:N	2.48	0.68
3:C:1553:LEU:HG	3:C:1559:TYR:HE1	1.55	0.68
4:D:494:TYR:CE2	4:D:560:LYS:HG2	2.29	0.68
4:I:550:TYR:CZ	4:I:654:ARG:HD3	2.29	0.67
3:C:1486:VAL:O	3:C:1490:ILE:HG12	1.94	0.67
1:A:475:ARG:HH11	1:A:475:ARG:CG	2.07	0.67
2:G:888:ARG:HH21	4:I:150:ARG:NH1	1.92	0.67
1:F:494:PRO:HG3	1:F:577:TRP:CE3	2.30	0.66
4:D:143:PRO:HG3	4:D:186:TRP:CZ2	2.29	0.66
4:D:298:LYS:HA	4:D:340:MET:HE3	1.78	0.66
4:I:337:VAL:HG12	4:I:341:MET:HE3	1.75	0.66
4:I:705:ARG:O	4:I:706:GLN:HB2	1.94	0.66
1:A:414:GLN:HG2	1:A:593:GLN:HE21	1.59	0.66
4:I:14:LEU:HD21	4:I:26:LEU:HD21	1.77	0.66
1:A:398:LEU:HD22	1:A:402:ARG:HB2	1.77	0.66
1:A:209:SER:HB3	1:A:222:HIS:HB2	1.77	0.65
1:A:526:LEU:HD22	2:B:771:SER:HB3	1.78	0.65
4:D:511:SER:C	4:D:512:ILE:HG13	2.21	0.65
1:F:107:PHE:HB3	1:F:571:ILE:HD11	1.78	0.65
4:I:143:PRO:HG3	4:I:186:TRP:CE2	2.31	0.65
3:H:1520:MET:HE3	3:H:1561:ILE:HD11	1.77	0.65
1:A:563:TYR:CE1	1:A:570:LYS:HE3	2.30	0.65
4:D:280:VAL:O	4:D:282:PRO:HD3	1.96	0.65
4:D:708:GLN:O	4:D:709:VAL:HG12	1.96	0.65
2:B:928:LEU:HD12	2:B:931:ARG:HD3	1.78	0.65
1:F:20:LEU:HD11	1:F:60:LEU:CD1	2.26	0.65
1:A:309:THR:HG22	1:A:310:GLU:H	1.60	0.65
4:I:477:ILE:O	4:I:478:ARG:HG3	1.96	0.65
4:I:668:ASN:HB2	4:I:699:VAL:HG11	1.79	0.65
1:F:247:ILE:HG23	1:F:290:HIS:NE2	2.12	0.64
4:I:158:LEU:O	4:I:159:GLU:HB2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:943:ILE:CD1	3:C:1301:MET:HE3	2.24	0.64
3:C:1578:ILE:HG22	3:C:1580:THR:HG23	1.80	0.64
1:F:13:THR:HG22	1:F:103:SER:OG	1.98	0.64
4:I:374:ILE:HD11	4:I:416:ALA:HB1	1.79	0.64
1:F:253:SER:O	1:F:255:PRO:HD3	1.98	0.64
4:D:700:CYS:HB3	4:D:701:LYS:HG2	1.81	0.63
4:D:713:ALA:O	4:D:714:ARG:HB2	1.99	0.63
1:F:77:ARG:O	1:F:78:GLN:HB2	1.97	0.63
4:I:385:TYR:HA	4:I:388:LYS:HD3	1.79	0.63
4:I:462:GLY:HA2	4:I:467:LYS:HE2	1.79	0.63
3:C:1478:LEU:HD13	3:C:1479:ASN:H	1.63	0.63
1:F:4:THR:HG22	1:F:608:THR:HG22	1.80	0.63
4:I:250:LEU:HD12	4:I:251:ASP:H	1.63	0.63
3:H:1367:GLY:HA2	3:H:1424:PHE:CE2	2.34	0.62
3:H:1517:ILE:HD13	3:H:1542:ILE:HG12	1.80	0.62
4:I:563:TYR:CZ	4:I:569:PRO:HG3	2.35	0.62
1:F:22:GLU:HG2	1:F:60:LEU:HD13	1.81	0.62
4:D:299:VAL:HG13	4:D:340:MET:CE	2.28	0.62
2:G:930:ASP:N	2:G:930:ASP:OD1	2.32	0.62
1:A:297:THR:HG23	1:A:308:VAL:HG22	1.81	0.62
4:D:432:ASP:HB2	4:D:435:ASN:HD22	1.64	0.61
4:I:313:GLN:O	4:I:316:GLU:HB2	1.99	0.61
4:I:549:ASP:OD1	4:I:654:ARG:HD2	2.00	0.61
2:G:720:ASP:CG	2:G:843:ARG:HH12	2.07	0.61
4:I:293:PRO:HG3	4:I:332:LYS:HB3	1.81	0.61
4:D:738:PHE:N	4:D:738:PHE:CD2	2.69	0.61
1:F:199:LEU:HB3	1:F:561:ALA:HB1	1.82	0.61
4:I:476:VAL:HG22	4:I:512:ILE:HG23	1.81	0.61
1:F:78:GLN:O	1:F:79:ASN:CG	2.43	0.61
3:C:1474:THR:HG22	3:C:1475:CYS:N	2.11	0.61
3:C:1476:SER:HB3	3:C:1551:LEU:HD13	1.81	0.61
3:C:1512:GLN:O	3:C:1515:ASN:HB2	2.01	0.61
4:D:35:TYR:HB2	4:D:47:GLN:O	2.01	0.61
4:D:44:TYR:OH	4:D:74:ARG:NH1	2.33	0.61
2:B:930:ASP:OD1	2:B:930:ASP:N	2.30	0.61
3:C:1478:LEU:HD13	3:C:1479:ASN:N	2.16	0.61
4:I:210:LEU:HG	4:I:443:MET:HE2	1.81	0.61
1:A:95:LYS:HD3	1:A:607:THR:HB	1.80	0.61
4:D:139:TYR:CE2	4:D:158:LEU:HD13	2.36	0.60
4:D:346:ASP:O	4:D:347:VAL:HG12	2.01	0.60
1:A:241:VAL:HG22	1:A:296:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:199:LEU:HD11	2:G:731:LYS:HD3	1.84	0.60
4:D:212:SER:HB2	4:D:424:GLU:OE1	2.02	0.60
4:I:633:ARG:HA	4:I:647:ILE:HD13	1.83	0.60
1:A:32:LEU:HD11	1:A:53:MET:HE3	1.84	0.60
4:D:634:ASP:HB2	4:D:714:ARG:HD2	1.83	0.60
4:I:34:GLU:HB2	4:I:48:THR:HG22	1.84	0.60
3:C:1553:LEU:HG	3:C:1559:TYR:CZ	2.37	0.60
4:D:44:TYR:HB3	4:D:45:PRO:CD	2.29	0.60
4:I:570:ILE:HD13	4:I:688:GLN:HB2	1.84	0.60
4:I:299:VAL:HG22	4:I:340:MET:HB3	1.83	0.59
1:F:416:GLN:HB3	1:F:508:GLU:HG3	1.83	0.59
3:H:1361:ASP:HB3	3:H:1435:LYS:HB2	1.83	0.59
4:I:82:HIS:HB3	4:I:150:ARG:NH1	2.16	0.59
4:D:738:PHE:N	4:D:738:PHE:HD2	2.01	0.59
3:C:1495:GLU:HB3	3:C:1498:VAL:HG23	1.83	0.59
3:C:1506:LEU:HB2	3:C:1559:TYR:HE2	1.66	0.59
3:C:1562:TRP:CD1	3:C:1562:TRP:O	2.55	0.59
4:I:285:GLY:HA3	4:I:340:MET:HE1	1.83	0.59
4:D:405:VAL:HG23	4:D:406:GLY:N	2.18	0.59
1:F:433:LYS:HG2	1:F:519:LYS:HD3	1.83	0.59
3:C:1540:GLN:O	3:C:1576:SER:HA	2.02	0.58
1:F:562:VAL:O	1:F:563:TYR:HB3	2.01	0.58
4:I:460:ARG:O	4:I:460:ARG:HG3	2.02	0.58
4:D:299:VAL:H	4:D:340:MET:HE3	1.69	0.58
1:F:524:GLY:HA3	1:F:548:ASP:OD2	2.02	0.58
3:H:1580:THR:HG22	3:H:1581:LYS:N	2.18	0.58
4:I:544:ILE:O	4:I:544:ILE:HG13	2.03	0.58
1:A:199:LEU:HD11	2:B:731:LYS:HD3	1.85	0.58
4:I:143:PRO:HG3	4:I:186:TRP:CZ2	2.39	0.58
3:H:1314:LYS:HG3	3:H:1317:VAL:HG22	1.85	0.58
4:I:705:ARG:HD2	4:I:705:ARG:N	2.17	0.58
4:D:570:ILE:HD13	4:D:688:GLN:HB2	1.86	0.58
1:A:563:TYR:HE1	1:A:570:LYS:HE3	1.69	0.57
4:D:347:VAL:HG13	4:D:347:VAL:O	2.04	0.57
4:I:629:GLY:O	4:I:633:ARG:HG3	2.03	0.57
4:I:705:ARG:O	4:I:706:GLN:CB	2.52	0.57
1:F:551:ALA:HA	2:G:773:THR:HG22	1.84	0.57
1:A:552:ARG:HE	2:B:737:THR:HG21	1.69	0.57
2:G:819:ASN:HA	2:G:853:LEU:CD1	2.35	0.57
4:I:61:LYS:HG2	4:I:62:THR:H	1.69	0.57
4:D:61:LYS:HB3	4:D:65:GLN:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:448:GLN:CG	4:I:449:SER:N	2.65	0.57
4:D:573:PRO:HB3	4:D:721:PHE:CE2	2.39	0.57
3:H:1314:LYS:HG3	3:H:1317:VAL:HG21	1.84	0.57
4:D:139:TYR:HE2	4:D:158:LEU:HD13	1.67	0.57
4:I:309:TRP:O	4:I:313:GLN:HG2	2.05	0.57
4:I:503:PHE:HE1	4:I:512:ILE:HG21	1.70	0.57
3:C:1553:LEU:CD1	3:C:1554:LYS:N	2.67	0.57
4:D:527:VAL:HG22	4:D:528:VAL:N	2.18	0.57
1:F:562:VAL:CG2	1:F:563:TYR:N	2.67	0.57
2:B:761:SER:HB2	2:B:765:TRP:CZ2	2.39	0.57
3:C:1482:GLU:O	3:C:1483:ARG:HD2	2.04	0.57
2:G:726:ARG:HB3	2:G:760:ASP:HB3	1.86	0.57
2:G:761:SER:HB2	2:G:765:TRP:CZ2	2.40	0.57
4:I:299:VAL:H	4:I:340:MET:HE3	1.69	0.57
4:D:696:VAL:HG12	4:D:697:VAL:HG23	1.87	0.56
4:I:494:TYR:CZ	4:I:560:LYS:HG3	2.39	0.56
3:C:1590:HIS:O	3:C:1591:GLU:CB	2.53	0.56
4:D:63:GLN:C	4:D:65:GLN:H	2.12	0.56
3:C:1284:LYS:C	3:C:1285:LEU:HD23	2.31	0.56
4:D:285:GLY:CA	4:D:340:MET:HE1	2.36	0.56
3:C:1589:PRO:HB2	3:C:1603:CYS:SG	2.45	0.56
1:F:74:THR:O	1:F:76:SER:N	2.37	0.56
2:G:728:ASP:O	2:G:730:PRO:HD3	2.05	0.56
4:I:209:PHE:HD2	4:I:443:MET:CE	2.18	0.56
3:H:1256:THR:HB	3:H:1292:THR:OG1	2.06	0.56
4:I:504:THR:HG23	4:I:505:VAL:H	1.71	0.56
4:I:653:PRO:HD2	4:I:654:ARG:NH2	2.21	0.56
4:I:373:PRO:HB2	4:I:417:LEU:HD21	1.87	0.56
4:D:343:TRP:O	4:D:345:ASP:N	2.39	0.56
3:H:1317:VAL:O	3:H:1317:VAL:HG23	2.04	0.56
1:F:618:SER:O	1:F:619:ALA:HB3	2.06	0.55
3:C:1383:ASP:HA	3:C:1406:ASN:ND2	2.21	0.55
1:F:17:GLU:OE1	1:F:466:LYS:HG2	2.06	0.55
4:I:45:PRO:HB3	4:I:62:THR:HG23	1.88	0.55
1:A:42:LYS:HE2	1:A:83:VAL:HG11	1.89	0.55
1:A:438:LEU:HD22	1:A:488:ILE:HD11	1.87	0.55
4:D:264:ALA:N	4:D:433:MET:HE2	2.22	0.55
4:D:463:THR:CG2	4:D:464:ASP:N	2.69	0.55
1:F:562:VAL:HG23	1:F:563:TYR:H	1.71	0.55
3:H:1311:LEU:H	3:H:1311:LEU:HD23	1.70	0.55
4:D:633:ARG:HA	4:D:647:ILE:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:233:LYS:NZ	4:D:233:LYS:HB3	2.22	0.55
4:I:303:ASP:O	4:I:304:SER:C	2.49	0.55
1:A:145:THR:HG22	1:A:175:TRP:CH2	2.42	0.54
3:C:1365:LEU:HB2	3:C:1368:PHE:CD2	2.43	0.54
4:I:270:ASN:HB3	4:I:444:ILE:HD11	1.89	0.54
1:A:89:PRO:O	1:A:90:GLN:HB2	2.06	0.54
1:F:559:ASP:OD1	2:G:763:THR:HG21	2.07	0.54
2:B:726:ARG:HB3	2:B:760:ASP:HB3	1.89	0.54
1:F:558:VAL:HG12	1:F:559:ASP:O	2.07	0.54
1:F:77:ARG:C	1:F:79:ASN:N	2.65	0.54
3:H:1349:TYR:CG	3:H:1355:SER:HB3	2.43	0.54
2:B:798:MET:HE2	2:B:810:ILE:HD13	1.89	0.54
3:C:1553:LEU:HD12	3:C:1554:LYS:H	1.71	0.54
4:D:19:ILE:HD11	4:D:23:SER:O	2.08	0.54
4:I:62:THR:HG22	4:I:63:GLN:H	1.73	0.54
4:D:540:LYS:HA	4:D:544:ILE:O	2.08	0.54
3:C:1478:LEU:HG	3:C:1553:LEU:CD2	2.38	0.53
3:C:1553:LEU:HD12	3:C:1554:LYS:N	2.22	0.53
4:D:347:VAL:N	4:D:348:PRO:HD3	2.23	0.53
4:D:351:GLY:HA2	4:D:354:ARG:NH1	2.23	0.53
2:G:763:THR:CG2	2:G:764:THR:N	2.54	0.53
4:D:714:ARG:NH1	4:D:714:ARG:CG	2.66	0.53
1:F:160:PHE:HE2	1:F:162:TRP:CE2	2.25	0.53
1:A:230:LEU:CD1	1:A:561:ALA:HB2	2.38	0.53
3:C:1383:ASP:HA	3:C:1406:ASN:HD22	1.73	0.53
2:G:796:LEU:HG	2:G:798:MET:HE2	1.89	0.53
3:H:1291:VAL:HG11	3:H:1301:MET:HE1	1.90	0.53
3:C:1516:ASP:HB3	3:C:1518:TYR:CE1	2.42	0.53
3:H:1367:GLY:HA2	3:H:1424:PHE:CZ	2.43	0.53
2:B:730:PRO:HG2	2:B:759:ARG:HG3	1.91	0.53
3:C:1545:ARG:O	3:C:1548:GLN:N	2.40	0.53
1:F:167:PRO:HD2	1:F:170:VAL:HG23	1.90	0.53
4:I:38:PRO:HG3	4:I:664:TYR:CE1	2.43	0.53
4:D:299:VAL:N	4:D:340:MET:HE3	2.24	0.53
4:I:215:GLU:OE1	4:I:237:VAL:HG21	2.09	0.53
2:G:728:ASP:OD2	2:G:759:ARG:HD2	2.09	0.53
1:A:524:GLY:HA3	1:A:548:ASP:OD2	2.09	0.53
3:C:1358:THR:HG22	3:C:1359:ILE:N	2.24	0.53
4:D:463:THR:HG22	4:D:464:ASP:N	2.24	0.53
4:D:475:SER:HB2	4:D:513:LYS:HG3	1.90	0.53
3:C:1291:VAL:HG21	3:C:1301:MET:SD	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:ARG:NH1	1:F:43:GLN:HG3	2.22	0.52
2:B:796:LEU:CD2	2:B:798:MET:HE3	2.39	0.52
3:H:1587:ARG:HH12	3:H:1589:PRO:HA	1.74	0.52
4:I:113:ARG:NH2	4:I:141:SER:HB2	2.24	0.52
1:A:541:MET:HE2	2:B:786:ILE:HD13	1.92	0.52
3:C:1545:ARG:O	3:C:1548:GLN:HB2	2.09	0.52
4:I:28:GLN:C	4:I:30:GLY:H	2.17	0.52
1:A:576:ILE:O	1:A:580:ILE:HG12	2.09	0.52
4:D:312:LYS:O	4:D:316:GLU:HG2	2.09	0.52
4:D:14:LEU:HD23	4:D:57:TRP:HZ2	1.74	0.52
4:I:59:THR:HG22	4:I:61:LYS:N	2.25	0.52
4:D:631:CYS:HA	4:D:714:ARG:NE	2.24	0.52
1:A:323:ILE:HD13	1:A:391:VAL:HG12	1.91	0.52
1:F:563:TYR:HE1	1:F:570:LYS:HE3	1.74	0.52
1:A:28:THR:O	1:A:30:LYS:HG3	2.10	0.52
1:A:167:PRO:HD2	1:A:170:VAL:HB	1.90	0.52
4:D:738:PHE:C	4:D:739:LEU:HD23	2.35	0.52
1:A:546:GLU:HG2	2:B:751:SER:HB2	1.92	0.52
2:B:798:MET:HE1	2:B:872:VAL:CB	2.39	0.52
3:C:1505:LYS:O	3:C:1507:LEU:HD23	2.10	0.52
4:D:48:THR:O	4:D:48:THR:OG1	2.27	0.52
2:G:729:PHE:CE2	2:G:889:LYS:HE2	2.45	0.52
1:A:251:LYS:HD3	1:A:293:TYR:CE2	2.45	0.51
4:D:195:ASP:HB2	4:D:198:MET:HG3	1.93	0.51
4:D:682:LYS:HG2	4:D:683:ARG:HG2	1.92	0.51
4:D:89:TYR:CE2	4:D:92:ARG:HG2	2.45	0.51
4:D:253:SER:HB3	4:D:327:GLY:O	2.10	0.51
2:G:796:LEU:HD22	2:G:874:ILE:HD12	1.92	0.51
4:I:699:VAL:HG22	4:I:699:VAL:O	2.09	0.51
4:I:709:VAL:HG13	4:I:710:PRO:HD2	1.93	0.51
1:A:437:ASN:HB3	1:A:485:ASN:OD1	2.11	0.51
1:A:475:ARG:CG	1:A:475:ARG:NH1	2.70	0.51
3:C:1340:ALA:O	3:C:1341:LEU:HD13	2.11	0.51
1:F:247:ILE:HG23	1:F:290:HIS:CE1	2.45	0.51
3:H:1255:ILE:HB	3:H:1268:TYR:HB2	1.92	0.51
1:A:530:GLY:HA3	2:B:784:TYR:CZ	2.46	0.51
2:B:939:THR:HB	3:C:1283:THR:CG2	2.40	0.51
4:D:504:THR:O	4:D:505:VAL:HB	2.10	0.51
2:G:896:GLU:H	2:G:896:GLU:CD	2.19	0.51
3:H:1311:LEU:H	3:H:1311:LEU:CD2	2.24	0.51
1:A:381:PRO:HB2	1:A:384:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1502:TYR:HB3	3:C:1522:VAL:HG13	1.92	0.51
3:H:1580:THR:HG22	3:H:1581:LYS:H	1.76	0.51
1:A:6:ILE:HG12	1:A:606:LEU:HD13	1.92	0.51
2:B:888:ARG:HH21	4:D:150:ARG:NH1	2.09	0.51
4:D:660:GLY:HA3	4:D:714:ARG:HH12	1.75	0.51
3:H:1364:MET:HA	3:H:1364:MET:HE2	1.92	0.51
4:I:603:ILE:HB	4:I:622:ILE:HB	1.92	0.51
4:D:579:THR:HG23	4:D:588:THR:HB	1.93	0.50
4:I:371:GLY:O	4:I:373:PRO:HD3	2.10	0.50
1:F:328:THR:CG2	1:F:341:THR:H	2.25	0.50
1:A:26:ASP:O	1:A:59:MET:HG3	2.11	0.50
1:A:180:LYS:HD3	6:A:9187:NAG:H81	1.93	0.50
1:A:222:HIS:ND1	1:A:269:LYS:HE2	2.27	0.50
4:D:209:PHE:CD2	4:D:443:MET:HE1	2.46	0.50
3:C:1388:ARG:HE	4:I:712:HIS:HB3	1.76	0.50
3:C:1590:HIS:O	3:C:1591:GLU:HB2	2.11	0.50
3:H:1316:ASN:O	3:H:1317:VAL:C	2.54	0.50
4:I:44:TYR:CD1	4:I:45:PRO:HA	2.47	0.50
3:C:1464:ILE:HD11	3:C:1569:LEU:HD13	1.93	0.50
3:C:1573:ASP:C	3:C:1574:LYS:HG2	2.36	0.50
4:D:289:TYR:CE1	4:D:330:THR:HA	2.47	0.50
3:C:1483:ARG:HH12	3:C:1601:LYS:HD3	1.77	0.50
3:C:1569:LEU:HD11	3:C:1578:ILE:CG1	2.42	0.50
4:I:61:LYS:CG	4:I:62:THR:H	2.24	0.50
4:D:26:LEU:O	4:D:27:LEU:HG	2.11	0.50
3:H:1469:ARG:NH1	3:H:1469:ARG:CG	2.64	0.50
3:H:1562:TRP:C	3:H:1562:TRP:CD1	2.90	0.50
3:H:1589:PRO:HG2	3:H:1602:LEU:HD23	1.94	0.50
4:D:739:LEU:HD23	4:D:739:LEU:N	2.27	0.50
1:F:336:MET:HE1	1:F:422:TYR:CB	2.42	0.50
1:A:169:LEU:HD21	3:C:1306:PHE:CD2	2.47	0.49
4:D:22:GLY:HA2	4:D:664:TYR:OH	2.12	0.49
1:F:247:ILE:O	1:F:248:ASP:HB2	2.12	0.49
1:F:39:PHE:CG	1:F:40:PRO:HA	2.47	0.49
4:I:702:ASN:O	4:I:704:LYS:N	2.45	0.49
3:C:1349:TYR:CD2	3:C:1355:SER:HB3	2.48	0.49
3:C:1506:LEU:HD13	3:C:1520:MET:HE2	1.94	0.49
2:G:730:PRO:HG2	2:G:759:ARG:HG3	1.94	0.49
1:A:2:LEU:HD23	1:A:24:HIS:CD2	2.47	0.49
3:H:1291:VAL:CG2	3:H:1301:MET:HE1	2.41	0.49
4:I:37:CYS:HB3	4:I:38:PRO:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:411:ILE:HG22	1:F:412:ALA:N	2.28	0.49
4:I:19:ILE:HG23	4:I:19:ILE:O	2.13	0.49
4:I:703:GLN:O	4:I:704:LYS:CB	2.60	0.49
4:D:713:ALA:O	4:D:714:ARG:CB	2.60	0.49
4:I:701:LYS:HB2	4:I:702:ASN:O	2.13	0.49
1:A:170:VAL:HG22	1:A:171:SER:N	2.27	0.49
2:G:942:ILE:HG13	3:H:1280:THR:HG22	1.94	0.49
4:I:250:LEU:HD12	4:I:251:ASP:N	2.26	0.49
1:A:459:TYR:C	1:A:460:LEU:HD12	2.38	0.49
2:B:795:ASP:HB3	2:B:813:ILE:HB	1.93	0.49
3:C:1547:CYS:C	3:C:1549:GLU:H	2.20	0.49
4:D:724:LEU:O	4:D:728:LYS:HG3	2.12	0.49
3:H:1316:ASN:ND2	3:H:1316:ASN:H	2.09	0.49
4:I:682:LYS:HG2	4:I:683:ARG:HG2	1.95	0.49
1:A:34:ILE:CD1	1:A:63:PRO:HG2	2.43	0.48
4:D:512:ILE:HG22	4:D:513:LYS:N	2.28	0.48
1:F:72:VAL:O	1:F:72:VAL:HG22	2.13	0.48
2:B:873:GLU:OE1	2:B:888:ARG:HD3	2.13	0.48
1:F:160:PHE:CE2	1:F:162:TRP:CE2	3.01	0.48
3:H:1313:GLU:OE1	3:H:1313:GLU:HA	2.12	0.48
4:I:113:ARG:HH21	4:I:141:SER:HB2	1.78	0.48
3:C:1355:SER:O	3:C:1407:LYS:HA	2.13	0.48
1:F:77:ARG:C	1:F:79:ASN:H	2.21	0.48
4:D:536:ILE:O	4:D:536:ILE:HG13	2.14	0.48
3:H:1545:ARG:C	3:H:1547:CYS:H	2.21	0.48
1:A:208:PRO:HD3	1:A:311:GLN:OE1	2.12	0.48
2:B:943:ILE:HD11	3:C:1301:MET:CE	2.33	0.48
4:D:629:GLY:O	4:D:633:ARG:HG3	2.13	0.48
1:F:328:THR:HG22	1:F:341:THR:O	2.13	0.48
1:A:333:LYS:HB3	1:A:336:MET:HE3	1.95	0.48
2:B:930:ASP:O	3:C:1310:GLN:HG2	2.14	0.48
4:D:510:HIS:C	4:D:512:ILE:H	2.22	0.48
4:I:295:ILE:HG21	4:I:298:LYS:HG2	1.94	0.48
3:C:1451:HIS:CG	3:C:1454:LYS:HD2	2.49	0.48
4:D:60:LEU:HB3	4:D:68:VAL:HB	1.94	0.48
1:F:309:THR:HG22	1:F:310:GLU:H	1.78	0.48
4:I:444:ILE:O	4:I:447:SER:HB3	2.14	0.48
4:D:543:GLY:O	4:D:545:PRO:HD3	2.13	0.48
1:F:211:LYS:HD2	1:F:211:LYS:HA	1.64	0.48
1:A:309:THR:HG22	1:A:310:GLU:N	2.27	0.48
1:A:560:LYS:O	1:A:564:VAL:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:236:ILE:HD12	4:D:280:VAL:HG21	1.96	0.48
1:A:230:LEU:HD13	1:A:561:ALA:HB2	1.95	0.48
3:C:1548:GLN:O	3:C:1549:GLU:HB3	2.14	0.48
4:I:195:ASP:HB2	4:I:198:MET:HG3	1.96	0.48
3:C:1593:GLU:O	3:C:1599:PHE:HB2	2.13	0.47
1:F:66:GLU:O	1:F:68:PRO:HD3	2.14	0.47
1:F:531:ASP:O	1:F:532:ASN:HB2	2.14	0.47
4:I:705:ARG:CG	4:I:707:LYS:HE2	2.40	0.47
3:C:1474:THR:CG2	3:C:1475:CYS:H	2.16	0.47
1:F:196:LYS:HG2	2:G:800:TYR:CZ	2.49	0.47
3:H:1330:ILE:HD11	3:H:1332:LEU:HD11	1.96	0.47
4:I:20:LYS:O	4:I:21:GLY:C	2.57	0.47
4:I:303:ASP:O	4:I:305:SER:N	2.47	0.47
1:A:395:HIS:HB3	1:A:398:LEU:HB2	1.97	0.47
4:D:59:THR:OG1	4:D:61:LYS:HE2	2.14	0.47
2:G:818:VAL:HG12	2:G:820:GLU:HG2	1.96	0.47
3:C:1451:HIS:HB3	3:C:1454:LYS:HB2	1.96	0.47
3:H:1259:LEU:HB3	3:H:1261:ASP:OD1	2.14	0.47
3:H:1518:TYR:CE1	3:H:1553:LEU:HD12	2.49	0.47
4:I:61:LYS:CG	4:I:65:GLN:HA	2.44	0.47
2:B:844:TYR:HE2	3:C:1430:GLN:HE21	1.62	0.47
1:A:460:LEU:HD12	1:A:460:LEU:N	2.29	0.47
2:B:822:ILE:HB	2:B:878:VAL:HG13	1.96	0.47
1:F:618:SER:O	1:F:619:ALA:CB	2.62	0.47
2:G:946:ASP:OD2	3:H:1298:LYS:HE3	2.14	0.47
1:A:419:SER:OG	1:A:508:GLU:OE2	2.26	0.47
2:B:933:PRO:O	2:B:934:ASP:HB2	2.14	0.47
4:D:42:TYR:HA	4:D:43:PRO:HD3	1.74	0.47
4:D:306:ASN:O	4:D:310:VAL:HG23	2.15	0.47
4:D:463:THR:HB	4:D:466:HIS:ND1	2.29	0.47
1:F:13:THR:O	1:F:67:ILE:HB	2.15	0.47
1:F:77:ARG:NH2	1:F:185:PRO:HA	2.30	0.47
1:F:160:PHE:HE2	1:F:162:TRP:NE1	2.12	0.47
4:I:293:PRO:CG	4:I:332:LYS:HB3	2.45	0.47
4:I:304:SER:O	4:I:306:ASN:N	2.47	0.47
4:I:462:GLY:HA2	4:I:467:LYS:CE	2.45	0.47
3:H:1395:MET:HE2	3:H:1421:LEU:CB	2.42	0.47
4:I:190:GLU:HA	4:I:191:PRO:HD3	1.79	0.47
4:D:293:PRO:HG3	4:D:332:LYS:HB3	1.97	0.47
1:F:453:GLN:O	1:F:455:LYS:HD3	2.15	0.47
2:G:908:LEU:HA	2:G:919:GLN:OE1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:705:ARG:CB	4:I:707:LYS:HG2	2.27	0.47
1:F:33:ASP:OD1	1:F:50:ARG:HG3	2.15	0.47
3:H:1316:ASN:O	3:H:1317:VAL:O	2.32	0.47
1:A:564:VAL:HG23	1:A:565:LEU:CD1	2.45	0.46
4:D:38:PRO:HG3	4:D:664:TYR:CE1	2.50	0.46
1:F:226:THR:HA	1:F:266:GLY:O	2.15	0.46
3:H:1451:HIS:HB3	3:H:1454:LYS:HB2	1.96	0.46
3:H:1543:SER:HB2	3:H:1579:ILE:HD12	1.97	0.46
3:H:1291:VAL:HG21	3:H:1301:MET:CE	2.42	0.46
4:I:189:THR:HG22	4:I:420:LYS:HB3	1.96	0.46
1:A:142:GLU:HB3	1:A:150:LEU:HD11	1.97	0.46
3:C:1520:MET:HB2	3:C:1539:HIS:O	2.16	0.46
4:D:14:LEU:HD23	4:D:57:TRP:CZ2	2.49	0.46
4:D:19:ILE:HG23	4:D:35:TYR:CE1	2.50	0.46
4:D:431:LYS:HG2	4:D:432:ASP:N	2.30	0.46
4:D:442:GLN:HG2	4:D:457:TRP:HZ3	1.80	0.46
1:F:339:GLU:HG2	1:F:377:ILE:HD11	1.97	0.46
1:F:596:LEU:O	1:F:600:GLU:HG3	2.16	0.46
3:H:1435:LYS:HA	3:H:1446:CYS:O	2.14	0.46
4:I:352:TRP:CG	4:I:353:ASN:N	2.83	0.46
1:A:35:PHE:HE1	1:A:48:GLN:NE2	2.14	0.46
1:A:212:PHE:CE2	1:A:320:PRO:HB3	2.51	0.46
4:D:261:PHE:CD2	4:D:319:TYR:HB2	2.50	0.46
4:D:504:THR:O	4:D:505:VAL:CB	2.63	0.46
3:H:1562:TRP:CD1	3:H:1562:TRP:O	2.69	0.46
4:I:544:ILE:O	4:I:544:ILE:CG1	2.63	0.46
3:C:1553:LEU:HD13	3:C:1553:LEU:HA	1.49	0.46
4:D:28:GLN:O	4:D:29:GLU:HB2	2.16	0.46
3:H:1416:LEU:HD12	3:H:1416:LEU:C	2.40	0.46
4:I:516:VAL:HG12	4:I:517:GLY:N	2.30	0.46
3:C:1485:ASP:OD1	3:C:1487:PRO:HD2	2.15	0.46
3:C:1549:GLU:O	3:C:1550:ALA:HB3	2.15	0.46
4:I:678:LEU:HD22	4:I:717:HIS:CD2	2.50	0.46
1:A:180:LYS:HD3	6:A:9187:NAG:C8	2.45	0.46
1:A:530:GLY:HA3	2:B:784:TYR:OH	2.15	0.46
4:I:474:ILE:O	4:I:485:SER:HA	2.16	0.46
1:A:233:GLU:HG3	2:B:817:TYR:CE1	2.50	0.46
4:D:433:MET:CE	4:D:436:LEU:HD23	2.46	0.46
1:F:423:LEU:HB2	1:F:502:TYR:CE2	2.51	0.46
3:H:1366:THR:OG1	3:H:1430:GLN:HB2	2.16	0.46
4:I:550:TYR:CE1	4:I:654:ARG:HD3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:LEU:HD22	1:A:389:ILE:HG21	1.97	0.46
3:C:1541:TYR:HB3	3:C:1579:ILE:HD11	1.97	0.46
4:I:516:VAL:O	4:I:519:GLU:HB2	2.16	0.46
1:A:225:ILE:HD12	1:A:261:ILE:HD11	1.98	0.46
4:D:61:LYS:C	4:D:63:GLN:H	2.23	0.46
4:D:296:TRP:CD2	4:D:317:ILE:HD13	2.51	0.46
4:D:433:MET:HE1	4:D:436:LEU:HD23	1.97	0.46
4:I:449:SER:C	4:I:451:SER:N	2.74	0.46
3:C:1512:GLN:OE1	3:C:1512:GLN:HA	2.15	0.45
4:I:343:TRP:HB2	4:I:344:PRO:HD2	1.98	0.45
4:I:552:VAL:HG13	4:I:718:ILE:HG21	1.98	0.45
1:A:87:THR:HA	1:A:91:VAL:O	2.16	0.45
4:D:205:VAL:HG22	4:D:428:PHE:CD1	2.50	0.45
1:F:122:LEU:HD23	1:F:163:PRO:HB3	1.99	0.45
1:A:251:LYS:HD3	1:A:293:TYR:CZ	2.51	0.45
4:D:674:SER:HA	4:D:692:ILE:HG22	1.99	0.45
1:F:261:ILE:HD11	1:F:270:ALA:HA	1.98	0.45
4:I:13:SER:O	4:I:57:TRP:NE1	2.49	0.45
4:I:214:THR:HG22	4:I:236:ILE:HG12	1.98	0.45
4:I:402:VAL:HG11	4:I:414:ILE:HB	1.99	0.45
1:F:199:LEU:HA	1:F:200:PRO:HD3	1.83	0.45
3:C:1254:ASP:CG	3:C:1269:ARG:HH21	2.25	0.45
1:F:261:ILE:CD1	1:F:270:ALA:HA	2.46	0.45
1:F:286:GLU:HG2	1:F:286:GLU:O	2.16	0.45
1:F:562:VAL:C	1:F:564:VAL:H	2.25	0.45
1:F:564:VAL:HG12	1:F:565:LEU:HD23	1.98	0.45
4:I:296:TRP:O	4:I:297:VAL:HG23	2.16	0.45
3:C:1506:LEU:HB2	3:C:1559:TYR:CE2	2.49	0.45
4:D:700:CYS:HA	4:D:701:LYS:HA	1.47	0.45
1:F:20:LEU:HD12	1:F:20:LEU:HA	1.77	0.45
1:A:112:LYS:HB3	1:A:562:VAL:HG11	1.98	0.45
4:D:265:LYS:O	4:D:269:VAL:HG23	2.17	0.45
2:G:922:VAL:O	2:G:922:VAL:HG12	2.16	0.45
1:F:484:MET:HE1	1:F:498:PHE:CZ	2.52	0.45
4:I:469:PRO:HD2	4:I:470:TRP:CE3	2.51	0.45
1:A:398:LEU:HD22	1:A:402:ARG:CB	2.47	0.45
3:C:1578:ILE:HG22	3:C:1580:THR:CG2	2.44	0.45
2:G:804:LYS:O	2:G:805:ASN:HB2	2.17	0.45
1:F:108:ILE:HD13	1:F:177:ILE:HG22	1.98	0.45
2:G:926:ARG:HD2	3:H:1305:THR:OG1	2.17	0.45
3:H:1514:GLY:HA2	3:H:1545:ARG:NH1	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:268:LEU:O	4:I:272:ILE:HG12	2.17	0.45
4:I:443:MET:C	4:I:445:ASP:H	2.25	0.45
3:C:1509:ILE:HG12	3:C:1518:TYR:CD1	2.51	0.44
4:D:654:ARG:HA	4:D:722:GLN:HG3	1.99	0.44
1:F:44:LYS:HG3	1:F:46:LEU:HD12	1.99	0.44
4:D:606:LEU:HD12	4:D:606:LEU:C	2.42	0.44
1:F:423:LEU:HB2	1:F:502:TYR:HE2	1.82	0.44
1:F:454:ILE:HD11	1:F:502:TYR:CE1	2.52	0.44
1:F:481:LEU:HD23	1:F:481:LEU:C	2.42	0.44
4:D:82:HIS:HB3	4:D:150:ARG:NH1	2.32	0.44
1:F:170:VAL:HG11	1:F:194:VAL:HG11	1.99	0.44
1:F:240:PHE:CE1	1:F:260:ARG:HG3	2.52	0.44
4:I:170:LEU:HD23	4:I:193:CYS:HB3	1.99	0.44
4:I:337:VAL:O	4:I:341:MET:HG3	2.17	0.44
3:C:1493:ALA:HB2	3:C:1562:TRP:CZ3	2.52	0.44
3:C:1569:LEU:HD11	3:C:1578:ILE:HG13	1.99	0.44
4:D:106:CYS:SG	4:D:112:LEU:HB2	2.58	0.44
4:D:298:LYS:HB2	4:D:301:GLU:HG3	1.99	0.44
1:F:77:ARG:O	1:F:78:GLN:CB	2.66	0.44
1:F:525:THR:HG22	1:F:526:LEU:N	2.32	0.44
3:H:1349:TYR:CD2	3:H:1355:SER:HB3	2.53	0.44
4:I:61:LYS:HG3	4:I:65:GLN:HA	1.99	0.44
1:F:13:THR:C	1:F:67:ILE:O	2.61	0.44
3:C:1462:ILE:HG13	3:C:1471:ALA:HB2	2.00	0.44
1:A:142:GLU:HB3	1:A:150:LEU:CD1	2.47	0.44
1:A:233:GLU:HG3	2:B:817:TYR:CZ	2.52	0.44
3:C:1349:TYR:CG	3:C:1355:SER:HB3	2.53	0.44
4:D:78:CYS:HA	4:D:79:PRO:HD3	1.83	0.44
1:A:98:LEU:HD12	1:A:99:LEU:H	1.83	0.44
3:C:1508:ARG:O	3:C:1509:ILE:HG13	2.18	0.44
4:D:294:LYS:HD2	4:D:294:LYS:HA	1.64	0.44
4:D:563:TYR:CZ	4:D:569:PRO:HG3	2.53	0.44
1:F:33:ASP:HB3	1:F:35:PHE:CE2	2.52	0.44
1:F:35:PHE:CE1	1:F:48:GLN:NE2	2.86	0.44
1:F:146:PRO:HD3	1:F:175:TRP:NE1	2.33	0.44
1:F:328:THR:CG2	1:F:341:THR:O	2.66	0.44
2:G:773:THR:OG1	2:G:776:LYS:HB2	2.17	0.44
3:C:1435:LYS:HA	3:C:1446:CYS:O	2.17	0.44
1:F:13:THR:CG2	1:F:103:SER:OG	2.63	0.44
4:I:709:VAL:CG1	4:I:710:PRO:HD2	2.47	0.44
2:B:915:VAL:C	2:B:917:GLY:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:523:LEU:CD1	4:D:561:LEU:HD21	2.48	0.43
1:F:5:LEU:HB3	1:F:607:THR:HG22	2.00	0.43
1:F:54:ASN:OD1	1:F:56:ALA:HB3	2.18	0.43
1:F:558:VAL:HG11	1:F:563:TYR:HB2	2.00	0.43
4:I:449:SER:O	4:I:452:LEU:N	2.50	0.43
4:I:606:LEU:HD12	4:I:606:LEU:O	2.17	0.43
4:I:656:LEU:HG	4:I:719:ASN:HB2	2.01	0.43
1:A:493:ILE:CG2	1:A:494:PRO:HA	2.48	0.43
1:F:170:VAL:HG22	1:F:171:SER:H	1.82	0.43
1:F:576:ILE:O	1:F:580:ILE:HG12	2.18	0.43
1:F:576:ILE:HG22	1:F:577:TRP:N	2.32	0.43
4:I:57:TRP:O	4:I:58:SER:HB2	2.18	0.43
3:C:1593:GLU:HB3	3:C:1599:PHE:CD1	2.53	0.43
4:D:35:TYR:CD2	4:D:47:GLN:O	2.72	0.43
4:D:63:GLN:C	4:D:65:GLN:N	2.71	0.43
4:D:348:PRO:HA	4:D:349:PRO:HD3	1.84	0.43
4:D:642:ASP:O	4:D:644:VAL:N	2.51	0.43
1:F:484:MET:HG2	1:F:485:ASN:O	2.19	0.43
4:I:27:LEU:HB2	4:I:32:ALA:O	2.18	0.43
4:I:475:SER:CB	4:I:513:LYS:HE3	2.41	0.43
4:I:638:ALA:HB2	4:I:696:VAL:HG13	2.01	0.43
1:A:18:GLN:HA	1:A:64:THR:HA	1.99	0.43
1:A:406:LYS:HG3	1:A:407:SER:N	2.33	0.43
3:C:1266:ILE:CD1	3:C:1281:VAL:HG11	2.48	0.43
3:C:1328:GLU:OE1	3:C:1344:LYS:HE2	2.18	0.43
3:C:1545:ARG:C	3:C:1547:CYS:N	2.73	0.43
3:C:1616:PHE:HD2	4:D:324:LEU:O	2.01	0.43
1:F:4:THR:OG1	1:F:22:GLU:HB2	2.18	0.43
3:H:1356:THR:O	3:H:1357:MET:C	2.61	0.43
4:I:678:LEU:HD22	4:I:717:HIS:CG	2.54	0.43
3:C:1555:VAL:HG12	3:C:1556:ASN:OD1	2.19	0.43
4:D:405:VAL:HG23	4:D:406:GLY:H	1.82	0.43
4:D:633:ARG:C	4:D:635:ALA:H	2.26	0.43
3:H:1332:LEU:HD12	3:H:1340:ALA:HB3	2.01	0.43
4:I:265:LYS:HD2	4:I:314:LEU:O	2.17	0.43
1:A:107:PHE:CE1	1:A:576:ILE:HA	2.54	0.43
1:A:375:LYS:C	1:A:376:LEU:HD23	2.43	0.43
1:A:578:ASP:O	1:A:582:LYS:HG2	2.18	0.43
2:B:844:TYR:CE2	3:C:1430:GLN:NE2	2.87	0.43
3:C:1266:ILE:HD13	3:C:1281:VAL:HG11	2.01	0.43
3:C:1545:ARG:O	3:C:1546:LYS:C	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:405:VAL:HG13	4:I:406:GLY:N	2.34	0.43
4:I:545:PRO:HB2	4:I:546:GLU:H	1.72	0.43
3:C:1478:LEU:HG	3:C:1553:LEU:HD23	2.01	0.43
4:I:49:ARG:HH21	4:I:58:SER:H	1.66	0.43
4:D:296:TRP:CE2	4:D:317:ILE:HD13	2.53	0.43
1:F:61:VAL:C	1:F:63:PRO:HD3	2.44	0.43
1:F:160:PHE:CD2	1:F:160:PHE:C	2.97	0.43
4:I:14:LEU:CD2	4:I:26:LEU:HD21	2.46	0.43
1:A:39:PHE:CG	1:A:40:PRO:HA	2.54	0.42
2:B:901:SER:HA	3:C:1305:THR:O	2.17	0.42
2:B:926:ARG:HD2	3:C:1305:THR:OG1	2.19	0.42
2:B:939:THR:HB	3:C:1283:THR:HG22	2.00	0.42
1:F:356:PRO:HA	1:F:367:THR:HA	2.01	0.42
3:C:1562:TRP:CD1	3:C:1562:TRP:C	2.97	0.42
4:D:372:ASP:OD2	4:D:374:ILE:HD12	2.19	0.42
1:F:230:LEU:HD22	1:F:560:LYS:HB3	2.01	0.42
2:G:821:ASP:OD1	2:G:851:LYS:HD2	2.19	0.42
4:I:703:GLN:HB3	4:I:704:LYS:H	1.69	0.42
4:I:724:LEU:HD23	4:I:724:LEU:HA	1.83	0.42
1:A:191:TYR:HB2	1:A:569:TYR:CD1	2.54	0.42
3:C:1366:THR:HG22	3:C:1426:VAL:HG21	2.01	0.42
1:F:12:ARG:O	1:F:13:THR:O	2.37	0.42
4:I:324:LEU:HG	4:I:325:LYS:HG3	2.01	0.42
4:I:358:VAL:HG22	4:I:399:ASP:HB2	2.02	0.42
4:I:461:LYS:HB3	4:I:461:LYS:HE2	1.68	0.42
2:B:715:ASP:C	2:B:717:PHE:H	2.27	0.42
1:F:423:LEU:HD12	1:F:424:HIS:N	2.34	0.42
4:I:33:LEU:C	4:I:33:LEU:HD12	2.44	0.42
4:I:78:CYS:HA	4:I:79:PRO:HD3	1.87	0.42
4:I:376:VAL:O	4:I:379:GLU:HB2	2.19	0.42
1:A:169:LEU:HD21	3:C:1306:PHE:CG	2.54	0.42
3:C:1463:CYS:C	3:C:1464:ILE:HD12	2.45	0.42
4:D:478:ARG:HA	4:D:479:PRO:HD2	1.81	0.42
4:D:631:CYS:HA	4:D:714:ARG:HE	1.83	0.42
4:I:12:CYS:HB2	4:I:57:TRP:CE2	2.55	0.42
4:I:352:TRP:C	4:I:354:ARG:H	2.27	0.42
4:I:457:TRP:HD1	4:I:459:HIS:NE2	2.18	0.42
1:A:111:ASP:OD2	1:A:112:LYS:HG3	2.19	0.42
3:C:1251:LEU:CD1	3:C:1297:GLY:HA3	2.41	0.42
3:C:1358:THR:CG2	3:C:1359:ILE:N	2.82	0.42
3:C:1588:TRP:O	3:C:1589:PRO:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:19:ILE:HD13	4:D:35:TYR:CD1	2.54	0.42
4:D:405:VAL:CG2	4:D:406:GLY:N	2.83	0.42
4:D:708:GLN:O	4:D:709:VAL:CG1	2.67	0.42
1:F:35:PHE:CE1	1:F:48:GLN:CD	2.98	0.42
4:I:557:LEU:HD13	4:I:561:LEU:HD21	2.01	0.42
1:A:34:ILE:O	1:A:48:GLN:HA	2.19	0.42
1:A:253:SER:C	1:A:255:PRO:HD3	2.43	0.42
3:C:1620:THR:OXT	4:D:253:SER:HB2	2.20	0.42
4:D:626:ASP:OD1	4:D:626:ASP:N	2.52	0.42
1:F:182:GLU:O	1:F:183:HIS:HB2	2.20	0.42
1:F:331:TYR:HA	1:F:411:ILE:O	2.20	0.42
4:D:164:TYR:CG	4:D:191:PRO:HG2	2.54	0.42
4:D:251:ASP:HA	4:D:289:TYR:CE2	2.55	0.42
4:D:439:VAL:HG12	4:D:443:MET:HE3	2.02	0.42
4:D:724:LEU:N	4:D:725:PRO:CD	2.82	0.42
1:F:170:VAL:HG22	1:F:171:SER:N	2.35	0.42
4:I:347:VAL:HA	4:I:348:PRO:HD3	1.86	0.42
1:A:166:LEU:HA	1:A:167:PRO:HD3	1.83	0.42
2:B:743:GLU:HA	2:B:744:PRO:HD3	1.91	0.42
4:D:402:VAL:HG11	4:D:414:ILE:HB	2.02	0.42
4:D:579:THR:CG2	4:D:588:THR:HB	2.50	0.42
4:D:728:LYS:O	4:D:732:GLN:HB3	2.20	0.42
1:F:293:TYR:CD1	1:F:293:TYR:C	2.98	0.42
2:G:910:PRO:HG2	3:H:1253:LEU:HD21	2.02	0.42
4:D:13:SER:HB2	4:D:15:GLU:OE1	2.20	0.42
1:F:182:GLU:O	1:F:183:HIS:CB	2.67	0.42
1:F:415:THR:HG22	1:F:421:ASN:O	2.19	0.42
3:H:1569:LEU:HD23	3:H:1570:PRO:HD2	2.02	0.42
4:I:493:GLU:HG2	4:I:563:TYR:OH	2.20	0.42
4:I:710:PRO:HB3	4:I:712:HIS:CD2	2.55	0.42
1:A:588:THR:OG1	1:A:601:ASP:HB3	2.19	0.41
3:H:1545:ARG:C	3:H:1547:CYS:N	2.77	0.41
4:I:203:GLN:HB3	4:I:458:GLU:HG3	2.02	0.41
4:I:452:LEU:HD23	4:I:455:MET:HG3	2.02	0.41
2:B:931:ARG:NH1	2:B:935:THR:O	2.53	0.41
4:D:190:GLU:HA	4:D:191:PRO:HD3	1.83	0.41
1:F:493:ILE:CG2	1:F:494:PRO:HA	2.51	0.41
2:G:946:ASP:HA	2:G:947:PRO:HD3	1.97	0.41
3:H:1589:PRO:HB2	3:H:1603:CYS:SG	2.60	0.41
4:I:363:THR:OG1	4:I:364:ASP:N	2.53	0.41
1:A:98:LEU:HD12	1:A:99:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:VAL:CG2	1:A:171:SER:N	2.83	0.41
4:D:269:VAL:HG22	4:D:314:LEU:HD23	2.01	0.41
1:F:339:GLU:HG2	1:F:377:ILE:CD1	2.50	0.41
4:I:597:LEU:O	4:I:599:PRO:HD2	2.20	0.41
1:A:157:ASP:O	1:A:159:ASN:N	2.51	0.41
1:A:556:VAL:HG23	2:B:735:TRP:HE3	1.86	0.41
2:B:931:ARG:HG2	2:B:932:VAL:O	2.21	0.41
3:C:1486:VAL:N	3:C:1487:PRO:CD	2.83	0.41
4:D:478:ARG:CZ	4:D:504:THR:HG23	2.50	0.41
4:D:498:THR:OG1	4:D:499:ALA:N	2.54	0.41
1:F:143:PHE:HB2	1:F:152:SER:HB3	2.02	0.41
3:H:1484:ILE:HB	3:H:1605:ASP:HB3	2.01	0.41
4:D:361:LEU:O	4:D:402:VAL:HA	2.20	0.41
4:D:611:GLU:O	4:D:612:GLU:HB2	2.20	0.41
4:D:636:GLN:OE1	4:D:647:ILE:HD11	2.21	0.41
2:G:941:ILE:HD11	3:H:1289:ILE:HD13	2.02	0.41
4:I:34:GLU:HG2	4:I:35:TYR:N	2.35	0.41
4:I:358:VAL:O	4:I:358:VAL:HG12	2.20	0.41
4:I:469:PRO:HD2	4:I:470:TRP:CZ3	2.56	0.41
2:B:728:ASP:C	2:B:730:PRO:HD3	2.45	0.41
4:D:199:TYR:CE1	4:D:429:LYS:HE2	2.56	0.41
1:F:107:PHE:CE1	1:F:576:ILE:HA	2.56	0.41
4:I:121:GLN:C	4:I:123:ASN:H	2.29	0.41
4:I:271:LEU:O	4:I:275:VAL:HG23	2.20	0.41
4:I:406:GLY:O	4:I:407:PRO:C	2.64	0.41
4:I:444:ILE:O	4:I:444:ILE:HG22	2.20	0.41
3:C:1365:LEU:HB2	3:C:1368:PHE:HD2	1.83	0.41
4:I:112:LEU:HD21	4:I:116:ALA:HA	2.03	0.41
4:I:393:PRO:O	4:I:394:ARG:HB2	2.20	0.41
2:B:888:ARG:HH21	4:D:150:ARG:HH11	1.68	0.41
3:C:1516:ASP:OD2	3:C:1548:GLN:HG2	2.21	0.41
4:D:732:GLN:HG3	4:D:733:ASP:OD1	2.20	0.41
3:H:1255:ILE:O	3:H:1267:ARG:HA	2.20	0.41
3:H:1315:ALA:O	3:H:1317:VAL:HG22	2.20	0.41
3:H:1500:TYR:O	3:H:1562:TRP:HB2	2.21	0.41
4:I:89:TYR:CE2	4:I:92:ARG:HG2	2.55	0.41
1:A:413:TYR:CD1	1:A:593:GLN:O	2.73	0.41
2:B:718:ILE:HD13	2:B:718:ILE:HA	1.87	0.41
3:C:1504:THR:O	3:C:1558:ASP:HA	2.21	0.41
3:C:1506:LEU:HD23	3:C:1554:LYS:O	2.21	0.41
4:D:164:TYR:CD2	4:D:191:PRO:HG2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:540:LYS:HE2	4:D:540:LYS:HB3	1.71	0.41
1:F:3:TYR:CG	1:F:91:VAL:HG22	2.56	0.41
1:F:119:SER:HB2	1:F:120:PRO:HD2	2.03	0.41
1:F:142:GLU:HB3	1:F:150:LEU:HD11	2.01	0.41
1:F:297:THR:HG23	1:F:308:VAL:HG22	2.03	0.41
1:F:432:ILE:HD13	1:F:438:LEU:HD11	2.02	0.41
1:F:530:GLY:HA3	2:G:784:TYR:CZ	2.55	0.41
2:G:897:GLY:HA2	3:H:1311:LEU:HD22	2.03	0.41
2:G:901:SER:HB3	3:H:1306:PHE:CD1	2.55	0.41
3:H:1610:SER:O	3:H:1614:THR:HG23	2.21	0.41
4:I:59:THR:HG22	4:I:60:LEU:N	2.36	0.41
4:I:407:PRO:O	4:I:408:LEU:CB	2.61	0.41
4:I:702:ASN:O	4:I:703:GLN:C	2.64	0.41
3:H:1330:ILE:HG13	3:H:1332:LEU:HG	2.03	0.41
4:I:18:GLU:O	4:I:19:ILE:HB	2.21	0.41
1:A:229:TYR:CZ	1:A:235:VAL:HG22	2.56	0.40
1:A:540:ALA:HB2	2:B:757:TYR:CE1	2.56	0.40
4:D:406:GLY:HA3	4:D:407:PRO:HD3	1.85	0.40
1:F:118:GLY:HA2	1:F:166:LEU:O	2.21	0.40
1:F:336:MET:HE1	1:F:422:TYR:HB2	2.03	0.40
4:I:350:GLU:O	4:I:350:GLU:HG3	2.20	0.40
1:A:95:LYS:HA	1:A:95:LYS:HD2	1.84	0.40
2:B:941:ILE:CG2	3:C:1301:MET:HE2	2.51	0.40
4:D:601:GLN:HG2	4:D:602:ASP:N	2.36	0.40
2:G:728:ASP:C	2:G:730:PRO:HD3	2.46	0.40
3:H:1333:ASN:OD1	3:H:1333:ASN:C	2.63	0.40
4:I:28:GLN:O	4:I:29:GLU:HB2	2.20	0.40
4:I:406:GLY:O	4:I:407:PRO:O	2.39	0.40
4:I:704:LYS:O	4:I:705:ARG:C	2.63	0.40
1:A:246:LYS:O	1:A:246:LYS:HG2	2.20	0.40
4:D:432:ASP:HB2	4:D:435:ASN:ND2	2.33	0.40
4:D:641:TYR:CD2	4:D:641:TYR:N	2.90	0.40
1:F:54:ASN:HB2	1:F:55:PRO:HD2	2.03	0.40
3:H:1353:VAL:HG23	3:H:1354:ASP:O	2.21	0.40
4:I:703:GLN:O	4:I:704:LYS:HB3	2.22	0.40
1:A:72:VAL:O	1:A:73:SER:HB3	2.21	0.40
1:A:102:GLN:HG3	1:A:186:GLU:HB2	2.04	0.40
1:F:44:LYS:HG3	1:F:46:LEU:CD1	2.52	0.40
4:I:251:ASP:OD1	4:I:251:ASP:C	2.64	0.40
4:I:522:ASP:OD1	4:I:522:ASP:N	2.52	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	607/627 (97%)	577 (95%)	26 (4%)	4 (1%)	18	53
1	F	613/627 (98%)	571 (93%)	36 (6%)	6 (1%)	12	45
2	B	231/252 (92%)	218 (94%)	13 (6%)	0	100	100
2	G	231/252 (92%)	218 (94%)	12 (5%)	1 (0%)	30	65
3	C	353/379 (93%)	318 (90%)	29 (8%)	6 (2%)	7	32
3	H	362/379 (96%)	333 (92%)	24 (7%)	5 (1%)	9	36
4	D	687/741 (93%)	608 (88%)	63 (9%)	16 (2%)	5	25
4	I	694/741 (94%)	605 (87%)	65 (9%)	24 (4%)	3	16
All	All	3778/3998 (94%)	3448 (91%)	268 (7%)	62 (2%)	7	34

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	247	ILE
4	D	44	TYR
4	D	46	VAL
4	D	344	PRO
4	D	505	VAL
4	D	539	LYS
4	D	713	ALA
1	F	13	THR
1	F	75	ASP
1	F	79	ASN
3	H	1313	GLU
3	H	1317	VAL
4	I	19	ILE
4	I	38	PRO
4	I	61	LYS
4	I	305	SER
4	I	407	PRO

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Mol	Chain	Res	Type
4	I	447	SER
4	I	448	GLN
4	I	449	SER
4	I	450	LEU
4	I	545	PRO
4	I	702	ASN
4	I	704	LYS
1	A	593	GLN
3	C	1549	GLU
3	C	1591	GLU
4	D	345	ASP
4	D	431	LYS
4	D	709	VAL
4	D	737	GLY
1	F	619	ALA
2	G	917	GLY
3	H	1357	MET
4	I	290	ALA
4	I	304	SER
4	I	462	GLY
4	I	465	TYR
4	I	703	GLN
4	I	706	GLN
4	I	737	GLY
1	A	158	LEU
4	D	58	SER
4	D	290	ALA
4	D	643	LYS
1	F	248	ASP
3	C	1318	CYS
4	D	714	ARG
1	F	77	ARG
3	H	1600	GLN
4	I	62	THR
4	I	408	LEU
4	I	705	ARG
1	A	249	ASP
3	C	1443	ASP
3	C	1550	ALA
4	D	20	LYS
3	H	1531	ASP
4	I	504	THR

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Mol	Chain	Res	Type
3	C	1427	GLY
4	D	511	SER
4	I	17	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	535/548 (98%)	524 (98%)	11 (2%)	47	75
1	F	539/548 (98%)	520 (96%)	19 (4%)	32	65
2	B	210/227 (92%)	197 (94%)	13 (6%)	16	49
2	G	210/227 (92%)	201 (96%)	9 (4%)	26	60
3	C	329/345 (95%)	310 (94%)	19 (6%)	18	51
3	H	335/345 (97%)	323 (96%)	12 (4%)	31	65
4	D	610/643 (95%)	587 (96%)	23 (4%)	29	63
4	I	615/643 (96%)	596 (97%)	19 (3%)	35	68
All	All	3383/3526 (96%)	3258 (96%)	125 (4%)	30	64

All (125) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	72	VAL
1	A	138	THR
1	A	219	GLU
1	A	235	VAL
1	A	400	ARG
1	A	427	ILE
1	A	475	ARG
1	A	476	ARG
1	A	514	VAL
1	A	536	MET
2	B	737	THR

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Mol	Chain	Res	Type
2	B	755	SER
2	B	810	ILE
2	B	824	VAL
2	B	826	VAL
2	B	828	LEU
2	B	862	ILE
2	B	898	VAL
2	B	915	VAL
2	B	923	ILE
2	B	926	ARG
2	B	928	LEU
2	B	930	ASP
3	C	1255	ILE
3	C	1326	SER
3	C	1341	LEU
3	C	1356	THR
3	C	1387	SER
3	C	1402	ILE
3	C	1421	LEU
3	C	1447	THR
3	C	1475	CYS
3	C	1478	LEU
3	C	1507	LEU
3	C	1544	GLN
3	C	1548	GLN
3	C	1551	LEU
3	C	1553	LEU
3	C	1562	TRP
3	C	1578	ILE
3	C	1585	ILE
3	C	1613	LEU
4	D	14	LEU
4	D	19	ILE
4	D	47	GLN
4	D	48	THR
4	D	64	ASP
4	D	98	VAL
4	D	111	THR
4	D	165	HIS
4	D	175	SER
4	D	201	THR
4	D	203	GLN

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Mol	Chain	Res	Type
4	D	429	LYS
4	D	430	VAL
4	D	505	VAL
4	D	541	GLU
4	D	608	VAL
4	D	654	ARG
4	D	699	VAL
4	D	709	VAL
4	D	714	ARG
4	D	728	LYS
4	D	738	PHE
4	D	739	LEU
1	F	13	THR
1	F	64	THR
1	F	74	THR
1	F	138	THR
1	F	159	ASN
1	F	233	GLU
1	F	261	ILE
1	F	295	SER
1	F	309	THR
1	F	328	THR
1	F	415	THR
1	F	483	THR
1	F	503	GLN
1	F	560	LYS
1	F	562	VAL
1	F	564	VAL
1	F	568	LYS
1	F	576	ILE
1	F	610	THR
2	G	715	ASP
2	G	753	THR
2	G	791	VAL
2	G	918	THR
2	G	922	VAL
2	G	926	ARG
2	G	928	LEU
2	G	930	ASP
2	G	943	ILE
3	H	1253	LEU
3	H	1311	LEU

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Mol	Chain	Res	Type
3	H	1312	GLN
3	H	1316	ASN
3	H	1320	LYS
3	H	1353	VAL
3	H	1356	THR
3	H	1402	ILE
3	H	1469	ARG
3	H	1478	LEU
3	H	1562	TRP
3	H	1578	ILE
4	I	18	GLU
4	I	62	THR
4	I	76	ILE
4	I	111	THR
4	I	130	THR
4	I	216	THR
4	I	239	ASP
4	I	342	SER
4	I	374	ILE
4	I	427	VAL
4	I	461	LYS
4	I	463	THR
4	I	468	GLN
4	I	505	VAL
4	I	608	VAL
4	I	654	ARG
4	I	697	VAL
4	I	703	GLN
4	I	705	ARG

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

Mol	Chain	Res	Type
1	A	54	ASN
1	A	437	ASN
1	A	593	GLN
2	B	819	ASN
2	B	870	HIS
3	C	1441	ASN
3	C	1528	GLN
3	C	1540	GLN
4	D	47	GLN

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Mol	Chain	Res	Type
4	D	537	ASN
4	D	601	GLN
1	F	90	GLN
1	F	395	HIS
1	F	437	ASN
1	F	443	ASN
1	F	453	GLN
1	F	473	GLN
1	F	506	ASN
1	F	593	GLN
2	G	815	HIS
3	H	1393	ASN
3	H	1540	GLN
4	I	565	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 ⓘ

4 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	E	1	5,4	14,14,15	0.50	0	17,19,21	1.86	5 (29%)
5	NAG	E	2	5	14,14,15	0.49	0	17,19,21	1.06	1 (5%)
5	NAG	J	1	5,4	14,14,15	0.42	0	17,19,21	1.13	1 (5%)
5	NAG	J	2	5	14,14,15	0.48	0	17,19,21	1.11	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	E	1	5,4	-	4/6/23/26	0/1/1/1
5	NAG	E	2	5	-	3/6/23/26	0/1/1/1
5	NAG	J	1	5,4	-	4/6/23/26	0/1/1/1
5	NAG	J	2	5	-	5/6/23/26	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1	NAG	C1-O5-C5	4.57	118.31	112.19
5	J	2	NAG	O5-C5-C6	3.22	113.92	107.66
5	J	1	NAG	C1-O5-C5	3.22	116.50	112.19
5	E	1	NAG	C2-N2-C7	2.98	126.90	122.90
5	E	1	NAG	C3-C4-C5	2.77	115.26	110.23
5	E	2	NAG	C1-O5-C5	2.67	115.77	112.19
5	E	1	NAG	O5-C5-C4	2.30	116.41	110.83
5	J	2	NAG	C1-O5-C5	2.09	114.99	112.19
5	E	1	NAG	C4-C3-C2	-2.06	108.00	111.02

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	1	NAG	C3-C2-N2-C7
5	E	2	NAG	C8-C7-N2-C2
5	E	2	NAG	O7-C7-N2-C2
5	J	1	NAG	C8-C7-N2-C2
5	J	1	NAG	O7-C7-N2-C2
5	J	2	NAG	C3-C2-N2-C7
5	J	2	NAG	C8-C7-N2-C2
5	J	2	NAG	O7-C7-N2-C2
5	J	2	NAG	C4-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
5	J	2	NAG	O5-C5-C6-O6
5	E	1	NAG	C4-C5-C6-O6
5	J	1	NAG	C4-C5-C6-O6
5	J	1	NAG	O5-C5-C6-O6

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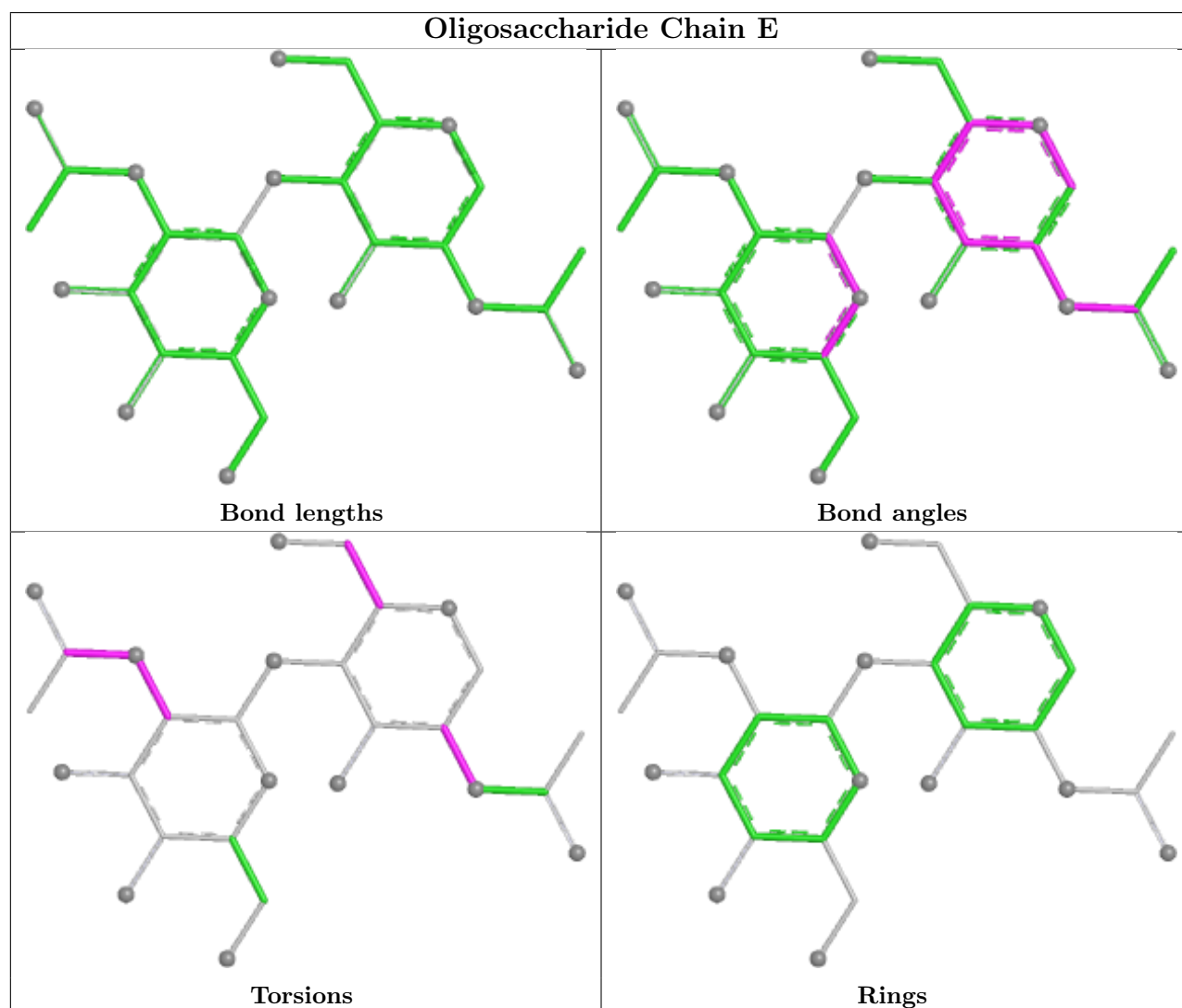
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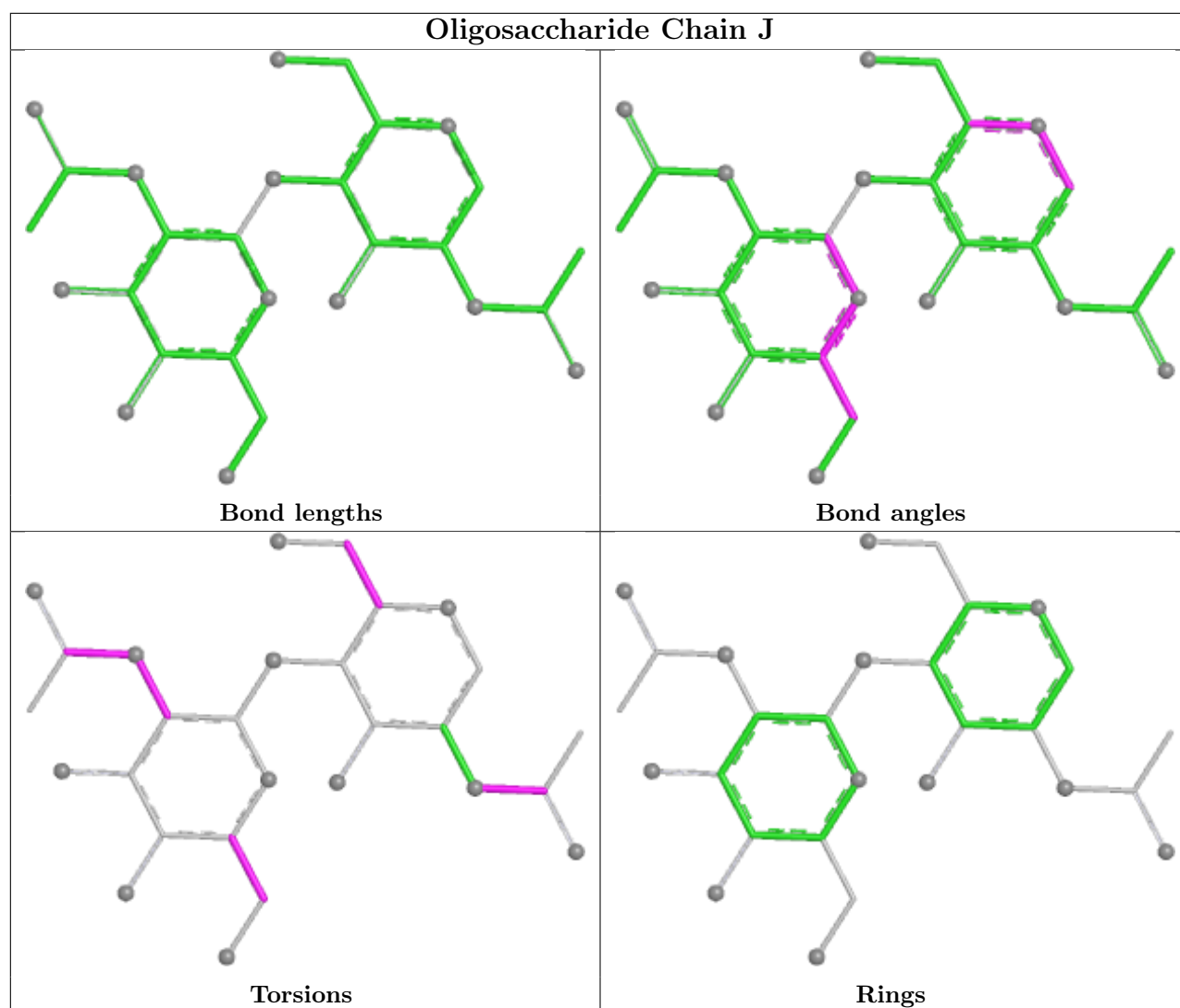
Mol	Chain	Res	Type	Atoms
5	E	1	NAG	C1-C2-N2-C7
5	E	2	NAG	C3-C2-N2-C7

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 [i](#)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

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	$\# Z > 2$
6	NAG	I	9117	4	14,14,15	0.44	0	17,19,21	1.10	1 (5%)
6	NAG	D	9117	4	14,14,15	0.36	0	17,19,21	2.45	4 (23%)
6	NAG	F	9187	1	14,14,15	0.44	0	17,19,21	1.37	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	D	9353	4	14,14,15	0.46	0	17,19,21	0.88	1 (5%)
6	NAG	A	9187	1	14,14,15	0.45	0	17,19,21	1.19	2 (11%)
6	NAG	C	9324	3	14,14,15	0.52	0	17,19,21	1.00	1 (5%)
6	NAG	H	9324	3	14,14,15	0.45	0	17,19,21	0.77	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	I	9117	4	-	4/6/23/26	0/1/1/1
6	NAG	D	9117	4	-	4/6/23/26	0/1/1/1
6	NAG	F	9187	1	-	3/6/23/26	0/1/1/1
6	NAG	D	9353	4	-	2/6/23/26	0/1/1/1
6	NAG	A	9187	1	-	3/6/23/26	0/1/1/1
6	NAG	C	9324	3	-	2/6/23/26	0/1/1/1
6	NAG	H	9324	3	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	9117	NAG	C1-O5-C5	8.61	123.73	112.19
6	F	9187	NAG	C1-O5-C5	3.84	117.33	112.19
6	A	9187	NAG	C1-O5-C5	3.43	116.79	112.19
6	I	9117	NAG	C1-O5-C5	3.42	116.76	112.19
6	C	9324	NAG	C1-O5-C5	3.24	116.52	112.19
6	D	9117	NAG	O5-C1-C2	3.00	115.93	111.29
6	D	9117	NAG	O5-C5-C4	2.73	117.46	110.83
6	D	9353	NAG	C1-O5-C5	2.71	115.82	112.19
6	A	9187	NAG	C2-N2-C7	-2.50	119.54	122.90
6	D	9117	NAG	C4-C3-C2	-2.43	107.45	111.02
6	F	9187	NAG	C3-C4-C5	2.31	114.42	110.23

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	9187	NAG	C8-C7-N2-C2
6	A	9187	NAG	O7-C7-N2-C2
6	C	9324	NAG	C8-C7-N2-C2
6	C	9324	NAG	O7-C7-N2-C2
6	D	9117	NAG	C8-C7-N2-C2
6	D	9117	NAG	O7-C7-N2-C2
6	D	9353	NAG	C8-C7-N2-C2
6	D	9353	NAG	O7-C7-N2-C2
6	H	9324	NAG	C8-C7-N2-C2
6	H	9324	NAG	O7-C7-N2-C2
6	I	9117	NAG	C8-C7-N2-C2
6	I	9117	NAG	O7-C7-N2-C2
6	D	9117	NAG	O5-C5-C6-O6
6	I	9117	NAG	O5-C5-C6-O6
6	F	9187	NAG	C8-C7-N2-C2
6	F	9187	NAG	O7-C7-N2-C2
6	D	9117	NAG	C4-C5-C6-O6
6	A	9187	NAG	O5-C5-C6-O6
6	I	9117	NAG	C4-C5-C6-O6
6	F	9187	NAG	O5-C5-C6-O6
6	H	9324	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	9187	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	613/627 (97%)	-0.69	0 100 100	31, 68, 125, 182	0
1	F	617/627 (98%)	-0.62	1 (0%) 91 83	37, 75, 132, 187	0
2	B	233/252 (92%)	-0.73	0 100 100	34, 63, 111, 123	0
2	G	233/252 (92%)	-0.69	0 100 100	33, 66, 115, 151	0
3	C	359/379 (94%)	-0.35	3 (0%) 82 64	40, 94, 210, 291	0
3	H	366/379 (96%)	-0.54	0 100 100	33, 81, 135, 216	0
4	D	699/741 (94%)	-0.36	1 (0%) 92 86	35, 88, 189, 233	0
4	I	704/741 (95%)	-0.41	1 (0%) 92 86	37, 91, 191, 244	0
All	All	3824/3998 (95%)	-0.52	6 (0%) 91 83	31, 79, 168, 291	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	1532	GLU	2.9
4	D	44	TYR	2.8
4	I	630	SER	2.4
3	C	1317	VAL	2.3
3	C	1552	ASN	2.2
1	F	13	THR	2.1

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

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

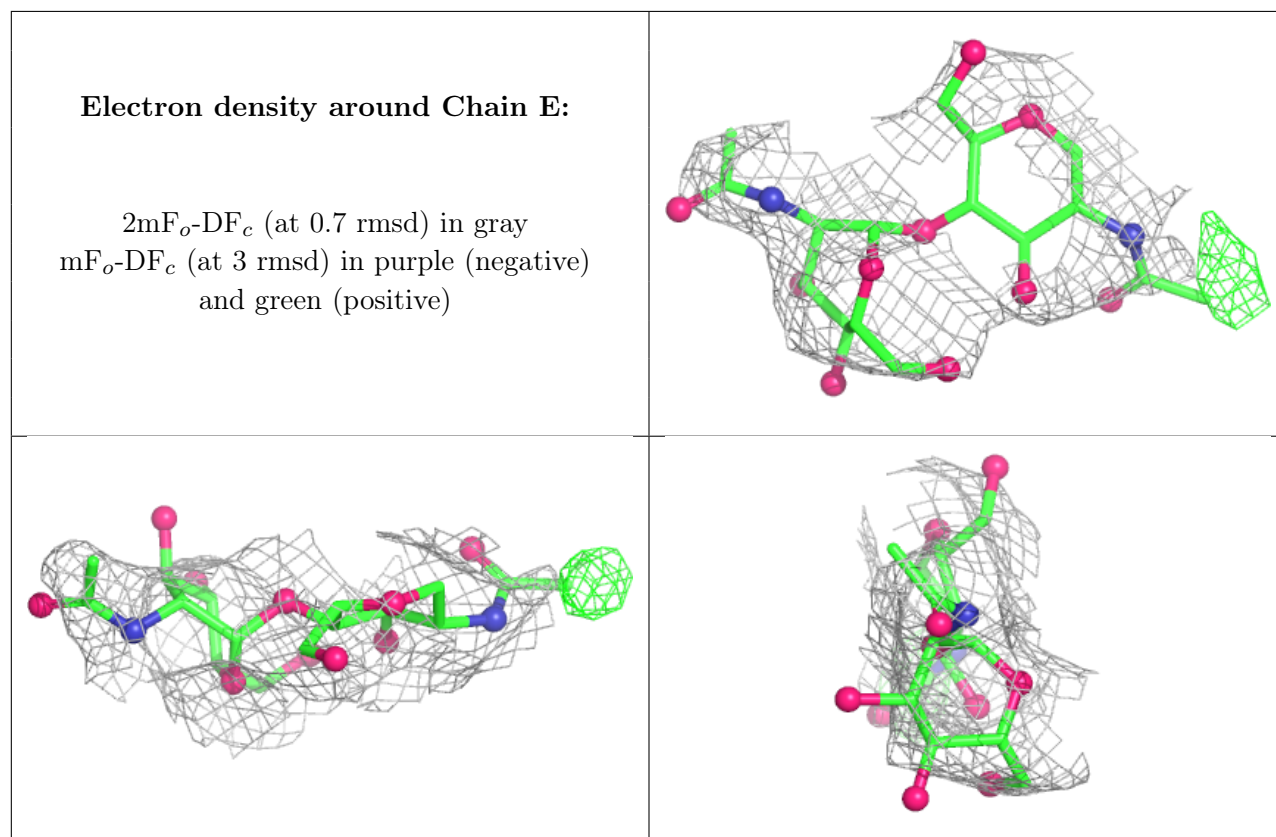
6.3 Carbohydrates ⓘ

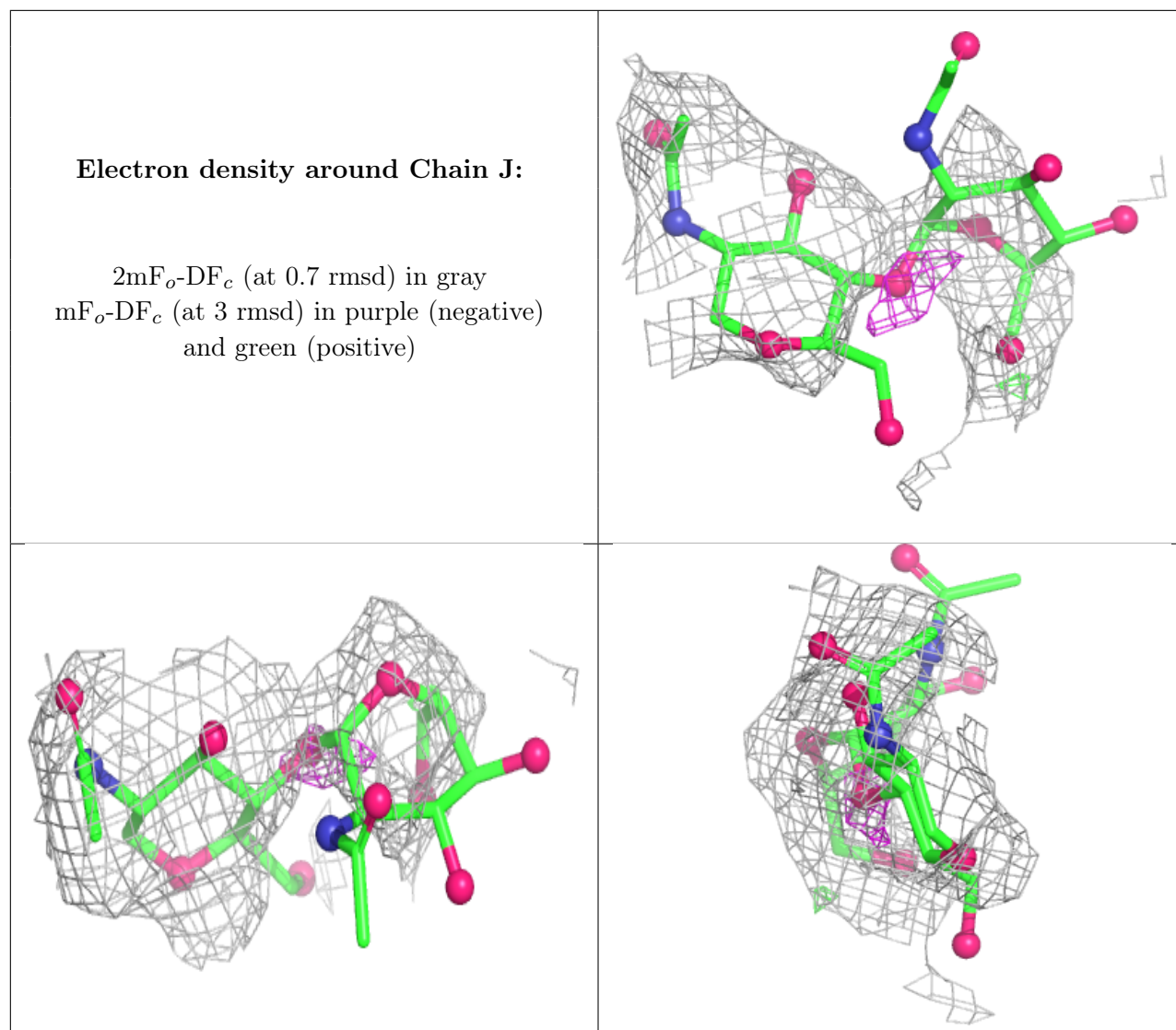
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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	E	1	14/15	-	-	136,146,153,163	0
5	NAG	E	2	14/15	-	-	161,168,182,183	0
5	NAG	J	2	14/15	0.50	0.12	173,184,194,201	0
5	NAG	J	1	14/15	0.71	0.10	126,139,157,173	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.





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
6	NAG	H	9324	14/15	0.24	0.16	129,140,144,146	0
6	NAG	C	9324	14/15	0.67	0.17	111,123,130,134	0
6	NAG	F	9187	14/15	0.69	0.14	106,116,125,127	0
6	NAG	D	9117	14/15	0.76	0.11	98,117,131,132	0
6	NAG	D	9353	14/15	0.78	0.08	122,136,142,146	0
6	NAG	A	9187	14/15	0.83	0.11	87,102,110,114	0
6	NAG	I	9117	14/15	0.83	0.10	116,129,142,143	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MG	F	628	1/1	0.98	0.07	73,73,73,73	0
7	MG	D	742	1/1	0.99	0.04	107,107,107,107	0
7	MG	A	628	1/1	0.99	0.05	105,105,105,105	0
7	MG	I	742	1/1	0.99	0.03	97,97,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.