



Full wwPDB EM Validation Report ⓘ

Oct 20, 2024 – 09:00 PM EDT

PDB ID : 8EYH
EMDB ID : EMD-28688
Title : SARS-CoV-2 spike protein bound with a nanobody
Authors : Laughlin, Z.T.; Patel, A.; Ortlund, E.A.
Deposited on : 2022-10-27
Resolution : 3.75 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

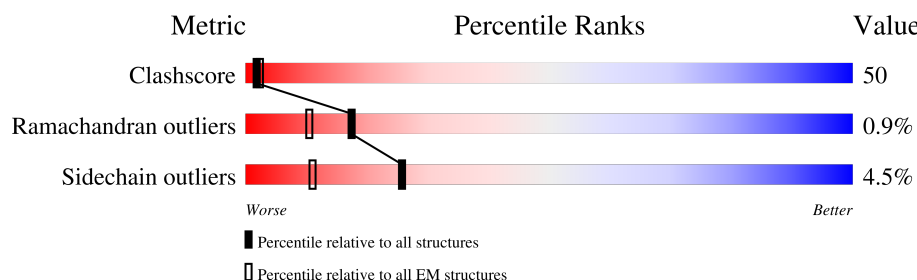
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	D	118	<div> <div>59%</div> <div>81%</div> <div>18%</div> <div>•</div> </div>
2	A	1136	<div> <div>37%</div> <div>37%</div> <div>54%</div> <div>• 6%</div> </div>
2	B	1136	<div> <div>36%</div> <div>35%</div> <div>57%</div> <div>• •</div> </div>
2	C	1136	<div> <div>42%</div> <div>36%</div> <div>54%</div> <div>• • 6%</div> </div>
3	E	2	<div> <div>50%</div> <div>100%</div> </div>
3	F	2	<div> <div>100%</div> <div>50%</div> <div>50%</div> </div>
3	G	2	<div> <div>50%</div> <div>50%</div> <div>50%</div> </div>
3	H	2	<div> <div>50%</div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
3	I	2	<div> <div>100%</div> <div>  </div> <div>100%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	I	1	-	-	X	-
4	NAG	C	1201	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 26575 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Nanobody.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	118	Total	C	N	O	S	0	0
			868	543	147	174	4		

- Molecule 2 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1088	Total	C	N	O	S	0	0
			8515	5436	1421	1620	38		
2	C	1067	Total	C	N	O	S	0	0
			8350	5327	1395	1589	39		
2	A	1069	Total	C	N	O	S	0	0
			8366	5339	1397	1591	39		

There are 18 discrepancies between the modelled and reference sequences:

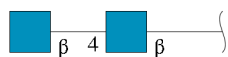
Chain	Residue	Modelled	Actual	Comment	Reference
B	817	PRO	PHE	conflict	UNP P0DTC2
B	892	PRO	ALA	conflict	UNP P0DTC2
B	899	PRO	ALA	conflict	UNP P0DTC2
B	942	PRO	ALA	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
C	817	PRO	PHE	conflict	UNP P0DTC2
C	892	PRO	ALA	conflict	UNP P0DTC2
C	899	PRO	ALA	conflict	UNP P0DTC2
C	942	PRO	ALA	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2
A	817	PRO	PHE	conflict	UNP P0DTC2
A	892	PRO	ALA	conflict	UNP P0DTC2
A	899	PRO	ALA	conflict	UNP P0DTC2
A	942	PRO	ALA	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2

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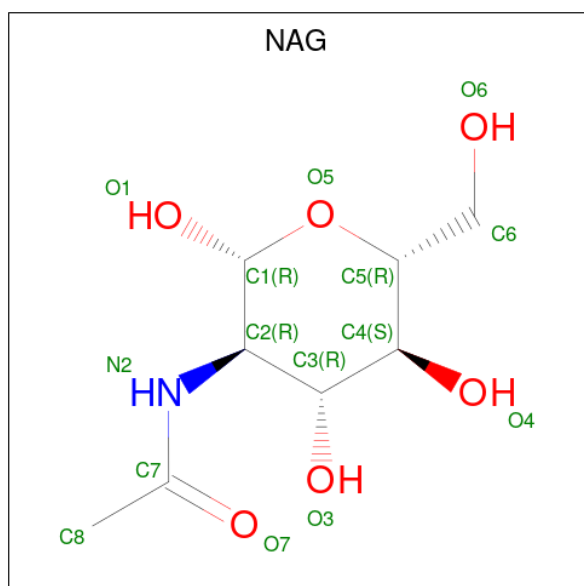
Chain	Residue	Modelled	Actual	Comment	Reference
A	987	PRO	VAL	conflict	UNP P0DTC2

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



Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		
3	G	2	Total	C	N	O	0	0
			28	16	2	10		
3	H	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



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

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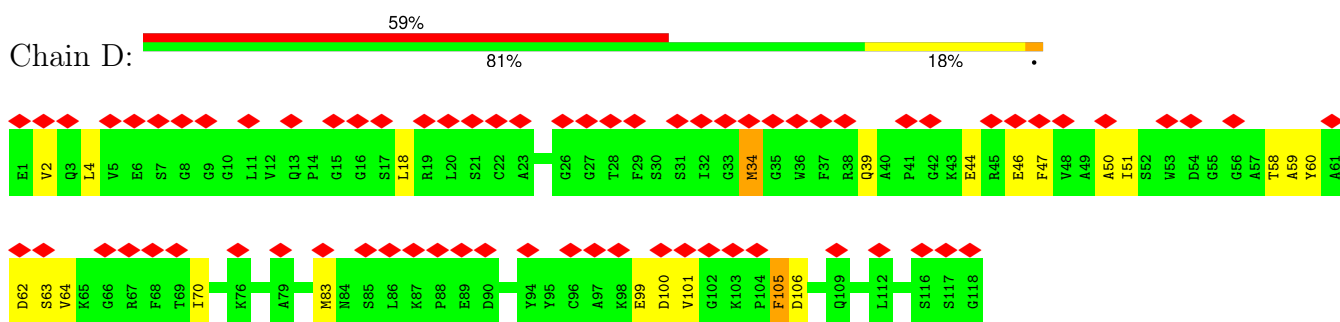
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Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	

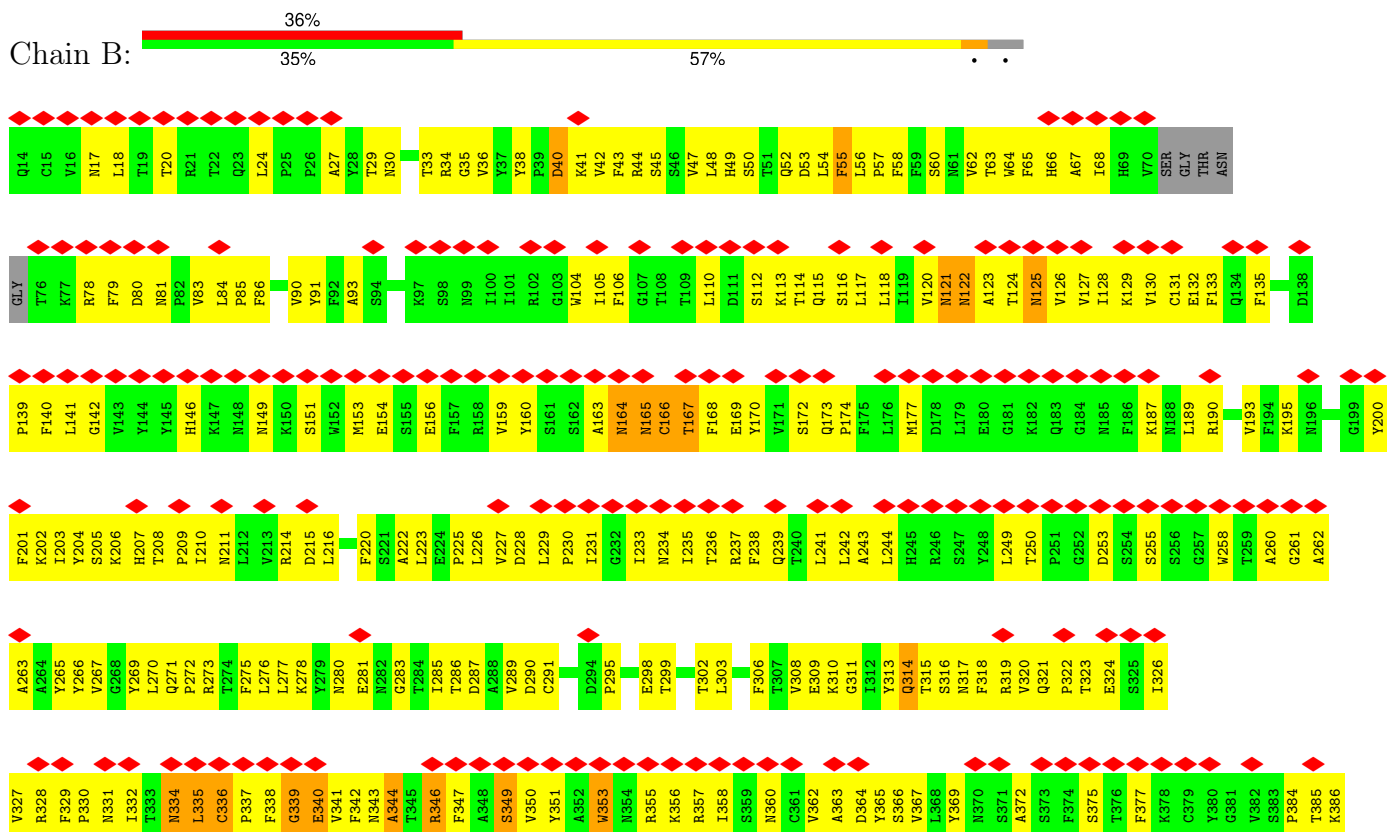
3 Residue-property plots

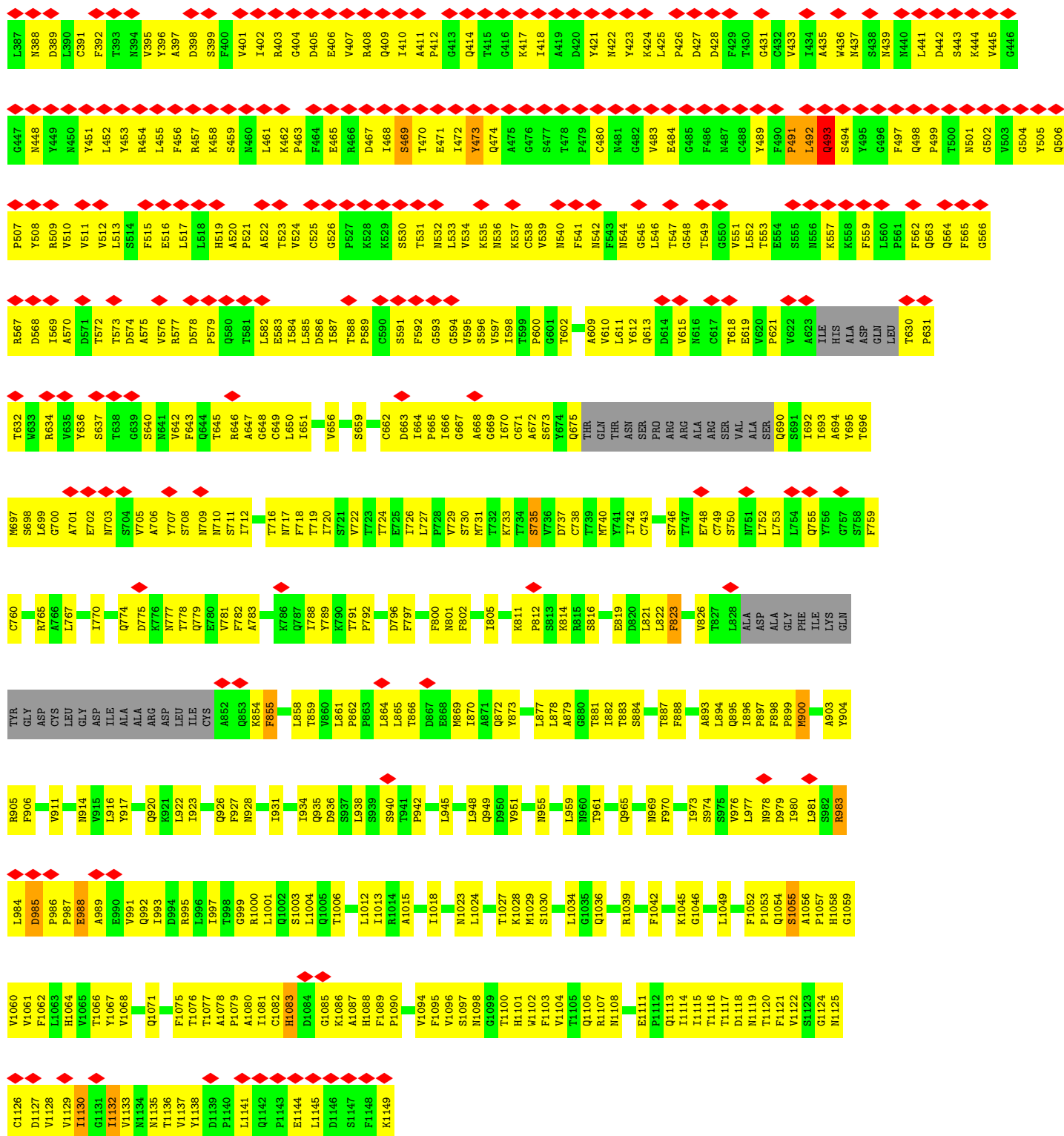
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Nanobody

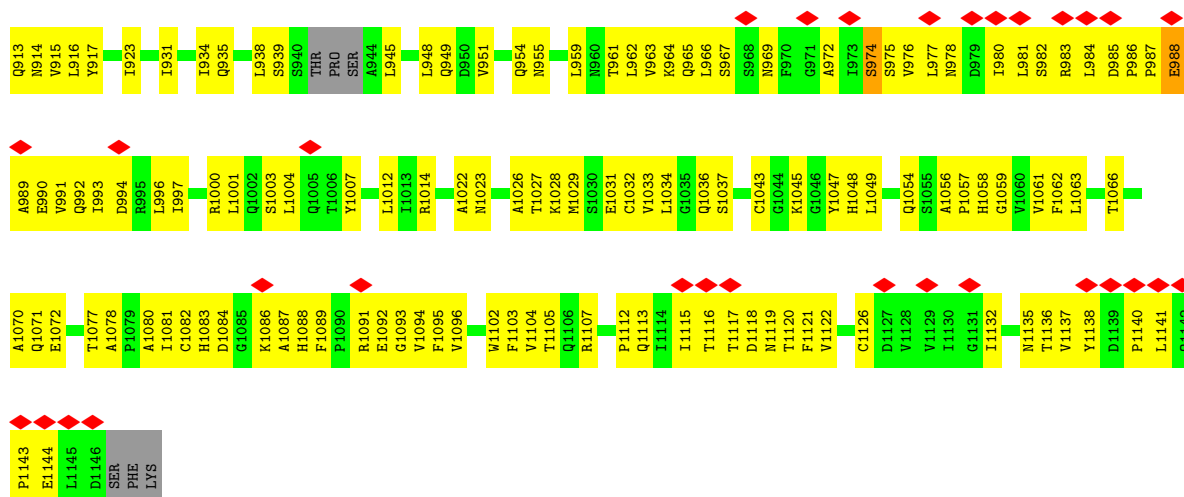


• Molecule 2: Spike glycoprotein

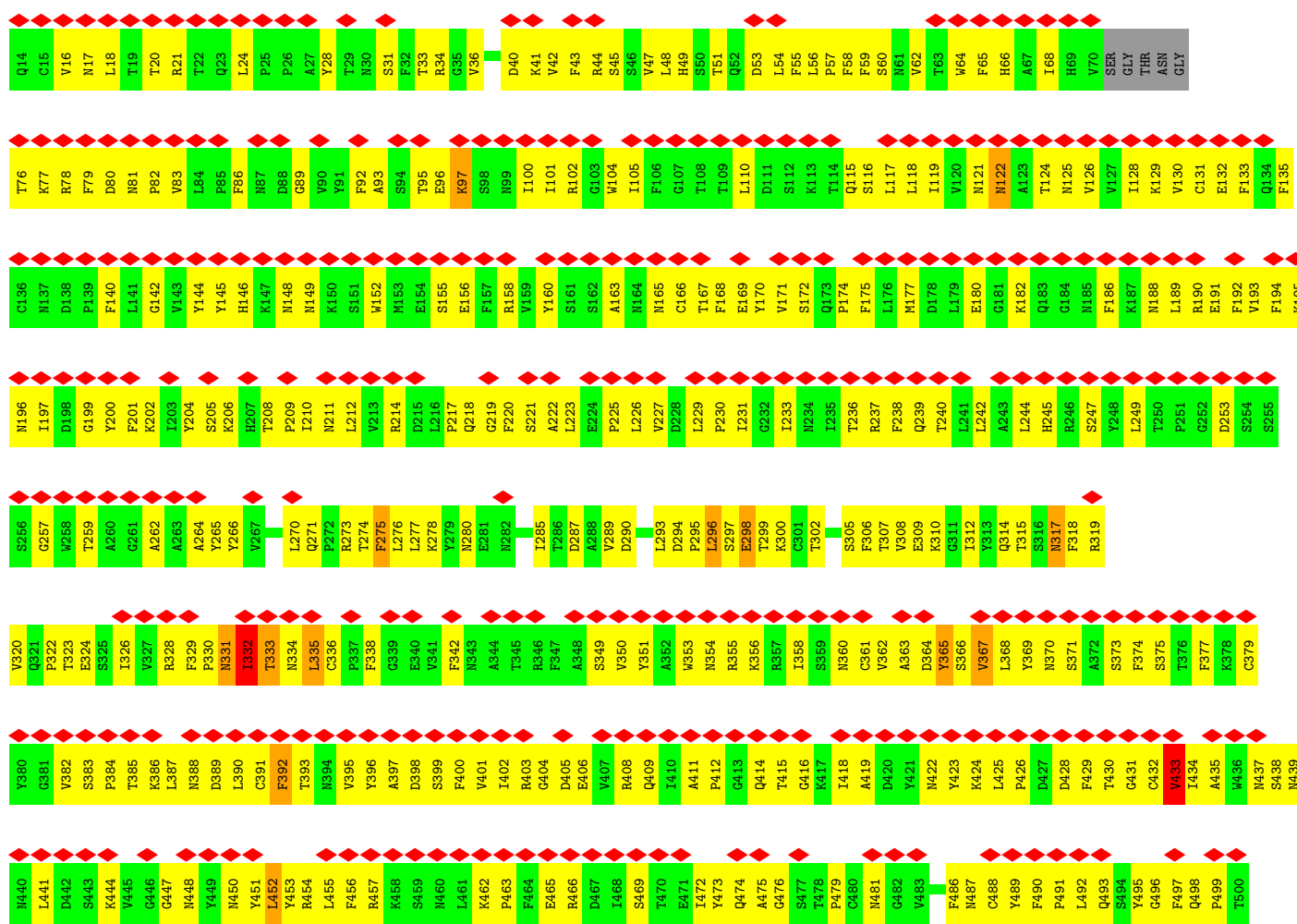


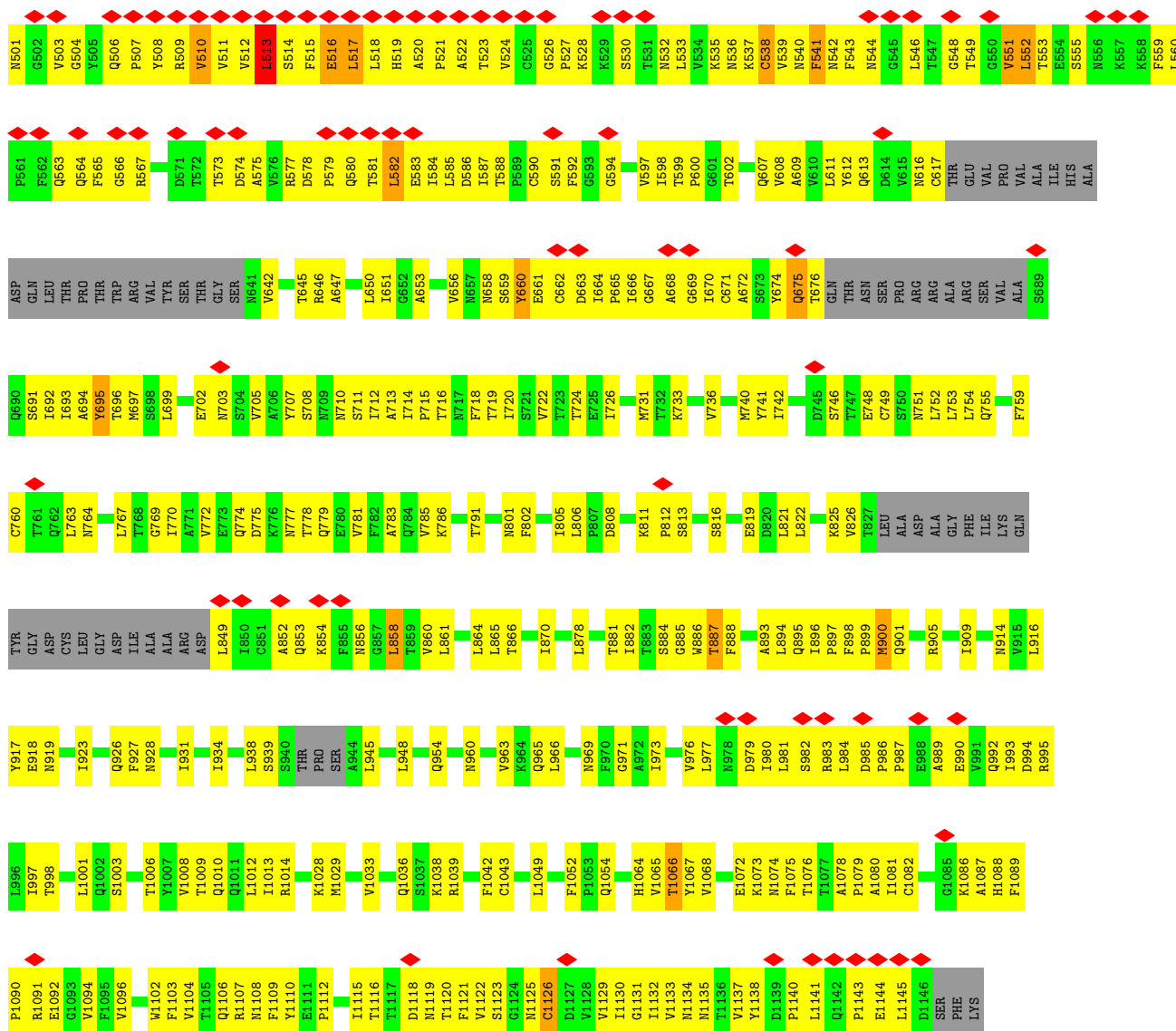






• Molecule 2: Spike glycoprotein





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



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



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



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	615492	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63.81	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	66.367	Depositor
Minimum map value	-45.933	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.755	Depositor
Recommended contour level	5	Depositor
Map size (Å)	444.7456, 444.7456, 444.7456	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0691, 1.0691, 1.0691	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	D	0.25	0/886	0.47	0/1198
2	A	0.29	0/8562	0.48	0/11654
2	B	0.29	0/8719	0.47	0/11874
2	C	0.30	0/8546	0.48	0/11632
All	All	0.29	0/26713	0.47	0/36358

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	D	868	0	831	18	0
2	A	8366	0	8167	880	0
2	B	8515	0	8324	1084	0
2	C	8350	0	8147	964	0
3	E	28	0	25	0	0
3	F	28	0	25	6	0
3	G	28	0	25	4	0
3	H	28	0	25	4	0
3	I	28	0	25	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	126	0	116	9	0
4	B	98	0	91	6	0
4	C	112	0	104	19	0
All	All	26575	0	25905	2628	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 50.

All (2628) 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)
2:B:343:ASN:HD21	3:I:1:NAG:C1	1.07	1.63
2:C:331:ASN:ND2	4:C:1201:NAG:C1	1.77	1.47
2:C:331:ASN:HD21	4:C:1201:NAG:C1	1.31	1.41
2:B:343:ASN:ND2	3:I:1:NAG:C1	1.93	1.30
2:A:334:ASN:HA	2:A:362:VAL:HG13	1.18	1.16
2:C:322:PRO:HB3	2:C:539:VAL:HA	1.28	1.14
2:A:546:LEU:HD21	2:A:573:THR:HG21	1.30	1.13
2:C:381:GLY:H	2:A:983:ARG:HB2	1.05	1.13
2:C:436:TRP:CH2	4:C:1208:NAG:H83	1.84	1.12
2:A:452:LEU:HD12	2:A:492:LEU:HB3	1.24	1.12
2:A:358:ILE:HB	2:A:395:VAL:HG21	1.31	1.11
2:C:724:THR:HG23	2:C:934:ILE:HD11	1.28	1.10
2:B:43:PHE:H	2:A:566:GLY:HA2	1.09	1.10
2:C:325:SER:HA	2:C:541:PHE:HA	1.09	1.08
2:C:600:PRO:HG3	2:C:692:ILE:HD11	1.24	1.08
2:B:570:ALA:HA	2:C:967:SER:HB2	1.35	1.07
2:C:410:ILE:HG13	2:C:425:LEU:HD21	1.31	1.07
2:C:805:ILE:HG22	2:C:878:LEU:HD21	1.34	1.07
2:B:322:PRO:HD3	2:C:745:ASP:HB2	1.32	1.06
2:C:391:CYS:HB2	2:C:525:CYS:HA	1.36	1.06
2:B:569:ILE:HG12	2:C:964:LYS:HG2	1.38	1.06
2:B:355:ARG:HB2	2:B:396:TYR:HB2	1.38	1.05
2:A:205:SER:HB3	2:A:226:LEU:HD22	1.39	1.04
2:B:386:LYS:HD2	2:C:983:ARG:HA	1.33	1.03
2:B:106:PHE:HB3	2:B:235:ILE:HD12	1.39	1.03
2:B:1121:PHE:HB2	2:C:1091:ARG:HD3	1.38	1.02
2:C:390:LEU:HD22	2:A:982:SER:HB3	1.42	1.01
2:C:436:TRP:HH2	4:C:1208:NAG:H83	1.15	1.00
2:B:775:ASP:HB3	2:B:864:LEU:HD12	1.42	1.00
2:A:206:LYS:HB2	2:A:223:LEU:HG	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1116:THR:HA	2:C:1138:TYR:H	1.25	0.99
2:B:203:ILE:HD12	2:B:227:VAL:HG23	1.44	0.98
2:B:410:ILE:HD12	2:B:425:LEU:HD13	1.42	0.98
2:C:187:LYS:HG3	2:C:211:ASN:HB2	1.45	0.98
2:A:770:ILE:HD11	2:A:1012:LEU:HA	1.43	0.98
2:A:34:ARG:HD3	2:A:219:GLY:HA3	1.42	0.97
2:C:858:LEU:HD21	2:C:962:LEU:HD22	1.47	0.97
2:C:328:ARG:HA	2:C:530:SER:HA	1.45	0.97
2:B:646:ARG:HA	2:C:862:PRO:HD2	1.43	0.97
2:C:733:LYS:HD2	2:C:771:ALA:HA	1.46	0.97
2:A:454:ARG:HB3	2:A:492:LEU:HD12	1.46	0.96
2:B:858:LEU:HD21	2:B:959:LEU:HD21	1.46	0.96
2:A:83:VAL:HG22	2:A:239:GLN:HB2	1.44	0.96
2:A:312:ILE:HG22	2:A:598:ILE:HG12	1.46	0.96
2:C:662:CYS:HB2	2:C:697:MET:HG3	1.47	0.96
2:A:329:PHE:HB2	2:A:528:LYS:HB3	1.48	0.96
2:B:895:GLN:HG2	2:A:705:VAL:HB	1.48	0.95
2:C:543:PHE:HZ	2:C:579:PRO:HD2	1.30	0.95
2:C:139:PRO:HB2	2:C:241:LEU:HD21	1.46	0.95
2:B:646:ARG:HB3	2:B:668:ALA:HB2	1.49	0.94
2:A:425:LEU:HD12	2:A:429:PHE:HA	1.47	0.93
2:C:1126:CYS:HB2	2:C:1132:ILE:HG21	1.51	0.93
2:B:552:LEU:HB3	2:B:585:LEU:HD21	1.47	0.93
2:B:822:LEU:HD21	2:B:1061:VAL:HG21	1.51	0.93
2:A:791:THR:HG21	2:A:806:LEU:HD13	1.49	0.93
2:C:485:GLY:H	2:C:488:CYS:HB2	1.34	0.92
2:B:86:PHE:HZ	2:B:238:PHE:HB3	1.32	0.92
2:C:331:ASN:HD22	4:C:1201:NAG:C1	1.75	0.92
2:B:709:ASN:HA	2:C:896:ILE:HG13	1.52	0.91
2:C:356:LYS:HB3	2:C:397:ALA:HB3	1.52	0.91
2:C:573:THR:HB	2:C:587:ILE:HG13	1.51	0.91
2:A:579:PRO:HB2	4:A:1202:NAG:H62	1.53	0.91
2:C:822:LEU:HD21	2:C:1061:VAL:HG21	1.53	0.90
2:C:381:GLY:N	2:A:983:ARG:HB2	1.85	0.90
2:B:48:LEU:HB3	2:B:276:LEU:HD11	1.53	0.90
2:C:331:ASN:ND2	4:C:1201:NAG:C2	2.35	0.90
2:A:559:PHE:HB2	2:A:577:ARG:HH21	1.36	0.90
2:A:650:LEU:HD11	2:A:666:ILE:HD13	1.51	0.90
2:C:308:VAL:HG22	2:C:602:THR:HG23	1.54	0.90
2:B:546:LEU:HD21	2:B:576:VAL:HG13	1.52	0.90
2:C:1115:ILE:HG22	2:C:1137:VAL:HA	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:334:ASN:H	2:B:362:VAL:HB	1.35	0.89
2:C:143:VAL:HG12	2:C:154:GLU:HG2	1.53	0.89
2:C:436:TRP:CH2	4:C:1208:NAG:C8	2.56	0.89
2:B:317:ASN:ND2	2:C:760:CYS:SG	2.46	0.89
2:C:24:LEU:HD12	2:C:25:PRO:HD2	1.53	0.88
2:C:472:ILE:HB	2:C:491:PRO:HB3	1.55	0.88
2:A:64:TRP:HE1	2:A:264:ALA:HB1	1.36	0.88
2:A:760:CYS:HB3	2:A:763:LEU:HD12	1.55	0.88
2:B:877:LEU:HD13	2:B:1029:MET:HE2	1.56	0.88
2:B:566:GLY:HA2	2:C:43:PHE:H	1.39	0.88
2:C:329:PHE:H	2:C:330:PRO:HD2	1.39	0.88
2:C:552:LEU:HD12	2:C:585:LEU:HB3	1.53	0.88
2:B:141:LEU:HD23	2:B:243:ALA:HB2	1.54	0.87
2:A:363:ALA:HB2	2:A:524:VAL:HB	1.56	0.87
2:B:499:PRO:HA	2:B:506:GLN:HG2	1.54	0.87
2:B:86:PHE:HB3	2:B:90:VAL:HG21	1.57	0.87
2:B:802:PHE:HD1	2:B:805:ILE:HD11	1.40	0.87
2:B:54:LEU:HD22	2:B:272:PRO:HB3	1.55	0.87
2:C:382:VAL:HG22	2:A:989:ALA:HB1	1.55	0.86
2:B:412:PRO:HA	2:B:427:ASP:HB3	1.56	0.86
2:C:452:LEU:HB3	2:C:492:LEU:HD21	1.57	0.86
2:A:1115:ILE:HG22	2:A:1137:VAL:HG12	1.57	0.86
2:C:325:SER:HA	2:C:541:PHE:CA	2.00	0.86
2:A:822:LEU:HD22	2:A:945:LEU:HD21	1.58	0.86
2:B:1145:LEU:HA	2:A:1145:LEU:HD21	1.58	0.86
2:C:328:ARG:HE	2:C:533:LEU:HD13	1.41	0.86
2:C:351:TYR:HB2	2:C:453:TYR:HA	1.58	0.86
2:B:336:CYS:H	2:B:363:ALA:HB2	1.40	0.85
2:A:535:LYS:HD2	2:A:536:ASN:HB2	1.58	0.85
2:C:390:LEU:HD11	2:A:983:ARG:HD2	1.57	0.85
2:B:27:ALA:HB3	2:B:64:TRP:HB3	1.58	0.85
2:B:437:ASN:HA	2:B:508:TYR:HB3	1.58	0.85
2:A:334:ASN:CA	2:A:362:VAL:HG13	2.05	0.84
2:B:57:PRO:HB3	2:B:273:ARG:HH12	1.43	0.84
2:B:326:ILE:HD12	2:B:533:LEU:HA	1.57	0.84
2:B:537:LYS:HG2	2:B:539:VAL:HG13	1.58	0.84
2:C:444:LYS:HB3	2:C:448:ASN:HB2	1.56	0.84
2:C:1083:HIS:ND1	2:C:1084:ASP:OD1	2.11	0.84
2:A:977:LEU:O	2:A:981:LEU:HD23	1.77	0.84
2:C:331:ASN:HD22	4:C:1201:NAG:C2	1.88	0.84
2:A:317:ASN:HA	2:A:594:GLY:HA2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:865:LEU:HD22	2:A:697:MET:HG3	1.59	0.84
2:B:567:ARG:HG2	2:B:573:THR:HA	1.57	0.83
2:C:216:LEU:HD21	2:C:266:TYR:HE2	1.43	0.83
2:A:1038:LYS:HA	2:A:1038:LYS:HE3	1.59	0.83
2:C:717:ASN:OD1	2:C:718:PHE:N	2.11	0.83
2:B:788:ILE:HG12	2:A:699:LEU:HB2	1.61	0.83
2:B:822:LEU:HD13	2:B:938:LEU:HD13	1.58	0.83
2:A:206:LYS:HZ1	2:A:221:SER:HB3	1.40	0.83
2:A:435:ALA:HB2	2:A:510:VAL:HB	1.59	0.83
2:B:409:GLN:HG3	2:B:418:ILE:HD11	1.60	0.82
2:C:391:CYS:CB	2:C:525:CYS:HA	2.08	0.82
2:C:733:LYS:HD2	2:C:771:ALA:CA	2.08	0.82
2:C:331:ASN:HD22	4:C:1201:NAG:H2	1.43	0.82
2:A:1116:THR:HG22	2:A:1118:ASP:H	1.42	0.82
2:B:338:PHE:HA	2:B:342:PHE:HD2	1.44	0.82
2:B:646:ARG:HB2	2:C:862:PRO:O	1.80	0.82
2:C:48:LEU:HG	2:C:278:LYS:HD3	1.59	0.82
2:B:1104:VAL:HG11	2:B:1119:ASN:HD21	1.44	0.82
2:B:349:SER:HB3	2:B:452:LEU:HG	1.63	0.81
2:A:140:PHE:HB2	2:A:244:LEU:HD13	1.62	0.81
2:A:278:LYS:HD3	2:A:287:ASP:HB2	1.61	0.81
2:C:980:ILE:HG21	2:C:993:ILE:HG13	1.62	0.81
2:B:331:ASN:HB2	4:B:1307:NAG:H2	1.62	0.81
2:A:324:GLU:H	2:A:539:VAL:HG12	1.43	0.81
2:A:328:ARG:HA	2:A:530:SER:HA	1.61	0.81
2:A:350:VAL:HA	2:A:400:PHE:HB2	1.63	0.80
2:B:439:ASN:HD21	2:B:443:SER:HA	1.46	0.80
2:B:742:ILE:HD13	2:B:1001:LEU:HD21	1.61	0.80
2:A:617:CYS:HA	4:A:1204:NAG:H82	1.61	0.80
2:C:325:SER:CA	2:C:541:PHE:HA	2.03	0.80
2:C:646:ARG:HH22	2:A:866:THR:HG23	1.44	0.80
2:C:594:GLY:HA3	2:C:613:GLN:HG2	1.63	0.80
2:B:424:LYS:HE2	2:B:462:LYS:HA	1.63	0.80
2:B:43:PHE:N	2:A:566:GLY:HA2	1.94	0.80
2:B:309:GLU:N	2:B:309:GLU:OE1	2.13	0.80
2:B:667:GLY:HA2	2:C:772:VAL:HA	1.63	0.80
2:C:113:LYS:HG3	2:C:114:THR:HG23	1.63	0.80
2:B:906:PHE:HE1	2:B:1049:LEU:HD21	1.46	0.80
2:C:83:VAL:HG12	2:C:239:GLN:HB2	1.64	0.80
2:C:115:GLN:HA	2:C:132:GLU:HG2	1.61	0.80
2:B:431:GLY:HA3	2:B:517:LEU:HG	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:125:ASN:HA	2:B:174:PRO:HD3	1.64	0.79
2:B:598:ILE:HD13	2:B:666:ILE:HD11	1.61	0.79
2:C:353:TRP:HB3	2:C:355:ARG:HH22	1.47	0.79
2:B:866:THR:HG23	2:A:669:GLY:HA3	1.64	0.79
2:B:642:VAL:HG22	2:B:651:ILE:CD1	2.12	0.79
2:C:83:VAL:HG21	2:C:237:ARG:HE	1.46	0.79
2:B:67:ALA:HB3	2:B:263:ALA:HB3	1.63	0.79
2:C:382:VAL:HB	2:A:981:LEU:HD13	1.65	0.79
2:A:454:ARG:CB	2:A:492:LEU:HD12	2.12	0.79
2:B:85:PRO:HA	2:B:236:THR:O	1.83	0.79
2:B:397:ALA:HB2	2:B:513:LEU:HG	1.65	0.79
2:B:65:PHE:CZ	2:B:84:LEU:HD11	2.18	0.79
2:B:588:THR:HG21	2:C:855:PHE:HB2	1.65	0.78
2:C:324:GLU:HB3	2:C:539:VAL:HG21	1.64	0.78
2:C:984:LEU:HB3	2:C:989:ALA:HB2	1.65	0.78
2:A:200:TYR:HA	2:A:230:PRO:HA	1.63	0.78
2:B:788:ILE:HD11	2:A:699:LEU:HD22	1.65	0.78
2:B:592:PHE:CZ	2:C:739:THR:HB	2.18	0.78
2:B:1100:THR:HG23	3:F:1:NAG:H83	1.66	0.78
2:C:277:LEU:HD23	2:C:277:LEU:H	1.49	0.78
2:B:126:VAL:HG23	2:B:174:PRO:HA	1.65	0.77
2:B:646:ARG:HG2	2:C:733:LYS:HE2	1.67	0.77
2:B:883:THR:HB	2:A:705:VAL:HG22	1.67	0.77
2:A:645:THR:HG23	2:A:647:ALA:H	1.49	0.77
2:C:277:LEU:HD12	2:C:285:ILE:HD11	1.66	0.77
2:A:472:ILE:HB	2:A:489:TYR:H	1.49	0.77
2:B:372:ALA:HA	2:B:377:PHE:CE2	2.19	0.77
2:B:326:ILE:O	2:B:542:ASN:HB3	1.85	0.77
2:C:399:SER:HA	2:C:511:VAL:HG12	1.66	0.77
2:C:1094:VAL:HG11	2:C:1107:ARG:HE	1.50	0.77
2:B:320:VAL:O	2:C:745:ASP:HB3	1.85	0.77
2:C:359:SER:HA	2:C:524:VAL:HB	1.65	0.77
2:A:93:ALA:HB3	2:A:266:TYR:HB2	1.66	0.77
2:B:131:CYS:HA	2:B:166:CYS:HA	1.65	0.76
2:C:443:SER:HB3	2:C:507:PRO:HG3	1.67	0.76
2:B:159:VAL:HG22	2:B:241:LEU:HD11	1.66	0.76
2:B:705:VAL:HG11	2:C:888:PHE:HA	1.67	0.76
2:B:1045:LYS:O	2:B:1066:THR:HG21	1.86	0.76
2:C:452:LEU:HB3	2:C:492:LEU:HD11	1.66	0.76
2:A:412:PRO:HB3	2:A:425:LEU:HD11	1.65	0.76
2:A:670:ILE:CG2	2:A:694:ALA:HB1	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:570:ALA:HA	2:C:967:SER:CB	2.15	0.76
2:B:878:LEU:HD21	2:B:1052:PHE:HB3	1.66	0.76
2:B:720:ILE:HD11	2:B:923:ILE:HD12	1.67	0.76
2:C:717:ASN:HB2	4:C:1206:NAG:H2	1.67	0.76
2:B:391:CYS:SG	2:B:522:ALA:N	2.56	0.76
2:B:437:ASN:HB2	2:B:508:TYR:CD2	2.20	0.76
2:C:39:PRO:HG3	2:C:51:THR:HG21	1.66	0.76
2:B:83:VAL:CG2	2:B:237:ARG:HB3	2.16	0.76
2:B:344:ALA:HB2	2:B:441:LEU:HD22	1.66	0.76
2:A:425:LEU:HD23	2:A:425:LEU:H	1.49	0.76
2:A:666:ILE:HD11	2:A:672:ALA:HB2	1.68	0.76
2:A:48:LEU:HD13	2:A:276:LEU:HD11	1.67	0.76
2:A:320:VAL:HG21	2:A:591:SER:HB3	1.67	0.75
2:B:426:PRO:HG3	2:B:463:PRO:HB3	1.66	0.75
2:B:391:CYS:HB2	2:B:524:VAL:HB	1.67	0.75
2:A:742:ILE:HD11	2:A:753:LEU:HD22	1.69	0.75
2:C:563:GLN:HB3	2:A:43:PHE:HB2	1.69	0.75
2:B:139:PRO:HB2	2:B:159:VAL:HA	1.67	0.75
2:A:360:ASN:HA	2:A:523:THR:HG21	1.68	0.75
1:D:44:GLU:N	1:D:44:GLU:OE2	2.19	0.75
2:C:358:ILE:HD12	2:C:395:VAL:HG11	1.68	0.75
2:B:735:SER:OG	2:A:314:GLN:NE2	2.20	0.75
2:C:89:GLY:HA3	2:C:270:LEU:HD12	1.68	0.75
2:B:364:ASP:O	2:B:367:VAL:HG22	1.87	0.75
2:A:472:ILE:HD11	2:A:475:ALA:HB2	1.68	0.75
2:B:347:PHE:HB3	2:B:399:SER:HB2	1.69	0.74
2:B:646:ARG:HD2	2:C:863:PRO:HA	1.69	0.74
2:B:705:VAL:CG1	2:C:888:PHE:HA	2.17	0.74
2:C:40:ASP:OD1	2:C:42:VAL:HG12	1.88	0.74
2:A:117:LEU:HG	2:A:130:VAL:HG22	1.69	0.74
2:A:411:ALA:HB1	2:A:412:PRO:HD2	1.68	0.74
2:A:453:TYR:HB3	2:A:493:GLN:HE21	1.51	0.74
2:C:436:TRP:HE1	2:C:509:ARG:HB2	1.53	0.74
2:B:130:VAL:HG21	2:B:231:ILE:CD1	2.17	0.74
2:A:736:VAL:O	2:A:764:ASN:ND2	2.20	0.74
2:C:449:TYR:O	2:C:451:TYR:N	2.21	0.74
2:A:444:LYS:HG2	2:A:448:ASN:HB2	1.69	0.74
2:B:705:VAL:HG11	2:C:888:PHE:CA	2.18	0.74
2:B:869:MET:SD	2:A:697:MET:HB2	2.27	0.74
2:C:779:GLN:OE1	2:C:865:LEU:HD11	1.88	0.74
2:C:37:TYR:HA	2:C:222:ALA:HB1	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:34:ARG:CD	2:A:219:GLY:HA3	2.18	0.74
2:B:567:ARG:HG3	2:C:42:VAL:HG21	1.70	0.73
2:C:247:SER:HB2	2:C:259:THR:HG21	1.69	0.73
2:A:377:PHE:CE2	2:A:379:CYS:HB3	2.23	0.73
2:B:615:VAL:HG23	2:B:649:CYS:HB2	1.69	0.73
2:C:736:VAL:CG1	2:C:858:LEU:HD23	2.17	0.73
2:B:541:PHE:CE2	2:B:576:VAL:HG21	2.24	0.73
2:C:976:VAL:O	2:C:980:ILE:HG12	1.89	0.73
2:B:362:VAL:CG2	2:B:524:VAL:HG13	2.18	0.73
2:C:434:ILE:HD11	2:C:511:VAL:CG2	2.19	0.73
2:B:424:LYS:HB2	2:B:461:LEU:HB2	1.70	0.73
2:A:560:LEU:HB2	2:A:563:GLN:HB2	1.70	0.73
2:C:384:PRO:HD3	2:A:985:ASP:HA	1.70	0.73
2:B:41:LYS:HD2	2:B:225:PRO:HG2	1.71	0.73
2:B:568:ASP:OD2	2:B:569:ILE:HG22	1.87	0.73
2:B:612:TYR:O	2:B:648:GLY:HA3	1.89	0.73
2:C:274:THR:O	2:C:291:CYS:HB2	1.88	0.73
2:A:453:TYR:O	2:A:493:GLN:N	2.22	0.73
2:B:866:THR:HG23	2:A:669:GLY:CA	2.19	0.72
2:A:664:ILE:HD11	2:A:672:ALA:HB3	1.71	0.72
2:B:58:PHE:CD2	2:B:290:ASP:HB2	2.24	0.72
2:B:577:ARG:HG3	2:B:583:GLU:H	1.54	0.72
2:B:719:THR:HG23	2:B:1068:VAL:HG13	1.70	0.72
2:B:1082:CYS:O	2:B:1083:HIS:ND1	2.21	0.72
2:C:380:TYR:HB2	2:A:984:LEU:HG	1.70	0.72
2:A:377:PHE:CE1	2:A:432:CYS:HA	2.23	0.72
2:C:1081:ILE:O	2:C:1088:HIS:N	2.22	0.72
2:A:579:PRO:HB2	4:A:1202:NAG:C6	2.18	0.72
2:C:329:PHE:N	2:C:330:PRO:HD2	2.04	0.72
2:C:654:GLU:OE1	2:C:654:GLU:N	2.18	0.72
2:B:128:ILE:HD13	2:B:229:LEU:HD11	1.71	0.72
2:C:357:ARG:HA	2:C:395:VAL:O	1.90	0.72
2:C:390:LEU:HD11	2:A:983:ARG:CD	2.18	0.72
2:C:430:THR:HG22	2:A:983:ARG:HH22	1.53	0.72
2:A:412:PRO:HA	2:A:425:LEU:HD21	1.71	0.72
2:A:905:ARG:HD3	2:A:1049:LEU:O	1.89	0.72
2:B:404:GLY:HA2	2:B:508:TYR:CD2	2.25	0.72
2:C:44:ARG:HB2	2:C:279:TYR:CE2	2.25	0.72
2:C:564:GLN:HB3	2:C:577:ARG:HB3	1.72	0.72
2:B:332:ILE:HG21	2:B:523:THR:O	1.90	0.72
2:B:402:ILE:HB	2:B:510:VAL:CG1	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:973:ILE:H	2:B:973:ILE:HD12	1.55	0.72
2:A:452:LEU:HD12	2:A:492:LEU:CB	2.14	0.72
2:A:985:ASP:O	2:A:989:ALA:N	2.23	0.72
2:B:659:SER:OG	2:B:698:SER:HB2	1.89	0.72
2:A:334:ASN:CG	2:A:362:VAL:HG11	2.09	0.72
2:A:767:LEU:HD21	2:A:1008:VAL:HG22	1.71	0.72
2:B:130:VAL:HG21	2:B:231:ILE:HD13	1.72	0.72
2:B:321:GLN:HA	2:C:745:ASP:CB	2.19	0.72
2:C:328:ARG:HA	2:C:530:SER:CA	2.18	0.72
2:B:613:GLN:NE2	2:C:768:THR:OG1	2.23	0.71
2:C:387:LEU:HD12	2:A:983:ARG:HA	1.73	0.71
2:A:567:ARG:HA	2:A:573:THR:HA	1.71	0.71
2:A:577:ARG:HG3	2:A:579:PRO:HD3	1.72	0.71
2:A:188:ASN:HA	2:A:209:PRO:HA	1.72	0.71
2:A:331:ASN:O	2:A:334:ASN:ND2	2.23	0.71
2:A:760:CYS:HB2	2:A:763:LEU:HB2	1.72	0.71
2:B:200:TYR:CE2	2:B:230:PRO:HB3	2.25	0.71
2:B:290:ASP:OD1	2:B:291:CYS:N	2.21	0.71
2:B:903:ALA:HB2	2:B:916:LEU:HD23	1.71	0.71
2:C:424:LYS:HB3	2:C:463:PRO:HB3	1.72	0.71
2:C:736:VAL:HG11	2:C:858:LEU:HD23	1.71	0.71
2:A:189:LEU:HD22	2:A:210:ILE:HD11	1.70	0.71
2:B:343:ASN:HD21	3:I:1:NAG:C2	1.98	0.71
2:C:375:SER:HB2	2:C:433:VAL:HG23	1.71	0.71
2:B:343:ASN:OD1	3:I:1:NAG:H2	1.91	0.71
2:B:362:VAL:HG22	2:B:524:VAL:HG13	1.72	0.71
2:B:564:GLN:HB2	2:C:41:LYS:HE2	1.73	0.71
2:B:973:ILE:HD13	2:B:984:LEU:HD11	1.72	0.71
2:A:201:PHE:HB2	2:A:231:ILE:HG12	1.70	0.71
2:B:299:THR:OG1	2:B:597:VAL:HG11	1.90	0.71
2:A:454:ARG:HH21	2:A:491:PRO:HA	1.55	0.71
2:B:42:VAL:CG1	2:A:567:ARG:HB2	2.20	0.71
2:B:540:ASN:HA	2:B:548:GLY:O	1.90	0.71
2:C:411:ALA:HB1	2:C:412:PRO:HD2	1.73	0.71
2:C:903:ALA:HB2	2:C:916:LEU:HD23	1.72	0.71
2:A:332:ILE:O	2:A:334:ASN:ND2	2.23	0.71
2:A:334:ASN:CG	2:A:362:VAL:CG1	2.59	0.71
2:B:106:PHE:HD2	2:B:235:ILE:HG21	1.55	0.70
2:B:865:LEU:CD2	2:A:697:MET:HG3	2.21	0.70
2:B:1114:ILE:H	2:B:1114:ILE:HD12	1.55	0.70
2:C:895:GLN:N	2:C:895:GLN:OE1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:214:ARG:HE	2:B:215:ASP:H	1.36	0.70
2:C:805:ILE:HD11	2:C:931:ILE:CD1	2.21	0.70
2:B:375:SER:HB3	2:B:437:ASN:H	1.56	0.70
2:C:472:ILE:HG21	2:C:489:TYR:O	1.91	0.70
2:B:589:PRO:HD2	2:C:856:ASN:HB3	1.72	0.70
2:B:540:ASN:HB3	2:B:549:THR:HG22	1.73	0.70
2:C:983:ARG:HG3	2:C:984:LEU:HD12	1.73	0.70
2:C:85:PRO:HB2	2:C:87:ASN:OD1	1.91	0.70
2:C:743:CYS:HB2	2:C:997:ILE:CD1	2.21	0.70
2:B:205:SER:OG	2:B:226:LEU:HD13	1.92	0.70
2:C:736:VAL:HG22	2:C:767:LEU:HD11	1.73	0.70
2:A:669:GLY:O	2:A:670:ILE:HD13	1.92	0.70
2:B:402:ILE:HB	2:B:510:VAL:HG11	1.74	0.69
2:B:436:TRP:HZ2	2:B:509:ARG:HD3	1.57	0.69
2:C:743:CYS:HB2	2:C:997:ILE:HD11	1.72	0.69
2:A:96:GLU:OE2	2:A:101:ILE:HG12	1.92	0.69
2:A:748:GLU:OE1	2:A:748:GLU:N	2.21	0.69
2:B:49:HIS:O	2:B:276:LEU:HA	1.91	0.69
2:B:135:PHE:CD1	2:B:160:TYR:HB3	2.27	0.69
2:B:742:ILE:HG22	2:B:1000:ARG:HB3	1.73	0.69
2:A:377:PHE:HB2	2:A:433:VAL:HG13	1.73	0.69
2:A:425:LEU:CD1	2:A:429:PHE:HA	2.22	0.69
2:B:866:THR:HG23	2:A:669:GLY:N	2.07	0.69
2:B:298:GLU:CG	2:B:315:THR:HB	2.22	0.69
2:A:104:TRP:CD1	2:A:240:THR:HG22	2.27	0.69
2:B:612:TYR:HB2	2:B:615:VAL:HG21	1.75	0.69
2:C:83:VAL:HG21	2:C:237:ARG:NE	2.08	0.69
2:C:472:ILE:HB	2:C:491:PRO:CB	2.22	0.69
2:C:53:ASP:HB3	2:C:55:PHE:CE1	2.28	0.69
2:C:724:THR:CG2	2:C:934:ILE:HD11	2.15	0.69
2:C:748:GLU:HB3	2:C:752:LEU:CD1	2.23	0.69
2:C:853:GLN:O	2:C:858:LEU:HB2	1.92	0.69
2:C:1091:ARG:HG2	2:C:1121:PHE:HD1	1.56	0.69
2:A:328:ARG:HG3	2:A:530:SER:CB	2.22	0.69
2:B:115:GLN:HG3	2:B:167:THR:HG21	1.74	0.69
2:C:905:ARG:HD3	2:C:1049:LEU:O	1.92	0.69
2:A:55:PHE:O	2:A:270:LEU:HB2	1.93	0.69
2:A:1116:THR:H	2:A:1119:ASN:HD21	1.40	0.69
2:B:646:ARG:HB3	2:B:668:ALA:CB	2.21	0.69
2:B:917:TYR:CD2	2:A:1079:PRO:HB3	2.27	0.69
2:C:322:PRO:CB	2:C:539:VAL:HA	2.17	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:543:PHE:CZ	2:C:579:PRO:HD2	2.22	0.69
2:A:20:THR:CG2	2:A:78:ARG:HA	2.22	0.69
2:A:131:CYS:SG	2:A:166:CYS:HA	2.33	0.69
2:A:612:TYR:HE2	2:A:651:ILE:HD11	1.56	0.69
2:B:33:THR:HG23	2:B:58:PHE:HE1	1.57	0.69
2:B:336:CYS:HB3	2:B:340:GLU:HB3	1.74	0.69
2:C:455:LEU:HG	2:C:456:PHE:HD1	1.57	0.69
2:A:849:LEU:N	2:A:852:ALA:O	2.25	0.69
2:C:376:THR:OG1	2:C:378:LYS:NZ	2.25	0.69
2:C:822:LEU:HD11	2:C:945:LEU:HD11	1.75	0.69
2:A:916:LEU:HD12	2:A:923:ILE:HD12	1.75	0.69
2:B:567:ARG:HA	2:B:572:THR:O	1.93	0.68
2:C:802:PHE:HB3	2:C:806:LEU:HD23	1.74	0.68
2:A:546:LEU:HD23	2:A:565:PHE:CD2	2.28	0.68
2:B:132:GLU:HB2	2:B:165:ASN:HB3	1.74	0.68
2:C:111:ASP:OD1	2:C:113:LYS:HG2	1.94	0.68
2:C:495:TYR:CE2	2:C:497:PHE:HB2	2.28	0.68
2:A:277:LEU:CD2	2:A:285:ILE:HD11	2.22	0.68
2:A:452:LEU:CD1	2:A:492:LEU:HB3	2.15	0.68
2:B:330:PRO:HG2	2:B:525:CYS:HB2	1.75	0.68
2:B:565:PHE:O	2:C:43:PHE:N	2.26	0.68
2:C:734:THR:HG21	2:C:959:LEU:HD22	1.75	0.68
2:A:298:GLU:HB3	2:A:315:THR:HG21	1.73	0.68
2:A:973:ILE:HG12	2:A:992:GLN:HE21	1.59	0.68
2:B:417:LYS:HA	2:B:421:TYR:HD2	1.57	0.68
2:B:717:ASN:OD1	2:B:718:PHE:N	2.27	0.68
2:B:717:ASN:HB2	3:G:1:NAG:H2	1.74	0.68
2:C:309:GLU:OE1	2:C:309:GLU:N	2.25	0.68
2:C:748:GLU:HB3	2:C:752:LEU:HD13	1.75	0.68
2:B:1071:GLN:OE1	3:G:1:NAG:H61	1.93	0.68
2:B:391:CYS:HB2	2:B:524:VAL:CB	2.22	0.68
2:B:716:THR:HG22	2:B:1071:GLN:O	1.93	0.68
2:C:402:ILE:HG23	2:C:404:GLY:H	1.58	0.68
2:A:393:THR:HG22	2:A:519:HIS:HB2	1.74	0.68
2:B:418:ILE:HA	2:B:422:ASN:HB3	1.76	0.68
2:B:700:GLY:HA3	2:C:786:LYS:HB3	1.75	0.68
2:C:1144:GLU:OE1	2:C:1144:GLU:N	2.27	0.68
2:A:33:THR:HG23	2:A:58:PHE:HE1	1.58	0.68
2:B:779:GLN:OE1	2:A:697:MET:HE2	1.94	0.68
2:C:521:PRO:HG3	2:C:546:LEU:HD23	1.76	0.68
2:C:573:THR:HB	2:C:587:ILE:CG1	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:200:TYR:HB3	2:B:228:ASP:OD1	1.92	0.68
2:B:1039:ARG:HG3	2:B:1039:ARG:HH11	1.57	0.68
2:C:854:LYS:HA	2:C:858:LEU:O	1.93	0.68
2:A:767:LEU:CD2	2:A:1008:VAL:HG22	2.24	0.68
2:B:54:LEU:CD2	2:B:272:PRO:HB3	2.23	0.68
2:B:456:PHE:HB2	2:B:491:PRO:HB3	1.76	0.68
2:C:86:PHE:HA	2:C:238:PHE:HE1	1.58	0.68
2:C:200:TYR:CD2	2:C:230:PRO:HB3	2.29	0.68
2:B:35:GLY:HA3	2:B:56:LEU:CD2	2.24	0.67
2:B:656:VAL:HG21	2:B:693:ILE:HD11	1.76	0.67
2:B:1029:MET:HE3	2:B:1053:PRO:HB3	1.75	0.67
2:B:948:LEU:HD21	2:B:1059:GLY:HA3	1.74	0.67
2:C:380:TYR:CB	2:A:984:LEU:HG	2.24	0.67
2:B:452:LEU:HA	2:B:494:SER:HA	1.74	0.67
2:C:860:VAL:O	2:C:861:LEU:HD23	1.95	0.67
2:A:126:VAL:HB	2:A:172:SER:OG	1.95	0.67
2:B:705:VAL:HG11	2:C:888:PHE:HB2	1.76	0.67
2:A:741:TYR:CE1	2:A:966:LEU:HD11	2.29	0.67
2:A:1090:PRO:HA	2:A:1120:THR:HG22	1.75	0.67
2:B:316:SER:O	2:B:595:VAL:HG12	1.93	0.67
2:B:726:ILE:O	2:B:727:LEU:HD23	1.94	0.67
2:C:349:SER:HB3	2:C:451:TYR:HA	1.76	0.67
2:C:1072:GLU:OE1	2:C:1072:GLU:N	2.26	0.67
2:A:555:SER:HB3	2:A:586:ASP:HB2	1.76	0.67
2:A:733:LYS:NZ	2:A:775:ASP:OD1	2.28	0.67
2:A:1072:GLU:OE1	2:A:1072:GLU:N	2.22	0.67
2:B:350:VAL:HG12	2:B:452:LEU:HB2	1.76	0.67
2:B:775:ASP:CB	2:B:864:LEU:HD12	2.22	0.67
2:B:903:ALA:N	2:B:916:LEU:HD22	2.10	0.67
2:C:354:ASN:HB2	2:C:399:SER:OG	1.94	0.67
2:B:501:ASN:O	2:B:505:TYR:HB2	1.93	0.67
2:B:552:LEU:CB	2:B:585:LEU:HD21	2.24	0.67
2:B:1088:HIS:HB3	2:B:1120:THR:HG21	1.76	0.67
2:C:578:ASP:HB3	2:C:583:GLU:H	1.60	0.67
2:C:969:ASN:HB3	2:C:975:SER:HB2	1.75	0.67
2:A:168:PHE:HE2	2:A:170:TYR:HB2	1.59	0.67
2:B:1083:HIS:CE1	2:B:1137:VAL:HG13	2.29	0.67
2:C:127:VAL:HG12	2:C:129:LYS:HG3	1.75	0.67
2:B:30:ASN:ND2	2:B:60:SER:O	2.27	0.67
2:C:775:ASP:HA	2:C:778:THR:HG22	1.75	0.67
2:A:320:VAL:CG2	2:A:591:SER:HB3	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:322:PRO:HD3	2:C:745:ASP:CB	2.20	0.67
2:B:20:THR:HG21	2:B:79:PHE:HB3	1.76	0.66
2:A:333:THR:C	2:A:334:ASN:HD22	1.97	0.66
2:B:402:ILE:HD11	2:B:406:GLU:OE1	1.95	0.66
2:B:646:ARG:HD2	2:C:863:PRO:CA	2.26	0.66
2:C:382:VAL:CB	2:A:981:LEU:HD13	2.24	0.66
2:C:805:ILE:HD11	2:C:931:ILE:HD12	1.78	0.66
2:C:336:CYS:HA	2:C:338:PHE:CZ	2.29	0.66
2:A:559:PHE:CE2	2:A:575:ALA:HB1	2.30	0.66
2:A:710:ASN:HB2	2:A:1076:THR:HG23	1.78	0.66
2:A:759:PHE:CD2	2:A:1001:LEU:HD11	2.29	0.66
2:B:90:VAL:HG12	2:B:91:TYR:H	1.61	0.66
2:B:743:CYS:HA	2:B:749:CYS:SG	2.36	0.66
2:B:931:ILE:O	2:B:934:ILE:HG22	1.94	0.66
2:C:353:TRP:HB2	2:C:355:ARG:HH12	1.60	0.66
2:C:353:TRP:HZ3	2:C:466:ARG:HA	1.60	0.66
2:A:201:PHE:HB2	2:A:231:ILE:CG1	2.25	0.66
2:A:498:GLN:HB3	2:A:499:PRO:HD2	1.77	0.66
2:B:330:PRO:HD3	2:B:544:ASN:HD21	1.61	0.66
2:B:418:ILE:HB	2:B:423:TYR:CE1	2.31	0.66
2:C:735:SER:HB3	2:C:861:LEU:HD11	1.77	0.66
2:A:560:LEU:HG	2:A:563:GLN:OE1	1.95	0.66
2:B:659:SER:HB2	2:B:696:THR:O	1.96	0.66
2:B:979:ASP:OD1	2:B:980:ILE:N	2.29	0.66
2:B:1122:VAL:HG22	2:C:1118:ASP:O	1.96	0.66
2:C:189:LEU:HG	2:C:191:GLU:OE1	1.96	0.66
2:C:435:ALA:HB2	2:C:510:VAL:CG2	2.26	0.66
2:A:365:TYR:CD2	2:A:387:LEU:HD13	2.30	0.66
2:B:801:ASN:HB2	3:H:1:NAG:H2	1.77	0.66
2:C:195:LYS:HZ2	2:C:197:ILE:HG22	1.61	0.66
2:A:354:ASN:HB2	2:A:399:SER:HB3	1.76	0.66
2:A:497:PHE:HB3	2:A:501:ASN:HD21	1.60	0.66
2:B:200:TYR:CD2	2:B:230:PRO:HB3	2.31	0.66
2:B:897:PRO:HG2	2:A:708:SER:O	1.96	0.66
2:C:294:ASP:HB2	2:C:295:PRO:HD2	1.78	0.66
2:A:349:SER:HA	2:A:451:TYR:CE1	2.31	0.66
1:D:99:GLU:N	1:D:99:GLU:OE1	2.28	0.66
2:B:355:ARG:HA	2:B:397:ALA:O	1.95	0.66
2:C:390:LEU:HD12	2:C:517:LEU:HD11	1.78	0.66
2:C:650:LEU:HD11	2:C:666:ILE:HD13	1.78	0.66
2:C:746:SER:OG	2:C:749:CYS:HB2	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:206:LYS:NZ	2:A:221:SER:HB3	2.09	0.66
2:B:33:THR:HG23	2:B:58:PHE:CE1	2.30	0.65
2:B:38:TYR:CE1	2:B:285:ILE:HG13	2.31	0.65
2:C:419:ALA:O	2:C:424:LYS:NZ	2.25	0.65
2:A:133:PHE:HB3	2:A:160:TYR:HB3	1.78	0.65
2:B:372:ALA:HA	2:B:377:PHE:CZ	2.31	0.65
2:B:777:ASN:O	2:B:781:VAL:HG23	1.97	0.65
2:B:1083:HIS:CE1	2:B:1136:THR:HA	2.30	0.65
2:C:656:VAL:HG11	2:C:693:ILE:HD11	1.79	0.65
2:A:336:CYS:HA	2:A:361:CYS:HB3	1.77	0.65
2:B:105:ILE:HG12	2:B:239:GLN:HB3	1.78	0.65
2:B:426:PRO:HG3	2:B:463:PRO:CB	2.26	0.65
2:B:788:ILE:CD1	2:A:699:LEU:HD22	2.26	0.65
2:C:191:GLU:HG2	2:C:206:LYS:HB3	1.78	0.65
2:C:962:LEU:HD11	2:C:1004:LEU:HD12	1.78	0.65
2:B:203:ILE:HD12	2:B:227:VAL:CG2	2.24	0.65
2:C:141:LEU:HD23	2:C:243:ALA:HB2	1.78	0.65
2:C:322:PRO:HB3	2:C:539:VAL:CA	2.15	0.65
2:C:195:LYS:CE	2:C:202:LYS:HD2	2.26	0.65
2:C:375:SER:CB	2:C:433:VAL:HG23	2.26	0.65
2:C:805:ILE:HG22	2:C:878:LEU:CD2	2.19	0.65
2:B:146:HIS:CE1	2:B:149:ASN:HB2	2.32	0.65
2:B:789:TYR:CD1	2:A:703:ASN:HB3	2.32	0.65
2:B:822:LEU:HD11	2:B:945:LEU:HD11	1.79	0.65
2:A:128:ILE:O	2:A:169:GLU:HA	1.96	0.65
2:A:719:THR:HG23	2:A:926:GLN:HE21	1.61	0.65
2:B:321:GLN:HA	2:C:745:ASP:HB2	1.78	0.65
2:B:360:ASN:HB3	2:B:524:VAL:HG22	1.77	0.65
2:B:566:GLY:N	2:B:575:ALA:HB3	2.12	0.65
2:B:709:ASN:CA	2:C:896:ILE:HG13	2.27	0.65
2:C:565:PHE:CD2	2:C:575:ALA:HB1	2.32	0.65
2:C:707:TYR:CE2	2:A:896:ILE:HA	2.32	0.65
2:A:415:THR:HG23	2:A:419:ALA:CB	2.26	0.65
2:B:753:LEU:HD13	2:B:997:ILE:HD13	1.78	0.65
2:B:951:VAL:O	2:B:955:ASN:ND2	2.26	0.65
2:C:390:LEU:CD2	2:A:982:SER:HB3	2.25	0.65
2:A:1003:SER:O	2:A:1006:THR:HG22	1.96	0.65
2:A:1081:ILE:HD12	2:A:1115:ILE:HD13	1.79	0.65
4:A:1207:NAG:O3	4:A:1207:NAG:O7	2.14	0.65
2:B:858:LEU:HD13	2:B:959:LEU:HD11	1.79	0.65
2:B:326:ILE:HG21	2:B:532:ASN:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:700:GLY:CA	2:C:786:LYS:HE3	2.27	0.65
2:C:348:ALA:O	2:C:401:VAL:N	2.30	0.65
2:A:105:ILE:HD11	2:A:239:GLN:HB3	1.79	0.65
2:A:453:TYR:O	2:A:493:GLN:HG3	1.96	0.65
2:A:785:VAL:HG11	2:A:888:PHE:HE2	1.62	0.65
2:C:358:ILE:HB	2:C:395:VAL:CB	2.27	0.64
2:C:381:GLY:O	2:A:984:LEU:HB2	1.97	0.64
2:A:168:PHE:CE2	2:A:170:TYR:HB2	2.32	0.64
2:A:451:TYR:O	2:A:495:TYR:HB2	1.97	0.64
2:B:436:TRP:CZ2	2:B:509:ARG:HB2	2.31	0.64
2:B:742:ILE:HD11	2:B:753:LEU:HD21	1.78	0.64
2:C:187:LYS:HG3	2:C:211:ASN:CB	2.23	0.64
2:C:981:LEU:HD12	2:C:982:SER:N	2.12	0.64
2:C:1043:CYS:HB2	2:C:1048:HIS:CD2	2.32	0.64
2:A:333:THR:O	2:A:334:ASN:ND2	2.30	0.64
2:B:128:ILE:HD12	2:B:170:TYR:CD2	2.33	0.64
2:B:551:VAL:HG22	2:B:588:THR:O	1.97	0.64
2:B:1024:LEU:HA	2:B:1027:THR:HG22	1.78	0.64
2:B:1081:ILE:HG22	2:B:1082:CYS:H	1.62	0.64
2:C:980:ILE:HG23	2:C:992:GLN:OE1	1.97	0.64
2:B:128:ILE:HD12	2:B:170:TYR:HD2	1.62	0.64
2:B:298:GLU:HG3	2:B:315:THR:HB	1.80	0.64
2:B:646:ARG:O	2:C:861:LEU:HB3	1.97	0.64
2:B:883:THR:HB	2:A:705:VAL:CG2	2.28	0.64
2:C:594:GLY:HA3	2:C:613:GLN:CG	2.28	0.64
4:C:1201:NAG:O7	4:C:1201:NAG:O4	2.05	0.64
2:B:65:PHE:HZ	2:B:84:LEU:HD11	1.62	0.64
2:B:146:HIS:HD2	2:B:153:MET:HG3	1.63	0.64
2:B:647:ALA:HB2	2:B:667:GLY:HA3	1.79	0.64
2:B:951:VAL:HG21	2:B:1018:ILE:HD11	1.80	0.64
4:B:1304:NAG:O7	4:B:1304:NAG:O3	2.13	0.64
2:C:316:SER:O	2:C:595:VAL:HG11	1.96	0.64
2:C:426:PRO:HD3	2:C:463:PRO:CB	2.28	0.64
2:B:894:LEU:HD13	2:A:1072:GLU:HG3	1.79	0.64
2:B:54:LEU:HB2	2:B:270:LEU:HD21	1.80	0.64
2:B:788:ILE:CG1	2:A:699:LEU:HB2	2.27	0.64
2:B:878:LEU:O	2:B:882:ILE:HG23	1.98	0.64
2:C:437:ASN:HA	2:C:508:TYR:CD1	2.33	0.64
2:A:672:ALA:HA	2:A:693:ILE:O	1.98	0.64
1:D:46:GLU:OE1	1:D:46:GLU:N	2.31	0.64
2:B:334:ASN:N	2:B:362:VAL:HB	2.10	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:44:ARG:HD3	2:C:49:HIS:CE1	2.33	0.64
2:C:277:LEU:HB2	2:C:285:ILE:HD12	1.79	0.64
2:C:347:PHE:HB2	2:C:401:VAL:HG23	1.78	0.64
2:C:356:LYS:O	2:C:397:ALA:N	2.30	0.64
2:B:461:LEU:HD21	2:B:467:ASP:HB2	1.79	0.64
2:C:48:LEU:HB3	2:C:276:LEU:HD11	1.79	0.64
2:C:347:PHE:CE2	2:C:509:ARG:HB3	2.33	0.64
2:C:406:GLU:HB3	2:C:409:GLN:CG	2.28	0.64
2:C:426:PRO:HD3	2:C:463:PRO:HB2	1.80	0.64
2:A:65:PHE:HB2	2:A:265:TYR:CE1	2.33	0.64
2:A:180:GLU:HG3	2:A:182:LYS:HG2	1.79	0.64
2:B:668:ALA:O	2:C:864:LEU:HB2	1.97	0.63
2:B:319:ARG:HA	2:B:592:PHE:CE1	2.33	0.63
2:B:324:GLU:OE1	2:B:537:LYS:HE3	1.97	0.63
2:B:611:LEU:HA	2:B:650:LEU:HA	1.79	0.63
2:C:535:LYS:NZ	2:C:536:ASN:OD1	2.29	0.63
2:A:323:THR:HG21	2:A:537:LYS:NZ	2.13	0.63
2:A:653:ALA:HB2	2:A:692:ILE:HG22	1.80	0.63
2:B:444:LYS:HB3	2:B:448:ASN:HD22	1.62	0.63
2:B:706:ALA:N	2:C:892:PRO:O	2.32	0.63
2:C:537:LYS:HG3	2:C:537:LYS:O	1.98	0.63
2:A:897:PRO:HD2	2:A:900:MET:HE3	1.79	0.63
2:B:270:LEU:HD12	2:B:271:GLN:H	1.62	0.63
2:B:1083:HIS:NE2	2:B:1137:VAL:HG22	2.14	0.63
2:C:390:LEU:HD11	2:A:983:ARG:CG	2.29	0.63
2:A:856:ASN:O	2:A:858:LEU:HD12	1.99	0.63
2:B:877:LEU:HD13	2:B:1029:MET:CE	2.28	0.63
2:B:883:THR:HG22	2:A:707:TYR:OH	1.99	0.63
2:C:398:ASP:HB2	2:C:512:VAL:HG13	1.79	0.63
2:C:733:LYS:NZ	2:C:775:ASP:OD1	2.32	0.63
2:C:1022:ALA:O	2:C:1026:ALA:N	2.25	0.63
2:B:984:LEU:HD22	2:B:988:GLU:HG3	1.81	0.63
2:C:564:GLN:HB3	2:C:577:ARG:CB	2.29	0.63
2:C:1126:CYS:CB	2:C:1132:ILE:HG21	2.24	0.63
2:B:726:ILE:HD12	2:B:1061:VAL:HG22	1.80	0.63
2:B:1066:THR:HG22	2:B:1067:TYR:H	1.64	0.63
2:C:900:MET:HB2	2:C:917:TYR:OH	1.98	0.63
2:A:367:VAL:HG22	2:A:368:LEU:H	1.64	0.63
2:B:642:VAL:HG22	2:B:651:ILE:HD12	1.79	0.63
2:C:106:PHE:HB3	2:C:235:ILE:HD12	1.80	0.63
2:C:916:LEU:HD12	2:C:923:ILE:HG13	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:20:THR:OG1	2:A:79:PHE:N	2.32	0.63
2:A:40:ASP:OD1	2:A:41:LYS:N	2.31	0.63
2:B:566:GLY:HA2	2:C:43:PHE:N	2.13	0.63
2:C:467:ASP:O	2:C:468:ILE:HD13	1.97	0.63
2:A:48:LEU:HB3	2:A:276:LEU:CD1	2.29	0.63
2:C:984:LEU:HD22	2:C:992:GLN:OE1	1.99	0.62
2:B:705:VAL:HG21	2:C:888:PHE:CB	2.29	0.62
2:A:354:ASN:O	2:A:398:ASP:HA	1.99	0.62
2:A:865:LEU:HD23	2:A:865:LEU:H	1.64	0.62
2:B:471:GLU:OE1	2:B:471:GLU:N	2.32	0.62
2:A:189:LEU:HD22	2:A:210:ILE:CD1	2.28	0.62
2:B:140:PHE:HD2	2:B:244:LEU:HD13	1.63	0.62
2:B:302:THR:HG23	2:B:303:LEU:HD12	1.81	0.62
2:B:313:TYR:O	2:B:597:VAL:N	2.32	0.62
2:B:338:PHE:HA	2:B:342:PHE:CD2	2.29	0.62
2:B:1003:SER:O	2:B:1006:THR:HG22	2.00	0.62
2:C:126:VAL:HG11	2:C:175:PHE:HE1	1.63	0.62
2:A:33:THR:HG23	2:A:58:PHE:CE1	2.34	0.62
2:B:129:LYS:HG2	2:B:169:GLU:HG3	1.82	0.62
2:B:277:LEU:HD22	2:B:285:ILE:HD13	1.82	0.62
2:B:436:TRP:CZ2	2:B:509:ARG:HD3	2.34	0.62
2:C:273:ARG:HB3	2:C:275:PHE:CE2	2.34	0.62
2:C:645:THR:HG22	2:C:647:ALA:H	1.63	0.62
2:A:86:PHE:HE2	2:A:196:ASN:HB3	1.63	0.62
2:A:295:PRO:O	2:A:299:THR:HG22	1.99	0.62
2:A:452:LEU:HG	2:A:492:LEU:HD23	1.81	0.62
2:A:455:LEU:HG	2:A:456:PHE:H	1.63	0.62
2:A:731:MET:HG2	2:A:774:GLN:OE1	1.98	0.62
2:B:402:ILE:CG2	2:B:510:VAL:HB	2.30	0.62
2:B:424:LYS:HE2	2:B:462:LYS:CA	2.29	0.62
2:B:1085:GLY:HA2	2:B:1126:CYS:CB	2.29	0.62
2:A:358:ILE:H	2:A:395:VAL:HB	1.63	0.62
2:B:105:ILE:O	2:B:238:PHE:HA	1.99	0.62
2:B:613:GLN:N	2:B:613:GLN:OE1	2.33	0.62
2:B:738:CYS:HB3	2:B:760:CYS:SG	2.40	0.62
2:C:341:VAL:HG11	2:C:397:ALA:HB1	1.81	0.62
2:C:655:HIS:HA	2:C:694:ALA:O	2.00	0.62
2:C:1103:PHE:CD2	2:C:1112:PRO:HB3	2.34	0.62
2:A:775:ASP:OD2	2:A:864:LEU:HD12	2.00	0.62
2:B:328:ARG:HB3	2:B:578:ASP:OD1	1.99	0.62
2:B:405:ASP:HB2	2:B:505:TYR:CD2	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:548:GLY:HA2	2:C:978:ASN:ND2	2.14	0.62
2:B:646:ARG:CB	2:B:668:ALA:HB2	2.26	0.62
2:B:826:VAL:HB	2:B:1057:PRO:HG2	1.82	0.62
2:C:331:ASN:ND2	4:C:1201:NAG:H2	2.10	0.62
2:A:20:THR:HG23	2:A:78:ARG:HA	1.82	0.62
2:B:417:LYS:O	2:B:421:TYR:N	2.32	0.62
2:B:706:ALA:CA	2:C:894:LEU:HB3	2.30	0.62
2:B:864:LEU:HD22	2:B:865:LEU:CD2	2.30	0.62
2:B:914:ASN:CB	2:A:1089:PHE:HE2	2.13	0.62
2:C:977:LEU:HD23	2:C:996:LEU:HD23	1.82	0.62
2:A:189:LEU:HB2	2:A:210:ILE:HG12	1.81	0.62
2:A:276:LEU:HB3	2:A:289:VAL:HG12	1.81	0.62
2:A:412:PRO:CB	2:A:425:LEU:HD11	2.30	0.62
2:A:712:ILE:CG2	2:A:1075:PHE:HB2	2.28	0.62
2:A:742:ILE:HD11	2:A:753:LEU:HD13	1.82	0.62
2:B:52:GLN:OE1	2:B:52:GLN:N	2.33	0.61
2:B:54:LEU:C	2:B:270:LEU:HD11	2.20	0.61
2:B:895:GLN:HG2	2:A:705:VAL:CB	2.26	0.61
2:C:791:THR:OG1	2:C:792:PRO:HD2	2.00	0.61
2:A:538:CYS:HB2	2:A:551:VAL:HG22	1.82	0.61
2:B:86:PHE:CZ	2:B:238:PHE:HB3	2.24	0.61
2:B:585:LEU:HD12	2:B:586:ASP:H	1.66	0.61
2:C:363:ALA:HB1	2:C:365:TYR:CE1	2.35	0.61
2:C:736:VAL:HG22	2:C:767:LEU:CD1	2.31	0.61
2:B:146:HIS:CD2	2:B:153:MET:HG3	2.35	0.61
2:B:567:ARG:HG3	2:C:42:VAL:CG2	2.30	0.61
2:B:666:ILE:HB	2:B:670:ILE:O	1.99	0.61
2:B:742:ILE:O	2:B:1000:ARG:NH1	2.33	0.61
2:B:973:ILE:CD1	2:B:992:GLN:HG2	2.30	0.61
2:C:707:TYR:HE2	2:A:897:PRO:HD3	1.65	0.61
2:B:700:GLY:HA3	2:C:786:LYS:HE3	1.81	0.61
2:B:711:SER:HA	2:B:1075:PHE:O	1.99	0.61
2:B:726:ILE:CD1	2:B:1061:VAL:HG22	2.31	0.61
2:C:984:LEU:CB	2:C:989:ALA:HB2	2.31	0.61
2:A:206:LYS:HE2	2:A:208:THR:OG1	2.00	0.61
2:B:24:LEU:HD21	2:B:78:ARG:HD3	1.83	0.61
2:B:321:GLN:HA	2:C:745:ASP:HB3	1.82	0.61
2:B:329:PHE:HA	2:B:544:ASN:ND2	2.16	0.61
2:B:572:THR:HG23	2:B:587:ILE:HD11	1.83	0.61
2:B:646:ARG:HG3	2:C:861:LEU:CB	2.30	0.61
2:B:887:THR:HG21	2:B:894:LEU:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:55:PHE:HB2	2:C:275:PHE:CE2	2.36	0.61
2:A:328:ARG:HG3	2:A:530:SER:HB3	1.81	0.61
2:B:472:ILE:HG13	2:B:483:VAL:O	2.00	0.61
2:B:592:PHE:HZ	2:C:739:THR:HB	1.62	0.61
2:B:707:TYR:CE2	2:C:896:ILE:HG21	2.35	0.61
2:C:277:LEU:HD12	2:C:285:ILE:CD1	2.30	0.61
2:A:472:ILE:HD12	2:A:473:TYR:H	1.65	0.61
2:B:770:ILE:O	2:B:774:GLN:NE2	2.22	0.61
2:C:909:ILE:HG13	2:C:911:VAL:HG23	1.83	0.61
2:A:48:LEU:HB3	2:A:276:LEU:HD11	1.82	0.61
2:A:617:CYS:HA	4:A:1204:NAG:C8	2.30	0.61
2:A:881:THR:HA	2:A:885:GLY:O	2.01	0.61
2:B:193:VAL:O	2:B:203:ILE:HA	2.01	0.61
2:B:439:ASN:OD1	2:B:442:ASP:HB2	2.01	0.61
2:B:567:ARG:NE	2:B:573:THR:HG22	2.16	0.61
2:B:673:SER:O	2:B:692:ILE:HD12	2.00	0.61
2:B:879:ALA:O	2:B:883:THR:HG23	2.01	0.61
2:C:170:TYR:HE2	2:C:175:PHE:HZ	1.48	0.61
2:C:523:THR:O	2:C:524:VAL:HG12	2.01	0.61
2:A:415:THR:HG23	2:A:419:ALA:HB3	1.83	0.61
2:A:1144:GLU:OE1	2:A:1144:GLU:N	2.33	0.61
2:C:39:PRO:HB3	2:C:55:PHE:HZ	1.64	0.61
2:C:96:GLU:OE1	2:C:101:ILE:HG12	2.01	0.61
2:C:380:TYR:CA	2:A:984:LEU:HG	2.31	0.61
2:C:421:TYR:HA	2:C:461:LEU:HB2	1.83	0.61
2:C:954:GLN:HB3	2:C:1014:ARG:NH1	2.15	0.61
2:A:542:ASN:HA	2:A:546:LEU:O	2.01	0.61
2:A:642:VAL:HA	2:A:651:ILE:HG22	1.82	0.61
2:C:139:PRO:HB2	2:C:241:LEU:CD2	2.27	0.60
2:C:434:ILE:HD11	2:C:511:VAL:HG23	1.82	0.60
2:A:350:VAL:HB	2:A:401:VAL:O	2.01	0.60
2:B:330:PRO:CD	2:B:544:ASN:HD21	2.12	0.60
2:B:346:ARG:HH12	2:B:442:ASP:HA	1.65	0.60
2:B:802:PHE:CD1	2:B:805:ILE:HD11	2.30	0.60
2:C:805:ILE:CG2	2:C:878:LEU:HD21	2.20	0.60
2:A:462:LYS:HD2	2:A:463:PRO:HD2	1.83	0.60
2:A:710:ASN:O	2:A:1076:THR:HA	2.01	0.60
2:C:1095:PHE:CD1	2:C:1104:VAL:HG22	2.36	0.60
2:A:308:VAL:H	2:A:602:THR:HB	1.66	0.60
2:B:822:LEU:HD21	2:B:1061:VAL:CG2	2.29	0.60
2:C:281:GLU:HG3	2:C:282:ASN:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:392:PHE:CD2	2:C:517:LEU:HD12	2.37	0.60
2:C:980:ILE:HG21	2:C:993:ILE:CG1	2.30	0.60
2:B:656:VAL:HG11	2:B:693:ILE:HD11	1.84	0.60
2:C:115:GLN:CA	2:C:132:GLU:HG2	2.29	0.60
2:C:457:ARG:O	2:C:461:LEU:HD21	2.01	0.60
2:A:674:TYR:HA	2:A:691:SER:O	2.00	0.60
2:B:141:LEU:N	2:B:242:LEU:O	2.35	0.60
2:C:403:ARG:NH2	2:C:493:GLN:OE1	2.35	0.60
2:C:407:VAL:HB	2:C:408:ARG:NH2	2.17	0.60
2:C:991:VAL:O	2:C:994:ASP:HB3	2.02	0.60
2:A:16:VAL:HG12	2:A:18:LEU:HG	1.84	0.60
2:A:402:ILE:HG13	2:A:404:GLY:H	1.66	0.60
2:B:234:ASN:O	2:B:235:ILE:HD13	2.02	0.60
2:B:329:PHE:HA	2:B:544:ASN:HD21	1.66	0.60
2:C:358:ILE:HB	2:C:395:VAL:HB	1.83	0.60
2:C:646:ARG:HD3	2:C:668:ALA:HB1	1.83	0.60
2:C:770:ILE:O	2:C:774:GLN:HG2	2.01	0.60
2:A:454:ARG:HG3	2:A:455:LEU:N	2.17	0.60
2:B:455:LEU:H	2:B:493:GLN:HG2	1.65	0.60
2:B:646:ARG:HD3	2:C:733:LYS:HZ1	1.66	0.60
2:C:415:THR:HG23	2:C:419:ALA:CB	2.32	0.60
2:A:105:ILE:CD1	2:A:110:LEU:HD13	2.32	0.60
2:B:141:LEU:HB3	2:B:243:ALA:HA	1.82	0.60
2:B:332:ILE:O	2:B:525:CYS:HB3	2.01	0.60
2:B:646:ARG:CG	2:C:733:LYS:HE2	2.31	0.60
2:B:864:LEU:HA	2:A:667:GLY:HA2	1.84	0.60
2:C:822:LEU:HD13	2:C:938:LEU:HD13	1.82	0.60
2:A:811:LYS:HZ2	2:A:813:SER:H	1.49	0.60
2:B:335:LEU:HD12	2:B:337:PRO:HD3	1.83	0.60
2:B:433:VAL:HA	2:B:513:LEU:O	2.01	0.60
2:B:437:ASN:CA	2:B:508:TYR:HB3	2.32	0.60
2:B:552:LEU:HB3	2:B:585:LEU:CD2	2.28	0.60
2:B:615:VAL:CG2	2:B:649:CYS:HB2	2.32	0.60
2:B:719:THR:CG2	2:B:1068:VAL:HG13	2.32	0.60
2:C:822:LEU:HD21	2:C:1061:VAL:CG2	2.29	0.60
2:A:205:SER:OG	2:A:226:LEU:HD13	2.02	0.60
2:A:722:VAL:HA	2:A:1064:HIS:O	2.02	0.60
2:B:710:ASN:HB2	2:B:1077:THR:O	2.02	0.59
2:C:452:LEU:HD22	2:C:492:LEU:HD21	1.84	0.59
2:C:972:ALA:HB1	2:C:992:GLN:HG3	1.84	0.59
2:C:983:ARG:O	2:C:984:LEU:HD12	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:287:ASP:HB3	2:A:306:PHE:CZ	2.37	0.59
2:A:584:ILE:O	2:A:585:LEU:HD23	2.02	0.59
2:A:377:PHE:CD1	2:A:432:CYS:HA	2.36	0.59
2:B:174:PRO:HB2	2:B:177:MET:SD	2.42	0.59
2:B:722:VAL:HA	2:B:1064:HIS:O	2.02	0.59
2:C:317:ASN:OD1	2:C:595:VAL:HG12	2.03	0.59
2:A:361:CYS:O	2:A:524:VAL:HA	2.01	0.59
2:A:396:TYR:CE1	2:A:398:ASP:HB3	2.37	0.59
2:B:170:TYR:CE2	2:B:172:SER:HB3	2.38	0.59
2:B:1085:GLY:HA2	2:B:1126:CYS:H	1.67	0.59
2:A:24:LEU:HD12	2:A:78:ARG:HH11	1.67	0.59
2:A:409:GLN:HG3	2:A:418:ILE:HB	1.85	0.59
2:B:386:LYS:HG2	2:B:386:LYS:O	2.03	0.59
2:B:403:ARG:HG2	2:B:405:ASP:H	1.67	0.59
2:C:106:PHE:HD2	2:C:235:ILE:HG21	1.67	0.59
2:C:555:SER:HA	2:C:586:ASP:OD2	2.03	0.59
2:B:402:ILE:HG22	2:B:508:TYR:O	2.02	0.59
2:B:646:ARG:NH2	2:C:732:THR:HA	2.17	0.59
2:C:517:LEU:HD13	2:A:983:ARG:NH1	2.17	0.59
2:B:299:THR:O	2:B:302:THR:HG22	2.02	0.59
2:B:491:PRO:HG2	2:B:492:LEU:HD12	1.83	0.59
2:B:705:VAL:HG11	2:C:888:PHE:CB	2.32	0.59
2:B:869:MET:SD	2:A:696:THR:HG22	2.43	0.59
2:C:216:LEU:HD21	2:C:266:TYR:CE2	2.33	0.59
2:C:524:VAL:HG13	2:C:524:VAL:O	2.02	0.59
2:C:666:ILE:HB	2:C:670:ILE:O	2.02	0.59
2:A:312:ILE:CG2	2:A:598:ILE:HG12	2.26	0.59
2:A:320:VAL:HG23	2:A:590:CYS:SG	2.42	0.59
2:B:439:ASN:HB2	2:B:506:GLN:HB3	1.84	0.59
2:B:731:MET:HB3	2:B:1018:ILE:HD13	1.83	0.59
2:C:131:CYS:HB2	2:C:133:PHE:CE2	2.37	0.59
2:A:377:PHE:HB3	2:A:433:VAL:O	2.03	0.59
2:A:425:LEU:HD12	2:A:429:PHE:CA	2.26	0.59
2:B:567:ARG:O	2:C:44:ARG:HG2	2.03	0.59
2:C:377:PHE:HD1	2:C:378:LYS:H	1.50	0.59
2:A:366:SER:O	2:A:367:VAL:HG12	2.03	0.59
2:A:775:ASP:CG	2:A:864:LEU:HB2	2.22	0.59
2:B:41:LYS:HE2	2:B:41:LYS:CA	2.33	0.59
2:B:323:THR:H	2:B:539:VAL:HG12	1.66	0.59
2:C:47:VAL:HB	2:C:49:HIS:HE1	1.66	0.59
2:C:381:GLY:H	2:A:983:ARG:CB	1.98	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:389:ASP:HB2	2:A:982:SER:OG	2.02	0.59
2:C:656:VAL:CG1	2:C:693:ILE:HD11	2.33	0.59
2:C:878:LEU:O	2:C:882:ILE:HD12	2.03	0.59
2:C:1086:LYS:HG3	2:C:1122:VAL:CG2	2.33	0.59
2:A:598:ILE:CD1	2:A:666:ILE:HG12	2.33	0.59
2:B:598:ILE:CD1	2:B:666:ILE:HD11	2.33	0.58
2:B:724:THR:HA	2:B:1062:PHE:O	2.03	0.58
2:B:864:LEU:HD22	2:B:865:LEU:HD23	1.84	0.58
2:C:24:LEU:CD1	2:C:25:PRO:HD2	2.31	0.58
2:C:305:SER:OG	2:C:306:PHE:N	2.35	0.58
2:C:877:LEU:HD13	2:C:1029:MET:SD	2.43	0.58
2:A:914:ASN:O	2:A:918:GLU:HG2	2.03	0.58
2:B:58:PHE:CE2	2:B:290:ASP:HB2	2.37	0.58
2:B:409:GLN:HG3	2:B:418:ILE:CD1	2.31	0.58
2:B:594:GLY:N	2:C:737:ASP:OD1	2.36	0.58
2:C:144:TYR:CZ	2:C:153:MET:HB2	2.38	0.58
2:A:131:CYS:HB2	2:A:133:PHE:CE1	2.38	0.58
2:A:206:LYS:CB	2:A:223:LEU:HG	2.28	0.58
2:A:309:GLU:OE1	2:A:309:GLU:N	2.35	0.58
2:A:1104:VAL:HG11	2:A:1119:ASN:OD1	2.03	0.58
2:B:298:GLU:HG2	2:B:315:THR:HB	1.84	0.58
2:B:392:PHE:CD2	2:B:515:PHE:HB3	2.39	0.58
2:B:562:PHE:CD2	2:C:224:GLU:HB3	2.38	0.58
2:C:273:ARG:HB3	2:C:275:PHE:CZ	2.38	0.58
2:C:452:LEU:HB3	2:C:492:LEU:CD2	2.32	0.58
2:A:133:PHE:HB3	2:A:160:TYR:CB	2.33	0.58
2:B:34:ARG:HD2	2:B:35:GLY:N	2.17	0.58
2:B:353:TRP:HB2	2:B:398:ASP:HB3	1.85	0.58
2:B:873:TYR:CE1	2:A:699:LEU:HD11	2.39	0.58
2:B:928:ASN:HB3	3:H:1:NAG:H61	1.84	0.58
2:B:961:THR:O	2:B:965:GLN:HG2	2.03	0.58
2:C:717:ASN:C	2:C:1070:ALA:HB3	2.23	0.58
2:C:886:TRP:HB3	2:C:905:ARG:NH2	2.18	0.58
2:A:208:THR:HG22	2:A:210:ILE:HG23	1.85	0.58
2:A:438:SER:N	2:A:506:GLN:HE22	2.01	0.58
2:A:457:ARG:HH21	2:A:469:SER:HB3	1.67	0.58
2:B:193:VAL:HG12	2:B:195:LYS:HG3	1.85	0.58
2:B:244:LEU:HD21	2:B:258:TRP:CE3	2.37	0.58
2:B:399:SER:HA	2:B:511:VAL:HG12	1.86	0.58
2:B:592:PHE:CG	2:C:740:MET:HB2	2.38	0.58
2:B:646:ARG:O	2:C:861:LEU:HD13	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:646:ARG:CD	2:C:733:LYS:HE2	2.33	0.58
2:B:1121:PHE:HE1	2:C:1092:GLU:HB2	1.68	0.58
2:C:393:THR:HG21	2:C:518:LEU:HG	1.86	0.58
2:C:457:ARG:NH1	2:C:467:ASP:OD1	2.36	0.58
2:C:707:TYR:CD1	2:C:711:SER:HB3	2.38	0.58
2:A:66:HIS:NE2	2:A:68:ILE:HB	2.18	0.58
2:A:66:HIS:O	2:A:78:ARG:NH1	2.37	0.58
2:A:104:TRP:HD1	2:A:240:THR:HG22	1.68	0.58
2:B:45:SER:O	2:B:47:VAL:HG23	2.03	0.58
2:B:569:ILE:CG1	2:C:964:LYS:HG2	2.26	0.58
2:B:570:ALA:HB1	2:C:966:LEU:C	2.23	0.58
2:B:742:ILE:CD1	2:B:1001:LEU:HD21	2.33	0.58
2:B:897:PRO:HG2	2:A:711:SER:HB3	1.86	0.58
2:C:36:VAL:HG11	2:C:220:PHE:CZ	2.38	0.58
2:B:117:LEU:HD23	2:B:118:LEU:N	2.18	0.58
2:B:551:VAL:N	2:B:588:THR:O	2.28	0.58
2:B:667:GLY:HA2	2:C:772:VAL:CA	2.34	0.58
2:B:821:LEU:HD21	2:B:935:GLN:HG3	1.85	0.58
2:B:973:ILE:HD12	2:B:992:GLN:HG2	1.85	0.58
2:C:90:VAL:HG21	2:C:238:PHE:CZ	2.37	0.58
2:C:396:TYR:HB3	2:C:514:SER:HB3	1.84	0.58
2:A:1038:LYS:HA	2:A:1038:LYS:CE	2.29	0.58
1:D:51:ILE:HG13	1:D:58:THR:HG22	1.85	0.58
2:B:35:GLY:HA3	2:B:56:LEU:HD21	1.86	0.58
2:B:86:PHE:CE2	2:B:235:ILE:HG22	2.38	0.58
2:B:426:PRO:HB2	2:B:428:ASP:OD1	2.04	0.58
2:B:577:ARG:CG	2:B:582:LEU:HA	2.34	0.58
2:B:646:ARG:HD3	2:C:733:LYS:NZ	2.18	0.58
2:B:702:GLU:OE1	2:C:787:GLN:HG3	2.04	0.58
2:C:331:ASN:ND2	4:C:1201:NAG:O5	2.34	0.58
2:A:476:GLY:N	2:A:487:ASN:HB2	2.18	0.58
2:B:948:LEU:O	2:B:951:VAL:HG12	2.04	0.58
2:C:734:THR:HG21	2:C:959:LEU:CD2	2.34	0.58
2:C:887:THR:O	2:C:887:THR:HG22	2.04	0.58
2:A:447:GLY:O	2:A:496:GLY:HA2	2.03	0.58
2:B:349:SER:HB2	2:B:351:TYR:CD1	2.39	0.58
2:B:765:ARG:HG2	2:B:765:ARG:HH11	1.69	0.58
2:B:899:PRO:O	2:B:916:LEU:HD21	2.04	0.58
2:C:611:LEU:HD12	2:C:650:LEU:HG	1.86	0.58
2:A:33:THR:O	2:A:34:ARG:HG2	2.04	0.58
2:A:579:PRO:HA	2:A:582:LEU:HD23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:662:CYS:HB3	2:A:695:TYR:HE2	1.68	0.58
2:A:994:ASP:O	2:A:998:THR:HG23	2.03	0.58
2:B:742:ILE:HD13	2:B:1001:LEU:CD2	2.34	0.57
2:B:906:PHE:CE1	2:B:1049:LEU:HD21	2.34	0.57
2:C:347:PHE:HB2	2:C:401:VAL:CG2	2.33	0.57
2:A:145:TYR:HB2	2:A:152:TRP:CZ3	2.38	0.57
2:A:342:PHE:HE1	2:A:511:VAL:HG21	1.69	0.57
2:A:567:ARG:O	2:A:574:ASP:HB3	2.04	0.57
2:B:193:VAL:N	2:B:204:TYR:O	2.37	0.57
2:B:598:ILE:HD13	2:B:666:ILE:CD1	2.34	0.57
2:B:854:LYS:HE2	2:A:592:PHE:HB3	1.86	0.57
2:B:1121:PHE:CB	2:C:1091:ARG:HD3	2.23	0.57
2:B:1141:LEU:HD23	2:B:1141:LEU:O	2.04	0.57
2:C:66:HIS:HE1	2:C:78:ARG:HH21	1.51	0.57
2:C:741:TYR:HD2	2:C:742:ILE:HD12	1.69	0.57
2:C:1071:GLN:OE1	4:C:1206:NAG:H61	2.04	0.57
2:A:48:LEU:CD1	2:A:276:LEU:HD11	2.32	0.57
2:A:566:GLY:HA3	2:A:575:ALA:HB3	1.86	0.57
2:B:86:PHE:HB3	2:B:90:VAL:CG2	2.32	0.57
2:B:706:ALA:CB	2:C:892:PRO:HG2	2.34	0.57
2:C:406:GLU:O	2:C:408:ARG:N	2.35	0.57
2:C:565:PHE:HA	2:C:575:ALA:HA	1.87	0.57
2:C:750:SER:O	2:C:754:LEU:HG	2.04	0.57
2:A:156:GLU:OE1	2:A:158:ARG:NH2	2.37	0.57
2:A:335:LEU:HB2	4:A:1202:NAG:C8	2.34	0.57
2:B:365:TYR:N	2:B:388:ASN:OD1	2.36	0.57
2:B:568:ASP:O	2:C:49:HIS:NE2	2.26	0.57
2:B:980:ILE:HG12	2:B:983:ARG:NH2	2.20	0.57
2:B:1066:THR:HG22	2:B:1067:TYR:N	2.19	0.57
2:C:53:ASP:OD1	2:C:54:LEU:N	2.32	0.57
2:C:146:HIS:CE1	2:C:148:ASN:HB3	2.39	0.57
2:C:410:ILE:HG13	2:C:425:LEU:CD2	2.19	0.57
2:A:105:ILE:HD11	2:A:110:LEU:HD13	1.85	0.57
2:A:326:ILE:HD11	2:A:532:ASN:C	2.25	0.57
2:A:454:ARG:NH2	2:A:491:PRO:HA	2.19	0.57
2:A:720:ILE:HD12	2:A:923:ILE:HG23	1.86	0.57
2:B:755:GLN:HB2	2:A:969:ASN:HD22	1.68	0.57
2:C:974:SER:H	2:C:992:GLN:HE21	1.51	0.57
2:A:217:PRO:HB2	2:A:218:GLN:OE1	2.05	0.57
2:A:670:ILE:HG21	2:A:694:ALA:HB1	1.87	0.57
2:A:759:PHE:HD2	2:A:1001:LEU:HD11	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:314:GLN:HA	2:B:596:SER:HA	1.85	0.57
2:B:375:SER:CB	2:B:437:ASN:H	2.17	0.57
2:B:882:ILE:HG13	2:A:707:TYR:OH	2.05	0.57
2:B:887:THR:HB	2:B:894:LEU:HG	1.86	0.57
2:C:399:SER:CA	2:C:511:VAL:HG12	2.33	0.57
2:C:406:GLU:HG2	2:C:418:ILE:HG13	1.85	0.57
2:C:568:ASP:OD1	2:A:47:VAL:HG21	2.04	0.57
2:C:646:ARG:HH22	2:A:866:THR:CG2	2.17	0.57
2:A:418:ILE:O	2:A:422:ASN:HB2	2.05	0.57
2:A:671:CYS:O	2:A:694:ALA:HA	2.04	0.57
2:B:767:LEU:HD12	2:B:770:ILE:HD13	1.87	0.57
2:B:869:MET:SD	2:A:697:MET:N	2.67	0.57
2:C:40:ASP:CG	2:C:42:VAL:HG12	2.25	0.57
2:A:276:LEU:HB3	2:A:289:VAL:CG1	2.35	0.57
2:B:207:HIS:NE2	2:B:209:PRO:HG3	2.20	0.57
2:B:591:SER:O	2:C:857:GLY:HA2	2.05	0.57
2:B:1082:CYS:HA	2:B:1086:LYS:O	2.05	0.57
2:A:310:LYS:NZ	2:A:663:ASP:HB3	2.19	0.57
2:A:360:ASN:HA	2:A:523:THR:CG2	2.35	0.57
2:A:472:ILE:HG12	2:A:488:CYS:HA	1.87	0.57
2:A:715:PRO:HG2	2:A:1108:ASN:O	2.05	0.57
2:B:594:GLY:O	2:B:612:TYR:HA	2.05	0.57
2:B:897:PRO:HB3	2:A:708:SER:H	1.70	0.57
2:C:371:SER:HB3	2:C:374:PHE:CZ	2.40	0.57
2:C:380:TYR:HB3	2:A:983:ARG:C	2.25	0.57
2:C:537:LYS:HG2	2:C:539:VAL:HB	1.86	0.57
2:C:672:ALA:HA	2:C:694:ALA:HA	1.87	0.57
2:A:748:GLU:HG3	2:A:981:LEU:HD11	1.87	0.57
2:B:277:LEU:HD22	2:B:285:ILE:CD1	2.35	0.57
2:B:706:ALA:HA	2:C:894:LEU:HB3	1.87	0.57
2:B:792:PRO:HG3	2:A:707:TYR:HE1	1.69	0.57
2:B:1080:ALA:O	2:B:1081:ILE:HD13	2.04	0.57
2:C:189:LEU:HD22	2:C:210:ILE:HD13	1.86	0.57
2:C:888:PHE:CE1	2:C:1034:LEU:HD22	2.40	0.57
2:B:105:ILE:HD12	2:B:110:LEU:CD2	2.35	0.56
2:B:646:ARG:HH21	2:C:733:LYS:H	1.53	0.56
2:B:705:VAL:HG21	2:C:888:PHE:HB2	1.87	0.56
2:C:741:TYR:HE1	2:C:966:LEU:HD11	1.69	0.56
2:A:452:LEU:HB2	2:A:493:GLN:O	2.04	0.56
2:B:326:ILE:CD1	2:B:533:LEU:HA	2.34	0.56
2:B:369:TYR:CE1	2:B:384:PRO:HG3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:410:ILE:CD1	2:B:425:LEU:HD13	2.27	0.56
2:B:1098:ASN:ND2	3:F:1:NAG:H61	2.19	0.56
2:C:45:SER:O	2:C:47:VAL:HG23	2.05	0.56
2:A:409:GLN:OE1	2:A:416:GLY:N	2.38	0.56
2:A:1038:LYS:HE3	2:A:1038:LYS:CA	2.26	0.56
2:B:68:ILE:HB	2:B:261:GLY:O	2.04	0.56
2:B:164:ASN:O	2:B:165:ASN:C	2.44	0.56
2:B:323:THR:H	2:B:539:VAL:CG1	2.18	0.56
2:B:343:ASN:ND2	3:I:1:NAG:C2	2.61	0.56
2:B:858:LEU:HD21	2:B:959:LEU:CD2	2.30	0.56
2:B:858:LEU:CD1	2:B:959:LEU:HD11	2.36	0.56
2:C:83:VAL:CG1	2:C:239:GLN:HB2	2.34	0.56
2:C:353:TRP:CZ3	2:C:466:ARG:HA	2.39	0.56
2:C:392:PHE:O	2:C:522:ALA:HB3	2.06	0.56
2:C:472:ILE:HD13	2:C:491:PRO:HA	1.87	0.56
2:A:193:VAL:HG12	2:A:195:LYS:HG3	1.87	0.56
2:A:650:LEU:HD12	2:A:666:ILE:HG21	1.87	0.56
2:A:1125:ASN:O	2:A:1126:CYS:HB3	2.05	0.56
2:B:57:PRO:HB3	2:B:273:ARG:NH1	2.17	0.56
2:B:610:VAL:O	2:B:651:ILE:N	2.25	0.56
2:B:646:ARG:HA	2:C:862:PRO:CD	2.28	0.56
2:C:141:LEU:HB3	2:C:243:ALA:HA	1.88	0.56
2:C:741:TYR:CE1	2:C:966:LEU:HD11	2.40	0.56
2:A:396:TYR:HE1	2:A:398:ASP:HB3	1.69	0.56
2:B:36:VAL:HG11	2:B:220:PHE:CE1	2.39	0.56
2:B:249:LEU:HD12	2:B:255:SER:O	2.05	0.56
2:B:643:PHE:HB3	2:B:650:LEU:HD21	1.87	0.56
2:B:897:PRO:HD2	2:B:900:MET:CE	2.34	0.56
2:B:1024:LEU:HA	2:B:1027:THR:CG2	2.36	0.56
2:A:31:SER:OG	2:A:60:SER:O	2.21	0.56
2:B:105:ILE:HD12	2:B:110:LEU:HD22	1.87	0.56
2:B:461:LEU:HD11	2:B:467:ASP:CB	2.35	0.56
2:B:552:LEU:HA	2:B:586:ASP:O	2.04	0.56
2:B:566:GLY:HA3	2:B:575:ALA:CB	2.36	0.56
2:B:788:ILE:O	2:A:702:GLU:HA	2.06	0.56
2:B:1100:THR:HG23	3:F:1:NAG:C8	2.35	0.56
2:A:116:SER:O	2:A:130:VAL:HA	2.06	0.56
2:A:334:ASN:OD1	2:A:362:VAL:HG11	2.06	0.56
2:B:360:ASN:HB3	2:B:524:VAL:CG2	2.35	0.56
2:B:642:VAL:HG22	2:B:651:ILE:HD11	1.87	0.56
2:B:673:SER:O	2:B:693:ILE:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1039:ARG:HG3	2:B:1039:ARG:NH1	2.20	0.56
2:C:964:LYS:HB3	2:C:964:LYS:HZ2	1.70	0.56
2:C:1116:THR:C	2:C:1137:VAL:HB	2.26	0.56
2:A:205:SER:CB	2:A:226:LEU:HD22	2.26	0.56
2:A:516:GLU:HG2	2:A:518:LEU:HB2	1.87	0.56
2:A:566:GLY:O	2:A:573:THR:HG22	2.05	0.56
2:B:27:ALA:O	2:B:64:TRP:N	2.39	0.56
2:A:454:ARG:HB3	2:A:492:LEU:CD1	2.26	0.56
2:A:726:ILE:HD13	2:A:945:LEU:HD23	1.88	0.56
2:B:83:VAL:HG21	2:B:237:ARG:HB3	1.88	0.56
2:B:670:ILE:HA	2:B:695:TYR:O	2.06	0.56
2:B:1085:GLY:HA2	2:B:1126:CYS:HB3	1.88	0.56
2:C:54:LEU:HD13	2:C:272:PRO:HB3	1.88	0.56
2:C:175:PHE:CB	2:C:176:LEU:HD12	2.36	0.56
2:C:380:TYR:HB2	2:A:984:LEU:CG	2.36	0.56
2:B:612:TYR:HB2	2:B:615:VAL:CG2	2.36	0.56
2:B:1013:ILE:HD11	2:A:1013:ILE:CD1	2.36	0.56
2:C:66:HIS:CE1	2:C:68:ILE:HD12	2.41	0.56
2:A:53:ASP:HB2	2:A:55:PHE:CE2	2.41	0.56
2:B:201:PHE:CE2	2:B:235:ILE:HG13	2.41	0.55
2:B:314:GLN:H	2:C:765:ARG:NE	2.03	0.55
2:B:408:ARG:O	2:B:409:GLN:HB2	2.06	0.55
2:B:873:TYR:CG	2:A:699:LEU:HD21	2.41	0.55
2:B:1130:ILE:HG13	2:C:917:TYR:CD2	2.41	0.55
2:C:109:THR:OG1	2:C:111:ASP:OD1	2.21	0.55
2:C:326:ILE:HD11	2:C:534:VAL:HB	1.88	0.55
2:C:375:SER:HB2	2:C:433:VAL:O	2.06	0.55
2:A:204:TYR:CD2	2:A:225:PRO:HA	2.41	0.55
2:B:222:ALA:C	2:B:223:LEU:HD12	2.25	0.55
2:C:581:THR:O	2:C:582:LEU:C	2.44	0.55
2:A:396:TYR:H	2:A:513:LEU:HD22	1.70	0.55
2:A:425:LEU:HB2	2:A:428:ASP:OD1	2.06	0.55
2:A:712:ILE:HG22	2:A:1075:PHE:H	1.70	0.55
2:A:779:GLN:O	2:A:783:ALA:HB3	2.06	0.55
2:B:40:ASP:N	2:B:40:ASP:OD1	2.39	0.55
2:B:47:VAL:O	2:B:48:LEU:HD13	2.06	0.55
2:B:643:PHE:HB3	2:B:650:LEU:CD2	2.35	0.55
2:B:646:ARG:HD2	2:C:863:PRO:N	2.22	0.55
2:B:854:LYS:NZ	2:A:591:SER:O	2.28	0.55
2:B:986:PRO:HG2	2:C:424:LYS:HG2	1.88	0.55
2:B:1095:PHE:CE2	2:B:1115:ILE:HD13	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:96:GLU:CD	2:C:99:ASN:HA	2.27	0.55
2:C:134:GLN:O	2:C:160:TYR:HA	2.06	0.55
2:C:189:LEU:HB2	2:C:210:ILE:CD1	2.37	0.55
2:A:21:ARG:HD2	2:A:76:THR:HG21	1.87	0.55
2:A:503:VAL:HG23	2:A:504:GLY:H	1.71	0.55
2:B:448:ASN:H	2:B:498:GLN:HE22	1.55	0.55
2:B:782:PHE:CZ	2:B:1060:VAL:HG22	2.42	0.55
2:B:862:PRO:HD3	2:A:647:ALA:HA	1.89	0.55
2:B:862:PRO:HG2	2:A:668:ALA:N	2.21	0.55
2:B:86:PHE:CB	2:B:90:VAL:HG21	2.33	0.55
2:B:319:ARG:HA	2:B:592:PHE:HE1	1.71	0.55
2:C:361:CYS:SG	2:C:524:VAL:HG23	2.46	0.55
2:C:805:ILE:HG23	2:C:1054:GLN:NE2	2.22	0.55
2:A:300:LYS:HG3	2:A:305:SER:O	2.06	0.55
2:A:338:PHE:HD1	2:A:358:ILE:HD12	1.71	0.55
2:A:653:ALA:CB	2:A:692:ILE:HG22	2.37	0.55
2:A:1086:LYS:NZ	2:A:1122:VAL:HG11	2.21	0.55
2:B:36:VAL:HG11	2:B:220:PHE:CZ	2.40	0.55
2:B:41:LYS:HE2	2:B:41:LYS:HA	1.89	0.55
2:B:564:GLN:N	2:C:41:LYS:O	2.35	0.55
2:B:570:ALA:C	2:C:967:SER:HA	2.27	0.55
2:B:878:LEU:CD2	2:B:1052:PHE:HB3	2.34	0.55
2:B:985:ASP:HB3	2:C:415:THR:OG1	2.07	0.55
2:B:1039:ARG:NH1	2:A:1039:ARG:HG2	2.20	0.55
2:B:1118:ASP:O	2:A:1091:ARG:NH2	2.40	0.55
2:C:144:TYR:HB3	2:C:246:ARG:HD3	1.89	0.55
2:C:330:PRO:HG2	2:C:530:SER:N	2.20	0.55
2:C:517:LEU:HD13	2:A:983:ARG:HH11	1.72	0.55
2:A:403:ARG:CZ	2:A:405:ASP:HB2	2.37	0.55
2:B:548:GLY:HA2	2:C:978:ASN:HD22	1.72	0.55
2:B:566:GLY:HA3	2:B:575:ALA:HB2	1.89	0.55
2:B:733:LYS:HG3	2:B:861:LEU:HB2	1.89	0.55
2:B:984:LEU:HB3	2:B:988:GLU:HB3	1.88	0.55
2:C:1045:LYS:O	2:C:1066:THR:HG21	2.07	0.55
2:A:144:TYR:HE1	2:A:155:SER:H	1.55	0.55
2:B:47:VAL:HG12	2:B:48:LEU:N	2.21	0.55
2:B:706:ALA:HA	2:C:894:LEU:N	2.22	0.55
2:B:748:GLU:OE1	2:B:981:LEU:HD13	2.06	0.55
2:C:53:ASP:HB3	2:C:55:PHE:HE1	1.72	0.55
2:C:707:TYR:HB3	2:A:895:GLN:NE2	2.21	0.55
2:C:983:ARG:C	2:C:984:LEU:HD12	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1082:CYS:HB3	2:C:1087:ALA:HA	1.88	0.55
4:C:1206:NAG:O7	4:C:1206:NAG:O3	2.17	0.55
2:A:760:CYS:HB3	2:A:763:LEU:CD1	2.33	0.55
2:B:343:ASN:CG	3:I:1:NAG:H2	2.27	0.55
2:B:408:ARG:HG2	2:B:409:GLN:H	1.72	0.55
2:B:439:ASN:ND2	2:B:499:PRO:HG3	2.22	0.55
2:C:433:VAL:HG12	2:C:512:VAL:HB	1.88	0.55
2:A:68:ILE:HG12	2:A:262:ALA:HB1	1.88	0.55
2:A:642:VAL:HG23	2:A:651:ILE:CG2	2.37	0.55
2:A:778:THR:HG21	2:A:870:ILE:HD11	1.88	0.55
2:B:1086:LYS:HD2	2:B:1122:VAL:HG21	1.89	0.55
2:C:353:TRP:HB3	2:C:355:ARG:NH2	2.20	0.55
2:C:384:PRO:HD3	2:A:986:PRO:HD3	1.89	0.55
2:A:89:GLY:HA3	2:A:194:PHE:O	2.07	0.55
2:B:458:LYS:HB3	2:B:473:TYR:HE1	1.72	0.54
2:B:928:ASN:HB3	3:H:1:NAG:C6	2.37	0.54
2:C:68:ILE:HG12	2:C:262:ALA:HA	1.88	0.54
2:C:106:PHE:CD2	2:C:235:ILE:HG21	2.42	0.54
2:A:318:PHE:H	2:A:594:GLY:HA2	1.72	0.54
2:A:367:VAL:O	2:A:369:TYR:N	2.40	0.54
2:A:995:ARG:HH11	2:A:995:ARG:HG3	1.72	0.54
2:B:35:GLY:HA3	2:B:56:LEU:HD22	1.88	0.54
2:B:397:ALA:CB	2:B:513:LEU:HG	2.35	0.54
2:B:444:LYS:HD3	2:B:448:ASN:CG	2.28	0.54
2:B:729:VAL:HG11	2:B:1060:VAL:HG23	1.90	0.54
2:B:985:ASP:OD1	2:B:987:PRO:HG2	2.08	0.54
2:C:1140:PRO:HG2	2:C:1141:LEU:HD22	1.89	0.54
2:B:62:VAL:HB	2:B:267:VAL:O	2.07	0.54
2:B:707:TYR:O	2:C:896:ILE:HB	2.08	0.54
2:B:922:LEU:O	2:B:926:GLN:HG3	2.07	0.54
2:B:1076:THR:HB	2:B:1097:SER:OG	2.07	0.54
2:C:358:ILE:HB	2:C:395:VAL:HG11	1.89	0.54
2:C:452:LEU:CB	2:C:492:LEU:HD21	2.33	0.54
2:C:538:CYS:HA	2:C:550:GLY:O	2.07	0.54
2:A:334:ASN:ND2	2:A:362:VAL:CG1	2.71	0.54
2:B:562:PHE:CZ	2:C:224:GLU:HG2	2.42	0.54
2:B:562:PHE:HD2	2:C:225:PRO:HD2	1.73	0.54
2:B:567:ARG:CG	2:C:42:VAL:HG21	2.37	0.54
2:B:905:ARG:HB3	2:B:1036:GLN:NE2	2.22	0.54
2:C:356:LYS:CB	2:C:397:ALA:HB3	2.32	0.54
2:C:440:ASN:OD1	2:C:441:LEU:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1102:TRP:CZ2	2:A:1133:VAL:HG21	2.43	0.54
2:B:470:THR:HA	2:B:492:LEU:HD11	1.88	0.54
2:B:541:PHE:CE1	2:B:552:LEU:HD21	2.43	0.54
2:B:613:GLN:HB3	2:C:735:SER:HB2	1.89	0.54
2:C:102:ARG:HG3	2:C:141:LEU:CD2	2.38	0.54
2:C:308:VAL:HG22	2:C:602:THR:CG2	2.34	0.54
2:C:650:LEU:HD11	2:C:666:ILE:CD1	2.38	0.54
2:A:452:LEU:CD1	2:A:492:LEU:HD23	2.37	0.54
2:A:1072:GLU:H	2:A:1072:GLU:CD	2.10	0.54
2:B:403:ARG:HD3	2:B:497:PHE:CZ	2.43	0.54
2:B:779:GLN:O	2:B:783:ALA:HB3	2.08	0.54
2:C:54:LEU:H	2:C:54:LEU:HD22	1.73	0.54
2:C:89:GLY:HA3	2:C:270:LEU:CD1	2.36	0.54
2:C:728:PRO:HB3	2:C:951:VAL:HG21	1.89	0.54
2:A:45:SER:OG	2:A:280:ASN:O	2.22	0.54
2:A:97:LYS:HG3	2:A:186:PHE:CD1	2.43	0.54
2:A:214:ARG:HB2	2:A:217:PRO:HG3	1.89	0.54
2:A:350:VAL:HA	2:A:400:PHE:CB	2.35	0.54
2:A:884:SER:HA	2:A:895:GLN:HA	1.88	0.54
2:B:80:ASP:OD1	2:B:81:ASN:N	2.41	0.54
2:B:613:GLN:HB3	2:C:735:SER:CB	2.38	0.54
2:C:736:VAL:HG12	2:C:858:LEU:HD23	1.89	0.54
2:A:44:ARG:NH1	2:A:49:HIS:HB2	2.23	0.54
2:A:117:LEU:CG	2:A:130:VAL:HG22	2.36	0.54
2:A:742:ILE:CD1	2:A:753:LEU:HD13	2.37	0.54
2:A:1140:PRO:O	2:A:1143:PRO:HD2	2.08	0.54
2:B:331:ASN:O	4:B:1307:NAG:H83	2.08	0.54
2:B:351:TYR:HB3	2:B:492:LEU:HD23	1.90	0.54
2:B:445:VAL:HA	2:B:498:GLN:HB3	1.90	0.54
2:B:708:SER:HA	2:C:895:GLN:O	2.07	0.54
2:B:742:ILE:HG22	2:B:1000:ARG:CB	2.37	0.54
2:B:1125:ASN:O	2:B:1129:VAL:HG23	2.08	0.54
2:C:381:GLY:C	2:A:984:LEU:HB2	2.29	0.54
2:C:934:ILE:HD13	2:C:1063:LEU:HD22	1.89	0.54
2:A:426:PRO:HG3	2:A:463:PRO:HB2	1.89	0.54
2:A:450:ASN:O	2:A:452:LEU:HD23	2.07	0.54
2:A:472:ILE:HD12	2:A:473:TYR:N	2.22	0.54
2:B:710:ASN:O	2:B:1077:THR:N	2.38	0.54
2:B:862:PRO:HG3	2:A:668:ALA:HB2	1.90	0.54
2:A:105:ILE:CD1	2:A:239:GLN:HB3	2.37	0.54
2:A:375:SER:O	2:A:434:ILE:HG12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:377:PHE:CD2	2:A:379:CYS:HB3	2.43	0.54
2:A:543:PHE:HB2	2:A:565:PHE:CE2	2.42	0.54
2:A:777:ASN:O	2:A:781:VAL:HG23	2.08	0.54
2:B:1119:ASN:ND2	2:B:1119:ASN:O	2.40	0.53
2:B:1144:GLU:HB3	2:A:1141:LEU:CD2	2.39	0.53
2:C:126:VAL:O	2:C:171:VAL:HA	2.07	0.53
2:C:328:ARG:CA	2:C:530:SER:HA	2.27	0.53
2:C:483:VAL:O	2:C:488:CYS:HB3	2.07	0.53
2:A:206:LYS:NZ	2:A:222:ALA:O	2.33	0.53
2:B:584:ILE:HD12	2:B:585:LEU:H	1.73	0.53
2:B:1071:GLN:NE2	3:G:1:NAG:O6	2.42	0.53
2:C:39:PRO:HB3	2:C:55:PHE:CZ	2.43	0.53
2:C:83:VAL:HG12	2:C:239:GLN:CB	2.34	0.53
2:C:211:ASN:C	2:C:212:LEU:HD22	2.29	0.53
2:C:415:THR:HG23	2:C:419:ALA:HB3	1.91	0.53
2:C:805:ILE:HD11	2:C:931:ILE:HD11	1.90	0.53
2:A:646:ARG:NH1	2:A:646:ARG:HB2	2.23	0.53
2:B:67:ALA:CB	2:B:263:ALA:HB3	2.36	0.53
2:B:123:ALA:O	2:B:174:PRO:HG3	2.08	0.53
2:B:206:LYS:HG3	2:B:208:THR:CG2	2.39	0.53
2:B:516:GLU:HB3	2:B:519:HIS:ND1	2.22	0.53
2:B:706:ALA:HB3	2:C:892:PRO:HG2	1.90	0.53
2:B:752:LEU:O	2:B:755:GLN:HG3	2.08	0.53
2:B:894:LEU:HD22	2:A:1072:GLU:OE2	2.08	0.53
2:B:976:VAL:HG12	2:B:978:ASN:H	1.73	0.53
2:C:308:VAL:CG2	2:C:602:THR:HG23	2.34	0.53
2:A:888:PHE:HA	2:A:893:ALA:HA	1.90	0.53
2:B:327:VAL:HG23	2:B:530:SER:HA	1.91	0.53
2:B:392:PHE:HD2	2:B:516:GLU:HB2	1.72	0.53
2:B:426:PRO:HD3	2:B:463:PRO:HA	1.90	0.53
2:B:646:ARG:HG3	2:C:861:LEU:C	2.27	0.53
2:C:360:ASN:OD1	2:C:523:THR:HB	2.09	0.53
2:C:543:PHE:HD2	2:C:546:LEU:HD11	1.73	0.53
2:C:822:LEU:CD1	2:C:945:LEU:HD11	2.39	0.53
2:A:516:GLU:HG2	2:A:518:LEU:CG	2.39	0.53
2:A:719:THR:HA	2:A:926:GLN:NE2	2.23	0.53
2:A:973:ILE:HG23	2:A:992:GLN:NE2	2.23	0.53
2:C:175:PHE:HB3	2:C:176:LEU:HD12	1.91	0.53
2:C:420:ASP:OD1	2:C:459:SER:HA	2.09	0.53
2:C:430:THR:O	2:C:514:SER:HA	2.09	0.53
2:C:530:SER:O	2:C:531:THR:C	2.47	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:140:PHE:CE2	2:A:158:ARG:HG3	2.44	0.53
2:B:41:LYS:HE2	2:B:41:LYS:N	2.24	0.53
2:B:326:ILE:HD11	2:B:534:VAL:HG12	1.88	0.53
2:B:386:LYS:CD	2:C:983:ARG:HA	2.22	0.53
2:B:498:GLN:HG2	2:B:501:ASN:HD21	1.73	0.53
2:B:563:GLN:HB3	2:C:41:LYS:O	2.08	0.53
2:B:1013:ILE:HD11	2:A:1013:ILE:HD12	1.91	0.53
2:C:380:TYR:CG	2:A:983:ARG:HB3	2.43	0.53
2:A:395:VAL:HA	2:A:513:LEU:HD11	1.91	0.53
2:A:430:THR:HB	2:A:515:PHE:HB2	1.89	0.53
2:A:536:ASN:O	2:A:537:LYS:HG3	2.09	0.53
2:A:594:GLY:HA3	2:A:613:GLN:NE2	2.24	0.53
2:B:208:THR:O	2:B:208:THR:OG1	2.25	0.53
2:B:314:GLN:HB3	2:C:765:ARG:HE	1.72	0.53
2:B:1090:PRO:HG3	2:B:1095:PHE:CE1	2.43	0.53
2:C:569:ILE:HD12	2:A:963:VAL:HG11	1.90	0.53
2:A:68:ILE:CG1	2:A:262:ALA:HB1	2.39	0.53
2:A:197:ILE:HD11	2:A:202:LYS:NZ	2.24	0.53
2:A:647:ALA:HB2	2:A:668:ALA:HB2	1.90	0.53
2:A:647:ALA:N	2:A:668:ALA:HB2	2.23	0.53
2:A:712:ILE:HG21	2:A:1075:PHE:HB2	1.90	0.53
2:B:701:ALA:O	2:C:786:LYS:HB2	2.08	0.53
2:C:394:ASN:O	2:C:515:PHE:HA	2.09	0.53
2:C:949:GLN:OE1	2:C:949:GLN:HA	2.09	0.53
2:C:954:GLN:HB3	2:C:1014:ARG:HH11	1.72	0.53
2:C:974:SER:HB2	2:C:980:ILE:CD1	2.39	0.53
2:A:218:GLN:HG2	2:A:219:GLY:N	2.24	0.53
2:A:330:PRO:HG2	2:A:544:ASN:ND2	2.24	0.53
2:A:411:ALA:O	2:A:425:LEU:HD21	2.09	0.53
2:A:598:ILE:HD11	2:A:666:ILE:HG12	1.91	0.53
2:A:1110:TYR:CZ	2:A:1112:PRO:HG3	2.43	0.53
2:B:214:ARG:HE	2:B:215:ASP:N	2.03	0.53
2:B:351:TYR:CD1	2:B:452:LEU:HD12	2.44	0.53
2:B:358:ILE:CG2	2:B:395:VAL:HB	2.39	0.53
2:B:458:LYS:HB3	2:B:473:TYR:CE1	2.44	0.53
2:B:700:GLY:HA3	2:C:786:LYS:CB	2.38	0.53
2:C:102:ARG:HG3	2:C:141:LEU:HD22	1.90	0.53
2:C:356:LYS:HB3	2:C:397:ALA:CB	2.32	0.53
2:C:452:LEU:CB	2:C:492:LEU:HD11	2.36	0.53
2:C:569:ILE:HD13	2:A:849:LEU:CD1	2.39	0.53
2:C:1071:GLN:NE2	4:C:1206:NAG:O6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:24:LEU:HD12	2:A:78:ARG:NH1	2.22	0.53
2:A:387:LEU:O	2:A:389:ASP:N	2.41	0.53
2:B:405:ASP:HB2	2:B:505:TYR:CE2	2.44	0.53
2:B:421:TYR:HA	2:B:457:ARG:HG2	1.90	0.53
2:B:439:ASN:OD1	2:B:507:PRO:HG2	2.09	0.53
2:B:1024:LEU:CD2	2:B:1028:LYS:HE2	2.39	0.53
2:C:56:LEU:HD21	2:C:91:TYR:CG	2.44	0.53
2:A:68:ILE:CD1	2:A:262:ALA:HB1	2.39	0.53
2:A:132:GLU:OE2	2:A:165:ASN:ND2	2.40	0.53
2:A:791:THR:HG21	2:A:806:LEU:CD1	2.30	0.53
2:A:816:SER:OG	2:A:819:GLU:HG3	2.08	0.53
2:B:346:ARG:HA	2:B:509:ARG:HH22	1.74	0.52
2:B:407:VAL:HG23	2:B:437:ASN:OD1	2.09	0.52
2:B:665:PRO:HB2	2:C:772:VAL:HG21	1.91	0.52
2:C:105:ILE:HD12	2:C:135:PHE:CE2	2.44	0.52
2:C:227:VAL:HG12	2:C:229:LEU:HG	1.91	0.52
2:A:131:CYS:HB2	2:A:133:PHE:CZ	2.43	0.52
2:A:247:SER:HB3	2:A:257:GLY:O	2.08	0.52
2:B:1023:ASN:O	2:B:1027:THR:HG22	2.09	0.52
2:B:1104:VAL:HG11	2:B:1119:ASN:ND2	2.21	0.52
2:C:215:ASP:OD1	2:C:215:ASP:N	2.41	0.52
2:C:770:ILE:HD11	2:C:1012:LEU:HA	1.90	0.52
2:A:439:ASN:O	2:A:441:LEU:HD23	2.09	0.52
2:A:760:CYS:CB	2:A:763:LEU:HD12	2.36	0.52
2:B:593:GLY:HA2	2:C:737:ASP:OD1	2.09	0.52
2:B:895:GLN:CG	2:A:705:VAL:HB	2.31	0.52
2:B:898:PHE:N	2:B:899:PRO:HD2	2.24	0.52
2:A:152:TRP:NE1	2:A:180:GLU:OE1	2.42	0.52
2:A:887:THR:HG21	2:A:894:LEU:HB2	1.90	0.52
2:B:411:ALA:HB3	2:B:414:GLN:NE2	2.25	0.52
2:B:669:GLY:C	2:C:864:LEU:HD12	2.29	0.52
2:B:869:MET:O	2:B:872:GLN:HB2	2.09	0.52
2:C:424:LYS:HB3	2:C:463:PRO:CB	2.36	0.52
2:C:717:ASN:O	2:C:1070:ALA:HB3	2.09	0.52
2:C:853:GLN:CB	2:C:963:VAL:HG21	2.39	0.52
2:C:1094:VAL:CG1	2:C:1107:ARG:HE	2.18	0.52
2:A:431:GLY:O	2:A:513:LEU:N	2.39	0.52
2:A:811:LYS:NZ	2:A:813:SER:H	2.07	0.52
2:A:1079:PRO:HG3	2:A:1130:ILE:O	2.10	0.52
2:A:1143:PRO:HG2	2:A:1144:GLU:OE1	2.10	0.52
2:B:54:LEU:O	2:B:270:LEU:HD11	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:343:ASN:OD1	3:I:1:NAG:C2	2.57	0.52
2:B:752:LEU:HD12	2:B:753:LEU:N	2.23	0.52
2:B:1141:LEU:HG	2:A:1141:LEU:HD13	1.90	0.52
2:C:66:HIS:NE2	2:C:68:ILE:HD12	2.24	0.52
2:C:327:VAL:HB	2:C:529:LYS:O	2.10	0.52
2:C:983:ARG:HG3	2:C:984:LEU:CD1	2.40	0.52
2:A:115:GLN:HE21	2:A:233:ILE:HG21	1.73	0.52
2:A:393:THR:CG2	2:A:519:HIS:HB2	2.40	0.52
2:A:719:THR:O	2:A:1068:VAL:HG22	2.10	0.52
2:B:216:LEU:HG	2:B:266:TYR:CZ	2.45	0.52
2:B:564:GLN:N	2:C:41:LYS:HB3	2.25	0.52
2:A:412:PRO:CA	2:A:425:LEU:HD11	2.40	0.52
2:A:719:THR:HG23	2:A:926:GLN:NE2	2.23	0.52
2:B:110:LEU:HD22	2:B:135:PHE:CD2	2.45	0.52
2:B:703:ASN:H	2:C:787:GLN:HB2	1.75	0.52
2:B:737:ASP:HB2	2:A:317:ASN:ND2	2.25	0.52
2:B:1124:GLY:HA2	2:C:1113:GLN:CD	2.30	0.52
2:C:578:ASP:HB3	2:C:583:GLU:N	2.24	0.52
2:C:986:PRO:HB2	2:C:987:PRO:HD3	1.91	0.52
2:A:676:THR:HG21	2:A:693:ILE:HG12	1.91	0.52
2:A:749:CYS:SG	2:A:997:ILE:HD11	2.49	0.52
2:A:1029:MET:HG3	2:A:1029:MET:O	2.08	0.52
2:B:125:ASN:HA	2:B:174:PRO:CD	2.39	0.52
2:B:461:LEU:HD11	2:B:467:ASP:HB2	1.90	0.52
2:B:887:THR:CB	2:B:894:LEU:HG	2.40	0.52
2:C:330:PRO:O	2:C:331:ASN:C	2.47	0.52
2:C:986:PRO:O	2:C:990:GLU:HG2	2.09	0.52
2:C:1095:PHE:CE1	2:C:1104:VAL:HG22	2.45	0.52
2:C:1115:ILE:CG2	2:C:1137:VAL:HA	2.35	0.52
2:A:308:VAL:CG1	2:A:602:THR:HB	2.40	0.52
2:B:905:ARG:HD3	2:B:1049:LEU:O	2.10	0.52
2:B:1145:LEU:HA	2:A:1145:LEU:CD2	2.34	0.52
2:C:358:ILE:H	2:C:395:VAL:HB	1.74	0.52
2:C:399:SER:CB	2:C:511:VAL:HG12	2.40	0.52
2:C:653:ALA:HB2	2:C:692:ILE:HG22	1.92	0.52
2:C:1062:PHE:O	2:C:1063:LEU:HD23	2.10	0.52
2:A:211:ASN:C	2:A:212:LEU:HD12	2.30	0.52
2:A:382:VAL:O	2:A:383:SER:OG	2.27	0.52
2:A:383:SER:OG	2:A:389:ASP:OD2	2.20	0.52
2:A:567:ARG:HA	2:A:573:THR:CA	2.40	0.52
2:B:565:PHE:C	2:C:42:VAL:HA	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1130:ILE:HG13	2:C:917:TYR:HD2	1.75	0.52
2:B:1145:LEU:HG	2:A:1145:LEU:HD21	1.92	0.52
2:C:294:ASP:OD1	2:C:296:LEU:N	2.41	0.52
2:C:303:LEU:HG	2:C:304:LYS:N	2.25	0.52
2:A:495:TYR:CD2	2:A:497:PHE:HE1	2.28	0.52
2:A:973:ILE:H	2:A:992:GLN:HE21	1.58	0.52
2:B:104:TRP:O	2:B:118:LEU:HD12	2.10	0.51
2:B:173:GLN:HB3	2:B:174:PRO:HD2	1.92	0.51
2:B:349:SER:CB	2:B:452:LEU:HG	2.35	0.51
2:B:670:ILE:HD12	2:B:695:TYR:O	2.10	0.51
2:C:177:MET:N	2:C:177:MET:SD	2.82	0.51
2:C:596:SER:N	2:C:611:LEU:O	2.43	0.51
2:C:822:LEU:CD1	2:C:945:LEU:HD21	2.41	0.51
2:C:1082:CYS:CB	2:C:1087:ALA:HA	2.40	0.51
2:A:68:ILE:HD13	2:A:262:ALA:HB1	1.90	0.51
2:A:332:ILE:O	2:A:333:THR:C	2.49	0.51
2:A:538:CYS:HA	2:A:551:VAL:HA	1.92	0.51
2:A:811:LYS:HD2	2:A:812:PRO:HD2	1.92	0.51
2:B:445:VAL:C	2:B:498:GLN:HE21	2.13	0.51
2:B:515:PHE:O	2:B:517:LEU:HD12	2.10	0.51
2:B:712:ILE:CG2	2:B:1077:THR:HB	2.40	0.51
2:B:805:ILE:HG22	2:B:1054:GLN:HE21	1.76	0.51
2:C:380:TYR:C	2:A:984:LEU:HG	2.31	0.51
2:C:407:VAL:HB	2:C:408:ARG:CZ	2.40	0.51
2:C:716:THR:HG22	2:C:1071:GLN:O	2.10	0.51
2:C:1102:TRP:O	2:C:1115:ILE:HD11	2.10	0.51
2:A:474:GLN:NE2	2:A:476:GLY:O	2.43	0.51
2:A:1028:LYS:NZ	2:A:1042:PHE:O	2.44	0.51
2:B:656:VAL:CG2	2:B:693:ILE:HD11	2.40	0.51
2:C:358:ILE:HB	2:C:395:VAL:CG1	2.40	0.51
2:A:358:ILE:CB	2:A:395:VAL:HG21	2.22	0.51
2:A:1129:VAL:O	2:A:1130:ILE:HD13	2.10	0.51
2:B:992:GLN:HE22	2:B:995:ARG:HE	1.59	0.51
2:B:1133:VAL:HG23	2:B:1135:ASN:HB3	1.91	0.51
2:C:65:PHE:CE1	2:C:84:LEU:HD21	2.46	0.51
2:C:126:VAL:N	2:C:172:SER:O	2.36	0.51
2:C:290:ASP:OD1	2:C:291:CYS:N	2.43	0.51
2:C:380:TYR:HB3	2:A:983:ARG:CB	2.40	0.51
2:C:805:ILE:HG23	2:C:1054:GLN:HE21	1.74	0.51
2:A:366:SER:HA	2:A:369:TYR:OH	2.10	0.51
2:A:566:GLY:C	2:A:574:ASP:H	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:712:ILE:HG22	2:A:1075:PHE:HB2	1.93	0.51
2:B:133:PHE:HA	2:B:163:ALA:HA	1.92	0.51
2:B:1130:ILE:HD11	2:C:913:GLN:HG3	1.93	0.51
2:C:133:PHE:CD1	2:C:163:ALA:HB2	2.45	0.51
2:C:373:SER:OG	2:C:436:TRP:HA	2.10	0.51
2:C:592:PHE:CD1	2:C:592:PHE:C	2.84	0.51
2:A:310:LYS:HZ3	2:A:663:ASP:HB3	1.75	0.51
2:A:426:PRO:HG3	2:A:463:PRO:CG	2.41	0.51
2:A:543:PHE:HB2	2:A:565:PHE:HE2	1.76	0.51
2:A:718:PHE:HE1	2:A:923:ILE:HG12	1.76	0.51
2:B:36:VAL:CG2	2:B:277:LEU:HD21	2.41	0.51
2:B:317:ASN:ND2	2:C:738:CYS:SG	2.83	0.51
2:B:334:ASN:HB2	2:B:362:VAL:H	1.75	0.51
2:B:353:TRP:CH2	2:B:423:TYR:HA	2.46	0.51
2:B:439:ASN:HD21	2:B:499:PRO:HG3	1.75	0.51
2:B:520:ALA:HB1	2:B:521:PRO:CD	2.41	0.51
2:B:537:LYS:HG2	2:B:539:VAL:CG1	2.36	0.51
2:B:567:ARG:HE	2:B:573:THR:HG22	1.74	0.51
2:B:690:GLN:N	2:B:690:GLN:OE1	2.44	0.51
2:B:712:ILE:O	2:B:1075:PHE:HB2	2.11	0.51
2:B:791:THR:OG1	2:B:792:PRO:HD2	2.10	0.51
2:B:903:ALA:HB2	2:B:916:LEU:CD2	2.39	0.51
2:C:646:ARG:CD	2:C:668:ALA:HB1	2.39	0.51
2:C:1086:LYS:HG3	2:C:1122:VAL:HG23	1.92	0.51
2:B:47:VAL:HG12	2:B:48:LEU:H	1.75	0.51
2:B:53:ASP:HB2	2:B:55:PHE:CZ	2.45	0.51
2:B:208:THR:O	2:B:210:ILE:HG12	2.11	0.51
2:B:334:ASN:OD1	2:B:362:VAL:HG23	2.10	0.51
2:C:290:ASP:O	2:C:297:SER:HB3	2.11	0.51
2:A:121:ASN:OD1	2:A:126:VAL:HG13	2.10	0.51
2:A:310:LYS:HB3	2:A:600:PRO:O	2.11	0.51
2:A:319:ARG:HG2	2:A:592:PHE:CD1	2.46	0.51
2:B:93:ALA:O	2:B:265:TYR:HB2	2.11	0.51
2:B:244:LEU:HD21	2:B:258:TRP:HE3	1.75	0.51
2:B:392:PHE:CD2	2:B:516:GLU:HB2	2.45	0.51
2:B:665:PRO:C	2:C:772:VAL:HG21	2.31	0.51
2:B:705:VAL:HG21	2:C:888:PHE:HB3	1.91	0.51
2:B:752:LEU:O	2:B:755:GLN:NE2	2.43	0.51
2:B:770:ILE:H	2:B:770:ILE:HD12	1.76	0.51
2:C:144:TYR:CB	2:C:246:ARG:HD3	2.40	0.51
2:A:330:PRO:HG2	2:A:544:ASN:HD22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:390:LEU:HD12	2:A:390:LEU:O	2.11	0.51
2:B:630:THR:HB	2:B:631:PRO:HD3	1.93	0.51
2:C:719:THR:O	2:C:719:THR:HG23	2.11	0.51
2:C:752:LEU:HA	2:C:755:GLN:HG2	1.93	0.51
2:C:886:TRP:HB3	2:C:905:ARG:HH22	1.76	0.51
2:A:454:ARG:HB2	2:A:492:LEU:HA	1.93	0.51
2:A:598:ILE:HB	2:A:609:ALA:O	2.10	0.51
2:A:822:LEU:HD21	2:A:938:LEU:HD13	1.92	0.51
2:B:502:GLY:HA3	2:B:505:TYR:CD1	2.45	0.51
2:C:193:VAL:CG1	2:C:204:TYR:HB2	2.41	0.51
2:C:396:TYR:O	2:C:513:LEU:HA	2.10	0.51
2:A:317:ASN:CA	2:A:594:GLY:HA2	2.35	0.51
2:A:373:SER:OG	2:A:374:PHE:N	2.42	0.51
2:A:659:SER:HB2	2:A:695:TYR:HB2	1.92	0.51
2:B:589:PRO:HG2	2:C:856:ASN:HB2	1.93	0.50
2:C:140:PHE:HB2	2:C:244:LEU:HD13	1.92	0.50
2:C:517:LEU:HD21	2:A:979:ASP:OD2	2.10	0.50
2:A:406:GLU:HG3	2:A:418:ILE:CG1	2.40	0.50
2:A:668:ALA:O	2:A:670:ILE:HG12	2.11	0.50
2:A:826:VAL:HG23	2:A:945:LEU:HD13	1.94	0.50
2:B:135:PHE:HD1	2:B:160:TYR:HB3	1.73	0.50
2:B:401:VAL:HB	2:B:451:TYR:CG	2.46	0.50
2:B:553:THR:O	2:B:585:LEU:HD12	2.10	0.50
2:B:566:GLY:O	2:B:574:ASP:N	2.44	0.50
2:B:914:ASN:HB3	2:A:1089:PHE:CE2	2.47	0.50
2:C:117:LEU:CD2	2:C:119:ILE:HG13	2.41	0.50
2:C:250:THR:N	2:C:253:ASP:OD2	2.43	0.50
2:A:453:TYR:HB3	2:A:493:GLN:NE2	2.24	0.50
2:A:490:PHE:CG	2:A:491:PRO:HD2	2.46	0.50
2:A:719:THR:HA	2:A:926:GLN:HE22	1.77	0.50
2:A:886:TRP:HZ3	2:A:901:GLN:HG3	1.75	0.50
2:B:314:GLN:OE1	2:C:761:THR:HA	2.11	0.50
2:B:453:TYR:CD2	2:B:455:LEU:HB2	2.46	0.50
2:B:506:GLN:HB2	2:B:508:TYR:CE1	2.47	0.50
2:B:538:CYS:SG	2:B:551:VAL:HG12	2.51	0.50
2:B:646:ARG:HD2	2:C:862:PRO:C	2.32	0.50
2:B:914:ASN:HB3	2:A:1089:PHE:HE2	1.77	0.50
2:B:1029:MET:HB2	2:B:1062:PHE:HZ	1.75	0.50
2:C:18:LEU:HB3	2:C:258:TRP:HZ2	1.75	0.50
2:C:963:VAL:O	2:C:966:LEU:HD13	2.12	0.50
2:A:323:THR:HG21	2:A:537:LYS:HZ2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1103:PHE:CD2	2:A:1112:PRO:HB3	2.47	0.50
2:B:349:SER:HB2	2:B:351:TYR:CE1	2.47	0.50
2:B:357:ARG:HB3	2:B:357:ARG:NH1	2.26	0.50
2:C:435:ALA:HB2	2:C:510:VAL:HG23	1.93	0.50
2:C:567:ARG:HE	2:A:42:VAL:HG21	1.77	0.50
2:C:779:GLN:O	2:C:783:ALA:HB3	2.11	0.50
2:C:802:PHE:CB	2:C:806:LEU:HD23	2.42	0.50
2:A:66:HIS:CE1	2:A:68:ILE:HB	2.46	0.50
2:A:616:ASN:O	4:A:1204:NAG:H82	2.10	0.50
2:B:559:PHE:CE1	2:B:563:GLN:HB2	2.47	0.50
2:B:984:LEU:HB3	2:B:989:ALA:N	2.27	0.50
2:B:1089:PHE:O	2:B:1120:THR:HG23	2.12	0.50
2:B:1121:PHE:CE1	2:C:1092:GLU:HB2	2.46	0.50
2:B:1145:LEU:HG	2:A:1145:LEU:HD11	1.92	0.50
2:C:230:PRO:C	2:C:231:ILE:HD12	2.32	0.50
2:A:80:ASP:OD1	2:A:82:PRO:HD3	2.12	0.50
2:A:495:TYR:HD2	2:A:497:PHE:HE1	1.60	0.50
2:B:372:ALA:HA	2:B:377:PHE:HE2	1.73	0.50
2:B:403:ARG:HE	2:B:405:ASP:HB3	1.77	0.50
2:C:44:ARG:HD3	2:C:49:HIS:NE2	2.26	0.50
2:C:1093:GLY:HA3	2:C:1105:THR:O	2.12	0.50
2:A:299:THR:O	2:A:302:THR:HG22	2.12	0.50
2:A:426:PRO:HG3	2:A:463:PRO:HG2	1.94	0.50
2:A:516:GLU:HG2	2:A:518:LEU:HG	1.93	0.50
2:A:733:LYS:HG3	2:A:861:LEU:HB2	1.94	0.50
2:A:1010:GLN:HG2	2:A:1014:ARG:NH2	2.27	0.50
2:B:68:ILE:O	2:B:262:ALA:HA	2.12	0.50
2:B:193:VAL:HB	2:B:204:TYR:HB2	1.93	0.50
2:B:358:ILE:HG22	2:B:395:VAL:H	1.77	0.50
2:B:696:THR:HA	2:C:864:LEU:HD11	1.93	0.50
2:B:709:ASN:HB2	2:C:900:MET:SD	2.52	0.50
2:C:30:ASN:HA	2:C:61:ASN:HA	1.92	0.50
2:C:117:LEU:HD21	2:C:119:ILE:HG13	1.93	0.50
2:C:402:ILE:HG23	2:C:404:GLY:N	2.26	0.50
2:C:735:SER:O	2:C:735:SER:OG	2.26	0.50
2:A:116:SER:HG	2:A:135:PHE:HE1	1.60	0.50
2:A:361:CYS:C	2:A:524:VAL:HG12	2.31	0.50
2:A:960:ASN:O	2:A:963:VAL:HG12	2.11	0.50
2:B:42:VAL:HG11	2:A:567:ARG:HB2	1.93	0.50
2:B:116:SER:HA	2:B:233:ILE:HD11	1.94	0.50
2:B:206:LYS:HB2	2:B:223:LEU:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:449:TYR:CD1	2:C:496:GLY:HA2	2.47	0.50
2:A:546:LEU:HD21	2:A:573:THR:CG2	2.22	0.50
2:A:597:VAL:CG1	2:A:608:VAL:HG11	2.42	0.50
2:B:57:PRO:HA	2:B:273:ARG:HH22	1.76	0.50
2:B:663:ASP:OD2	2:B:673:SER:HA	2.12	0.50
2:C:424:LYS:HB3	2:C:463:PRO:CA	2.41	0.50
2:C:770:ILE:HD11	2:C:1012:LEU:HD23	1.93	0.50
2:C:977:LEU:CD2	2:C:996:LEU:HD23	2.42	0.50
2:A:332:ILE:HG23	2:A:333:THR:N	2.25	0.50
2:A:472:ILE:CD1	2:A:475:ALA:HB2	2.41	0.50
2:A:670:ILE:HG22	2:A:671:CYS:N	2.27	0.50
2:B:491:PRO:HG2	2:B:492:LEU:CD1	2.42	0.49
2:B:591:SER:OG	2:B:619:GLU:OE2	2.24	0.49
2:B:897:PRO:HA	2:A:707:TYR:CD2	2.47	0.49
2:B:974:SER:HB2	2:B:983:ARG:HH12	1.76	0.49
2:C:611:LEU:HD12	2:C:650:LEU:CD2	2.43	0.49
2:A:971:GLY:HA3	2:A:995:ARG:NH2	2.27	0.49
2:B:347:PHE:CZ	2:B:511:VAL:HG21	2.47	0.49
2:B:662:CYS:HB2	2:B:697:MET:SD	2.51	0.49
2:B:731:MET:HB3	2:B:1018:ILE:CD1	2.42	0.49
2:B:862:PRO:HG3	2:A:647:ALA:CA	2.42	0.49
2:C:299:THR:OG1	2:C:597:VAL:HG21	2.12	0.49
2:C:330:PRO:HG2	2:C:530:SER:H	1.77	0.49
2:C:562:PHE:C	2:A:41:LYS:HE2	2.33	0.49
2:A:48:LEU:HD22	2:A:278:LYS:HA	1.94	0.49
2:A:811:LYS:NZ	2:A:812:PRO:HD2	2.26	0.49
2:B:278:LYS:HG2	2:B:287:ASP:O	2.12	0.49
2:C:159:VAL:HG23	2:C:160:TYR:HD1	1.76	0.49
2:C:452:LEU:HB3	2:C:492:LEU:CD1	2.39	0.49
2:C:742:ILE:HA	2:C:1000:ARG:HB3	1.94	0.49
2:C:885:GLY:HA2	2:C:901:GLN:NE2	2.27	0.49
2:C:967:SER:O	2:C:975:SER:OG	2.24	0.49
2:B:646:ARG:HH21	2:C:732:THR:HA	1.77	0.49
2:C:389:ASP:HB2	2:A:982:SER:CB	2.42	0.49
2:A:270:LEU:HD23	2:A:270:LEU:H	1.77	0.49
2:A:533:LEU:HD13	2:A:583:GLU:HG2	1.94	0.49
2:B:140:PHE:CD2	2:B:244:LEU:HD13	2.45	0.49
2:C:48:LEU:CG	2:C:278:LYS:HD3	2.36	0.49
2:C:68:ILE:O	2:C:78:ARG:HG2	2.13	0.49
2:C:406:GLU:HB3	2:C:409:GLN:HG2	1.95	0.49
2:C:749:CYS:O	2:C:753:LEU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:190:ARG:HD3	2:A:192:PHE:HE2	1.78	0.49
2:A:353:TRP:CD1	2:A:466:ARG:HD2	2.48	0.49
2:A:457:ARG:HE	2:A:469:SER:CB	2.25	0.49
2:B:91:TYR:OH	2:B:93:ALA:HB2	2.12	0.49
2:B:350:VAL:HG12	2:B:452:LEU:CB	2.42	0.49
2:B:439:ASN:HA	2:B:507:PRO:O	2.12	0.49
2:B:538:CYS:HB3	2:B:551:VAL:HG12	1.95	0.49
2:B:667:GLY:O	2:B:668:ALA:HB3	2.13	0.49
2:B:1028:LYS:HA	2:B:1042:PHE:HE2	1.77	0.49
2:B:1141:LEU:CG	2:A:1141:LEU:HD13	2.43	0.49
2:C:44:ARG:HD3	2:C:49:HIS:CD2	2.48	0.49
2:C:105:ILE:HD12	2:C:135:PHE:CD2	2.47	0.49
2:C:338:PHE:HE1	2:C:361:CYS:HG	1.60	0.49
2:C:380:TYR:HB3	2:A:984:LEU:N	2.28	0.49
2:C:420:ASP:O	2:C:461:LEU:HD23	2.12	0.49
2:C:804:GLN:NE2	2:C:935:GLN:OE1	2.46	0.49
2:C:1028:LYS:HG3	2:C:1032:CYS:SG	2.52	0.49
2:C:1078:ALA:HB2	2:C:1102:TRP:CH2	2.47	0.49
2:A:140:PHE:O	2:A:158:ARG:HB2	2.12	0.49
2:B:58:PHE:HD2	2:B:290:ASP:HB2	1.75	0.49
2:B:330:PRO:HD3	2:B:544:ASN:ND2	2.28	0.49
2:B:520:ALA:HB1	2:B:521:PRO:HD2	1.94	0.49
2:B:770:ILE:HG22	2:B:774:GLN:NE2	2.27	0.49
2:B:864:LEU:HG	2:A:665:PRO:CB	2.42	0.49
2:C:565:PHE:HA	2:C:575:ALA:CB	2.43	0.49
2:A:752:LEU:HD12	2:A:990:GLU:OE1	2.12	0.49
2:A:1066:THR:OG1	2:A:1067:TYR:N	2.45	0.49
2:B:195:LYS:O	2:B:201:PHE:HA	2.12	0.49
2:B:698:SER:C	2:B:699:LEU:HD12	2.33	0.49
2:B:1030:SER:O	2:B:1034:LEU:HB2	2.12	0.49
2:B:1055:SER:OG	2:B:1056:ALA:N	2.46	0.49
2:C:573:THR:CB	2:C:587:ILE:HG13	2.33	0.49
2:C:1091:ARG:HG2	2:C:1121:PHE:CD1	2.44	0.49
2:A:64:TRP:NE1	2:A:264:ALA:HB1	2.17	0.49
2:A:476:GLY:H	2:A:487:ASN:HB2	1.77	0.49
2:A:539:VAL:O	2:A:549:THR:HA	2.12	0.49
2:A:611:LEU:HD22	2:A:666:ILE:HG23	1.94	0.49
2:B:339:GLY:O	2:B:343:ASN:HB2	2.12	0.49
2:B:391:CYS:HB2	2:B:524:VAL:CG1	2.43	0.49
2:B:706:ALA:HB1	2:C:894:LEU:HB3	1.94	0.49
2:B:936:ASP:O	2:B:940:SER:N	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1124:GLY:HA2	2:C:1113:GLN:NE2	2.28	0.49
2:C:204:TYR:CD1	2:C:225:PRO:HA	2.47	0.49
2:C:726:ILE:CD1	2:C:1061:VAL:HG22	2.42	0.49
2:A:79:PHE:CE2	2:A:242:LEU:HD11	2.48	0.49
2:A:430:THR:CB	2:A:515:PHE:HB2	2.43	0.49
2:A:566:GLY:CA	2:A:575:ALA:HB3	2.43	0.49
2:B:44:ARG:O	2:B:283:GLY:HA2	2.12	0.49
2:B:206:LYS:HG3	2:B:208:THR:HG22	1.95	0.49
2:B:666:ILE:HG22	2:B:667:GLY:O	2.13	0.49
2:B:742:ILE:HD11	2:B:753:LEU:CD2	2.41	0.49
2:C:83:VAL:HG12	2:C:239:GLN:CG	2.42	0.49
2:C:403:ARG:HD3	2:C:495:TYR:CE1	2.48	0.49
2:C:406:GLU:HB3	2:C:409:GLN:HG3	1.95	0.49
2:C:470:THR:HG23	2:C:471:GLU:HG3	1.95	0.49
2:C:520:ALA:HB3	2:C:521:PRO:HD3	1.93	0.49
2:C:566:GLY:H	2:C:575:ALA:CA	2.26	0.49
2:C:566:GLY:HA3	2:C:574:ASP:HB2	1.95	0.49
2:C:641:ASN:ND2	2:C:641:ASN:O	2.46	0.49
2:C:742:ILE:HG23	2:C:997:ILE:HG23	1.93	0.49
2:C:822:LEU:HD12	2:C:945:LEU:HD21	1.95	0.49
2:A:44:ARG:CZ	2:A:49:HIS:HB2	2.43	0.49
2:A:160:TYR:HE2	2:A:163:ALA:HB2	1.78	0.49
2:B:38:TYR:CD2	2:A:560:LEU:HD11	2.47	0.48
2:C:739:THR:O	2:C:740:MET:C	2.51	0.48
2:A:308:VAL:HG12	2:A:602:THR:HB	1.95	0.48
2:A:715:PRO:HA	2:A:1072:GLU:HA	1.95	0.48
1:D:2:VAL:O	1:D:2:VAL:HG22	2.13	0.48
2:B:34:ARG:HH11	2:B:35:GLY:HA2	1.79	0.48
2:B:566:GLY:CA	2:C:42:VAL:HG22	2.43	0.48
2:C:281:GLU:HG3	2:C:282:ASN:OD1	2.13	0.48
2:C:804:GLN:HA	2:C:817:PRO:HG2	1.93	0.48
2:C:985:ASP:N	2:C:988:GLU:OE1	2.46	0.48
2:B:349:SER:HB3	2:B:452:LEU:CG	2.39	0.48
2:B:480:CYS:HB2	2:B:483:VAL:CG2	2.43	0.48
2:B:548:GLY:HA2	2:C:978:ASN:CB	2.44	0.48
2:B:577:ARG:HD3	2:B:582:LEU:CA	2.43	0.48
2:B:705:VAL:HG13	2:C:789:TYR:OH	2.14	0.48
2:B:748:GLU:OE2	2:B:981:LEU:HB2	2.14	0.48
2:B:862:PRO:CG	2:A:647:ALA:HB2	2.43	0.48
2:B:1086:LYS:HD2	2:B:1122:VAL:CG2	2.42	0.48
2:B:1088:HIS:HB3	2:B:1120:THR:CG2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:382:VAL:HB	2:A:981:LEU:HA	1.94	0.48
2:C:462:LYS:HD3	2:C:465:GLU:HG3	1.95	0.48
2:C:742:ILE:O	2:C:1000:ARG:HD2	2.13	0.48
2:C:985:ASP:O	2:C:986:PRO:C	2.52	0.48
2:A:516:GLU:HG2	2:A:518:LEU:CB	2.43	0.48
2:A:754:LEU:HD12	2:A:755:GLN:N	2.28	0.48
2:B:146:HIS:HE1	2:B:149:ASN:HB2	1.77	0.48
2:B:672:ALA:HB1	2:B:692:ILE:HD11	1.94	0.48
2:C:189:LEU:HD12	2:C:190:ARG:N	2.29	0.48
2:C:664:ILE:HG13	2:C:672:ALA:O	2.12	0.48
2:C:1091:ARG:HH21	2:C:1121:PHE:HB3	1.79	0.48
2:A:362:VAL:O	2:A:364:ASP:N	2.46	0.48
2:A:403:ARG:NE	2:A:405:ASP:HB2	2.28	0.48
2:A:479:PRO:HG2	2:A:481:ASN:OD1	2.13	0.48
2:A:566:GLY:O	2:A:567:ARG:HG3	2.12	0.48
2:A:740:MET:O	2:A:740:MET:HG3	2.12	0.48
2:A:986:PRO:HB2	2:A:987:PRO:HD3	1.94	0.48
2:B:129:LYS:HE2	2:B:169:GLU:OE2	2.13	0.48
2:B:341:VAL:HG21	2:B:515:PHE:CZ	2.48	0.48
2:B:646:ARG:HG3	2:C:861:LEU:HB3	1.95	0.48
2:B:916:LEU:O	2:B:920:GLN:N	2.46	0.48
2:C:70:VAL:HG22	2:C:77:LYS:HB3	1.94	0.48
2:C:119:ILE:HG12	2:C:128:ILE:HG12	1.94	0.48
2:C:328:ARG:O	2:C:329:PHE:HB3	2.14	0.48
2:C:403:ARG:HB2	2:C:406:GLU:OE1	2.14	0.48
2:B:401:VAL:HG23	2:B:451:TYR:CE1	2.49	0.48
2:B:462:LYS:H	2:B:465:GLU:HB2	1.77	0.48
2:B:630:THR:HB	2:B:631:PRO:CD	2.43	0.48
2:B:897:PRO:CB	2:A:708:SER:H	2.27	0.48
2:B:1100:THR:CG2	3:F:1:NAG:H83	2.40	0.48
2:A:20:THR:HG23	2:A:77:LYS:O	2.13	0.48
2:A:1039:ARG:HD2	2:A:1042:PHE:CD2	2.48	0.48
2:B:811:LYS:CG	2:B:812:PRO:HD2	2.44	0.48
2:B:897:PRO:HD2	2:B:900:MET:HE1	1.96	0.48
2:C:126:VAL:CG2	2:C:174:PRO:HA	2.43	0.48
2:C:1054:GLN:OE1	2:C:1054:GLN:HA	2.13	0.48
2:A:544:ASN:HD21	2:A:565:PHE:HE1	1.62	0.48
2:A:760:CYS:CB	2:A:763:LEU:HB2	2.43	0.48
2:A:1010:GLN:HG2	2:A:1014:ARG:HH22	1.79	0.48
2:B:392:PHE:HD2	2:B:516:GLU:H	1.62	0.48
2:C:36:VAL:O	2:C:222:ALA:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:115:GLN:HA	2:C:132:GLU:CG	2.40	0.48
2:C:489:TYR:OH	2:A:368:LEU:HD11	2.13	0.48
2:C:542:ASN:HA	2:C:547:THR:HG22	1.96	0.48
2:C:714:ILE:HD12	2:C:1096:VAL:HG11	1.94	0.48
2:A:81:ASN:O	2:A:239:GLN:NE2	2.47	0.48
2:A:355:ARG:HA	2:A:397:ALA:O	2.14	0.48
2:A:566:GLY:O	2:A:573:THR:HA	2.14	0.48
2:A:900:MET:HA	2:A:917:TYR:OH	2.14	0.48
2:A:954:GLN:HE22	2:A:1014:ARG:NH2	2.11	0.48
2:B:90:VAL:HG12	2:B:91:TYR:N	2.27	0.48
2:B:358:ILE:HG21	2:B:395:VAL:HB	1.96	0.48
2:B:362:VAL:HG23	2:B:524:VAL:HG13	1.95	0.48
2:B:452:LEU:HD13	2:B:492:LEU:HB3	1.95	0.48
2:B:480:CYS:HB2	2:B:483:VAL:HG23	1.95	0.48
2:B:726:ILE:CG2	2:B:948:LEU:HG	2.44	0.48
2:B:746:SER:HB3	2:B:749:CYS:HB3	1.95	0.48
2:B:1104:VAL:O	2:B:1104:VAL:HG13	2.13	0.48
2:C:68:ILE:HD13	2:C:262:ALA:HB1	1.96	0.48
2:C:577:ARG:O	2:C:582:LEU:HA	2.14	0.48
2:C:712:ILE:CG2	2:C:1077:THR:HB	2.44	0.48
2:A:105:ILE:CG1	2:A:239:GLN:HB3	2.44	0.48
2:A:653:ALA:HA	2:A:692:ILE:O	2.13	0.48
2:A:1043:CYS:HB3	2:A:1064:HIS:CE1	2.49	0.48
2:B:775:ASP:OD1	2:B:864:LEU:HB2	2.12	0.48
2:C:368:LEU:HD23	2:C:434:ILE:HG22	1.95	0.48
2:C:1033:VAL:HG12	2:C:1034:LEU:HD23	1.95	0.48
2:A:430:THR:HB	2:A:515:PHE:CD2	2.49	0.48
2:A:662:CYS:HA	2:A:695:TYR:OH	2.14	0.48
2:A:825:LYS:CG	2:A:945:LEU:HD12	2.44	0.48
2:B:882:ILE:HG13	2:A:707:TYR:HH	1.79	0.47
2:B:1090:PRO:HG3	2:B:1095:PHE:HE1	1.77	0.47
2:C:117:LEU:HD21	2:C:119:ILE:CD1	2.44	0.47
2:A:20:THR:HG21	2:A:78:ARG:HG3	1.94	0.47
2:A:377:PHE:CZ	2:A:432:CYS:HA	2.49	0.47
2:A:401:VAL:CG1	2:A:507:PRO:HB2	2.44	0.47
2:B:104:TRP:HB3	2:B:238:PHE:HD2	1.79	0.47
2:B:116:SER:O	2:B:130:VAL:HG13	2.15	0.47
2:B:202:LYS:C	2:B:203:ILE:HG13	2.34	0.47
2:B:720:ILE:CD1	2:B:923:ILE:HG23	2.44	0.47
2:B:800:PHE:CD1	2:B:927:PHE:HD2	2.32	0.47
2:B:811:LYS:HG3	2:B:812:PRO:HD2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:417:LYS:HD2	2:C:417:LYS:O	2.13	0.47
2:C:977:LEU:HD22	2:C:993:ILE:HD13	1.96	0.47
2:C:1117:THR:OG1	2:C:1137:VAL:HG21	2.13	0.47
2:A:452:LEU:CG	2:A:492:LEU:HD23	2.42	0.47
2:B:231:ILE:HG22	2:B:233:ILE:HG22	1.95	0.47
2:B:755:GLN:HB2	2:A:969:ASN:ND2	2.28	0.47
2:B:1081:ILE:O	2:B:1087:ALA:HA	2.13	0.47
2:C:393:THR:HG21	2:C:518:LEU:CD2	2.43	0.47
2:C:573:THR:HB	2:C:587:ILE:CB	2.44	0.47
2:A:472:ILE:HD13	2:A:489:TYR:HB2	1.96	0.47
2:A:598:ILE:HG23	2:A:664:ILE:HD12	1.97	0.47
2:A:759:PHE:CD2	2:A:1001:LEU:HD21	2.49	0.47
1:D:47:PHE:CE1	2:A:486:PHE:HB2	2.50	0.47
2:B:289:VAL:HB	2:B:306:PHE:CE1	2.49	0.47
2:B:426:PRO:HG3	2:B:463:PRO:HG3	1.95	0.47
2:B:462:LYS:HE3	2:B:465:GLU:CD	2.34	0.47
2:B:770:ILE:HD11	2:B:1012:LEU:HD21	1.96	0.47
2:B:1046:GLY:HA3	2:B:1066:THR:HG21	1.96	0.47
2:C:206:LYS:NZ	2:C:221:SER:HB3	2.29	0.47
2:A:146:HIS:CE1	2:A:148:ASN:HB3	2.49	0.47
2:A:552:LEU:CD1	2:A:587:ILE:HG12	2.44	0.47
2:B:589:PRO:HB2	2:C:856:ASN:HB2	1.96	0.47
2:B:712:ILE:HG21	2:B:1077:THR:HB	1.97	0.47
2:C:312:ILE:HG13	2:C:598:ILE:CD1	2.45	0.47
2:A:454:ARG:HH21	2:A:491:PRO:CA	2.25	0.47
2:B:50:SER:HA	2:B:275:PHE:O	2.14	0.47
2:B:822:LEU:CD1	2:B:945:LEU:HD21	2.44	0.47
2:B:985:ASP:OD1	2:B:988:GLU:HB2	2.14	0.47
2:C:707:TYR:HE1	2:C:711:SER:O	1.97	0.47
2:A:712:ILE:HG12	2:A:713:ALA:H	1.79	0.47
2:A:989:ALA:O	2:A:993:ILE:HG12	2.14	0.47
2:A:1106:GLN:NE2	2:A:1109:PHE:HB3	2.30	0.47
1:D:34:MET:HE3	1:D:51:ILE:HG23	1.96	0.47
2:B:91:TYR:CZ	2:B:93:ALA:HB2	2.49	0.47
2:B:410:ILE:N	2:B:414:GLN:OE1	2.47	0.47
2:B:517:LEU:H	2:B:519:HIS:CE1	2.33	0.47
2:B:562:PHE:HZ	2:C:38:TYR:CE1	2.33	0.47
2:B:589:PRO:CG	2:C:856:ASN:HB2	2.44	0.47
2:B:671:CYS:HB2	2:B:695:TYR:CE1	2.49	0.47
2:B:719:THR:HG22	2:B:1068:VAL:O	2.14	0.47
2:C:347:PHE:CD2	2:C:509:ARG:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:529:LYS:C	2:C:531:THR:H	2.18	0.47
2:C:562:PHE:HA	2:A:41:LYS:HE2	1.96	0.47
2:C:668:ALA:O	2:C:670:ILE:HD12	2.14	0.47
2:C:705:VAL:HG21	2:A:894:LEU:HA	1.96	0.47
2:C:962:LEU:O	2:C:962:LEU:HD23	2.15	0.47
2:C:1140:PRO:O	2:C:1143:PRO:HD2	2.14	0.47
2:A:18:LEU:HD13	2:A:79:PHE:CE2	2.49	0.47
2:A:24:LEU:HB2	2:A:78:ARG:NH1	2.30	0.47
2:A:275:PHE:HB3	2:A:289:VAL:O	2.15	0.47
2:A:322:PRO:HA	2:A:538:CYS:O	2.14	0.47
2:A:375:SER:O	2:A:434:ILE:HG23	2.15	0.47
2:A:506:GLN:HG3	2:A:508:TYR:HE1	1.79	0.47
2:A:598:ILE:HD13	2:A:666:ILE:HG12	1.97	0.47
2:A:733:LYS:CD	2:A:861:LEU:HB2	2.44	0.47
2:A:965:GLN:OE1	2:A:1003:SER:HB2	2.14	0.47
2:A:973:ILE:H	2:A:992:GLN:NE2	2.13	0.47
2:A:1086:LYS:HZ3	2:A:1122:VAL:HG11	1.78	0.47
2:A:1087:ALA:HB1	2:A:1089:PHE:HE1	1.79	0.47
2:B:570:ALA:O	2:C:967:SER:HA	2.15	0.47
2:B:592:PHE:CD1	2:C:740:MET:HB2	2.50	0.47
2:B:992:GLN:HE22	2:B:995:ARG:NE	2.13	0.47
2:B:1004:LEU:O	2:B:1004:LEU:HD12	2.14	0.47
2:C:294:ASP:OD1	2:C:296:LEU:HB3	2.15	0.47
2:A:322:PRO:HB2	2:A:539:VAL:HA	1.96	0.47
2:A:574:ASP:HA	2:A:587:ILE:CG1	2.45	0.47
2:B:121:ASN:HA	2:B:126:VAL:HA	1.95	0.47
2:B:135:PHE:HA	2:B:160:TYR:HA	1.97	0.47
2:B:159:VAL:HG22	2:B:241:LEU:CD1	2.40	0.47
2:B:562:PHE:CD2	2:C:225:PRO:HD2	2.49	0.47
2:B:577:ARG:HD3	2:B:582:LEU:HA	1.97	0.47
2:B:697:MET:HB2	2:C:779:GLN:CD	2.35	0.47
2:B:789:TYR:HD1	2:A:703:ASN:HB3	1.78	0.47
2:B:893:ALA:O	2:B:894:LEU:HD23	2.14	0.47
2:C:424:LYS:HB3	2:C:463:PRO:HA	1.96	0.47
2:C:462:LYS:HB2	2:C:465:GLU:HG3	1.97	0.47
2:A:66:HIS:HE1	2:A:68:ILE:HD12	1.80	0.47
2:A:584:ILE:C	2:A:585:LEU:HD23	2.34	0.47
2:A:716:THR:HG22	2:A:1110:TYR:CB	2.44	0.47
2:A:985:ASP:OD2	2:A:987:PRO:HD2	2.15	0.47
2:B:41:LYS:CD	2:B:225:PRO:HG2	2.43	0.47
2:B:455:LEU:H	2:B:493:GLN:CG	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:615:VAL:HG23	2:B:649:CYS:CB	2.40	0.47
2:B:621:PRO:HG3	2:B:637:SER:O	2.14	0.47
2:B:896:ILE:HG13	2:B:900:MET:CE	2.45	0.47
2:B:1100:THR:HG23	3:F:1:NAG:N2	2.30	0.47
2:C:384:PRO:HD3	2:A:986:PRO:CD	2.44	0.47
2:A:367:VAL:HG13	2:A:368:LEU:N	2.29	0.47
2:A:650:LEU:CD1	2:A:666:ILE:HG21	2.45	0.47
2:A:769:GLY:O	2:A:772:VAL:HG12	2.14	0.47
2:A:770:ILE:CD1	2:A:1012:LEU:HA	2.29	0.47
2:B:577:ARG:HH22	2:B:584:ILE:HD13	1.79	0.46
2:C:337:PRO:HG2	2:C:358:ILE:HG12	1.97	0.46
2:C:563:GLN:HB3	2:A:43:PHE:CB	2.43	0.46
2:C:962:LEU:HD12	2:C:1007:TYR:CB	2.45	0.46
2:A:402:ILE:HG13	2:A:404:GLY:N	2.30	0.46
2:A:406:GLU:HB2	2:A:409:GLN:HB3	1.96	0.46
2:A:1091:ARG:NH1	2:A:1121:PHE:HB3	2.30	0.46
3:I:1:NAG:O6	3:I:2:NAG:N2	2.48	0.46
2:B:730:SER:O	2:B:1058:HIS:HB3	2.16	0.46
2:B:743:CYS:O	2:B:977:LEU:HD22	2.16	0.46
2:B:755:GLN:OE1	2:A:969:ASN:HB2	2.14	0.46
2:B:783:ALA:HA	2:B:873:TYR:CE2	2.49	0.46
2:B:883:THR:O	2:A:705:VAL:HG21	2.15	0.46
2:B:1100:THR:HG23	3:F:1:NAG:C7	2.44	0.46
2:B:1122:VAL:HG22	2:C:1119:ASN:HA	1.97	0.46
2:C:48:LEU:N	2:C:48:LEU:HD12	2.30	0.46
2:C:436:TRP:NE1	2:C:509:ARG:HB2	2.25	0.46
2:C:550:GLY:HA3	2:C:589:PRO:HA	1.96	0.46
2:A:81:ASN:HB2	2:A:239:GLN:HE21	1.80	0.46
2:A:322:PRO:CB	2:A:539:VAL:HA	2.46	0.46
2:A:363:ALA:HB1	2:A:365:TYR:CE1	2.51	0.46
2:A:406:GLU:OE2	2:A:418:ILE:HD11	2.15	0.46
2:B:86:PHE:CD2	2:B:235:ILE:HG22	2.50	0.46
2:B:334:ASN:HB2	2:B:362:VAL:N	2.30	0.46
2:B:577:ARG:HD3	2:B:582:LEU:CB	2.45	0.46
2:B:979:ASP:OD1	2:B:980:ILE:HG13	2.14	0.46
2:C:898:PHE:N	2:C:899:PRO:HD2	2.30	0.46
2:A:81:ASN:N	2:A:81:ASN:OD1	2.48	0.46
2:A:146:HIS:HB3	2:A:149:ASN:HB2	1.96	0.46
2:A:476:GLY:CA	2:A:487:ASN:HB2	2.45	0.46
2:A:1087:ALA:HB1	2:A:1089:PHE:CE1	2.51	0.46
2:B:110:LEU:HD22	2:B:135:PHE:HD2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:720:ILE:HD12	2:B:923:ILE:HG23	1.97	0.46
2:B:743:CYS:SG	2:B:750:SER:HA	2.55	0.46
2:C:328:ARG:NE	2:C:533:LEU:HD13	2.21	0.46
2:C:472:ILE:HB	2:C:491:PRO:CA	2.46	0.46
2:C:888:PHE:CZ	2:C:1034:LEU:HD22	2.51	0.46
2:C:974:SER:HB2	2:C:980:ILE:HD13	1.96	0.46
2:A:36:VAL:HG23	2:A:36:VAL:O	2.15	0.46
2:A:95:THR:HG22	2:A:189:LEU:HD12	1.96	0.46
2:A:119:ILE:HG12	2:A:128:ILE:HG12	1.97	0.46
2:A:722:VAL:HG23	2:A:934:ILE:HD11	1.96	0.46
2:B:17:ASN:O	2:B:18:LEU:HD23	2.16	0.46
2:B:40:ASP:C	2:B:41:LYS:HE2	2.36	0.46
2:B:142:GLY:O	2:B:156:GLU:HB2	2.16	0.46
2:B:433:VAL:HG23	2:B:513:LEU:O	2.16	0.46
2:B:708:SER:OG	2:C:894:LEU:HG	2.16	0.46
2:B:1129:VAL:HA	2:C:914:ASN:OD1	2.15	0.46
2:A:121:ASN:OD1	2:A:126:VAL:HG22	2.15	0.46
2:B:24:LEU:HD13	2:B:66:HIS:HB3	1.97	0.46
2:B:343:ASN:ND2	3:I:1:NAG:H2	2.30	0.46
2:B:353:TRP:CZ3	2:B:423:TYR:HA	2.51	0.46
2:C:117:LEU:HD21	2:C:119:ILE:HD11	1.97	0.46
2:C:332:ILE:H	2:C:332:ILE:HG12	1.55	0.46
2:C:948:LEU:HD21	2:C:1059:GLY:HA3	1.98	0.46
2:A:211:ASN:N	2:A:211:ASN:OD1	2.49	0.46
2:A:353:TRP:CH2	2:A:423:TYR:HB2	2.51	0.46
2:A:559:PHE:HB2	2:A:577:ARG:NH2	2.17	0.46
2:A:720:ILE:CD1	2:A:923:ILE:HG23	2.45	0.46
2:B:577:ARG:HH21	2:B:584:ILE:HA	1.80	0.46
2:B:598:ILE:HB	2:B:609:ALA:HB3	1.98	0.46
2:B:634:ARG:HD2	2:B:637:SER:OG	2.15	0.46
2:B:826:VAL:CB	2:B:1057:PRO:HG2	2.44	0.46
2:B:1000:ARG:HA	2:B:1003:SER:OG	2.16	0.46
2:C:51:THR:OG1	2:C:52:GLN:N	2.49	0.46
2:C:193:VAL:HG12	2:C:204:TYR:HB2	1.98	0.46
2:C:742:ILE:CG2	2:C:997:ILE:HG23	2.46	0.46
2:C:1027:THR:O	2:C:1031:GLU:HG3	2.15	0.46
2:B:29:THR:HG22	2:B:30:ASN:H	1.81	0.46
2:B:65:PHE:CE2	2:B:84:LEU:HD11	2.51	0.46
2:B:139:PRO:CB	2:B:159:VAL:HA	2.39	0.46
2:B:310:LYS:HD2	2:B:663:ASP:OD1	2.16	0.46
2:B:330:PRO:HB3	2:B:579:PRO:CB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:656:VAL:HG11	2:B:693:ILE:CD1	2.45	0.46
2:B:1078:ALA:HB2	2:B:1102:TRP:CH2	2.50	0.46
2:B:1083:HIS:NE2	2:B:1137:VAL:HG13	2.30	0.46
2:C:115:GLN:HG2	2:C:233:ILE:HD12	1.98	0.46
2:C:742:ILE:HG12	2:C:1001:LEU:HD12	1.98	0.46
2:C:775:ASP:O	2:C:779:GLN:HG2	2.15	0.46
2:C:898:PHE:N	2:C:899:PRO:CD	2.78	0.46
2:C:909:ILE:CG2	2:C:1036:GLN:HE22	2.27	0.46
2:A:578:ASP:O	2:A:581:THR:N	2.45	0.46
2:B:278:LYS:HD3	2:B:286:THR:HG23	1.97	0.46
2:B:454:ARG:HD2	2:B:492:LEU:H	1.81	0.46
2:B:865:LEU:HB2	2:B:870:ILE:CG1	2.46	0.46
2:B:1141:LEU:HD21	2:A:1141:LEU:HD13	1.98	0.46
2:C:529:LYS:HE2	2:C:529:LYS:HB2	1.43	0.46
2:C:730:SER:O	2:C:1058:HIS:HB3	2.16	0.46
2:C:916:LEU:CD1	2:C:923:ILE:HG13	2.45	0.46
2:C:1086:LYS:HG3	2:C:1122:VAL:HG21	1.98	0.46
2:C:1132:ILE:HD13	2:C:1132:ILE:HA	1.82	0.46
2:A:227:VAL:CG1	2:A:229:LEU:HG	2.46	0.46
2:A:365:TYR:HD1	2:A:365:TYR:H	1.64	0.46
2:A:374:PHE:CE2	2:A:434:ILE:HD13	2.51	0.46
2:B:68:ILE:HD13	2:B:260:ALA:HB3	1.98	0.46
2:B:342:PHE:CE1	2:B:513:LEU:HD22	2.51	0.46
2:B:351:TYR:HD1	2:B:452:LEU:HD12	1.79	0.46
2:B:407:VAL:HG23	2:B:437:ASN:CG	2.36	0.46
2:B:566:GLY:CA	2:C:43:PHE:H	2.20	0.46
2:B:577:ARG:HD3	2:B:582:LEU:HB3	1.98	0.46
2:B:663:ASP:OD1	2:B:663:ASP:C	2.54	0.46
2:B:748:GLU:OE2	2:B:981:LEU:HD22	2.16	0.46
2:B:1144:GLU:HB3	2:A:1141:LEU:HD23	1.97	0.46
2:C:414:GLN:O	2:C:414:GLN:HG3	2.15	0.46
2:C:460:ASN:O	2:C:460:ASN:ND2	2.49	0.46
2:C:550:GLY:CA	2:C:589:PRO:HA	2.45	0.46
2:C:825:LYS:NZ	2:C:939:SER:HA	2.31	0.46
2:C:907:ASN:HA	2:C:911:VAL:O	2.16	0.46
2:A:242:LEU:N	2:A:242:LEU:HD23	2.31	0.46
2:A:338:PHE:HA	2:A:358:ILE:CD1	2.46	0.46
2:A:476:GLY:HA3	2:A:487:ASN:HB2	1.98	0.46
2:A:724:THR:CG2	2:A:934:ILE:HD12	2.46	0.46
2:A:825:LYS:HG2	2:A:945:LEU:HD12	1.98	0.46
2:B:656:VAL:CG1	2:B:693:ILE:HD11	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:767:LEU:O	2:B:770:ILE:HD12	2.16	0.45
2:B:904:TYR:HA	2:A:1107:ARG:NH2	2.31	0.45
2:C:396:TYR:HB3	2:C:514:SER:CB	2.45	0.45
2:A:124:THR:CA	2:A:174:PRO:HG3	2.46	0.45
2:A:444:LYS:CG	2:A:448:ASN:HB2	2.43	0.45
2:A:805:ILE:HB	2:A:1054:GLN:NE2	2.31	0.45
2:B:168:PHE:HB3	2:B:231:ILE:HD11	1.97	0.45
2:B:330:PRO:HG2	2:B:525:CYS:CB	2.46	0.45
2:B:391:CYS:HB2	2:B:524:VAL:HG12	1.98	0.45
2:B:767:LEU:HA	2:B:770:ILE:CD1	2.46	0.45
2:B:969:ASN:O	2:B:970:PHE:HB2	2.17	0.45
2:B:973:ILE:CD1	2:B:984:LEU:HD11	2.45	0.45
2:B:1080:ALA:HB1	2:B:1088:HIS:O	2.15	0.45
2:B:1088:HIS:CD2	2:B:1122:VAL:HG12	2.51	0.45
2:B:1132:ILE:HG13	2:B:1132:ILE:O	2.12	0.45
2:C:521:PRO:HG2	2:C:565:PHE:HE2	1.82	0.45
2:C:697:MET:HB2	2:C:697:MET:HE3	1.88	0.45
2:C:707:TYR:HD1	2:C:711:SER:HB3	1.81	0.45
2:A:226:LEU:HG	2:A:227:VAL:HG23	1.98	0.45
2:A:396:TYR:H	2:A:513:LEU:CD2	2.28	0.45
2:A:670:ILE:HG22	2:A:671:CYS:H	1.81	0.45
2:B:29:THR:HG22	2:B:30:ASN:N	2.31	0.45
2:B:36:VAL:O	2:B:222:ALA:HA	2.17	0.45
2:B:141:LEU:HD11	2:B:154:GLU:OE2	2.17	0.45
2:B:737:ASP:HB2	2:A:317:ASN:HD21	1.81	0.45
2:B:884:SER:HB2	2:B:894:LEU:H	1.81	0.45
2:B:1056:ALA:HB1	2:B:1057:PRO:CD	2.45	0.45
2:C:1080:ALA:HB1	2:C:1088:HIS:O	2.16	0.45
2:A:105:ILE:HG12	2:A:239:GLN:HB3	1.98	0.45
2:A:453:TYR:C	2:A:493:GLN:HG3	2.37	0.45
2:A:591:SER:O	2:A:592:PHE:HB3	2.17	0.45
2:B:699:LEU:HD22	2:C:783:ALA:O	2.16	0.45
2:B:906:PHE:CD1	2:B:1049:LEU:HD11	2.51	0.45
2:C:102:ARG:NE	2:C:243:ALA:HB2	2.32	0.45
2:C:330:PRO:HG3	2:C:528:LYS:C	2.35	0.45
2:C:358:ILE:CD1	2:C:395:VAL:HG11	2.43	0.45
2:C:368:LEU:HD22	2:C:368:LEU:HA	1.74	0.45
2:A:96:GLU:OE1	2:A:100:ILE:HB	2.17	0.45
2:A:97:LYS:HG3	2:A:186:PHE:CE1	2.51	0.45
2:A:294:ASP:OD1	2:A:297:SER:HB3	2.17	0.45
2:A:328:ARG:HG3	2:A:530:SER:OG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:452:LEU:HD12	2:A:492:LEU:HD23	1.98	0.45
2:C:28:TYR:CD1	2:C:63:THR:HG22	2.52	0.45
2:C:444:LYS:CB	2:C:448:ASN:HB2	2.37	0.45
2:C:775:ASP:HA	2:C:778:THR:CG2	2.46	0.45
2:A:409:GLN:NE2	2:A:414:GLN:O	2.50	0.45
2:A:674:TYR:HD1	2:A:692:ILE:HG12	1.82	0.45
2:A:699:LEU:HD12	2:A:699:LEU:N	2.31	0.45
2:A:1126:CYS:SG	2:A:1132:ILE:HD12	2.57	0.45
2:B:106:PHE:HB2	2:B:117:LEU:HB3	1.98	0.45
2:B:106:PHE:CB	2:B:235:ILE:HD12	2.29	0.45
2:B:308:VAL:HG22	2:B:602:THR:OG1	2.16	0.45
2:B:347:PHE:CD2	2:B:511:VAL:HG11	2.52	0.45
2:B:566:GLY:CA	2:B:575:ALA:HB3	2.47	0.45
2:B:613:GLN:HB3	2:C:735:SER:OG	2.17	0.45
2:B:1096:VAL:HG23	2:B:1103:PHE:HB2	1.98	0.45
2:C:204:TYR:HA	2:C:225:PRO:HA	1.98	0.45
2:C:383:SER:OG	2:A:982:SER:HA	2.16	0.45
2:C:577:ARG:HG2	2:C:579:PRO:HD3	1.98	0.45
2:C:767:LEU:HD23	2:C:767:LEU:O	2.17	0.45
2:C:1116:THR:CA	2:C:1137:VAL:HB	2.46	0.45
2:A:54:LEU:HD12	2:A:54:LEU:N	2.31	0.45
2:A:408:ARG:NH1	2:A:411:ALA:HB3	2.31	0.45
2:B:341:VAL:HG21	2:B:515:PHE:HZ	1.82	0.45
2:B:409:GLN:HA	2:B:414:GLN:NE2	2.32	0.45
2:B:595:VAL:CG2	2:B:610:VAL:HG13	2.46	0.45
2:C:335:LEU:O	2:C:361:CYS:HB2	2.17	0.45
2:C:379:CYS:O	2:A:983:ARG:NH2	2.50	0.45
2:A:356:LYS:N	2:A:397:ALA:HB3	2.32	0.45
2:A:878:LEU:HD21	2:A:1052:PHE:HB3	1.98	0.45
2:A:1096:VAL:HG22	2:A:1103:PHE:O	2.16	0.45
2:B:120:VAL:HG12	2:B:122:ASN:HD22	1.82	0.45
2:B:461:LEU:HD11	2:B:467:ASP:HB3	1.99	0.45
2:B:706:ALA:CB	2:C:894:LEU:HB3	2.46	0.45
2:B:897:PRO:CG	2:A:708:SER:H	2.29	0.45
2:B:1083:HIS:HE1	2:B:1136:THR:HA	1.79	0.45
2:C:295:PRO:HB3	2:C:610:VAL:CG2	2.47	0.45
2:C:335:LEU:H	2:C:335:LEU:HD12	1.81	0.45
2:C:382:VAL:CG2	2:A:993:ILE:HD11	2.46	0.45
2:C:733:LYS:HE3	2:C:771:ALA:HB1	1.99	0.45
2:A:437:ASN:HB2	2:A:439:ASN:OD1	2.17	0.45
2:A:498:GLN:OE1	2:A:498:GLN:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:754:LEU:HD12	2:A:754:LEU:C	2.37	0.45
2:B:29:THR:O	2:B:62:VAL:HG22	2.16	0.45
2:B:48:LEU:HB3	2:B:276:LEU:CD1	2.36	0.45
2:B:104:TRP:HA	2:B:239:GLN:O	2.16	0.45
2:B:106:PHE:CD2	2:B:235:ILE:HG21	2.43	0.45
2:B:121:ASN:HB3	2:B:126:VAL:HG22	1.99	0.45
2:B:349:SER:HB3	2:B:452:LEU:H	1.81	0.45
2:B:435:ALA:HB2	2:B:512:VAL:HG12	1.98	0.45
2:B:498:GLN:HG2	2:B:501:ASN:ND2	2.32	0.45
2:B:1130:ILE:HD12	2:C:914:ASN:HA	1.98	0.45
2:A:191:GLU:HB2	2:A:206:LYS:HB3	1.98	0.45
2:A:335:LEU:N	4:A:1202:NAG:H81	2.32	0.45
2:A:428:ASP:O	2:A:430:THR:HG23	2.16	0.45
2:B:557:LYS:HD3	2:C:45:SER:CB	2.47	0.45
2:B:862:PRO:CD	2:A:647:ALA:HA	2.47	0.45
2:B:864:LEU:HD11	2:A:665:PRO:HB3	1.99	0.45
2:B:1029:MET:HB2	2:B:1062:PHE:CZ	2.52	0.45
2:C:267:VAL:HG12	2:C:268:GLY:N	2.32	0.45
2:C:328:ARG:HD3	2:C:328:ARG:N	2.32	0.45
2:C:577:ARG:HH11	2:C:577:ARG:H	1.64	0.45
2:A:423:TYR:O	2:A:424:LYS:HD2	2.16	0.45
3:H:2:NAG:H3	3:H:2:NAG:O7	2.17	0.45
2:B:189:LEU:HD12	2:B:190:ARG:N	2.32	0.44
2:B:541:PHE:O	2:B:547:THR:HA	2.17	0.44
2:B:646:ARG:CG	2:C:861:LEU:CB	2.95	0.44
2:B:970:PHE:CD2	2:B:999:GLY:HA3	2.53	0.44
2:C:90:VAL:HG21	2:C:238:PHE:CE1	2.52	0.44
2:C:382:VAL:O	2:A:983:ARG:N	2.51	0.44
2:C:656:VAL:HG21	2:C:693:ILE:HD11	2.00	0.44
2:A:132:GLU:CD	2:A:165:ASN:HD22	2.19	0.44
2:A:566:GLY:N	2:A:575:ALA:HB3	2.32	0.44
2:A:662:CYS:HB3	2:A:695:TYR:CE2	2.50	0.44
2:A:1078:ALA:HB1	2:A:1131:GLY:O	2.16	0.44
2:B:63:THR:HG1	2:B:65:PHE:HE2	1.64	0.44
2:B:280:ASN:ND2	2:B:281:GLU:OE2	2.50	0.44
2:B:1111:GLU:O	2:B:1113:GLN:HG3	2.17	0.44
2:C:239:GLN:HG2	2:C:240:THR:N	2.33	0.44
2:A:86:PHE:HA	2:A:238:PHE:CE1	2.52	0.44
2:A:400:PHE:CE2	2:A:510:VAL:HG13	2.52	0.44
2:A:995:ARG:HG3	2:A:995:ARG:NH1	2.31	0.44
2:B:347:PHE:CE2	2:B:511:VAL:HG11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:574:ASP:HB2	2:B:586:ASP:HA	1.99	0.44
2:B:705:VAL:CB	2:C:888:PHE:HA	2.48	0.44
2:B:1062:PHE:HB3	2:B:1064:HIS:CD2	2.53	0.44
2:C:594:GLY:HA3	2:C:613:GLN:CB	2.47	0.44
2:C:726:ILE:CG2	2:C:948:LEU:HG	2.47	0.44
2:C:911:VAL:CG1	2:C:915:VAL:HG21	2.48	0.44
2:C:961:THR:O	2:C:965:GLN:HB2	2.18	0.44
2:C:986:PRO:CA	2:C:990:GLU:HG2	2.48	0.44
2:A:218:GLN:HG2	2:A:219:GLY:H	1.82	0.44
2:B:351:TYR:O	2:B:468:ILE:HG23	2.18	0.44
2:B:426:PRO:HG3	2:B:463:PRO:CG	2.47	0.44
2:B:441:LEU:HD12	2:B:441:LEU:H	1.83	0.44
2:B:707:TYR:CD2	2:C:896:ILE:HG21	2.52	0.44
2:B:866:THR:HG23	2:A:668:ALA:C	2.37	0.44
2:B:873:TYR:CD2	2:A:699:LEU:HD21	2.53	0.44
2:C:126:VAL:HG11	2:C:175:PHE:CE1	2.49	0.44
2:C:358:ILE:O	2:C:395:VAL:HB	2.18	0.44
2:C:724:THR:HG22	2:C:1063:LEU:HD23	1.99	0.44
2:C:1091:ARG:HG3	2:C:1120:THR:HA	1.99	0.44
2:C:1116:THR:OG1	2:C:1138:TYR:O	2.22	0.44
4:C:1206:NAG:HO3	4:C:1206:NAG:C7	2.22	0.44
2:A:227:VAL:HG12	2:A:229:LEU:HG	1.99	0.44
2:A:533:LEU:HD23	2:A:543:PHE:HZ	1.82	0.44
2:A:582:LEU:HD22	2:A:582:LEU:HA	1.74	0.44
2:A:712:ILE:HD11	2:A:1094:VAL:HG21	2.00	0.44
2:A:1081:ILE:HD13	2:A:1135:ASN:HB3	2.00	0.44
2:B:869:MET:SD	2:A:697:MET:CB	3.04	0.44
2:C:430:THR:OG1	2:C:516:GLU:N	2.50	0.44
2:C:490:PHE:CE2	2:C:492:LEU:HB3	2.51	0.44
2:C:980:ILE:O	2:C:984:LEU:HB2	2.17	0.44
2:A:822:LEU:CD2	2:A:938:LEU:HD13	2.48	0.44
2:A:886:TRP:CZ3	2:A:901:GLN:HG3	2.52	0.44
2:A:985:ASP:CG	2:A:987:PRO:HD2	2.37	0.44
2:B:27:ALA:HB3	2:B:64:TRP:CB	2.40	0.44
2:B:113:LYS:HG3	2:B:114:THR:HG23	2.00	0.44
2:B:412:PRO:HA	2:B:427:ASP:CB	2.38	0.44
2:B:442:ASP:OD1	2:B:509:ARG:NH1	2.48	0.44
2:B:547:THR:O	2:C:978:ASN:HB2	2.17	0.44
2:B:670:ILE:CG2	2:B:694:ALA:HB1	2.47	0.44
2:C:712:ILE:HG22	2:C:1077:THR:HB	2.00	0.44
2:C:853:GLN:HB3	2:C:963:VAL:HG21	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:881:THR:HA	2:C:885:GLY:O	2.18	0.44
2:A:17:ASN:O	2:A:18:LEU:HD23	2.17	0.44
2:A:59:PHE:HE1	2:A:293:LEU:HD21	1.82	0.44
2:A:432:CYS:O	2:A:432:CYS:SG	2.75	0.44
2:A:444:LYS:HG2	2:A:448:ASN:CB	2.44	0.44
2:A:898:PHE:N	2:A:899:PRO:HD2	2.32	0.44
2:B:57:PRO:HB3	2:B:273:ARG:HH22	1.82	0.44
2:B:164:ASN:HB2	2:B:165:ASN:H	1.58	0.44
2:B:457:ARG:NH1	2:B:459:SER:HB2	2.32	0.44
2:B:708:SER:O	2:C:896:ILE:HD12	2.17	0.44
2:B:748:GLU:CD	2:B:981:LEU:HD22	2.38	0.44
2:B:866:THR:CG2	2:A:669:GLY:HA3	2.42	0.44
2:B:949:GLN:HA	2:B:949:GLN:NE2	2.33	0.44
2:C:383:SER:HA	2:A:986:PRO:HD3	1.99	0.44
2:C:808:ASP:OD2	2:C:811:LYS:HG2	2.18	0.44
2:C:931:ILE:O	2:C:934:ILE:HG22	2.18	0.44
2:C:1087:ALA:O	2:C:1122:VAL:HG23	2.18	0.44
2:A:51:THR:O	2:A:274:THR:HA	2.18	0.44
2:A:527:PRO:O	2:A:528:LYS:HB2	2.17	0.44
2:A:541:PHE:N	2:A:548:GLY:O	2.50	0.44
2:A:645:THR:HG23	2:A:647:ALA:N	2.25	0.44
2:A:1073:LYS:HG2	2:A:1074:ASN:N	2.33	0.44
2:B:43:PHE:H	2:A:566:GLY:CA	2.01	0.44
2:B:83:VAL:HG22	2:B:237:ARG:HB3	1.96	0.44
2:B:250:THR:N	2:B:253:ASP:OD2	2.49	0.44
2:B:454:ARG:NH2	2:B:467:ASP:OD2	2.50	0.44
2:B:707:TYR:CE2	2:C:885:GLY:HA3	2.53	0.44
2:B:864:LEU:HG	2:A:665:PRO:HB2	1.99	0.44
2:C:329:PHE:N	2:C:330:PRO:CD	2.77	0.44
2:C:377:PHE:HD1	2:C:378:LYS:N	2.13	0.44
2:C:435:ALA:HB2	2:C:510:VAL:HB	1.98	0.44
2:C:559:PHE:C	2:C:560:LEU:HD12	2.38	0.44
2:C:769:GLY:HA2	2:C:772:VAL:HG12	2.00	0.44
2:C:912:THR:O	2:C:915:VAL:HG22	2.17	0.44
2:C:986:PRO:O	2:C:987:PRO:C	2.56	0.44
2:A:275:PHE:HD1	2:A:290:ASP:CB	2.31	0.44
2:A:1115:ILE:CG2	2:A:1137:VAL:HG12	2.37	0.44
2:B:27:ALA:CB	2:B:64:TRP:HB3	2.38	0.44
2:B:168:PHE:CE2	2:B:170:TYR:HB2	2.53	0.44
2:B:362:VAL:HG13	2:B:526:GLY:HA2	1.99	0.44
2:B:577:ARG:CD	2:B:582:LEU:HD12	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:588:THR:HG23	2:B:589:PRO:HD2	2.00	0.44
2:B:1024:LEU:CA	2:B:1027:THR:HG22	2.46	0.44
2:C:421:TYR:OH	2:C:453:TYR:HB2	2.17	0.44
2:C:430:THR:OG1	2:C:515:PHE:N	2.49	0.44
2:C:539:VAL:HG22	2:C:540:ASN:H	1.82	0.44
2:C:993:ILE:O	2:C:993:ILE:HG22	2.18	0.44
2:A:332:ILE:HD12	2:A:332:ILE:HA	1.73	0.44
2:A:406:GLU:O	2:A:409:GLN:HB3	2.18	0.44
2:A:426:PRO:CG	2:A:463:PRO:HG2	2.48	0.44
2:A:742:ILE:HD11	2:A:753:LEU:CD2	2.46	0.44
2:B:386:LYS:O	2:B:386:LYS:CG	2.66	0.43
2:B:417:LYS:O	2:B:421:TYR:HB2	2.18	0.43
2:B:484:GLU:HG2	2:B:489:TYR:O	2.18	0.43
2:B:566:GLY:N	2:C:42:VAL:HG23	2.33	0.43
2:B:595:VAL:HA	2:B:611:LEU:O	2.18	0.43
2:C:83:VAL:O	2:C:84:LEU:HD23	2.18	0.43
2:C:195:LYS:NZ	2:C:197:ILE:HG22	2.32	0.43
2:C:351:TYR:HD1	2:C:421:TYR:HH	1.66	0.43
2:C:738:CYS:HA	2:C:1004:LEU:CD2	2.48	0.43
2:C:806:LEU:HD21	2:C:882:ILE:HD13	1.99	0.43
2:A:497:PHE:CD1	2:A:507:PRO:HD3	2.53	0.43
2:A:535:LYS:HE2	2:A:535:LYS:HB3	1.90	0.43
2:A:746:SER:HB3	2:A:749:CYS:HB3	2.01	0.43
2:A:770:ILE:O	2:A:774:GLN:HG2	2.18	0.43
2:A:806:LEU:HD21	2:A:882:ILE:CD1	2.48	0.43
1:D:39:GLN:OE1	1:D:39:GLN:N	2.51	0.43
2:B:577:ARG:HH21	2:B:584:ILE:CA	2.31	0.43
4:B:1301:NAG:O7	4:B:1301:NAG:O3	2.24	0.43
2:C:326:ILE:HB	2:C:531:THR:OG1	2.18	0.43
2:C:337:PRO:O	2:C:340:GLU:HB3	2.18	0.43
2:C:376:THR:O	2:C:432:CYS:HB2	2.18	0.43
2:C:435:ALA:CB	2:C:510:VAL:HB	2.48	0.43
2:C:565:PHE:HA	2:C:575:ALA:CA	2.46	0.43
2:C:751:ASN:O	2:C:755:GLN:NE2	2.51	0.43
2:A:336:CYS:HB3	2:A:363:ALA:N	2.33	0.43
2:A:338:PHE:HA	2:A:358:ILE:HD13	2.00	0.43
2:A:980:ILE:HD11	2:A:993:ILE:HD13	2.00	0.43
2:B:91:TYR:CE1	2:B:93:ALA:HB2	2.53	0.43
2:B:146:HIS:CE1	2:B:151:SER:HB2	2.52	0.43
2:B:873:TYR:CZ	2:A:699:LEU:HG	2.53	0.43
2:B:897:PRO:CG	2:A:711:SER:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:351:TYR:HB2	2:C:453:TYR:CA	2.41	0.43
2:C:533:LEU:HD12	2:C:534:VAL:N	2.33	0.43
2:A:125:ASN:HB2	2:A:171:VAL:HG13	2.00	0.43
2:A:392:PHE:HD2	2:A:515:PHE:HA	1.82	0.43
2:A:497:PHE:CB	2:A:501:ASN:HD21	2.30	0.43
2:A:546:LEU:HD23	2:A:565:PHE:CG	2.53	0.43
2:A:986:PRO:HA	2:A:989:ALA:HB3	2.00	0.43
2:B:105:ILE:CG1	2:B:239:GLN:HB3	2.44	0.43
2:B:141:LEU:HB3	2:B:243:ALA:CA	2.48	0.43
2:B:708:SER:OG	2:C:894:LEU:CG	2.67	0.43
2:B:775:ASP:HB3	2:B:864:LEU:CD1	2.30	0.43
2:C:189:LEU:HB2	2:C:210:ILE:HD11	1.99	0.43
2:C:322:PRO:HB3	2:C:539:VAL:HG23	2.01	0.43
2:C:355:ARG:NE	2:C:355:ARG:HA	2.33	0.43
2:C:1080:ALA:O	2:C:1081:ILE:HG13	2.19	0.43
2:A:307:THR:HA	2:A:602:THR:HG21	2.00	0.43
2:A:726:ILE:HG21	2:A:948:LEU:HG	2.00	0.43
2:B:29:THR:HG21	2:B:216:LEU:HD12	2.01	0.43
2:C:646:ARG:HD3	2:C:668:ALA:CB	2.46	0.43
2:A:56:LEU:HD23	2:A:57:PRO:O	2.19	0.43
2:A:62:VAL:HG21	2:A:266:TYR:CG	2.53	0.43
2:A:277:LEU:HD22	2:A:285:ILE:CD1	2.48	0.43
2:A:335:LEU:HD22	4:A:1202:NAG:H83	2.00	0.43
1:D:50:ALA:O	1:D:59:ALA:N	2.42	0.43
2:B:56:LEU:O	2:B:56:LEU:HD23	2.18	0.43
2:B:116:SER:O	2:B:130:VAL:HA	2.18	0.43
2:B:133:PHE:CD2	2:B:163:ALA:HB2	2.53	0.43
2:B:717:ASN:HB2	3:G:1:NAG:C2	2.43	0.43
2:B:792:PRO:HG3	2:A:707:TYR:CE1	2.51	0.43
2:B:1015:ALA:O	2:B:1018:ILE:HG22	2.17	0.43
2:B:1141:LEU:CD2	2:A:1141:LEU:HD13	2.49	0.43
2:C:173:GLN:HB3	2:C:174:PRO:HD2	2.01	0.43
2:C:377:PHE:CD1	2:C:378:LYS:N	2.81	0.43
2:C:1113:GLN:OE1	2:C:1113:GLN:HA	2.19	0.43
2:A:142:GLY:HA2	2:A:244:LEU:O	2.18	0.43
2:A:300:LYS:HE2	2:A:300:LYS:HB2	1.84	0.43
2:A:577:ARG:HH12	2:A:582:LEU:HD13	1.84	0.43
2:A:659:SER:OG	2:A:696:THR:O	2.36	0.43
2:A:751:ASN:O	2:A:754:LEU:HG	2.19	0.43
2:B:41:LYS:NZ	2:B:225:PRO:HD3	2.33	0.43
2:B:132:GLU:OE1	2:B:132:GLU:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:156:GLU:OE1	2:B:156:GLU:N	2.51	0.43
2:B:646:ARG:O	2:C:861:LEU:HD22	2.19	0.43
2:B:646:ARG:CG	2:C:861:LEU:HB3	2.49	0.43
2:B:1079:PRO:HG3	2:C:913:GLN:NE2	2.33	0.43
4:B:1307:NAG:H82	4:B:1307:NAG:O3	2.18	0.43
2:C:48:LEU:HG	2:C:278:LYS:CD	2.39	0.43
2:C:426:PRO:HD3	2:C:463:PRO:HB3	1.99	0.43
2:C:492:LEU:HD23	2:C:493:GLN:N	2.34	0.43
2:C:611:LEU:HD12	2:C:650:LEU:CG	2.47	0.43
2:C:780:GLU:OE1	2:C:780:GLU:HA	2.18	0.43
2:C:1054:GLN:HB2	2:C:1061:VAL:O	2.18	0.43
2:A:329:PHE:CE1	2:A:544:ASN:HB3	2.54	0.43
2:A:714:ILE:HD12	2:A:1096:VAL:HG11	2.01	0.43
2:A:726:ILE:CG2	2:A:948:LEU:HG	2.48	0.43
2:B:778:THR:HG22	2:B:865:LEU:HD12	1.99	0.43
2:B:985:ASP:HB2	2:B:987:PRO:HD2	2.00	0.43
2:C:176:LEU:H	2:C:177:MET:CE	2.31	0.43
2:C:346:ARG:HA	2:C:509:ARG:NH2	2.34	0.43
2:C:393:THR:CG2	2:C:518:LEU:HG	2.48	0.43
2:C:430:THR:O	2:C:515:PHE:N	2.52	0.43
2:C:451:TYR:O	2:C:452:LEU:HD23	2.19	0.43
2:A:92:PHE:HZ	2:A:238:PHE:CE2	2.37	0.43
2:B:335:LEU:HD13	2:B:335:LEU:HA	1.79	0.43
2:B:531:THR:HG22	2:B:532:ASN:N	2.33	0.43
2:B:549:THR:H	2:C:978:ASN:ND2	2.16	0.43
2:B:646:ARG:CD	2:C:863:PRO:HA	2.43	0.43
2:B:864:LEU:CD1	2:A:665:PRO:HB3	2.49	0.43
2:B:877:LEU:O	2:B:881:THR:HG22	2.19	0.43
2:C:390:LEU:HD11	2:A:983:ARG:HG3	2.00	0.43
2:C:777:ASN:O	2:C:781:VAL:HG23	2.19	0.43
2:C:1089:PHE:O	2:C:1120:THR:HB	2.18	0.43
2:A:105:ILE:O	2:A:105:ILE:HG13	2.18	0.43
2:A:177:MET:H	2:A:177:MET:HG3	1.70	0.43
2:A:290:ASP:C	2:A:290:ASP:OD1	2.57	0.43
2:A:331:ASN:O	2:A:332:ILE:HG22	2.18	0.43
2:A:392:PHE:CE2	2:A:515:PHE:HB3	2.54	0.43
2:A:976:VAL:HB	2:A:979:ASP:HB3	2.01	0.43
2:B:424:LYS:CB	2:B:461:LEU:HB2	2.45	0.43
2:B:985:ASP:O	2:B:986:PRO:C	2.58	0.43
2:B:1046:GLY:HA3	2:B:1066:THR:CG2	2.49	0.43
2:C:366:SER:HA	2:C:369:TYR:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:520:ALA:HB3	2:C:521:PRO:CD	2.49	0.43
2:C:853:GLN:HA	2:C:856:ASN:HD21	1.84	0.43
2:A:444:LYS:H	2:A:448:ASN:HB2	1.83	0.43
2:A:1009:THR:O	2:A:1013:ILE:HG12	2.19	0.43
2:B:38:TYR:HE2	2:A:560:LEU:HD21	1.84	0.42
2:B:353:TRP:HZ3	2:B:423:TYR:HB3	1.84	0.42
2:B:491:PRO:O	2:B:492:LEU:C	2.57	0.42
2:B:498:GLN:H	2:B:501:ASN:HD22	1.65	0.42
2:B:1087:ALA:HB2	2:B:1129:VAL:CG2	2.49	0.42
2:C:68:ILE:HD13	2:C:262:ALA:CB	2.49	0.42
2:C:102:ARG:HE	2:C:243:ALA:HB2	1.84	0.42
2:C:119:ILE:HG12	2:C:128:ILE:HG23	2.01	0.42
2:C:143:VAL:HG23	2:C:245:HIS:ND1	2.34	0.42
2:C:1096:VAL:HG23	2:C:1103:PHE:HB2	2.01	0.42
2:A:249:LEU:HB3	2:A:253:ASP:OD2	2.18	0.42
2:A:426:PRO:CA	2:A:463:PRO:HG2	2.49	0.42
2:A:520:ALA:HB3	2:A:521:PRO:HD3	2.01	0.42
2:A:693:ILE:HD12	2:A:695:TYR:HD1	1.84	0.42
2:A:801:ASN:N	2:A:928:ASN:OD1	2.49	0.42
2:A:802:PHE:HZ	2:A:898:PHE:CZ	2.37	0.42
2:B:318:PHE:HZ	2:B:615:VAL:CG1	2.31	0.42
2:B:618:THR:CG2	4:B:1303:NAG:H61	2.49	0.42
2:B:1100:THR:HG1	2:B:1101:HIS:CE1	2.36	0.42
2:C:69:HIS:HB2	2:C:78:ARG:O	2.19	0.42
2:C:146:HIS:HB3	2:C:149:ASN:HB2	2.01	0.42
2:C:196:ASN:HB2	2:C:201:PHE:CD2	2.54	0.42
2:C:247:SER:CB	2:C:259:THR:HG21	2.46	0.42
2:C:335:LEU:HB2	2:C:361:CYS:HA	2.01	0.42
2:C:402:ILE:HG12	2:C:403:ARG:H	1.84	0.42
2:C:424:LYS:CB	2:C:463:PRO:HA	2.49	0.42
2:C:599:THR:HB	2:C:608:VAL:HG12	2.01	0.42
2:C:707:TYR:CE2	2:C:708:SER:O	2.72	0.42
2:C:734:THR:O	2:C:767:LEU:HD21	2.19	0.42
2:C:752:LEU:HD21	2:C:990:GLU:OE1	2.19	0.42
2:C:858:LEU:HD22	2:C:959:LEU:HD11	2.01	0.42
2:C:860:VAL:HG22	2:C:861:LEU:N	2.34	0.42
2:A:102:ARG:HB3	2:A:119:ILE:O	2.18	0.42
2:A:236:THR:HG23	2:A:237:ARG:HG3	2.01	0.42
2:A:412:PRO:CA	2:A:425:LEU:HD21	2.45	0.42
2:A:656:VAL:HG13	2:A:695:TYR:HB3	2.00	0.42
2:A:865:LEU:HD23	2:A:865:LEU:N	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:295:PRO:HG3	2:B:636:TYR:CE2	2.55	0.42
2:B:705:VAL:HB	2:C:887:THR:O	2.19	0.42
2:B:706:ALA:HB1	2:C:894:LEU:CB	2.49	0.42
2:B:719:THR:HG23	2:B:719:THR:O	2.20	0.42
2:B:742:ILE:HG13	2:B:743:CYS:N	2.34	0.42
2:C:565:PHE:O	2:A:43:PHE:HB3	2.19	0.42
2:A:57:PRO:HB3	2:A:273:ARG:NH1	2.34	0.42
2:A:426:PRO:CB	2:A:463:PRO:HG2	2.50	0.42
2:A:462:LYS:HB3	2:A:465:GLU:OE1	2.19	0.42
2:A:928:ASN:O	2:A:931:ILE:HG22	2.19	0.42
2:A:971:GLY:HA3	2:A:995:ARG:HH22	1.83	0.42
2:A:980:ILE:O	2:A:980:ILE:HG13	2.19	0.42
1:D:105:PHE:CD1	1:D:105:PHE:N	2.85	0.42
2:B:42:VAL:HG13	2:A:566:GLY:C	2.39	0.42
2:B:386:LYS:HE2	2:B:389:ASP:OD2	2.19	0.42
2:B:498:GLN:H	2:B:501:ASN:ND2	2.17	0.42
2:B:574:ASP:HA	2:B:587:ILE:HG23	2.01	0.42
2:B:887:THR:CG2	2:B:894:LEU:HD12	2.49	0.42
2:B:1106:GLN:H	2:B:1106:GLN:HG2	1.64	0.42
2:B:1144:GLU:CD	2:A:1141:LEU:HD23	2.40	0.42
2:C:54:LEU:N	2:C:54:LEU:HD22	2.34	0.42
2:C:326:ILE:HD12	2:C:532:ASN:CG	2.39	0.42
2:C:362:VAL:O	2:C:527:PRO:HD3	2.19	0.42
2:C:472:ILE:CB	2:C:491:PRO:HB3	2.37	0.42
2:C:523:THR:O	2:C:524:VAL:CG1	2.68	0.42
2:C:578:ASP:OD1	2:C:580:GLN:HB3	2.18	0.42
2:C:741:TYR:CD2	2:C:742:ILE:HD12	2.53	0.42
2:C:785:VAL:HG21	2:C:789:TYR:HE1	1.85	0.42
2:A:218:GLN:OE1	2:A:218:GLN:N	2.52	0.42
2:A:811:LYS:HD2	2:A:811:LYS:HA	1.72	0.42
2:A:927:PHE:HE2	2:A:1065:VAL:HG21	1.84	0.42
2:B:131:CYS:HB2	2:B:163:ALA:HB1	2.01	0.42
2:B:310:LYS:HG3	2:B:600:PRO:HA	2.02	0.42
2:B:385:THR:HG23	2:C:985:ASP:HB3	2.02	0.42
2:B:386:LYS:HD2	2:C:983:ARG:CA	2.25	0.42
2:B:453:TYR:HD2	2:B:455:LEU:HB2	1.83	0.42
2:B:506:GLN:HB3	2:B:507:PRO:HD2	2.00	0.42
2:B:566:GLY:HA2	2:C:42:VAL:HG22	2.01	0.42
2:B:595:VAL:HG23	2:B:610:VAL:HG13	2.00	0.42
2:B:816:SER:OG	2:B:819:GLU:HG3	2.20	0.42
2:B:855:PHE:CD2	2:B:858:LEU:HD23	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1116:THR:HG23	2:B:1138:TYR:O	2.19	0.42
2:C:31:SER:OG	2:C:60:SER:O	2.27	0.42
2:C:104:TRP:HA	2:C:240:THR:HA	2.01	0.42
2:C:189:LEU:CD2	2:C:210:ILE:HD13	2.48	0.42
2:C:211:ASN:O	2:C:212:LEU:HD13	2.20	0.42
2:C:443:SER:HB3	2:C:507:PRO:CG	2.43	0.42
2:C:582:LEU:HA	2:C:582:LEU:HD22	1.85	0.42
2:A:490:PHE:CD1	2:A:491:PRO:HD2	2.55	0.42
2:A:708:SER:HB3	2:A:711:SER:HB2	2.01	0.42
1:D:100:ASP:OD1	1:D:101:VAL:N	2.47	0.42
2:B:207:HIS:CD2	2:B:209:PRO:HD3	2.55	0.42
2:B:456:PHE:HB2	2:B:491:PRO:CB	2.47	0.42
2:B:546:LEU:HD11	2:B:576:VAL:CG1	2.49	0.42
2:B:797:PHE:O	2:B:800:PHE:HD2	2.02	0.42
2:B:893:ALA:C	2:B:894:LEU:HD23	2.40	0.42
2:B:1029:MET:HE3	2:B:1053:PRO:CB	2.47	0.42
2:C:538:CYS:HA	2:C:551:VAL:HA	2.01	0.42
2:C:718:PHE:CD1	2:C:718:PHE:C	2.93	0.42
2:C:980:ILE:HG23	2:C:992:GLN:CD	2.39	0.42
2:C:1047:TYR:O	2:C:1066:THR:HA	2.18	0.42
2:A:118:LEU:N	2:A:129:LYS:O	2.37	0.42
2:A:329:PHE:HD1	2:A:528:LYS:HB2	1.85	0.42
2:A:354:ASN:HB2	2:A:399:SER:CB	2.46	0.42
2:A:454:ARG:CG	2:A:455:LEU:N	2.83	0.42
2:A:456:PHE:CZ	2:A:489:TYR:HD2	2.38	0.42
2:A:540:ASN:HA	2:A:548:GLY:O	2.19	0.42
2:A:599:THR:HA	2:A:608:VAL:HG22	2.01	0.42
2:B:168:PHE:HD2	2:B:231:ILE:HD11	1.83	0.42
2:B:562:PHE:CG	2:C:224:GLU:HB3	2.55	0.42
2:B:862:PRO:HG2	2:A:668:ALA:H	1.83	0.42
2:B:951:VAL:HG21	2:B:1018:ILE:CD1	2.48	0.42
2:B:1145:LEU:CA	2:A:1145:LEU:HD21	2.40	0.42
2:C:328:ARG:HG2	2:C:328:ARG:HH11	1.85	0.42
2:C:475:ALA:HB1	2:A:386:LYS:HD3	2.01	0.42
2:A:320:VAL:HG22	2:A:592:PHE:H	1.84	0.42
2:A:370:ASN:O	2:A:371:SER:HB2	2.20	0.42
2:A:428:ASP:OD1	2:A:429:PHE:N	2.53	0.42
1:D:62:ASP:OD1	1:D:63:SER:N	2.53	0.42
2:B:112:SER:HA	2:B:132:GLU:OE2	2.20	0.42
2:B:117:LEU:HA	2:B:130:VAL:HG22	2.01	0.42
2:B:122:ASN:O	2:B:174:PRO:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:541:PHE:HE2	2:B:576:VAL:HG21	1.78	0.42
2:B:706:ALA:HB2	2:C:892:PRO:C	2.40	0.42
2:B:986:PRO:N	2:B:987:PRO:HD2	2.35	0.42
2:C:54:LEU:C	2:C:55:PHE:HD1	2.22	0.42
2:C:367:VAL:O	2:C:369:TYR:N	2.52	0.42
2:C:371:SER:HB3	2:C:374:PHE:HZ	1.84	0.42
2:C:474:GLN:HB3	2:C:480:CYS:SG	2.59	0.42
2:C:821:LEU:HD23	2:C:821:LEU:C	2.40	0.42
2:C:1056:ALA:HB1	2:C:1057:PRO:HD2	2.00	0.42
2:C:1091:ARG:HE	2:C:1121:PHE:HB3	1.83	0.42
2:A:193:VAL:HG12	2:A:195:LYS:CG	2.49	0.42
2:A:391:CYS:O	2:A:392:PHE:HB2	2.20	0.42
2:A:786:LYS:O	2:A:786:LYS:HG3	2.20	0.42
2:A:1144:GLU:C	2:A:1145:LEU:HD12	2.40	0.42
2:B:135:PHE:CE1	2:B:159:VAL:HG12	2.54	0.42
2:B:643:PHE:CE2	2:B:645:THR:HB	2.55	0.42
2:C:126:VAL:HG23	2:C:174:PRO:HA	2.02	0.42
2:C:145:TYR:HB2	2:C:245:HIS:CE1	2.54	0.42
2:C:560:LEU:HB3	2:C:561:PRO:HD2	2.02	0.42
2:C:726:ILE:HD13	2:C:1061:VAL:HG22	2.01	0.42
2:A:433:VAL:HA	2:A:512:VAL:HG22	2.02	0.42
2:A:577:ARG:HH11	2:A:582:LEU:HD22	1.85	0.42
2:A:1029:MET:HA	2:A:1033:VAL:HG12	2.02	0.42
2:B:20:THR:HG21	2:B:79:PHE:CB	2.48	0.42
2:B:38:TYR:HE1	2:B:285:ILE:HG13	1.82	0.42
2:B:403:ARG:HD3	2:B:497:PHE:CE2	2.54	0.42
2:C:76:THR:O	2:C:78:ARG:NH1	2.52	0.42
2:C:382:VAL:CG2	2:A:981:LEU:HD13	2.50	0.42
2:C:442:ASP:OD2	2:C:451:TYR:OH	2.38	0.42
2:C:461:LEU:O	2:C:465:GLU:HB2	2.20	0.42
2:C:475:ALA:HB3	2:A:385:THR:OG1	2.20	0.42
2:A:242:LEU:HD23	2:A:242:LEU:H	1.85	0.42
2:A:245:HIS:HB2	2:A:259:THR:O	2.19	0.42
2:A:472:ILE:HG21	2:A:488:CYS:HA	2.02	0.42
1:D:64:VAL:O	1:D:64:VAL:HG23	2.20	0.41
2:B:42:VAL:HG11	2:A:567:ARG:HD2	2.02	0.41
2:B:338:PHE:HA	2:B:342:PHE:HB2	2.02	0.41
2:B:410:ILE:HD11	2:B:423:TYR:HE2	1.85	0.41
2:B:564:GLN:HB2	2:C:41:LYS:CE	2.47	0.41
2:B:983:ARG:HE	2:B:983:ARG:HB2	1.38	0.41
2:C:571:ASP:N	2:C:571:ASP:OD1	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:732:THR:HG23	2:C:955:ASN:ND2	2.35	0.41
2:A:66:HIS:CE1	2:A:68:ILE:HD12	2.55	0.41
2:A:300:LYS:HD2	2:A:306:PHE:HA	2.01	0.41
2:A:326:ILE:HD11	2:A:532:ASN:O	2.19	0.41
2:A:379:CYS:SG	2:A:430:THR:HG22	2.60	0.41
2:A:402:ILE:HG12	2:A:508:TYR:O	2.19	0.41
2:A:574:ASP:HA	2:A:587:ILE:HG13	2.02	0.41
2:A:692:ILE:HD13	2:A:692:ILE:HA	1.96	0.41
2:A:1087:ALA:CB	2:A:1089:PHE:HE1	2.33	0.41
2:B:170:TYR:HE2	2:B:172:SER:HB3	1.84	0.41
2:B:318:PHE:O	2:B:592:PHE:CE1	2.74	0.41
2:B:323:THR:N	2:B:539:VAL:HG12	2.34	0.41
2:B:366:SER:HB2	2:B:388:ASN:HB3	2.02	0.41
2:B:458:LYS:NZ	2:B:474:GLN:HB2	2.35	0.41
2:B:502:GLY:O	2:B:504:GLY:N	2.53	0.41
2:B:564:GLN:H	2:C:41:LYS:HB3	1.83	0.41
2:B:900:MET:HB3	2:B:900:MET:HE2	1.75	0.41
2:B:973:ILE:HD12	2:B:973:ILE:N	2.31	0.41
2:C:206:LYS:HA	2:C:206:LYS:HD2	1.74	0.41
2:C:986:PRO:C	2:C:990:GLU:HG2	2.40	0.41
2:A:475:ALA:HB3	2:A:487:ASN:O	2.20	0.41
2:A:909:ILE:HG23	2:A:1036:GLN:NE2	2.35	0.41
2:B:391:CYS:SG	2:B:521:PRO:HA	2.60	0.41
2:B:664:ILE:HG13	2:B:672:ALA:O	2.20	0.41
2:C:197:ILE:HD12	2:C:198:ASP:H	1.84	0.41
2:C:277:LEU:H	2:C:277:LEU:CD2	2.24	0.41
2:C:337:PRO:HG2	2:C:358:ILE:HG23	2.01	0.41
2:C:454:ARG:NH1	2:C:491:PRO:HB2	2.35	0.41
2:C:656:VAL:CG2	2:C:693:ILE:HD11	2.50	0.41
2:C:880:GLY:O	2:C:884:SER:OG	2.30	0.41
2:C:974:SER:H	2:C:992:GLN:NE2	2.18	0.41
2:A:169:GLU:O	2:A:169:GLU:HG2	2.20	0.41
2:A:374:PHE:CE2	2:A:434:ILE:HG21	2.55	0.41
2:A:392:PHE:CE2	2:A:517:LEU:HD22	2.55	0.41
2:A:580:GLN:OE1	2:A:581:THR:HG23	2.19	0.41
2:A:612:TYR:CE2	2:A:651:ILE:HD11	2.44	0.41
2:A:919:ASN:O	2:A:923:ILE:HG13	2.21	0.41
2:A:1082:CYS:O	2:A:1134:ASN:HA	2.20	0.41
1:D:47:PHE:CD1	2:A:486:PHE:HB2	2.55	0.41
2:B:125:ASN:HB2	2:B:172:SER:O	2.20	0.41
2:B:444:LYS:O	2:B:498:GLN:NE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:569:ILE:O	2:B:570:ALA:HB3	2.19	0.41
2:B:592:PHE:CD2	2:C:737:ASP:HB2	2.55	0.41
2:B:630:THR:N	2:B:631:PRO:HD2	2.34	0.41
2:B:823:PHE:CD1	2:B:823:PHE:C	2.94	0.41
2:B:1116:THR:HG22	2:B:1117:THR:N	2.35	0.41
2:C:62:VAL:CG1	2:C:268:GLY:HA2	2.50	0.41
2:C:278:LYS:HB3	2:C:287:ASP:O	2.20	0.41
2:C:362:VAL:O	2:C:363:ALA:HB3	2.21	0.41
2:C:538:CYS:HA	2:C:551:VAL:CA	2.50	0.41
2:C:858:LEU:HD21	2:C:962:LEU:CD2	2.34	0.41
2:C:1071:GLN:CD	4:C:1206:NAG:H61	2.41	0.41
2:A:664:ILE:O	2:A:664:ILE:CG1	2.69	0.41
2:A:808:ASP:OD1	2:A:808:ASP:N	2.52	0.41
2:A:1122:VAL:O	2:A:1123:SER:OG	2.33	0.41
2:B:535:LYS:HG3	2:B:536:ASN:CG	2.39	0.41
2:B:862:PRO:HG3	2:A:647:ALA:HA	2.02	0.41
2:B:988:GLU:HA	2:B:991:VAL:HG12	2.02	0.41
2:C:403:ARG:NH2	2:C:495:TYR:HA	2.35	0.41
2:C:788:ILE:HG23	2:C:788:ILE:O	2.20	0.41
2:A:116:SER:O	2:A:131:CYS:N	2.47	0.41
2:A:388:ASN:OD1	2:A:526:GLY:HA3	2.20	0.41
2:A:425:LEU:O	2:A:425:LEU:HG	2.20	0.41
2:A:607:GLN:HB3	2:A:674:TYR:CE1	2.55	0.41
2:A:712:ILE:HG22	2:A:1075:PHE:N	2.34	0.41
1:D:60:TYR:OH	1:D:70:ILE:N	2.46	0.41
2:B:346:ARG:HA	2:B:346:ARG:HD2	1.66	0.41
2:B:469:SER:O	2:B:492:LEU:HD21	2.20	0.41
2:B:491:PRO:HB2	2:B:492:LEU:H	1.77	0.41
2:B:740:MET:C	2:B:740:MET:SD	2.99	0.41
2:B:906:PHE:HB3	2:B:911:VAL:HG23	2.02	0.41
2:C:196:ASN:HA	2:C:200:TYR:O	2.20	0.41
2:C:329:PHE:O	2:C:330:PRO:C	2.59	0.41
2:C:470:THR:OG1	2:C:471:GLU:N	2.53	0.41
2:C:667:GLY:O	2:C:668:ALA:HB3	2.21	0.41
2:C:705:VAL:HG23	2:A:895:GLN:OE1	2.20	0.41
2:C:1023:ASN:O	2:C:1027:THR:HG22	2.21	0.41
2:A:130:VAL:HB	2:A:167:THR:OG1	2.20	0.41
2:A:335:LEU:HD12	2:A:335:LEU:HA	1.83	0.41
2:A:336:CYS:HB3	2:A:363:ALA:H	1.84	0.41
2:A:349:SER:HA	2:A:451:TYR:CD1	2.55	0.41
2:A:426:PRO:HG3	2:A:463:PRO:CB	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:748:GLU:HG3	2:A:981:LEU:CD1	2.49	0.41
1:D:101:VAL:HG23	1:D:101:VAL:O	2.21	0.41
2:B:42:VAL:CG1	2:A:567:ARG:CB	2.97	0.41
2:B:364:ASP:OD1	2:B:367:VAL:HG13	2.21	0.41
2:B:441:LEU:HD12	2:B:441:LEU:N	2.36	0.41
2:B:911:VAL:HG12	2:B:1108:ASN:HB2	2.03	0.41
2:C:752:LEU:O	2:C:755:GLN:HG2	2.21	0.41
2:C:858:LEU:CD2	2:C:959:LEU:HD11	2.50	0.41
2:C:988:GLU:O	2:C:988:GLU:HG2	2.21	0.41
2:A:594:GLY:O	2:A:612:TYR:HD1	2.03	0.41
2:A:650:LEU:CD1	2:A:666:ILE:HD13	2.36	0.41
2:B:311:GLY:HA2	2:B:664:ILE:HG23	2.02	0.41
2:B:356:LYS:O	2:B:396:TYR:HA	2.21	0.41
2:B:611:LEU:HD23	2:B:611:LEU:C	2.41	0.41
2:B:709:ASN:OD1	2:B:709:ASN:N	2.53	0.41
2:B:710:ASN:O	2:B:1077:THR:HG22	2.20	0.41
2:C:156:GLU:N	2:C:156:GLU:OE1	2.54	0.41
2:C:273:ARG:HG2	2:C:274:THR:N	2.35	0.41
2:C:707:TYR:HB3	2:A:895:GLN:CD	2.40	0.41
2:C:774:GLN:OE1	2:C:774:GLN:HA	2.21	0.41
2:C:851:CYS:HB3	2:C:853:GLN:NE2	2.36	0.41
2:C:964:LYS:HB3	2:C:964:LYS:NZ	2.31	0.41
2:A:384:PRO:O	2:A:385:THR:OG1	2.33	0.41
2:A:453:TYR:O	2:A:492:LEU:HG	2.20	0.41
2:A:462:LYS:HD2	2:A:463:PRO:CD	2.48	0.41
2:A:1080:ALA:HB1	2:A:1088:HIS:O	2.21	0.41
2:B:33:THR:HA	2:B:58:PHE:HD1	1.86	0.41
2:B:271:GLN:OE1	2:B:272:PRO:HD2	2.21	0.41
2:B:402:ILE:HB	2:B:510:VAL:CB	2.50	0.41
2:B:471:GLU:O	2:B:491:PRO:HG3	2.21	0.41
2:B:480:CYS:HB2	2:B:483:VAL:O	2.21	0.41
2:B:545:GLY:O	2:B:547:THR:HG23	2.21	0.41
2:B:735:SER:O	2:B:859:THR:HG22	2.20	0.41
2:B:770:ILE:HD11	2:B:1012:LEU:CD2	2.51	0.41
2:B:903:ALA:H	2:B:916:LEU:HD22	1.83	0.41
2:B:948:LEU:CD2	2:B:1059:GLY:HA3	2.45	0.41
2:B:1028:LYS:HA	2:B:1042:PHE:CE2	2.54	0.41
2:B:1094:VAL:HG13	2:B:1107:ARG:HG2	2.03	0.41
2:B:1149:LYS:C	2:A:1145:LEU:HD23	2.41	0.41
2:C:54:LEU:CD1	2:C:272:PRO:HB3	2.50	0.41
2:C:117:LEU:HD21	2:C:119:ILE:CG1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:151:SER:HB2	2:C:153:MET:CE	2.51	0.41
2:C:200:TYR:HA	2:C:230:PRO:HA	2.03	0.41
2:C:278:LYS:HB2	2:C:306:PHE:CZ	2.55	0.41
2:C:290:ASP:OD2	2:C:293:LEU:HB2	2.20	0.41
2:C:365:TYR:CD2	2:C:387:LEU:HD23	2.55	0.41
2:C:382:VAL:HG13	2:A:986:PRO:HA	2.03	0.41
2:C:396:TYR:N	2:C:514:SER:O	2.37	0.41
2:C:411:ALA:HB1	2:C:412:PRO:CD	2.46	0.41
2:C:569:ILE:HD13	2:A:849:LEU:HD12	2.03	0.41
2:C:642:VAL:HG23	2:C:651:ILE:CD1	2.50	0.41
2:C:825:LYS:HE2	2:C:939:SER:HA	2.03	0.41
2:C:990:GLU:OE1	2:C:990:GLU:HA	2.20	0.41
2:C:1115:ILE:HG21	2:C:1136:THR:O	2.20	0.41
2:C:1116:THR:HA	2:C:1137:VAL:HB	2.02	0.41
2:A:330:PRO:O	2:A:331:ASN:HB3	2.21	0.41
2:A:391:CYS:SG	2:A:522:ALA:HB3	2.60	0.41
2:A:516:GLU:CG	2:A:518:LEU:HB2	2.50	0.41
2:A:821:LEU:HD12	2:A:821:LEU:O	2.20	0.41
2:A:897:PRO:HG2	2:A:900:MET:CE	2.50	0.41
2:B:53:ASP:HB2	2:B:55:PHE:CE1	2.56	0.41
2:B:364:ASP:CG	2:B:367:VAL:HG13	2.41	0.41
2:B:696:THR:HB	2:C:864:LEU:HD21	2.02	0.41
2:B:884:SER:OG	2:B:888:PHE:HD2	2.04	0.41
2:B:1078:ALA:HB2	2:B:1102:TRP:CZ3	2.56	0.41
2:B:1118:ASP:OD1	2:A:1091:ARG:NH2	2.53	0.41
2:C:127:VAL:HG22	2:C:171:VAL:HG22	2.03	0.41
2:C:308:VAL:O	2:C:601:GLY:HA2	2.21	0.41
2:C:380:TYR:CB	2:A:983:ARG:HB3	2.50	0.41
2:C:383:SER:N	2:A:984:LEU:O	2.53	0.41
2:C:459:SER:O	2:C:461:LEU:HD22	2.21	0.41
2:C:743:CYS:HB2	2:C:997:ILE:HD12	1.99	0.41
2:C:1104:VAL:O	2:C:1113:GLN:HG2	2.21	0.41
2:A:115:GLN:HE21	2:A:233:ILE:CG2	2.35	0.41
2:A:329:PHE:CD1	2:A:528:LYS:HB2	2.56	0.41
2:A:393:THR:N	2:A:522:ALA:HB2	2.36	0.41
2:A:418:ILE:HA	2:A:422:ASN:OD1	2.21	0.41
2:A:503:VAL:HG23	2:A:504:GLY:N	2.34	0.41
2:A:642:VAL:HG23	2:A:651:ILE:HG22	2.02	0.41
2:A:853:GLN:O	2:A:854:LYS:HB2	2.21	0.41
2:A:860:VAL:O	2:A:860:VAL:HG23	2.21	0.41
1:D:2:VAL:HG22	1:D:4:LEU:HD21	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:LEU:HD12	1:D:18:LEU:N	2.37	0.40
2:B:346:ARG:CZ	2:B:509:ARG:HH12	2.34	0.40
2:B:458:LYS:O	2:B:459:SER:OG	2.32	0.40
2:B:675:GLN:O	2:B:690:GLN:N	2.54	0.40
2:C:36:VAL:HG12	2:C:221:SER:O	2.21	0.40
2:C:329:PHE:H	2:C:330:PRO:CD	2.20	0.40
2:C:380:TYR:HB2	2:A:984:LEU:CD2	2.51	0.40
2:C:393:THR:HG21	2:C:518:LEU:CG	2.51	0.40
2:A:515:PHE:N	2:A:515:PHE:CD1	2.87	0.40
2:A:566:GLY:HA3	2:A:575:ALA:CB	2.50	0.40
2:A:821:LEU:HD21	2:A:939:SER:OG	2.21	0.40
2:A:886:TRP:C	2:A:888:PHE:H	2.23	0.40
2:A:986:PRO:CB	2:A:987:PRO:HD3	2.51	0.40
2:B:534:VAL:CG2	2:B:537:LYS:HB3	2.51	0.40
2:B:646:ARG:NE	2:C:733:LYS:HE2	2.36	0.40
2:B:659:SER:CB	2:B:696:THR:HG23	2.52	0.40
2:B:706:ALA:HA	2:C:894:LEU:CB	2.52	0.40
2:C:304:LYS:O	2:C:304:LYS:HD2	2.21	0.40
2:C:334:ASN:O	2:C:335:LEU:C	2.58	0.40
2:C:392:PHE:CE2	2:C:517:LEU:HD12	2.55	0.40
2:A:199:GLY:O	2:A:231:ILE:N	2.47	0.40
2:A:412:PRO:HA	2:A:425:LEU:HD11	2.04	0.40
2:B:431:GLY:CA	2:B:517:LEU:HG	2.41	0.40
2:B:770:ILE:O	2:B:774:GLN:HG2	2.21	0.40
2:C:18:LEU:HB3	2:C:258:TRP:CZ2	2.56	0.40
2:C:86:PHE:CD1	2:C:90:VAL:HG23	2.56	0.40
2:C:327:VAL:HG22	2:C:542:ASN:O	2.22	0.40
2:C:370:ASN:O	2:C:371:SER:C	2.59	0.40
2:C:435:ALA:HB2	2:C:510:VAL:CB	2.52	0.40
2:C:865:LEU:HD12	2:C:865:LEU:H	1.86	0.40
2:A:122:ASN:HD22	2:A:122:ASN:H	1.67	0.40
2:B:993:ILE:HD13	2:B:993:ILE:HA	1.91	0.40
2:B:1081:ILE:HD11	2:B:1095:PHE:CE2	2.57	0.40
2:C:328:ARG:HH12	2:C:580:GLN:HB3	1.86	0.40
2:C:351:TYR:OH	2:C:468:ILE:HA	2.22	0.40
2:C:427:ASP:O	2:C:429:PHE:N	2.55	0.40
2:C:668:ALA:H	2:A:864:LEU:HG	1.85	0.40
2:C:1037:SER:O	2:C:1037:SER:OG	2.39	0.40
2:C:1083:HIS:HB3	2:C:1135:ASN:O	2.22	0.40
2:A:197:ILE:HD11	2:A:202:LYS:HZ2	1.86	0.40
2:A:451:TYR:C	2:A:495:TYR:HB2	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:653:ALA:HB2	2:A:692:ILE:CG2	2.51	0.40
2:A:1089:PHE:O	2:A:1120:THR:HB	2.20	0.40
2:B:187:LYS:HB3	2:B:211:ASN:HB3	2.02	0.40
2:B:327:VAL:HB	2:B:329:PHE:HE1	1.87	0.40
2:B:402:ILE:HB	2:B:510:VAL:HB	2.03	0.40
2:B:570:ALA:HB1	2:C:966:LEU:HB2	2.03	0.40
2:B:821:LEU:HD21	2:B:935:GLN:CG	2.51	0.40
2:B:896:ILE:HG13	2:B:900:MET:HE1	2.02	0.40
2:B:992:GLN:NE2	2:B:992:GLN:HA	2.36	0.40
2:C:105:ILE:HD12	2:C:135:PHE:CZ	2.57	0.40
2:C:290:ASP:HB3	2:C:293:LEU:HB2	2.03	0.40
2:C:457:ARG:O	2:C:458:LYS:HB3	2.21	0.40
2:C:709:ASN:OD1	4:C:1205:NAG:H2	2.21	0.40
2:A:296:LEU:HD12	2:A:296:LEU:HA	1.81	0.40
2:A:659:SER:OG	2:A:660:TYR:N	2.54	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 PDB entries followed by that with respect to all EM entries.

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	D	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
2	A	1057/1136 (93%)	957 (90%)	90 (8%)	10 (1%)	14	47
2	B	1078/1136 (95%)	963 (89%)	110 (10%)	5 (0%)	25	58
2	C	1055/1136 (93%)	933 (88%)	107 (10%)	15 (1%)	9	39
All	All	3306/3526 (94%)	2963 (90%)	313 (10%)	30 (1%)	17	47

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	329	PHE
2	C	330	PRO
2	C	450	ASN
2	A	332	ILE
2	A	367	VAL
2	A	513	LEU
2	B	165	ASN
2	C	384	PRO
2	C	531	THR
2	C	582	LEU
2	A	675	GLN
2	B	344	ALA
2	B	491	PRO
2	C	368	LEU
2	A	433	VAL
2	A	514	SER
2	B	493	GLN
2	C	387	LEU
2	C	389	ASP
2	C	530	SER
2	C	739	THR
2	A	331	ASN
2	A	392	PHE
2	A	887	THR
2	C	331	ASN
2	C	576	VAL
2	A	333	THR
2	C	332	ILE
2	B	339	GLY
2	C	383	SER

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 PDB entries followed by that with respect to all EM entries.

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	D	89/89 (100%)	85 (96%)	4 (4%)	23	49
2	A	937/990 (95%)	897 (96%)	40 (4%)	25	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	954/990 (96%)	912 (96%)	42 (4%)	24	50
2	C	935/990 (94%)	889 (95%)	46 (5%)	21	47
All	All	2915/3059 (95%)	2783 (96%)	132 (4%)	26	49

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	34	MET
1	D	83	MET
1	D	105	PHE
1	D	106	ASP
2	B	40	ASP
2	B	55	PHE
2	B	121	ASN
2	B	122	ASN
2	B	124	THR
2	B	125	ASN
2	B	127	VAL
2	B	164	ASN
2	B	166	CYS
2	B	167	THR
2	B	269	TYR
2	B	314	GLN
2	B	334	ASN
2	B	335	LEU
2	B	336	CYS
2	B	340	GLU
2	B	346	ARG
2	B	349	SER
2	B	353	TRP
2	B	469	SER
2	B	473	TYR
2	B	492	LEU
2	B	493	GLN
2	B	632	THR
2	B	640	SER
2	B	735	SER
2	B	759	PHE
2	B	796	ASP
2	B	814	LYS
2	B	823	PHE

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Mol	Chain	Res	Type
2	B	855	PHE
2	B	900	MET
2	B	942	PRO
2	B	983	ARG
2	B	985	ASP
2	B	988	GLU
2	B	1055	SER
2	B	1083	HIS
2	B	1127	ASP
2	B	1128	VAL
2	B	1130	ILE
2	B	1132	ILE
2	C	30	ASN
2	C	58	PHE
2	C	64	TRP
2	C	92	PHE
2	C	192	PHE
2	C	206	LYS
2	C	259	THR
2	C	266	TYR
2	C	269	TYR
2	C	287	ASP
2	C	310	LYS
2	C	325	SER
2	C	328	ARG
2	C	330	PRO
2	C	332	ILE
2	C	338	PHE
2	C	340	GLU
2	C	341	VAL
2	C	343	ASN
2	C	366	SER
2	C	367	VAL
2	C	368	LEU
2	C	386	LYS
2	C	387	LEU
2	C	391	CYS
2	C	417	LYS
2	C	423	TYR
2	C	436	TRP
2	C	513	LEU
2	C	514	SER

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Mol	Chain	Res	Type
2	C	516	GLU
2	C	529	LYS
2	C	530	SER
2	C	571	ASP
2	C	577	ARG
2	C	582	LEU
2	C	592	PHE
2	C	605	SER
2	C	718	PHE
2	C	740	MET
2	C	820	ASP
2	C	823	PHE
2	C	873	TYR
2	C	974	SER
2	C	988	GLU
2	C	1003	SER
2	A	28	TYR
2	A	97	LYS
2	A	122	ASN
2	A	175	PHE
2	A	220	PHE
2	A	271	GLN
2	A	275	PHE
2	A	296	LEU
2	A	298	GLU
2	A	317	ASN
2	A	332	ILE
2	A	335	LEU
2	A	351	TYR
2	A	365	TYR
2	A	433	VAL
2	A	452	LEU
2	A	509	ARG
2	A	510	VAL
2	A	513	LEU
2	A	516	GLU
2	A	517	LEU
2	A	538	CYS
2	A	541	PHE
2	A	551	VAL
2	A	552	LEU
2	A	553	THR

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Mol	Chain	Res	Type
2	A	564	GLN
2	A	582	LEU
2	A	588	THR
2	A	658	ASN
2	A	660	TYR
2	A	661	GLU
2	A	675	GLN
2	A	695	TYR
2	A	858	LEU
2	A	900	MET
2	A	1066	THR
2	A	1092	GLU
2	A	1126	CYS
2	A	1138	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	146	HIS
2	B	165	ASN
2	B	207	HIS
2	B	448	ASN
2	B	498	GLN
2	B	501	ASN
2	B	544	ASN
2	B	804	GLN
2	B	954	GLN
2	B	1071	GLN
2	B	1119	ASN
2	C	66	HIS
2	C	149	ASN
2	C	331	ASN
2	C	487	ASN
2	C	804	GLN
2	C	1036	GLN
2	C	1071	GLN
2	A	66	HIS
2	A	115	GLN
2	A	239	GLN
2	A	271	GLN
2	A	334	ASN
2	A	487	ASN

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Mol	Chain	Res	Type
2	A	493	GLN
2	A	506	GLN
2	A	544	ASN
2	A	658	ASN
2	A	804	GLN
2	A	926	GLN
2	A	969	ASN
2	A	992	GLN
2	A	1119	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	E	1	3,2	14,14,15	0.25	0	17,19,21	0.45	0
3	NAG	E	2	3	14,14,15	0.25	0	17,19,21	0.44	0
3	NAG	F	1	3,2	14,14,15	0.67	1 (7%)	17,19,21	0.98	1 (5%)
3	NAG	F	2	3	14,14,15	0.24	0	17,19,21	0.45	0
3	NAG	G	1	3,2	14,14,15	0.39	0	17,19,21	0.49	0
3	NAG	G	2	3	14,14,15	0.26	0	17,19,21	0.41	0
3	NAG	H	1	3,2	14,14,15	0.64	1 (7%)	17,19,21	0.64	0
3	NAG	H	2	3	14,14,15	0.27	0	17,19,21	0.44	0
3	NAG	I	1	3	14,14,15	0.48	0	17,19,21	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	I	2	3	14,14,15	0.36	0	17,19,21	0.41	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	3,2	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	3,2	-	3/6/23/26	0/1/1/1
3	NAG	F	2	3	-	3/6/23/26	0/1/1/1
3	NAG	G	1	3,2	-	3/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	3/6/23/26	0/1/1/1
3	NAG	I	1	3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	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)
3	H	1	NAG	O5-C1	-2.22	1.40	1.43
3	F	1	NAG	O5-C1	2.14	1.47	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	NAG	C1-O5-C5	3.73	117.18	112.19

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1	NAG	C1-C2-N2-C7
3	F	2	NAG	C4-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6

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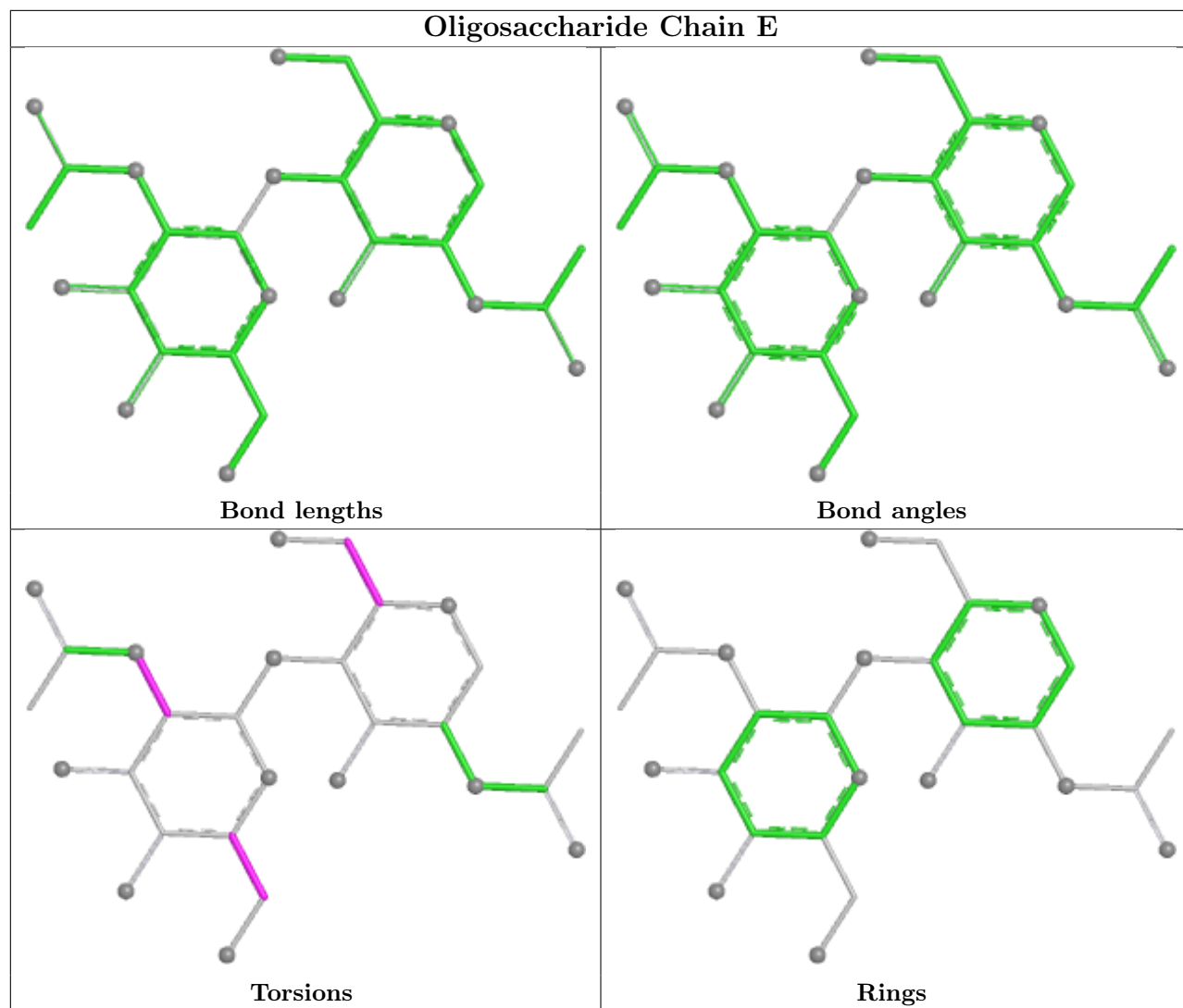
Mol	Chain	Res	Type	Atoms
3	H	2	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
3	I	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O7-C7-N2-C2
3	F	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6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

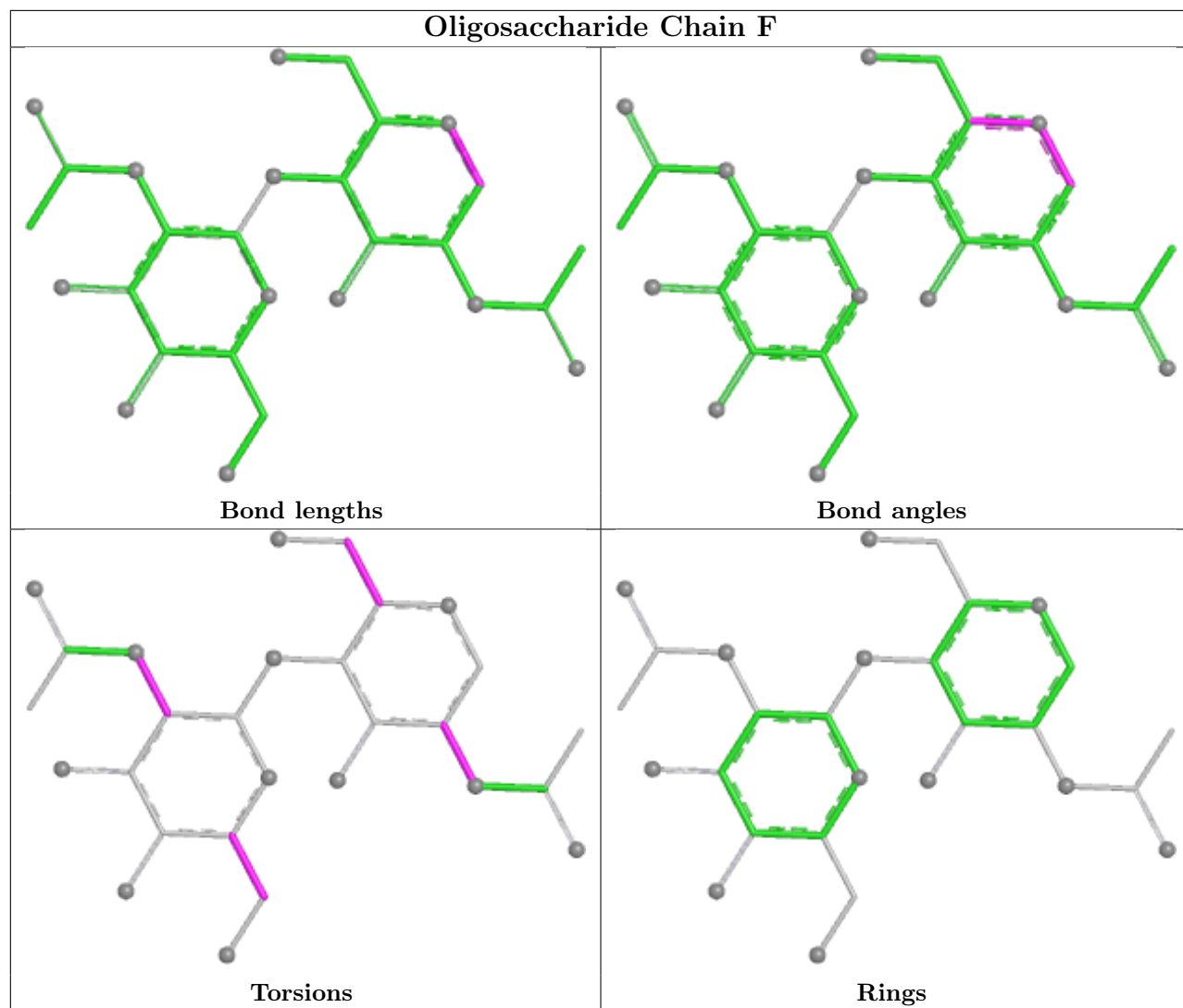
There are no ring outliers.

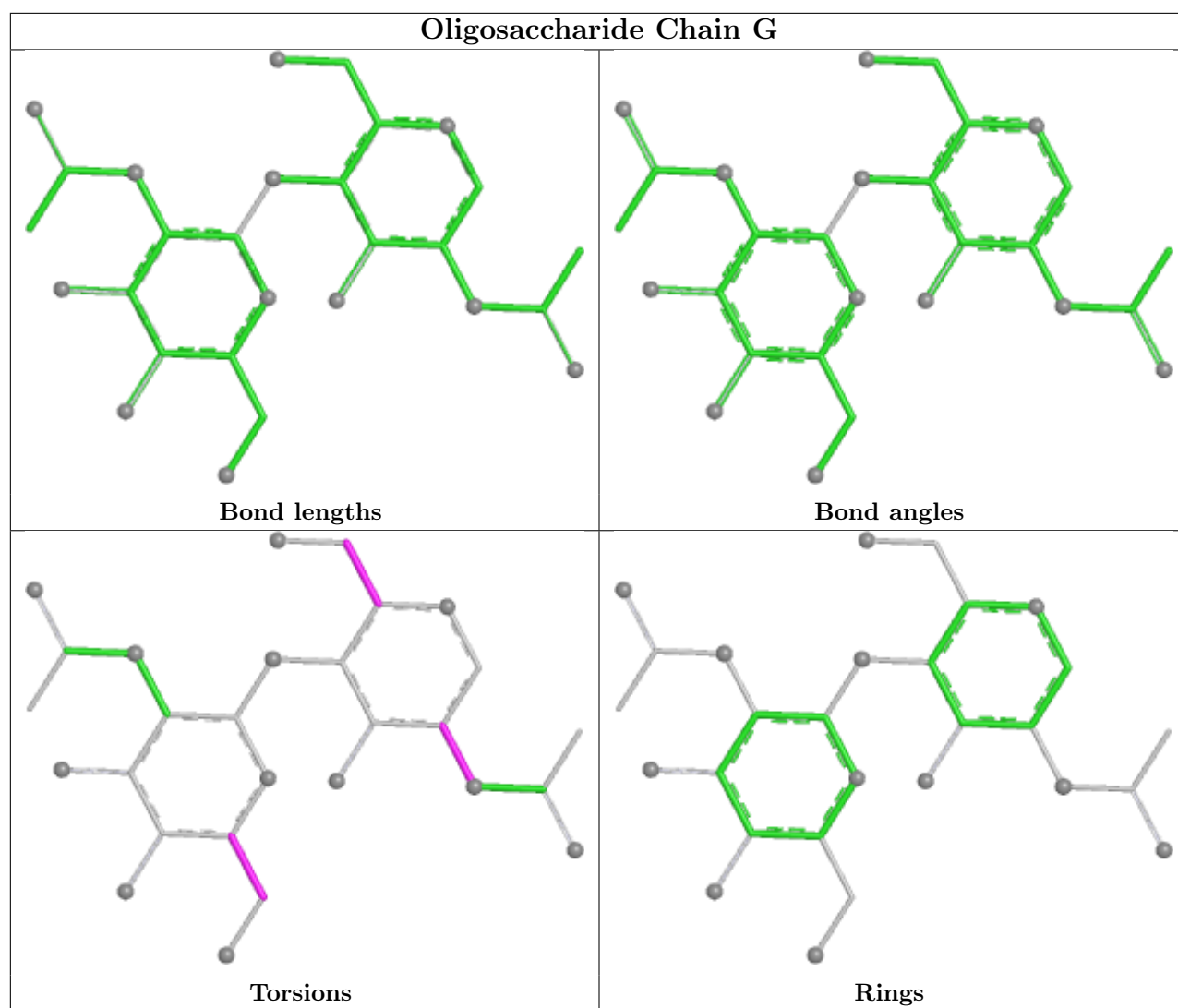
6 monomers are involved in 23 short contacts:

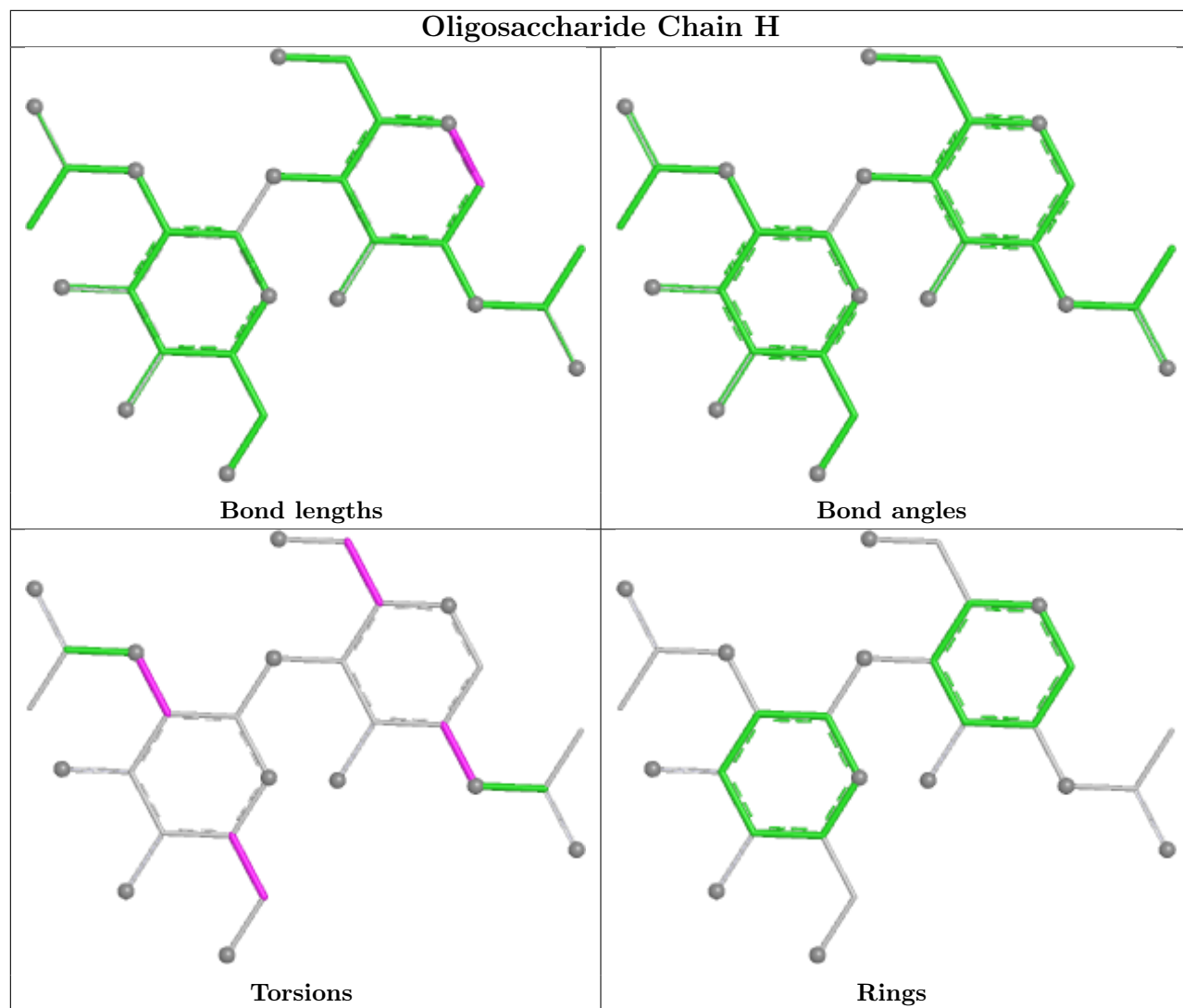
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	2	NAG	1	0
3	G	1	NAG	4	0
3	I	1	NAG	9	0
3	I	2	NAG	1	0
3	H	1	NAG	3	0
3	F	1	NAG	6	0

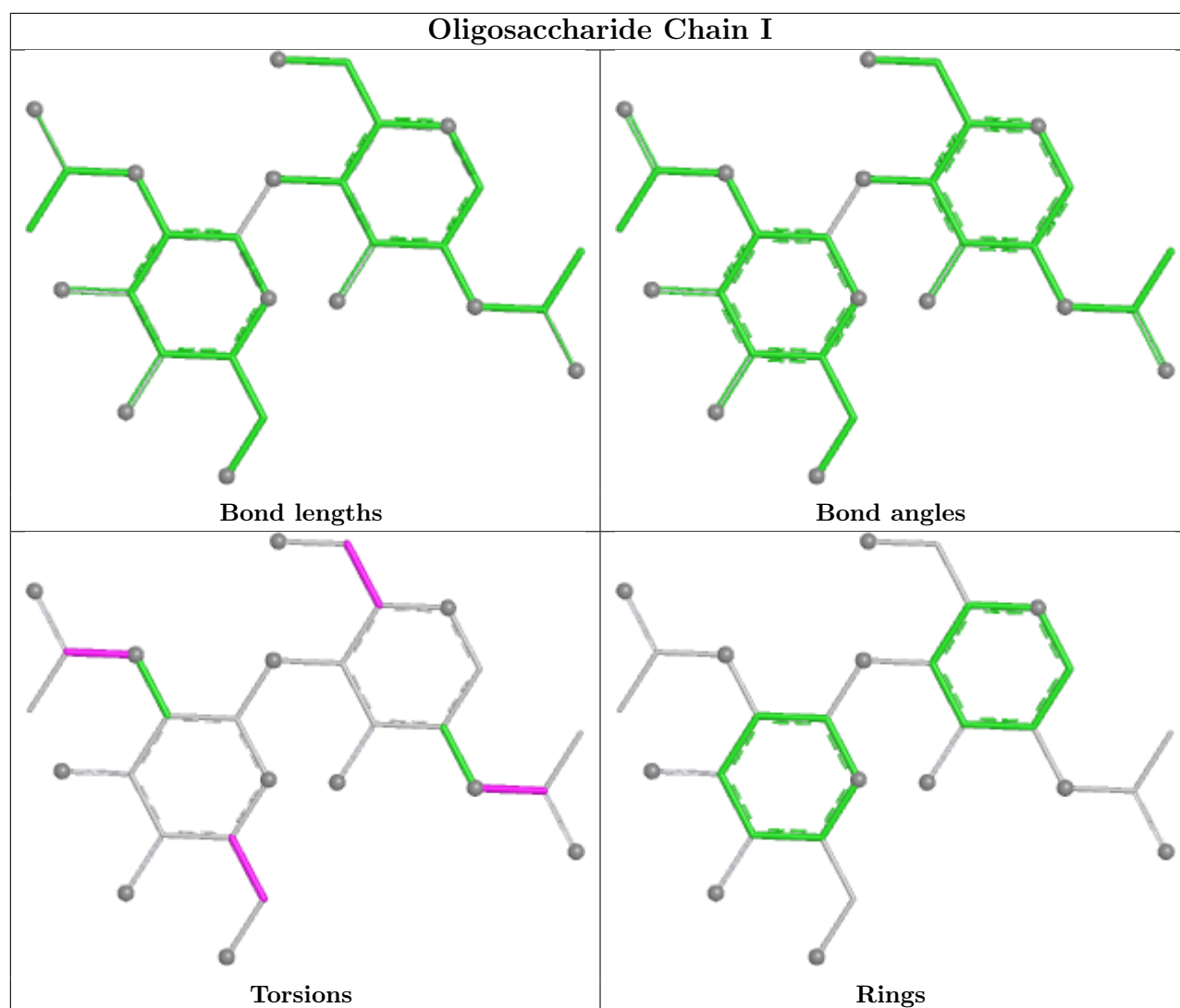
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	1208	-	14,14,15	0.99	0	17,19,21	0.94	1 (5%)
4	NAG	B	1302	2	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	A	1205	2	14,14,15	0.25	0	17,19,21	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1202	-	14,14,15	2.70	7 (50%)	17,19,21	1.23	2 (11%)
4	NAG	C	1206	2	14,14,15	0.31	0	17,19,21	0.34	0
4	NAG	A	1208	2	14,14,15	0.23	0	17,19,21	0.46	0
4	NAG	A	1206	2	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1205	2	14,14,15	0.21	0	17,19,21	0.40	0
4	NAG	B	1303	2	14,14,15	0.28	0	17,19,21	0.43	0
4	NAG	A	1203	2	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1306	2	14,14,15	0.23	0	17,19,21	0.42	0
4	NAG	A	1201	2	14,14,15	0.50	0	17,19,21	0.76	1 (5%)
4	NAG	C	1207	2	14,14,15	0.24	0	17,19,21	0.50	0
4	NAG	C	1202	2	14,14,15	0.53	0	17,19,21	0.79	1 (5%)
4	NAG	C	1204	2	14,14,15	0.25	0	17,19,21	0.42	0
4	NAG	A	1209	2	14,14,15	0.43	0	17,19,21	0.35	0
4	NAG	C	1203	2	14,14,15	0.24	0	17,19,21	0.43	0
4	NAG	B	1304	2	14,14,15	0.28	0	17,19,21	0.40	0
4	NAG	C	1201	-	14,14,15	0.61	0	17,19,21	0.58	0
4	NAG	A	1204	2	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1301	2	14,14,15	0.58	0	17,19,21	0.82	1 (5%)
4	NAG	B	1307	2	14,14,15	0.26	0	17,19,21	0.45	0
4	NAG	B	1305	-	14,14,15	1.65	2 (14%)	17,19,21	1.23	3 (17%)
4	NAG	A	1207	2	14,14,15	0.27	0	17,19,21	0.42	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
4	NAG	C	1208	-	-	4/6/23/26	0/1/1/1
4	NAG	B	1302	2	-	4/6/23/26	0/1/1/1
4	NAG	A	1205	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1202	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1206	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1208	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1206	2	-	1/6/23/26	0/1/1/1
4	NAG	C	1205	2	-	1/6/23/26	0/1/1/1
4	NAG	B	1303	2	-	4/6/23/26	0/1/1/1
4	NAG	A	1203	2	-	4/6/23/26	0/1/1/1
4	NAG	B	1306	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1201	2	-	4/6/23/26	0/1/1/1
4	NAG	C	1207	2	-	2/6/23/26	0/1/1/1
4	NAG	C	1202	2	-	1/6/23/26	0/1/1/1
4	NAG	C	1204	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1209	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1203	2	-	3/6/23/26	0/1/1/1
4	NAG	B	1304	2	-	4/6/23/26	0/1/1/1
4	NAG	C	1201	-	-	4/6/23/26	0/1/1/1
4	NAG	A	1204	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1301	2	-	4/6/23/26	0/1/1/1
4	NAG	B	1307	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1305	-	-	2/6/23/26	0/1/1/1
4	NAG	A	1207	2	-	3/6/23/26	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1305	NAG	C1-C2	5.23	1.59	1.52
4	A	1202	NAG	O5-C5	4.45	1.52	1.43
4	A	1202	NAG	C3-C2	4.25	1.61	1.52
4	A	1202	NAG	C8-C7	-3.49	1.43	1.50
4	A	1202	NAG	C2-N2	-3.48	1.40	1.46
4	A	1202	NAG	O5-C1	-3.30	1.38	1.43
4	A	1202	NAG	O4-C4	3.29	1.51	1.43
4	B	1305	NAG	O5-C1	2.78	1.48	1.43
4	A	1202	NAG	C7-N2	2.22	1.41	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1301	NAG	C1-O5-C5	3.04	116.27	112.19
4	A	1202	NAG	O7-C7-C8	-2.95	116.80	122.05
4	C	1202	NAG	C1-O5-C5	2.88	116.05	112.19
4	A	1201	NAG	C1-O5-C5	2.75	115.87	112.19
4	B	1305	NAG	O5-C5-C4	-2.72	104.20	110.83
4	B	1305	NAG	C3-C4-C5	-2.64	105.44	110.23
4	B	1305	NAG	C1-O5-C5	2.49	115.52	112.19
4	A	1202	NAG	O7-C7-N2	2.45	126.31	121.98
4	C	1208	NAG	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1204	NAG	C4-C5-C6-O6
4	A	1209	NAG	C4-C5-C6-O6
4	B	1301	NAG	C4-C5-C6-O6
4	A	1203	NAG	C4-C5-C6-O6
4	A	1205	NAG	O5-C5-C6-O6
4	C	1204	NAG	O5-C5-C6-O6
4	B	1301	NAG	O5-C5-C6-O6
4	A	1209	NAG	O5-C5-C6-O6
4	B	1302	NAG	C4-C5-C6-O6
4	C	1203	NAG	C4-C5-C6-O6
4	C	1207	NAG	C4-C5-C6-O6
4	C	1208	NAG	O5-C5-C6-O6
4	A	1208	NAG	C4-C5-C6-O6
4	B	1306	NAG	O5-C5-C6-O6
4	A	1203	NAG	O5-C5-C6-O6
4	B	1305	NAG	O5-C5-C6-O6
4	B	1303	NAG	O5-C5-C6-O6
4	B	1306	NAG	C4-C5-C6-O6
4	B	1302	NAG	O5-C5-C6-O6
4	B	1304	NAG	C4-C5-C6-O6
4	C	1203	NAG	O5-C5-C6-O6
4	A	1205	NAG	C4-C5-C6-O6
4	C	1201	NAG	O5-C5-C6-O6
4	C	1207	NAG	O5-C5-C6-O6
4	A	1201	NAG	O5-C5-C6-O6
4	A	1208	NAG	O5-C5-C6-O6
4	C	1201	NAG	C4-C5-C6-O6
4	B	1305	NAG	C4-C5-C6-O6
4	C	1208	NAG	C4-C5-C6-O6
4	A	1201	NAG	C4-C5-C6-O6
4	B	1304	NAG	O5-C5-C6-O6
4	B	1307	NAG	C8-C7-N2-C2
4	B	1307	NAG	O7-C7-N2-C2
4	C	1208	NAG	C8-C7-N2-C2
4	C	1208	NAG	O7-C7-N2-C2
4	A	1206	NAG	O5-C5-C6-O6
4	A	1204	NAG	O5-C5-C6-O6
4	A	1204	NAG	C4-C5-C6-O6
4	C	1205	NAG	O5-C5-C6-O6
4	A	1207	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	C	1202	NAG	O5-C5-C6-O6
4	B	1303	NAG	C4-C5-C6-O6
4	B	1302	NAG	C1-C2-N2-C7
4	B	1303	NAG	C1-C2-N2-C7
4	B	1304	NAG	C1-C2-N2-C7
4	C	1201	NAG	C1-C2-N2-C7
4	A	1207	NAG	C1-C2-N2-C7
4	B	1301	NAG	C3-C2-N2-C7
4	B	1304	NAG	C3-C2-N2-C7
4	C	1201	NAG	C3-C2-N2-C7
4	C	1206	NAG	C3-C2-N2-C7
4	A	1201	NAG	C3-C2-N2-C7
4	A	1203	NAG	C3-C2-N2-C7
4	A	1207	NAG	C3-C2-N2-C7
4	B	1301	NAG	C1-C2-N2-C7
4	C	1206	NAG	C1-C2-N2-C7
4	A	1201	NAG	C1-C2-N2-C7
4	A	1203	NAG	C1-C2-N2-C7
4	B	1302	NAG	C3-C2-N2-C7
4	B	1303	NAG	C3-C2-N2-C7
4	C	1203	NAG	C3-C2-N2-C7
4	A	1209	NAG	C3-C2-N2-C7

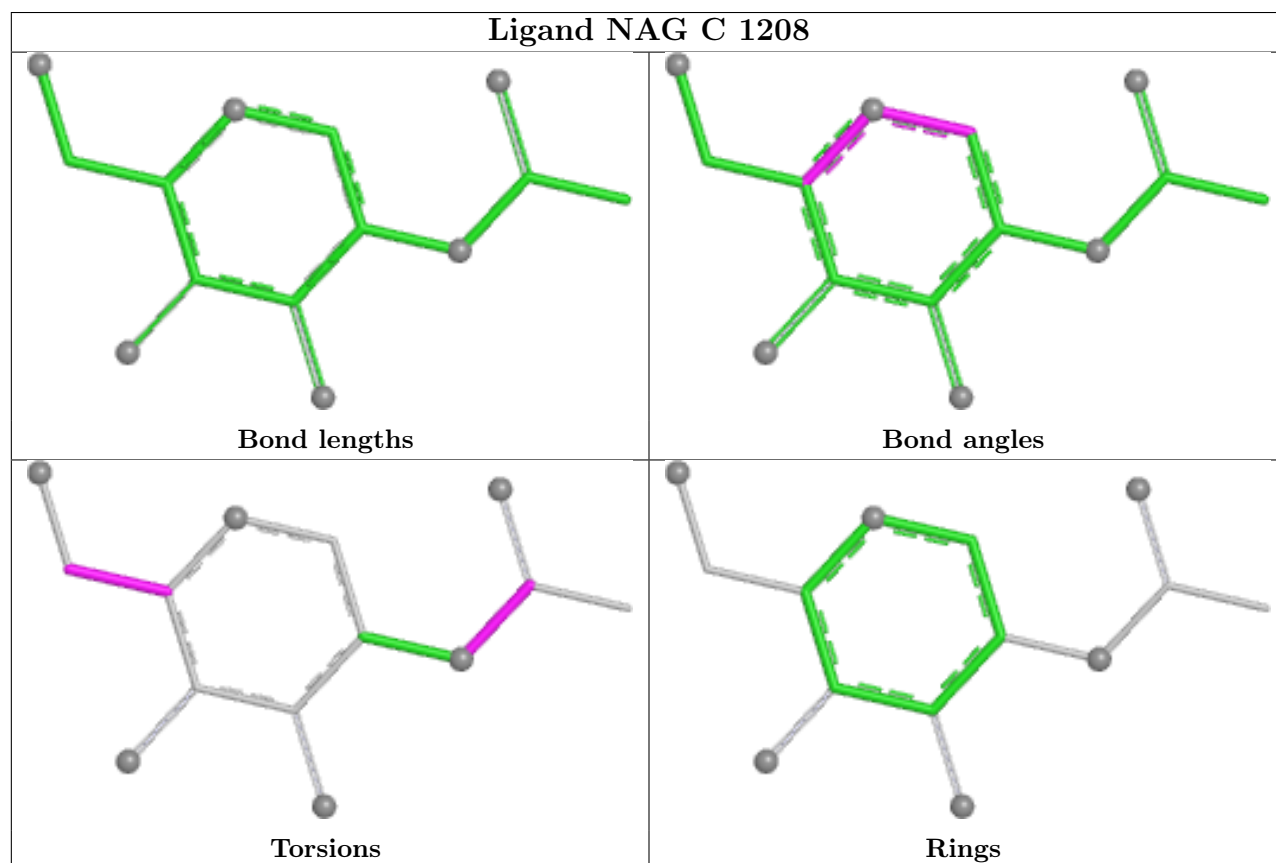
There are no ring outliers.

11 monomers are involved in 34 short contacts:

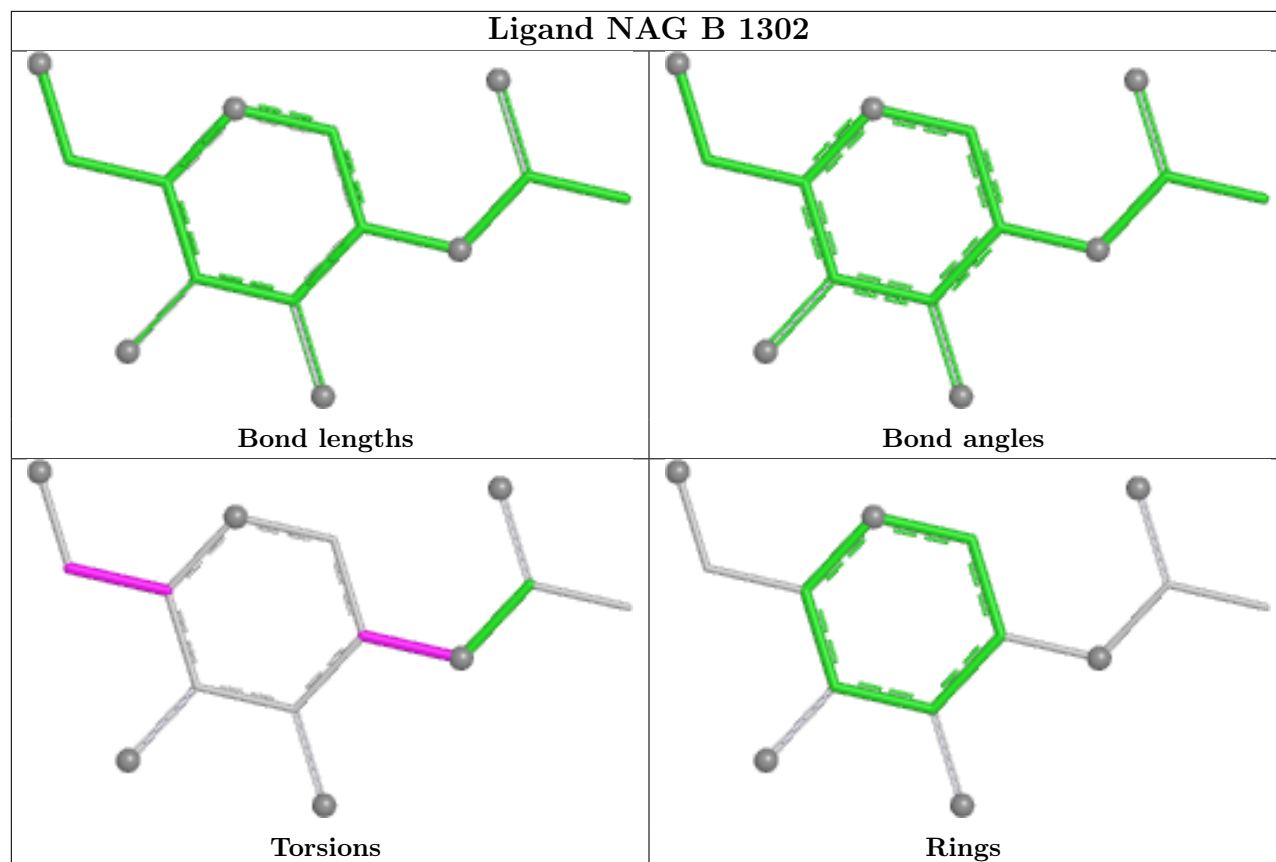
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1208	NAG	3	0
4	A	1202	NAG	5	0
4	C	1206	NAG	6	0
4	C	1205	NAG	1	0
4	B	1303	NAG	1	0
4	B	1304	NAG	1	0
4	C	1201	NAG	9	0
4	A	1204	NAG	3	0
4	B	1301	NAG	1	0
4	B	1307	NAG	3	0
4	A	1207	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

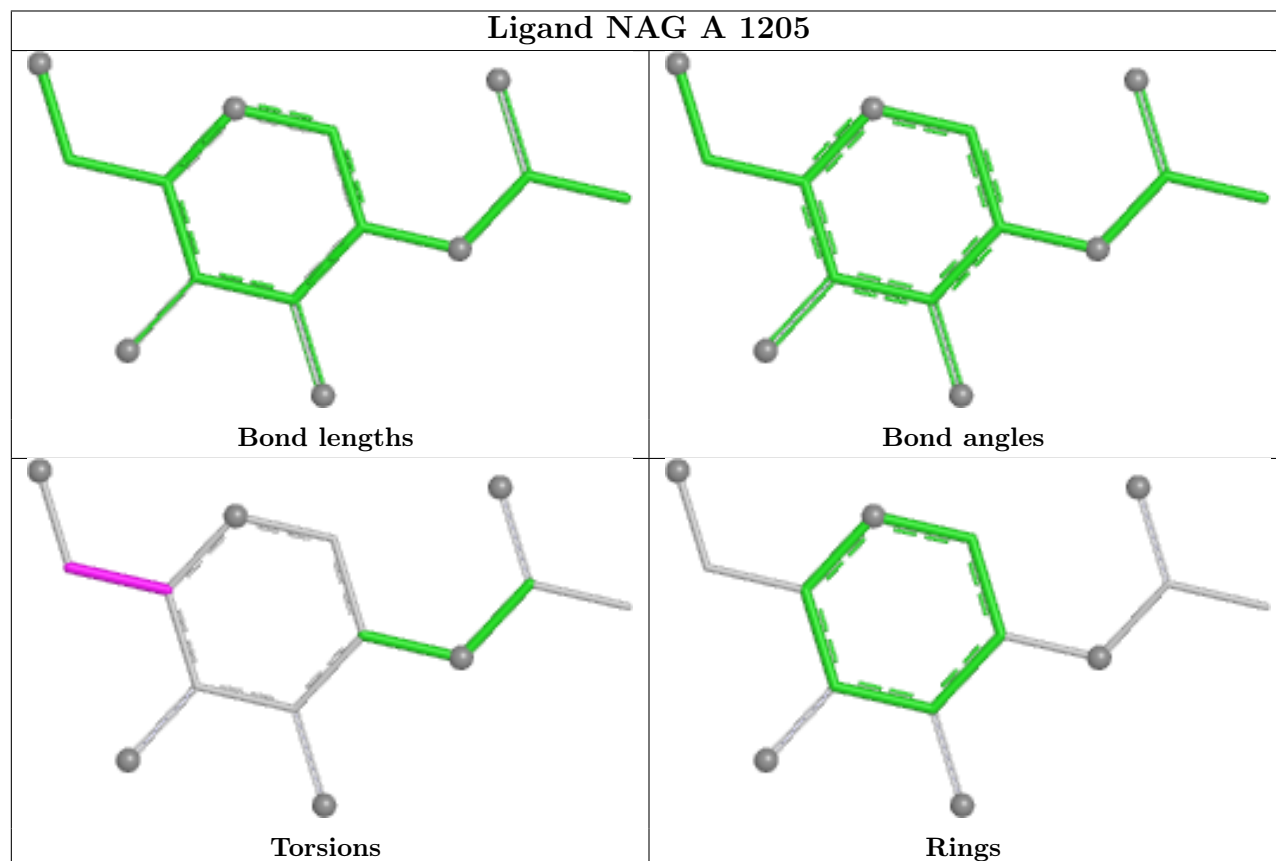
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



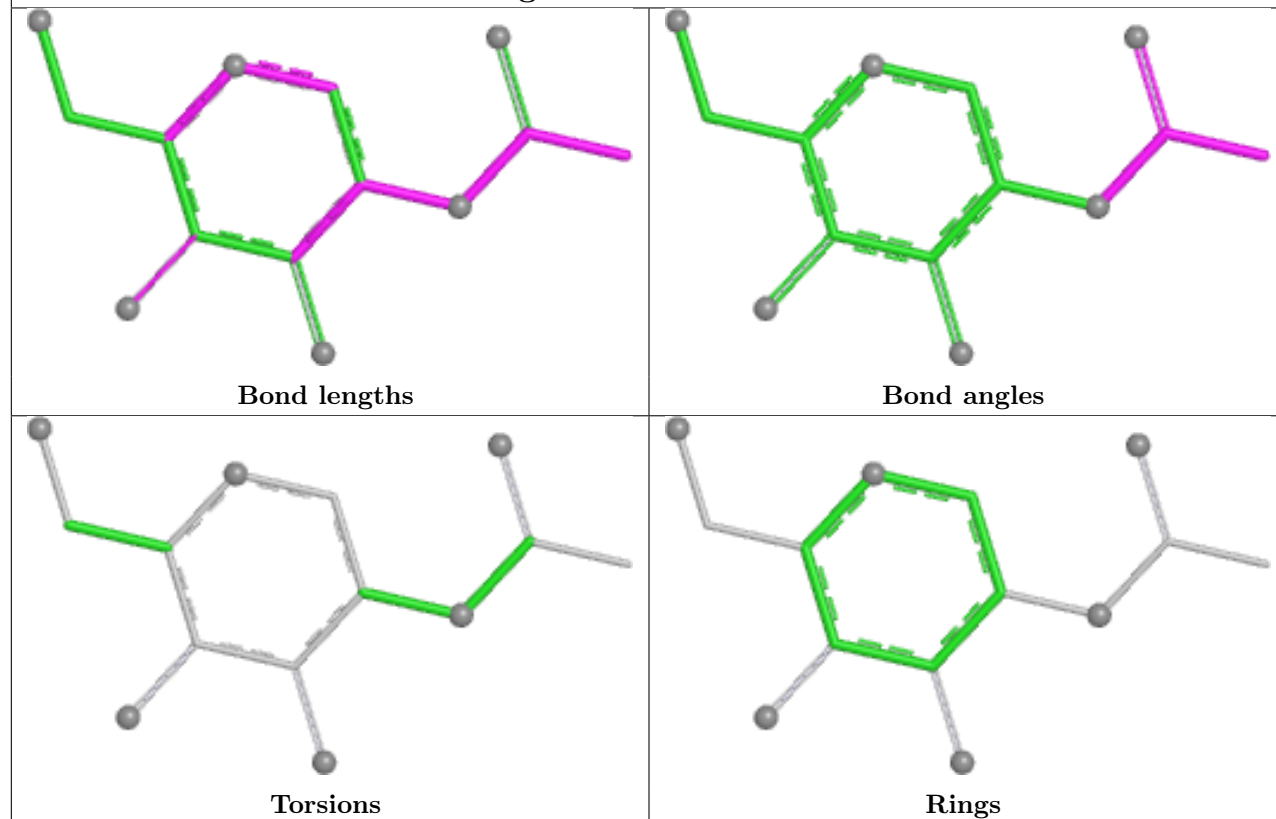
Ligand NAG B 1302



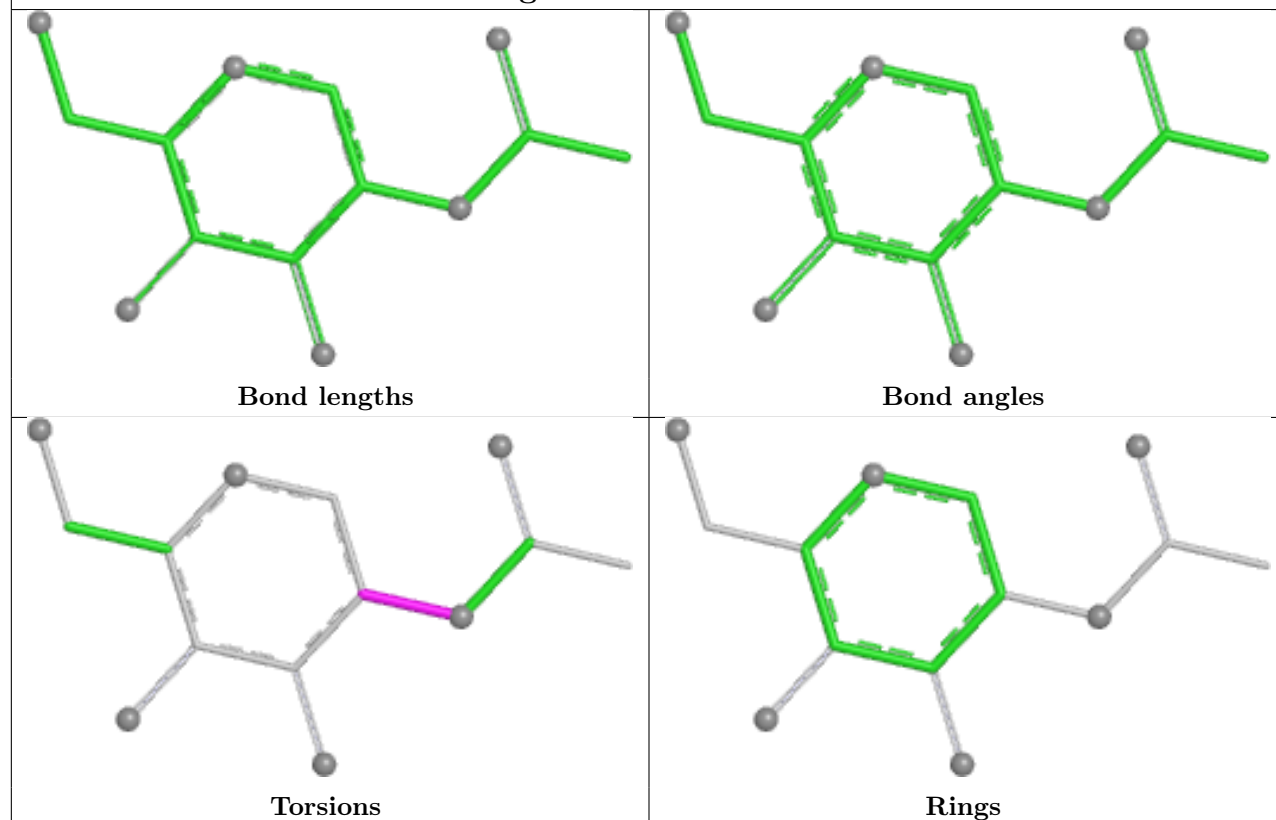
Ligand NAG A 1205

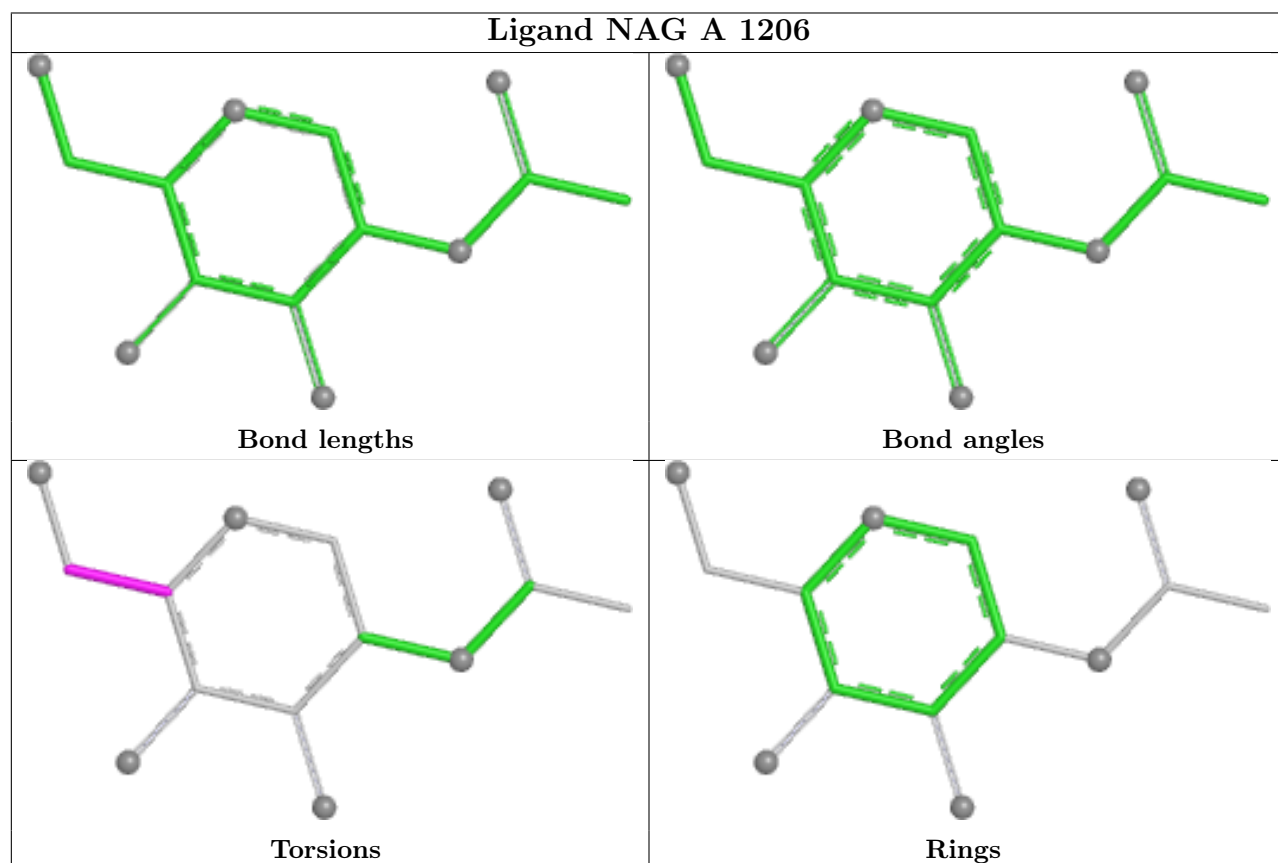
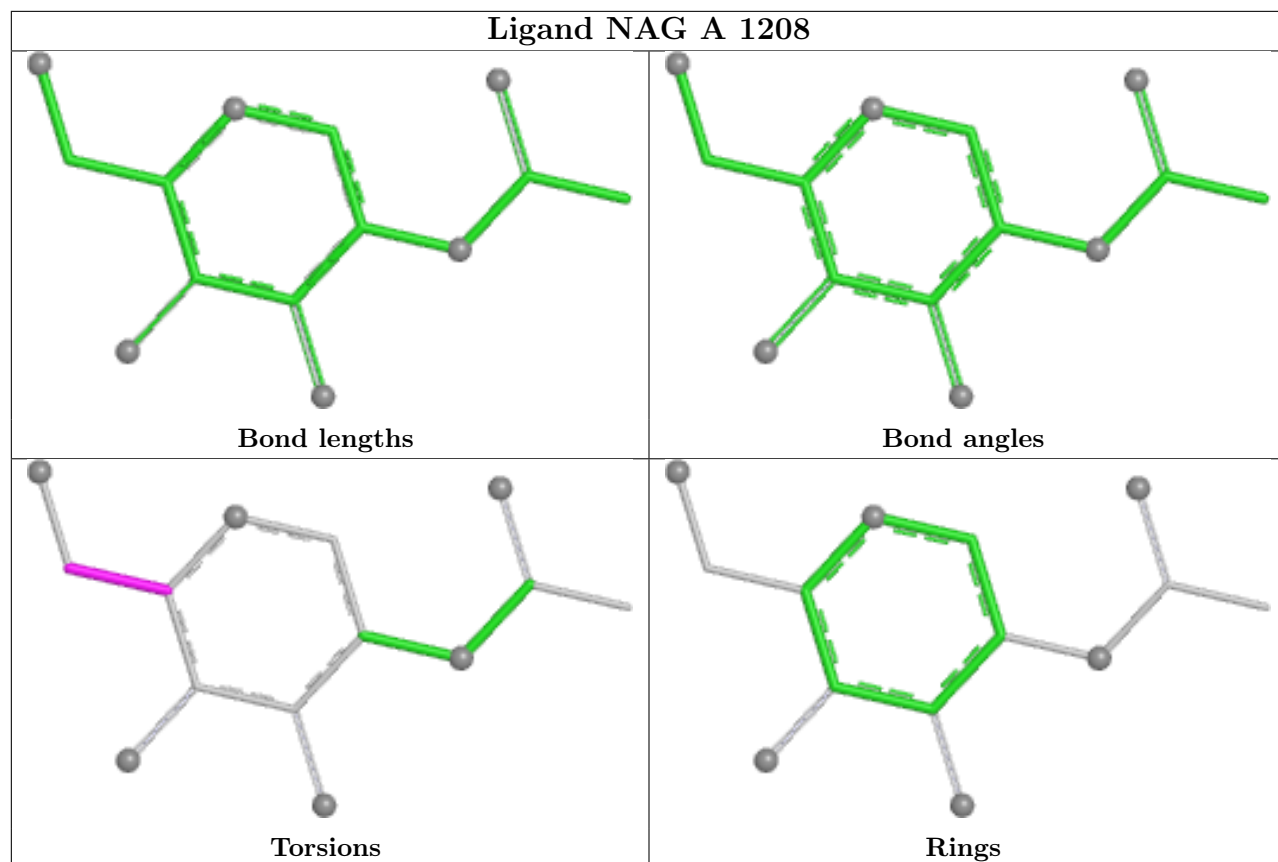


Ligand NAG A 1202

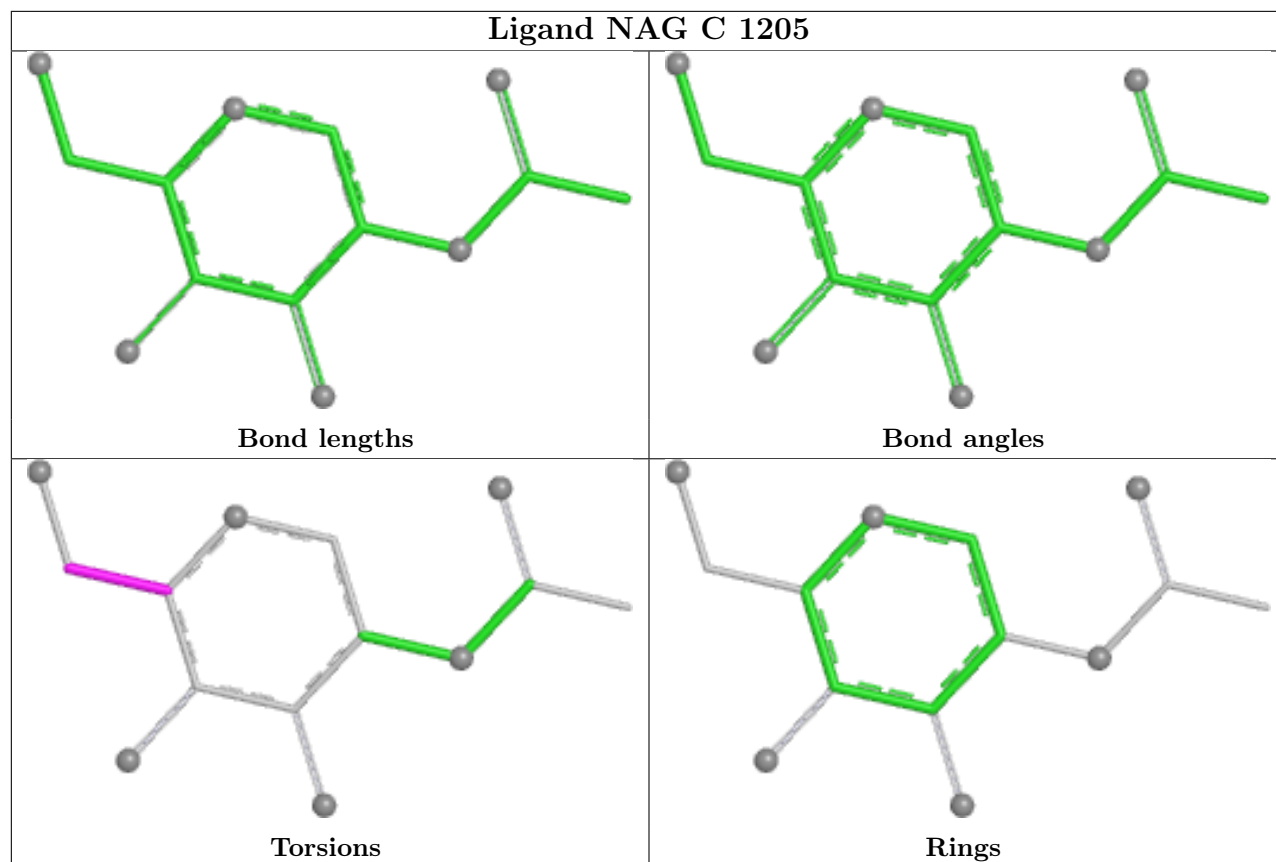


Ligand NAG C 1206

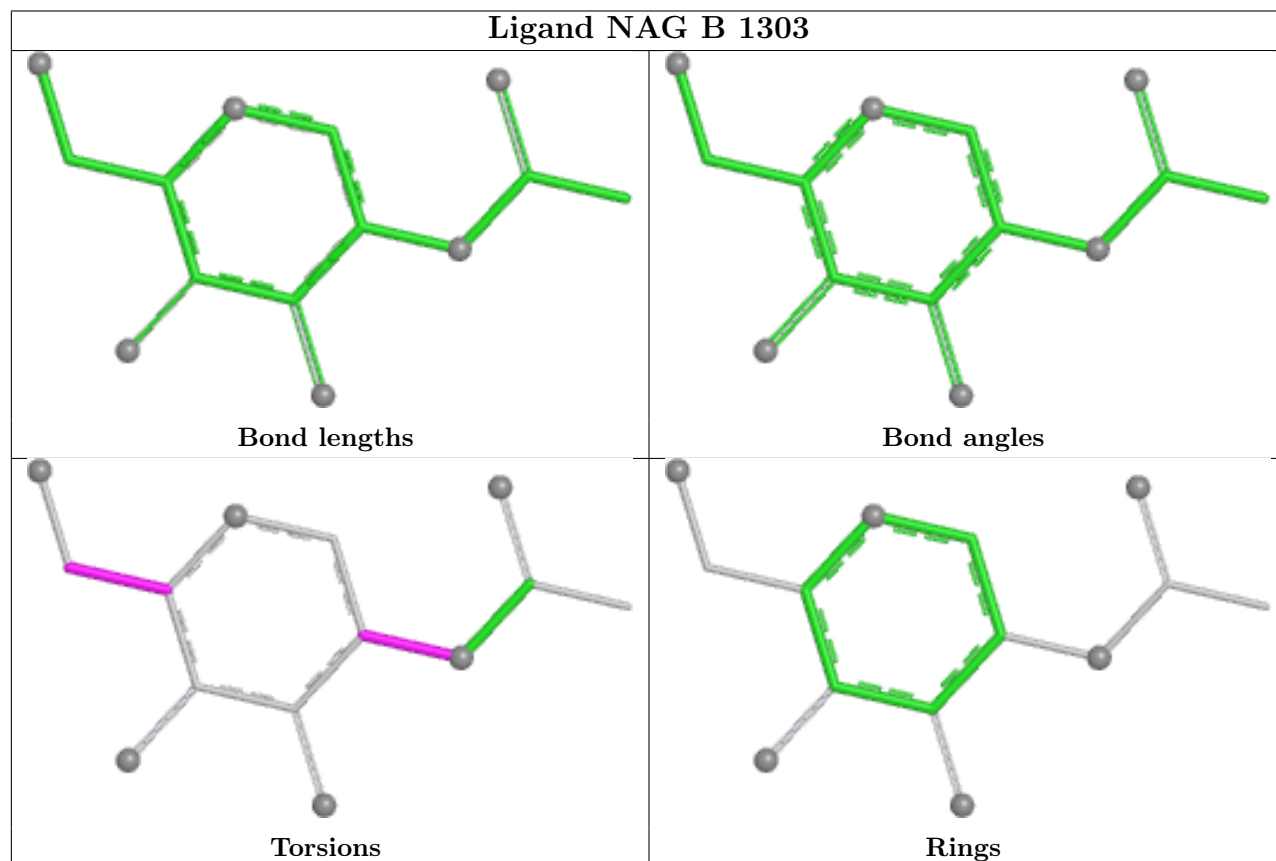




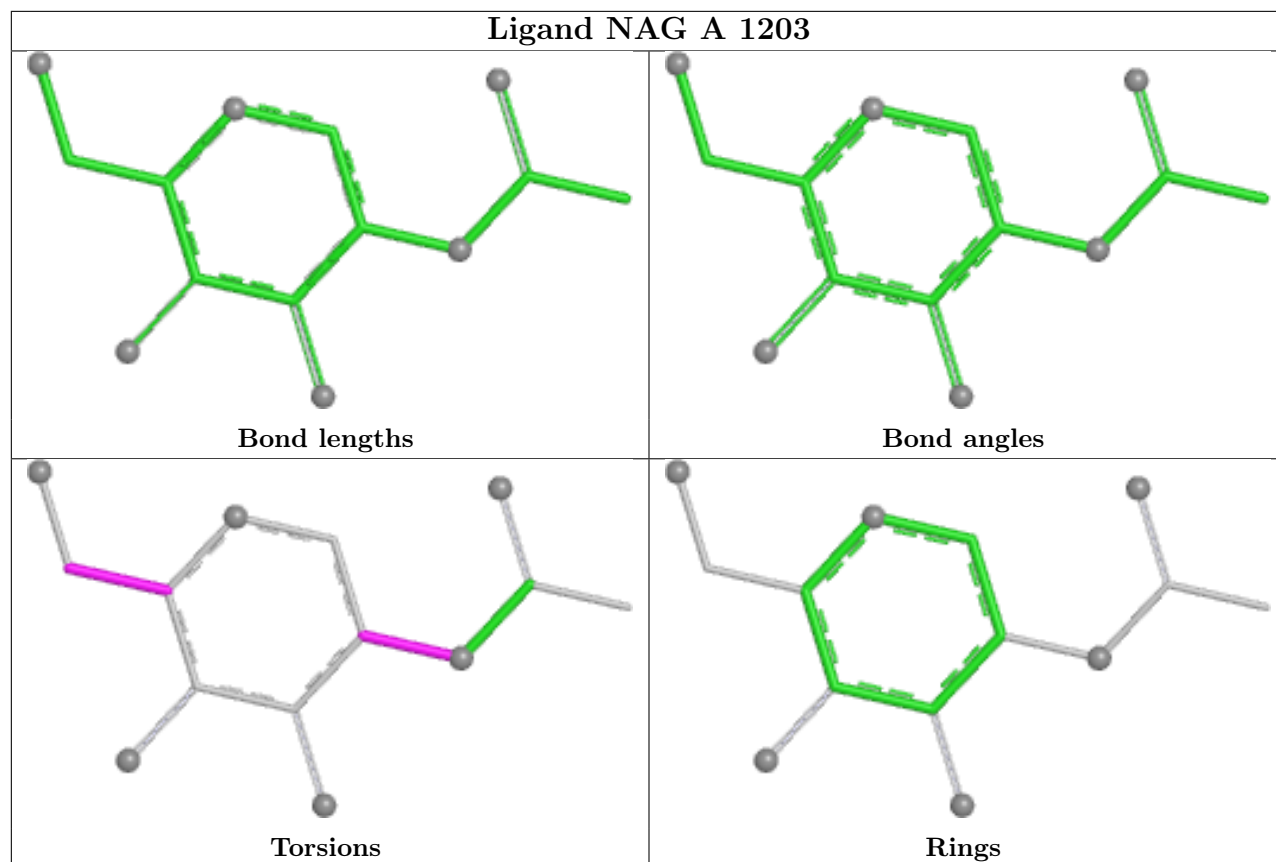
Ligand NAG C 1205



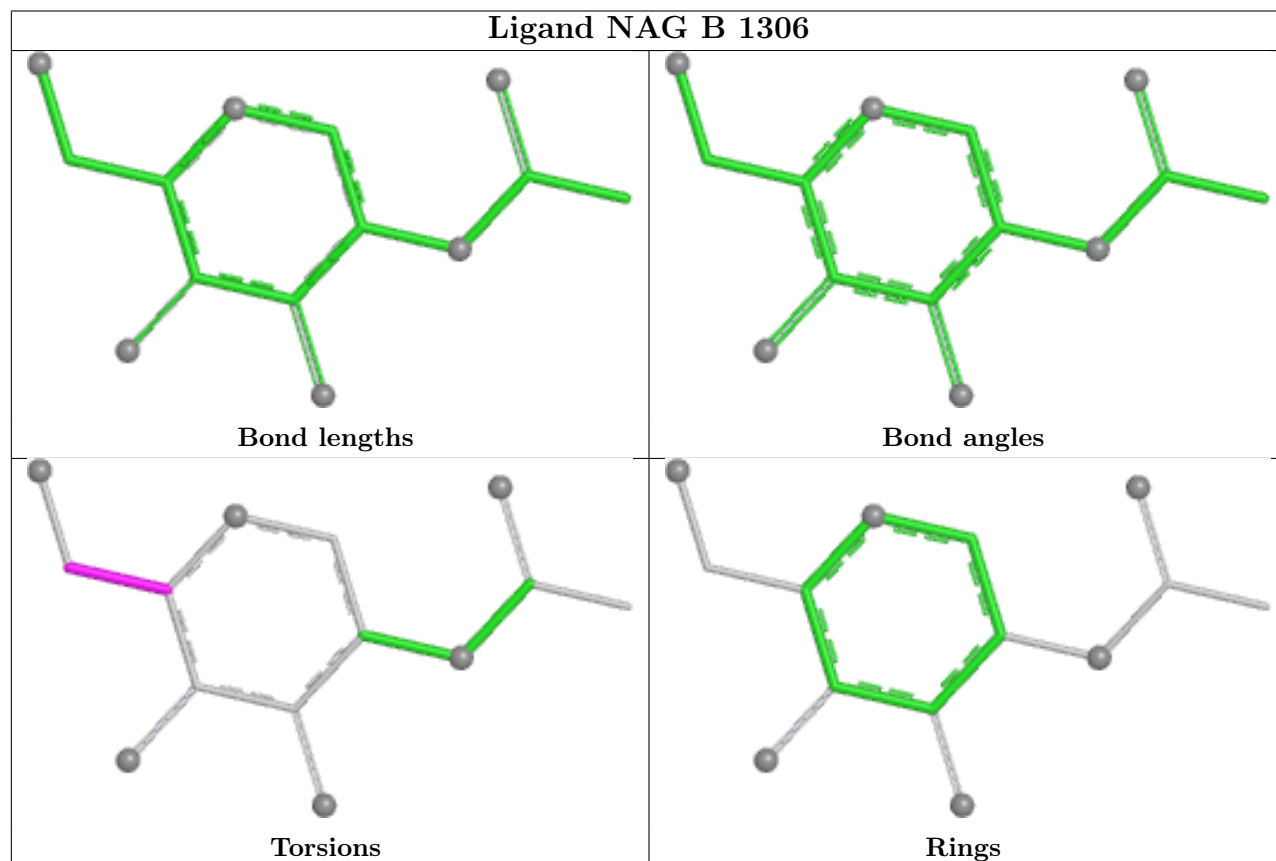
Ligand NAG B 1303



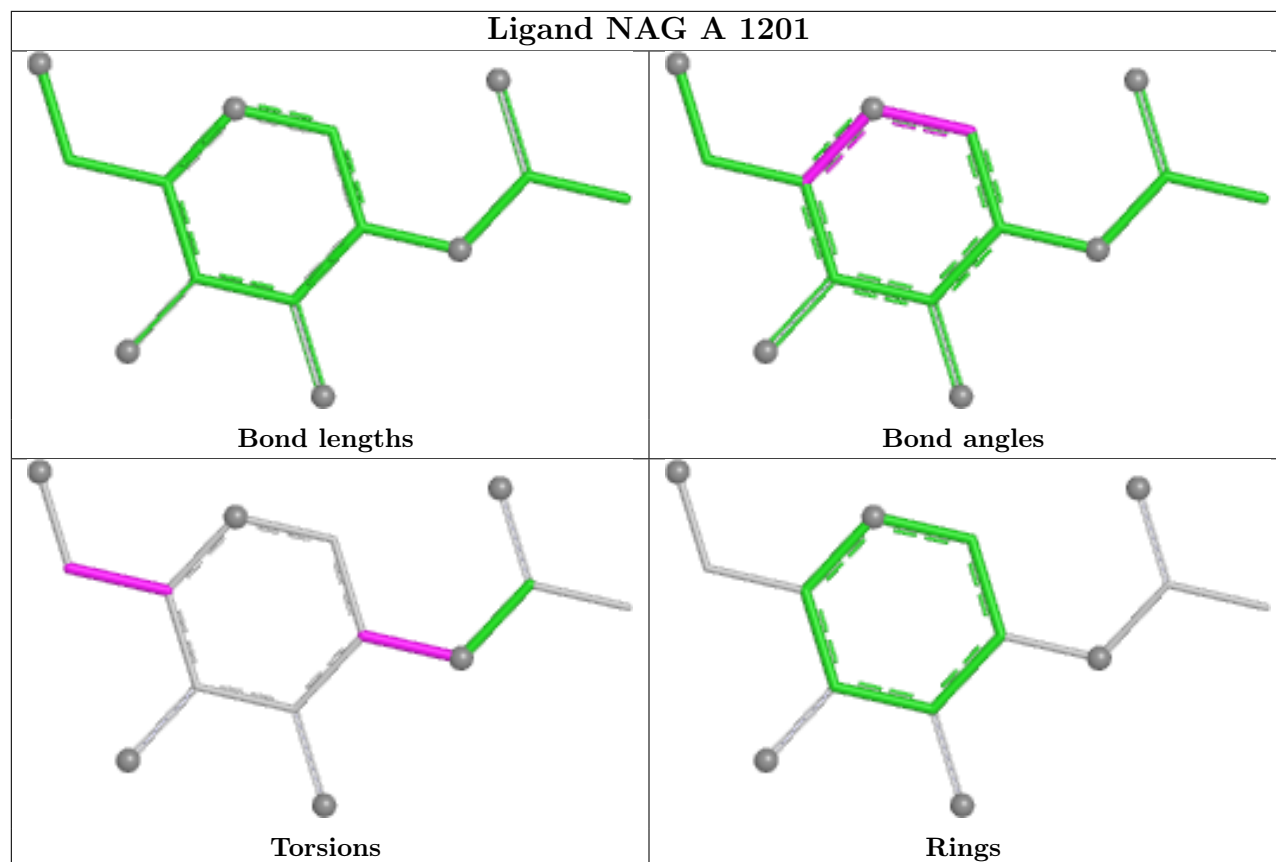
Ligand NAG A 1203



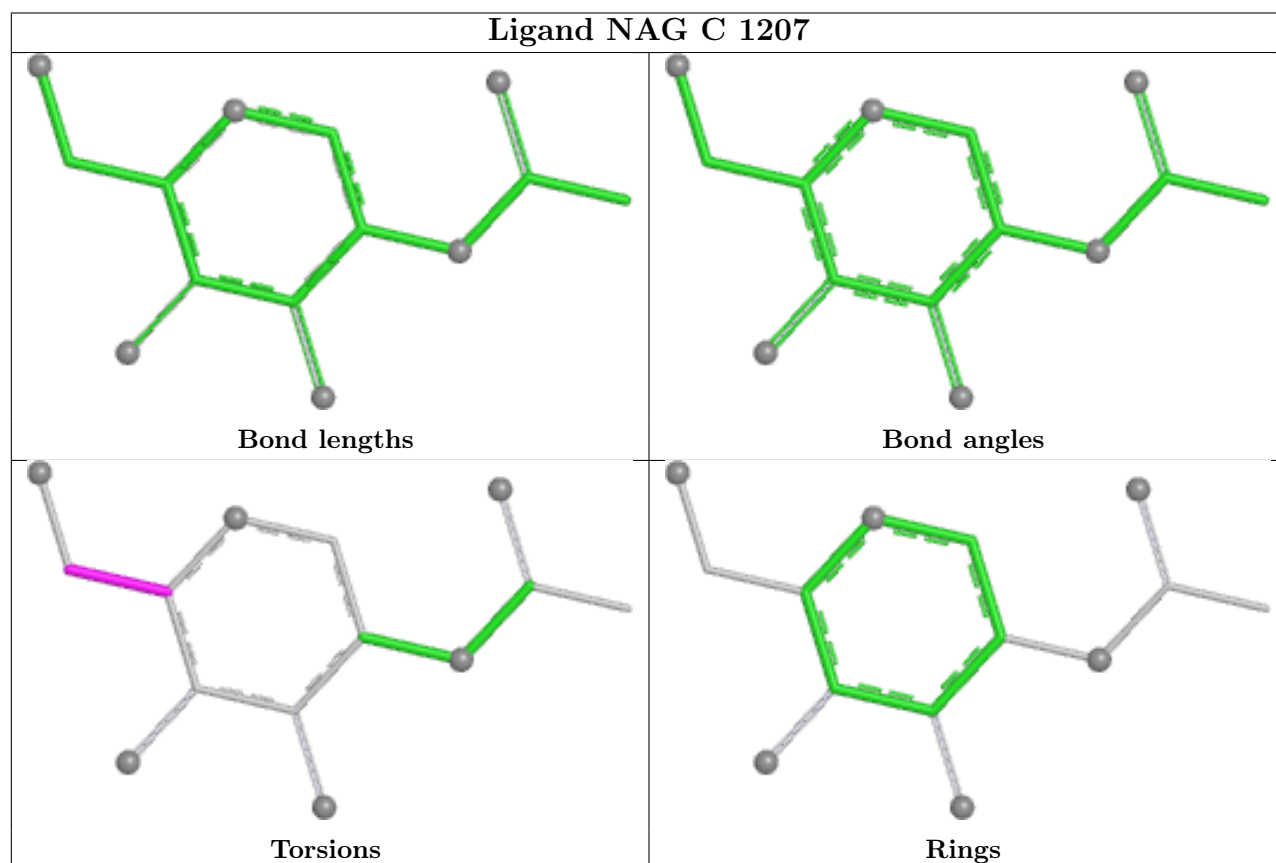
Ligand NAG B 1306

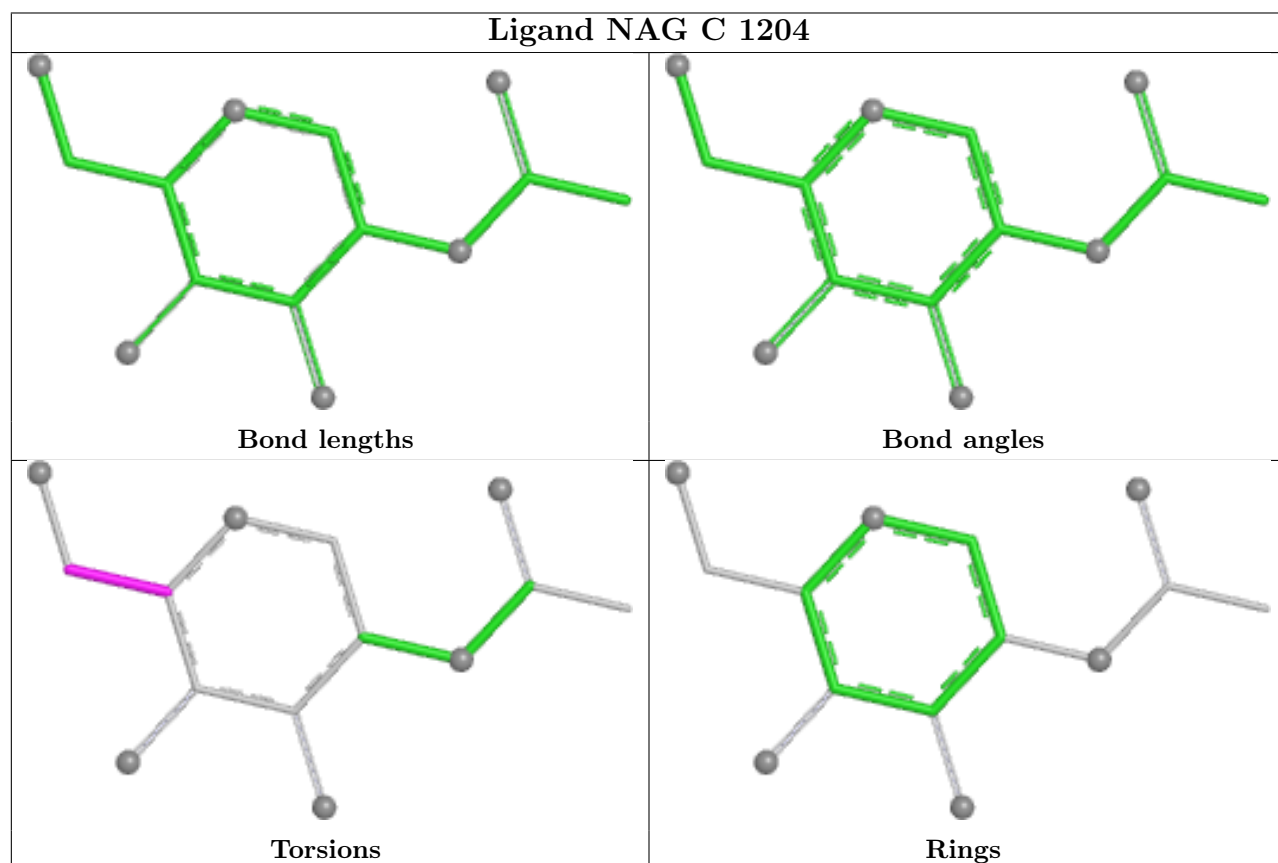
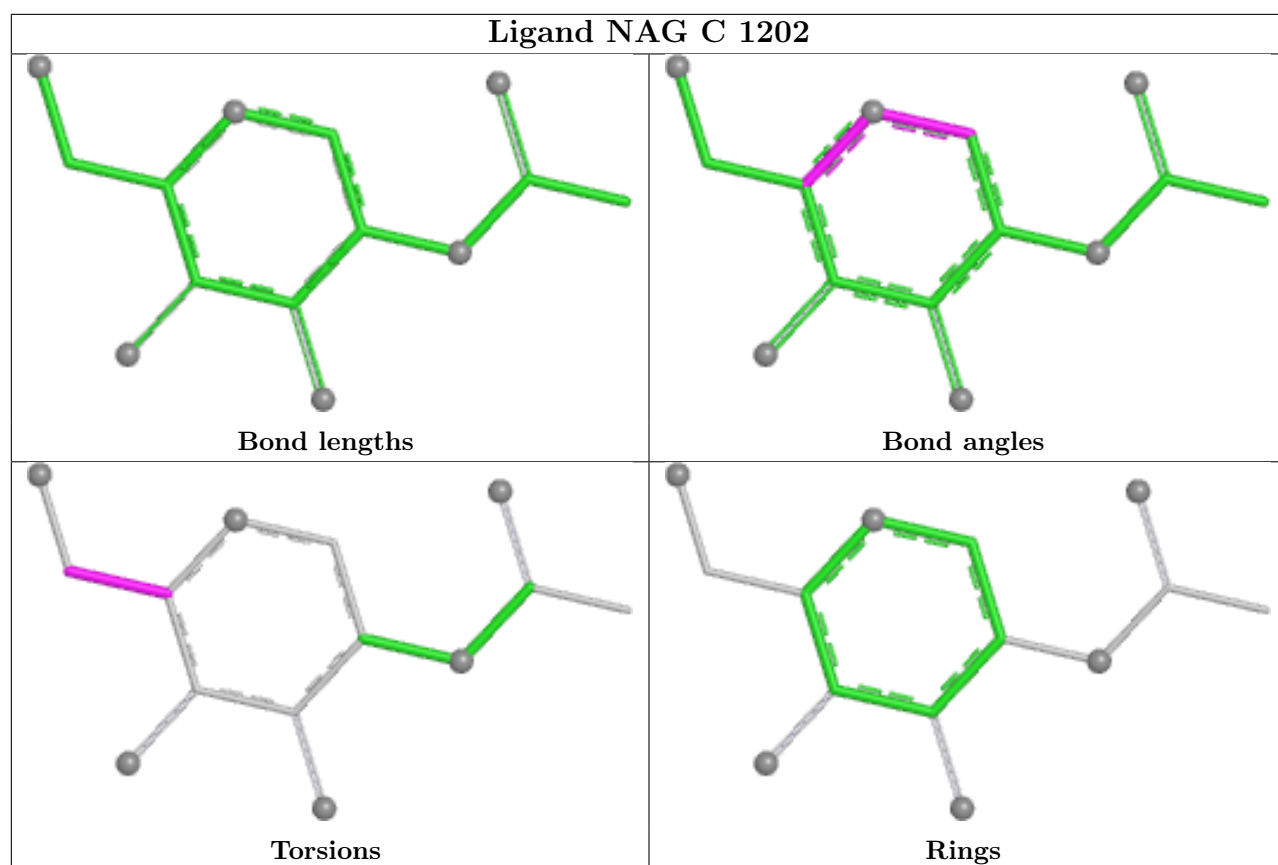


Ligand NAG A 1201

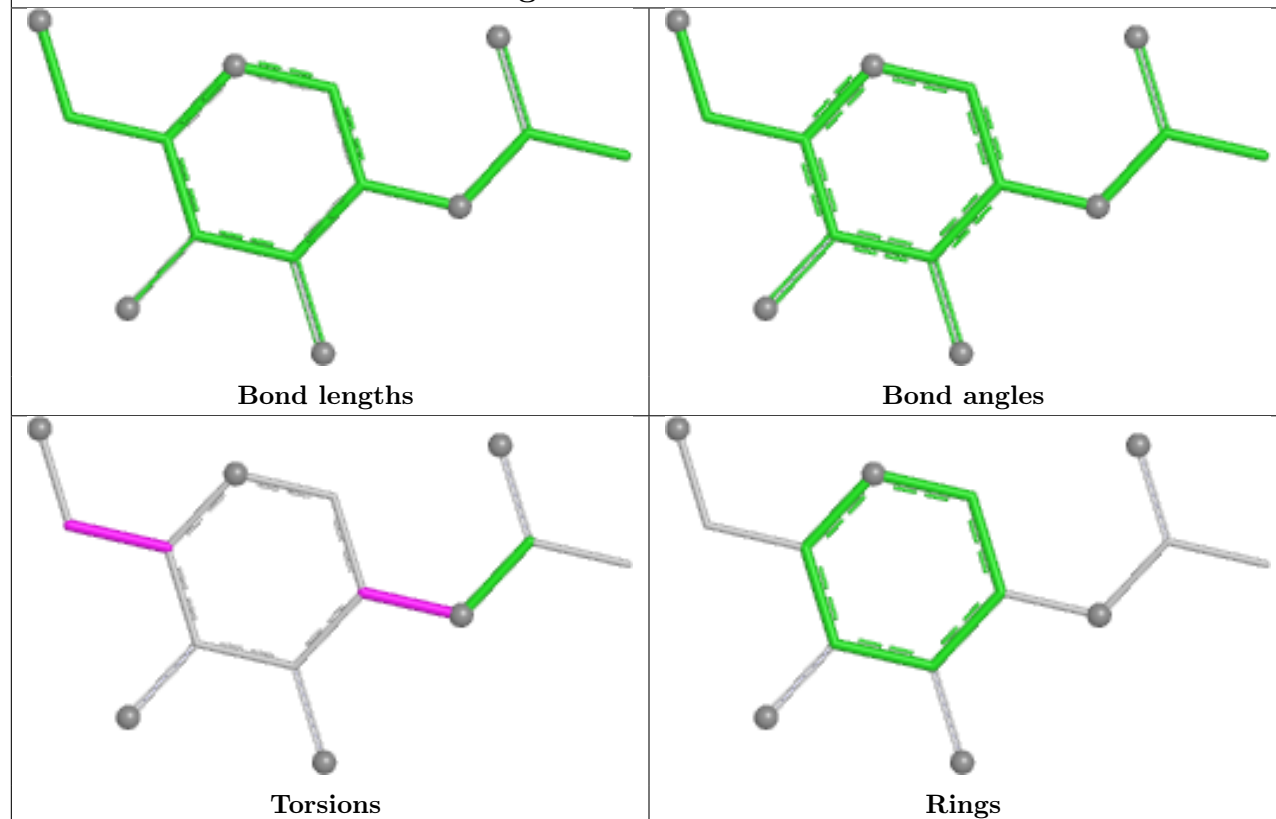


Ligand NAG C 1207

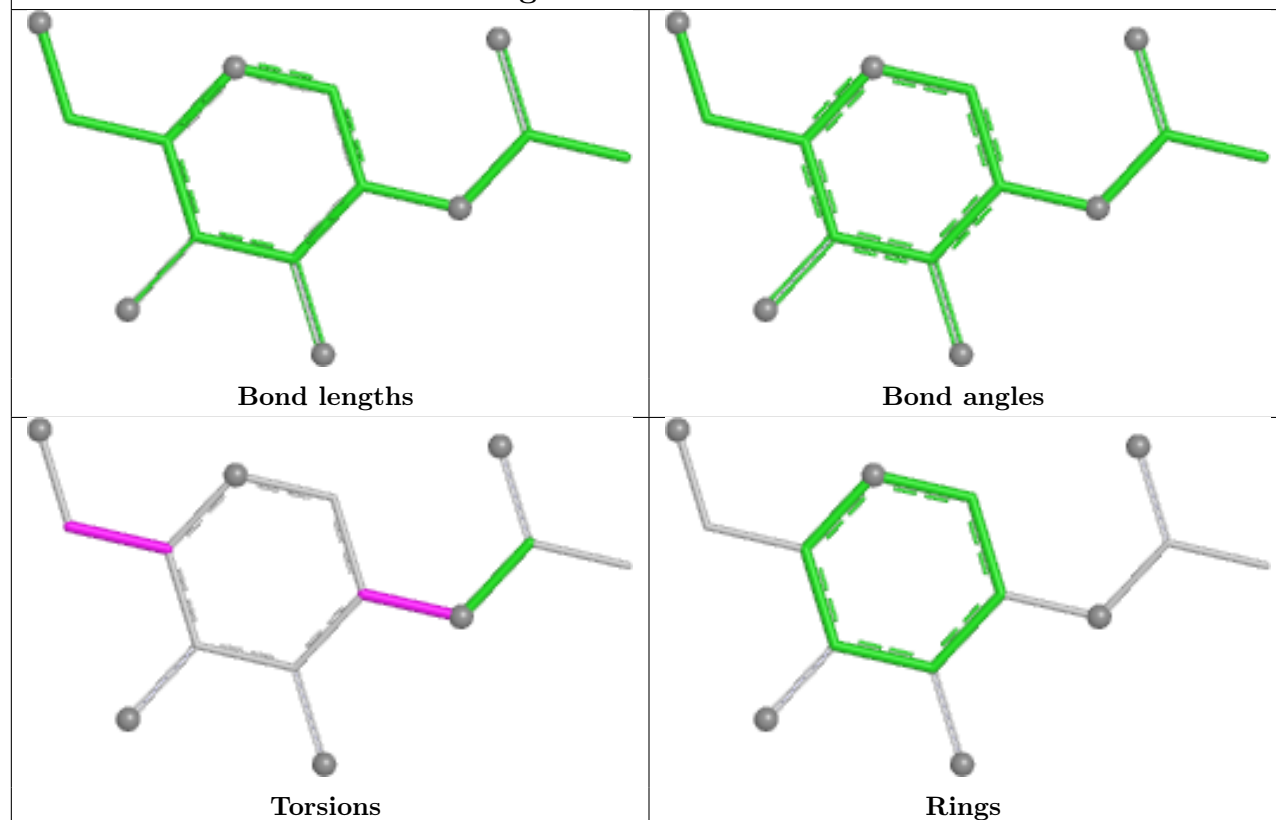




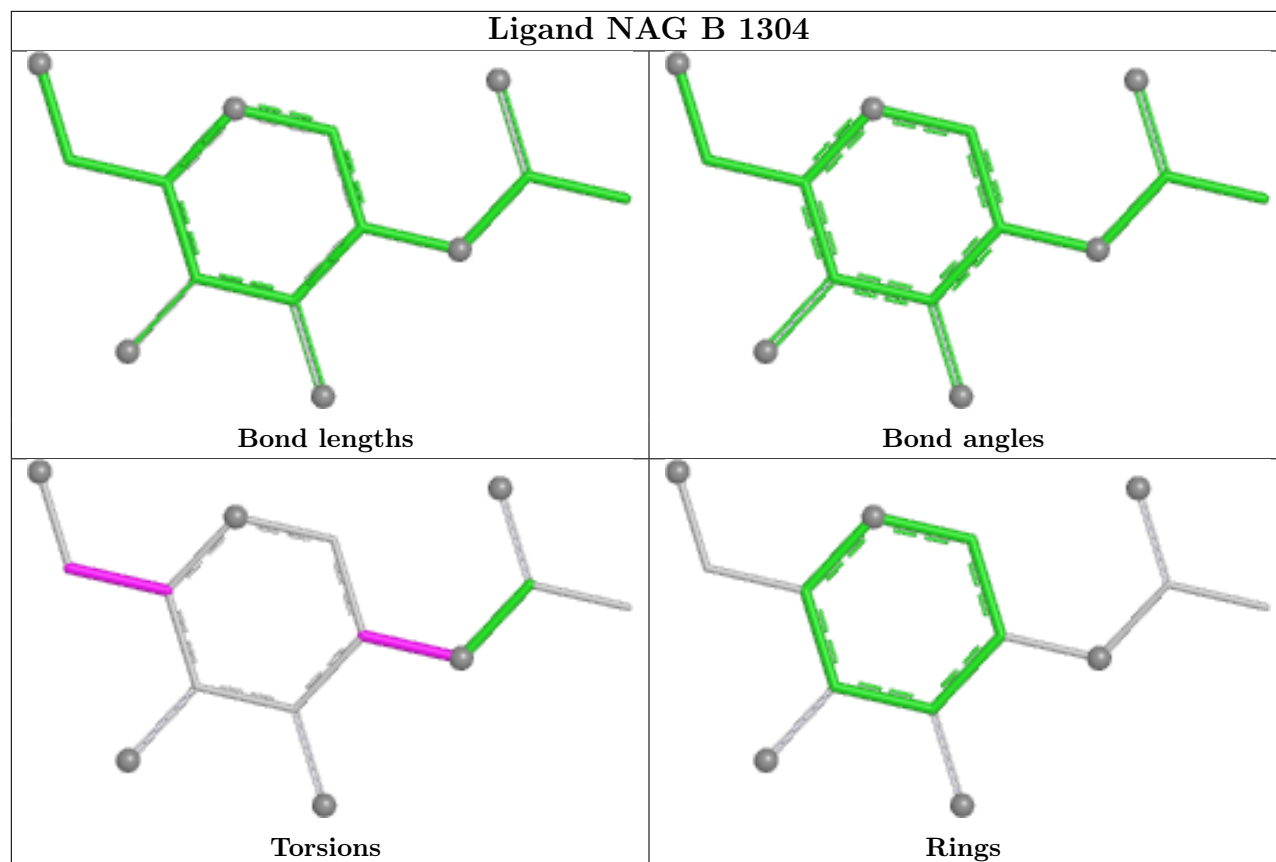
Ligand NAG A 1209



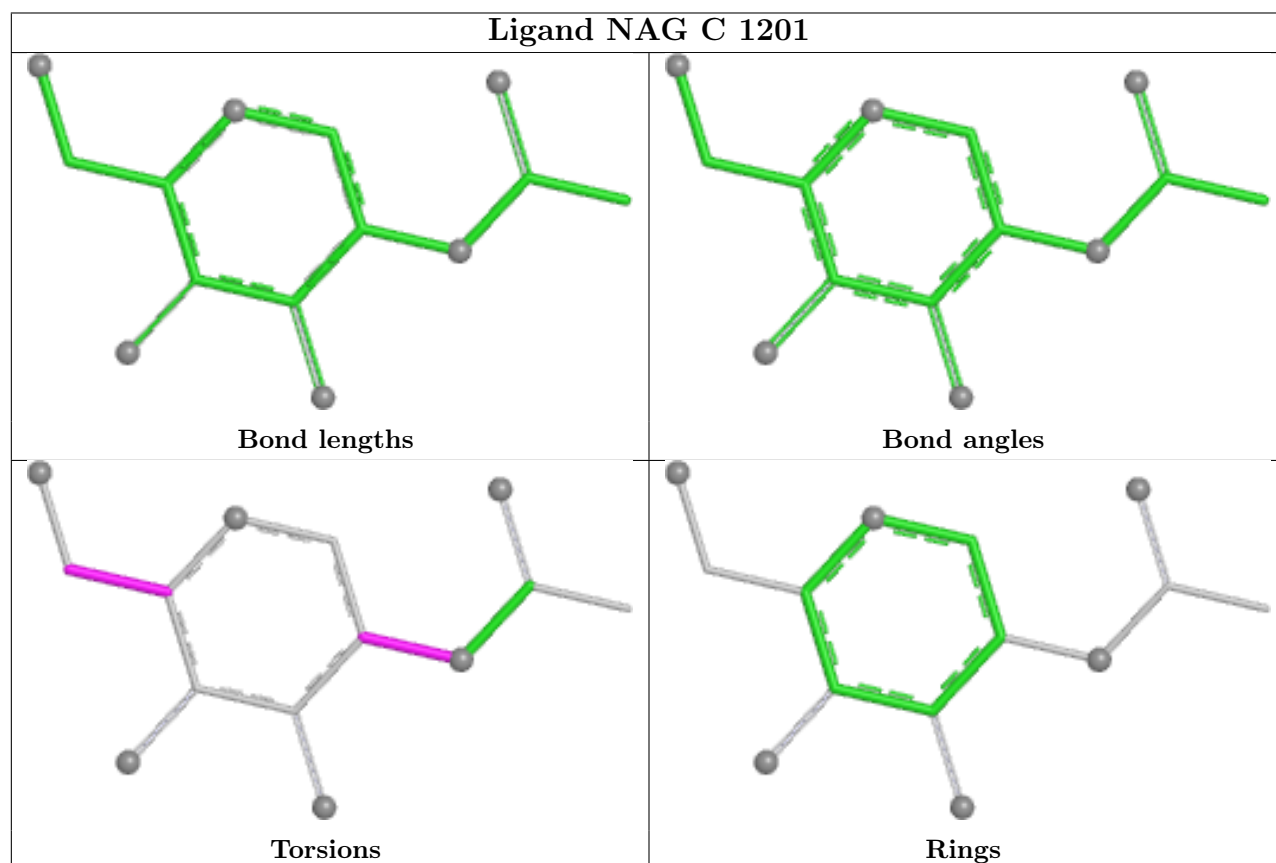
Ligand NAG C 1203



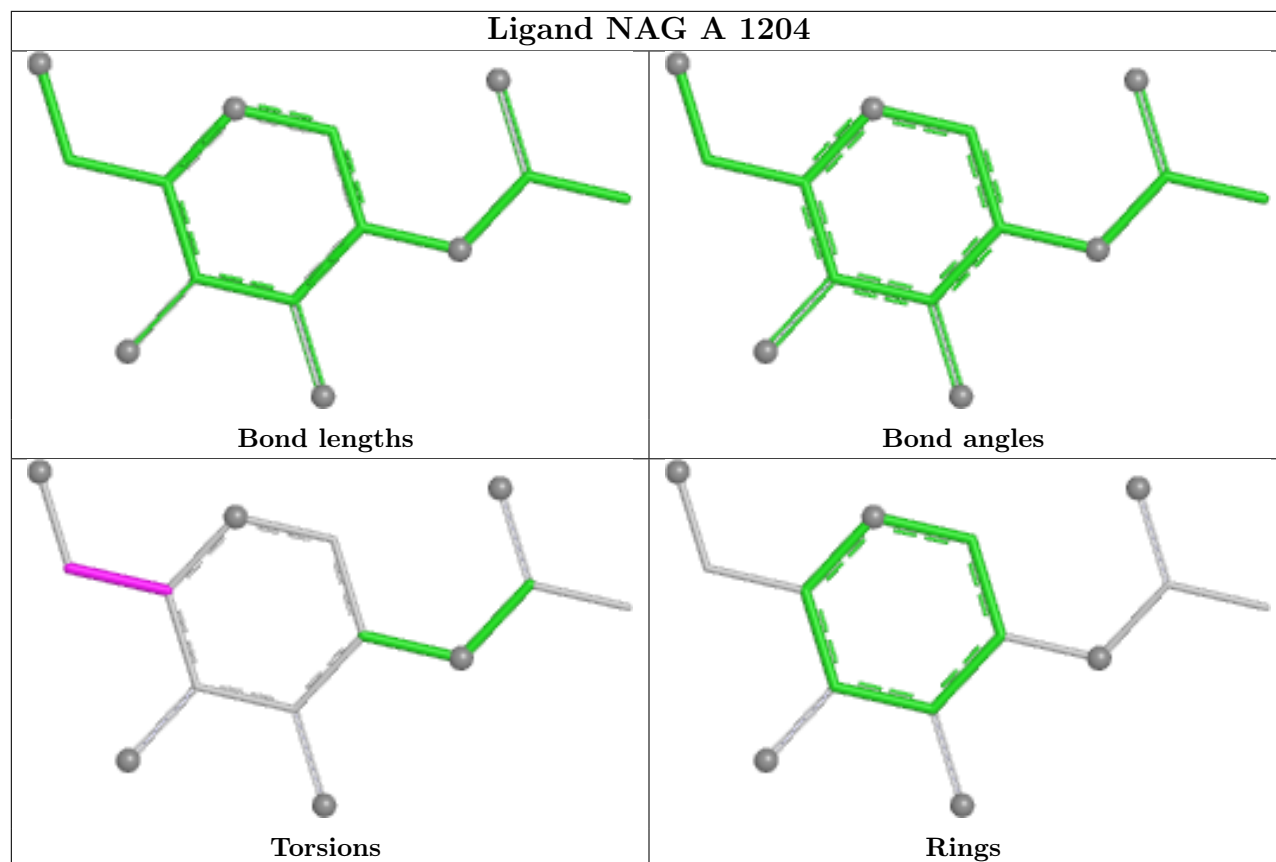
Ligand NAG B 1304



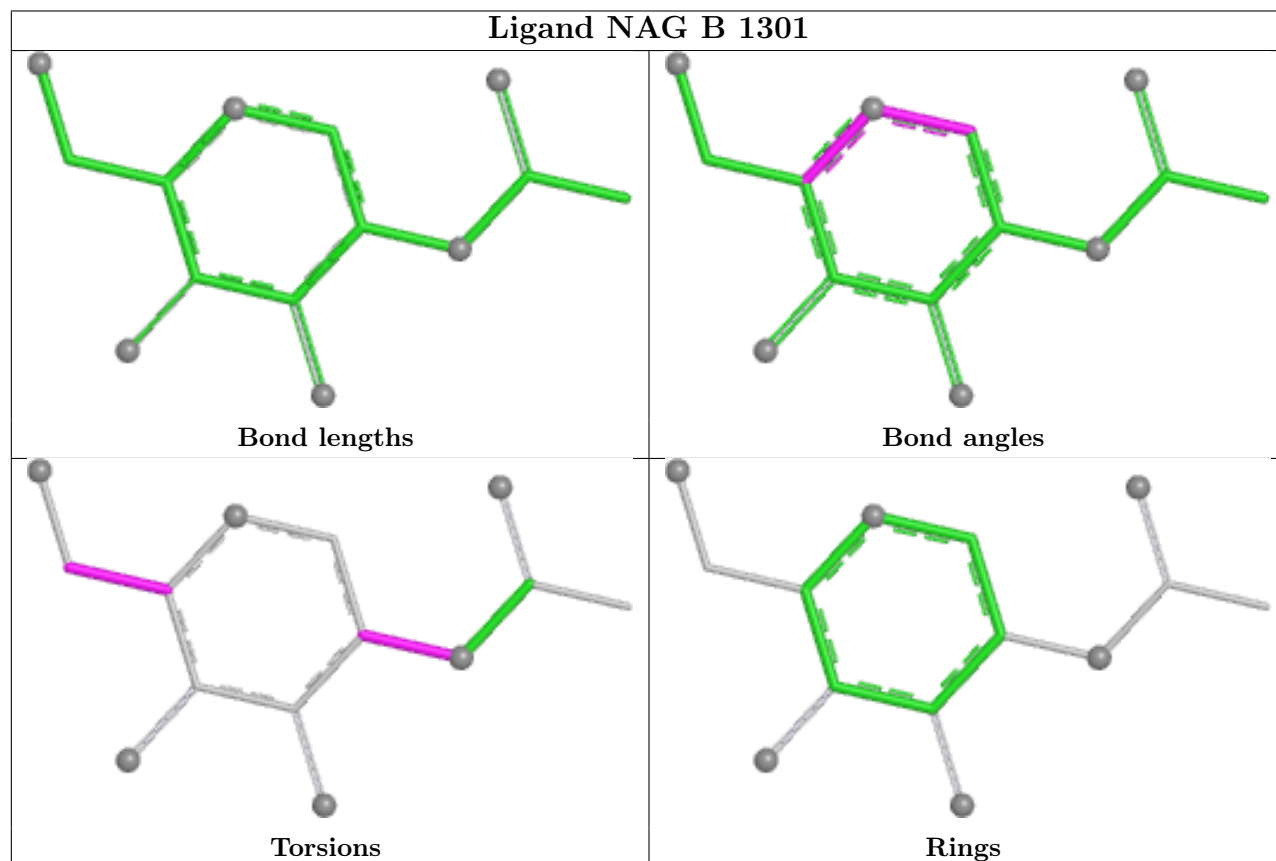
Ligand NAG C 1201



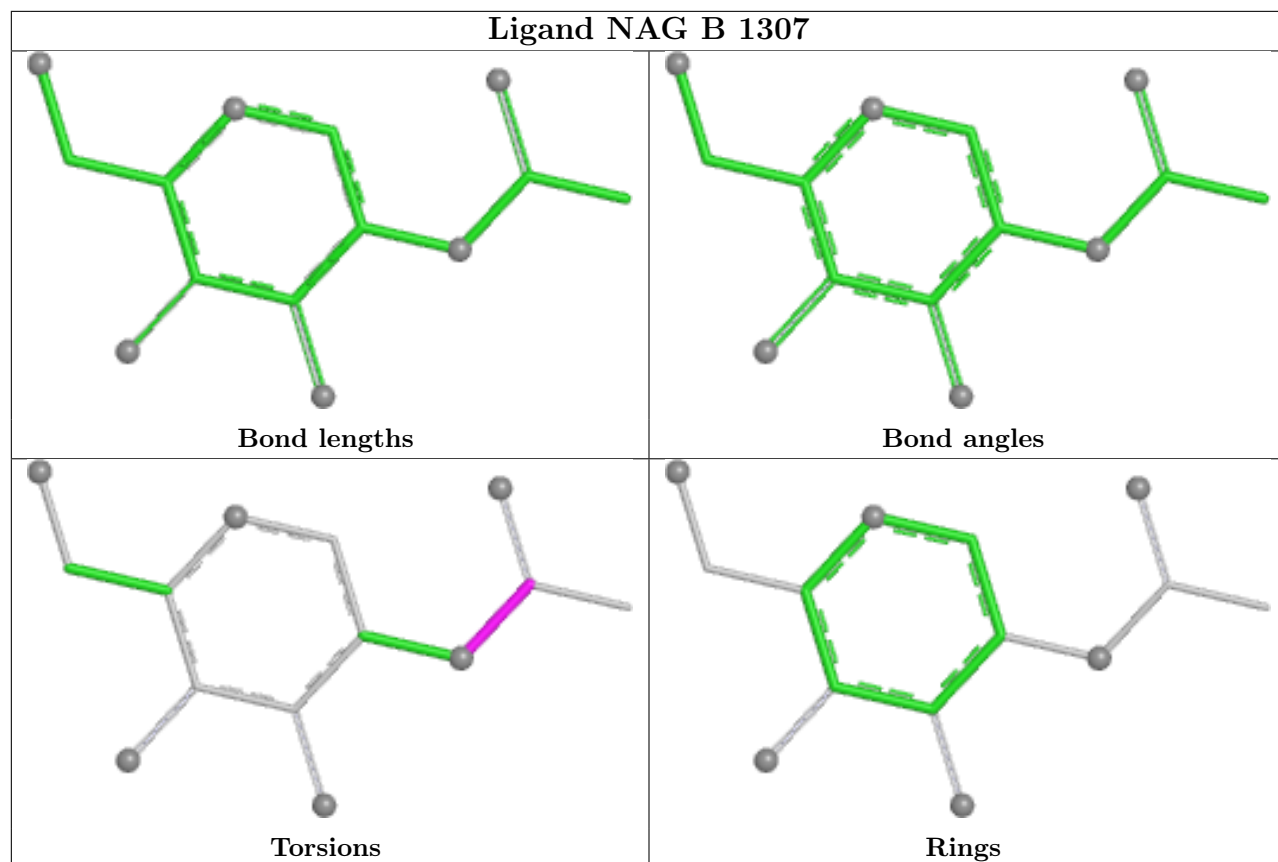
Ligand NAG A 1204



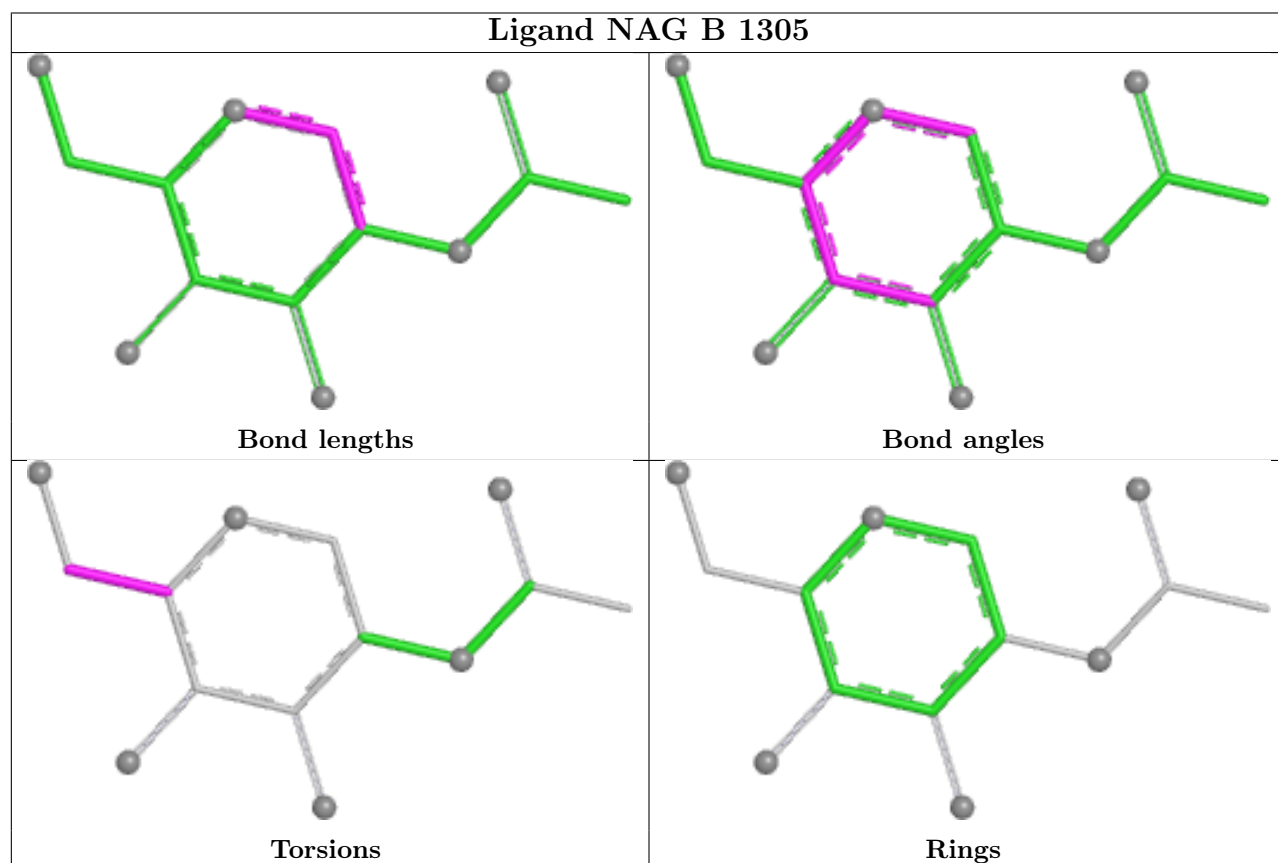
Ligand NAG B 1301

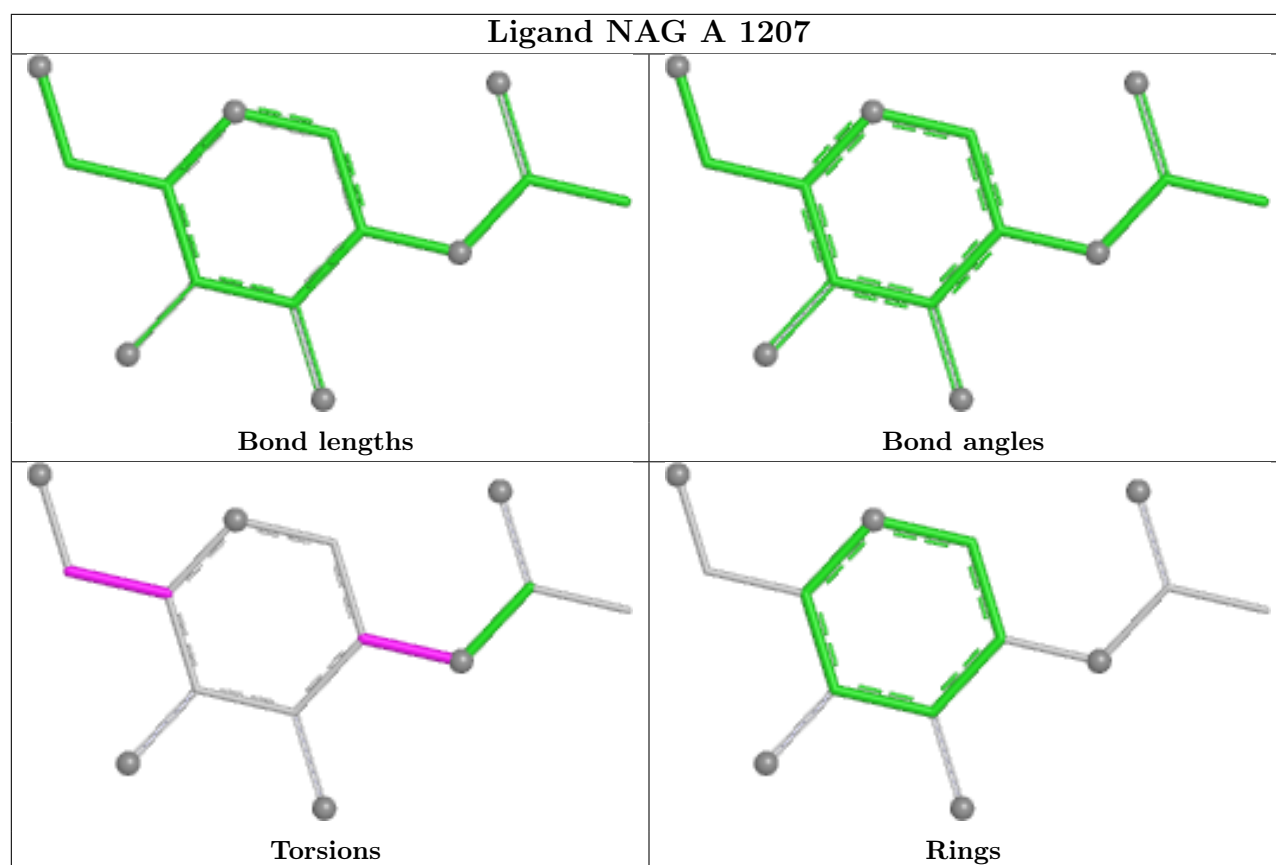


Ligand NAG B 1307



Ligand NAG B 1305





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.

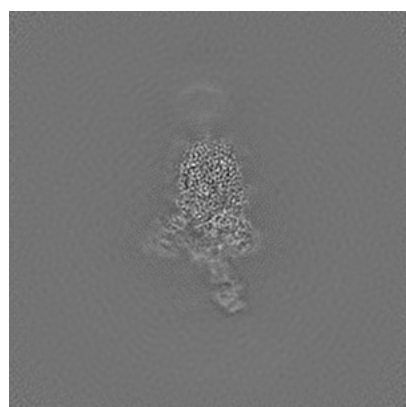
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28688. These allow visual inspection of the internal detail of the map and identification of artifacts.

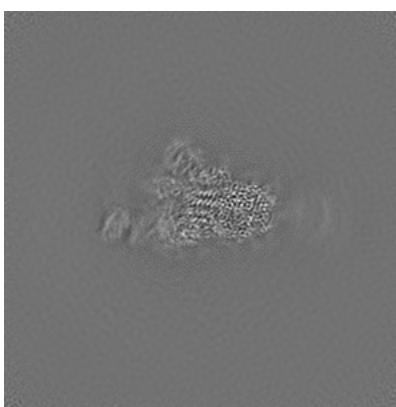
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

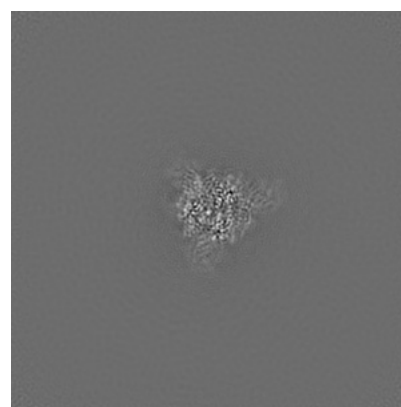
6.1.1 Primary map



X



Y

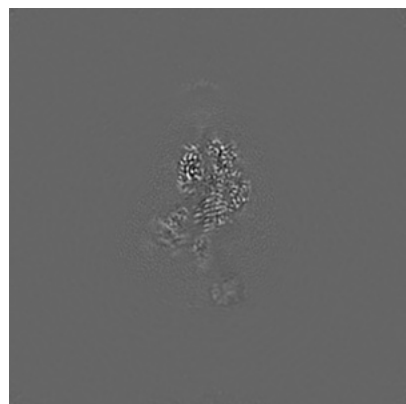


Z

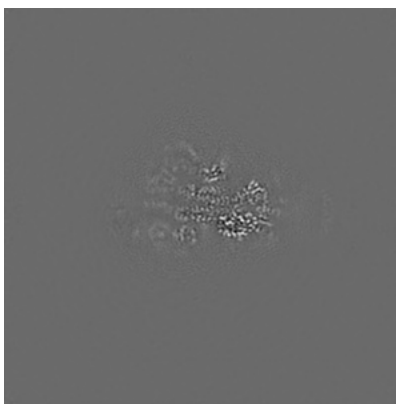
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

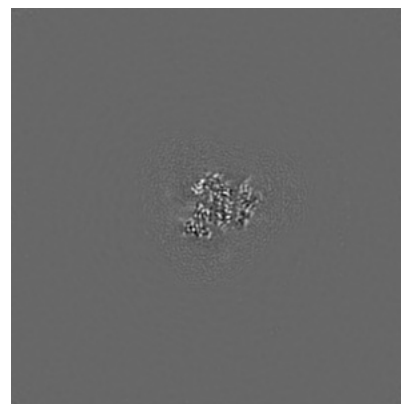
6.2.1 Primary map



X Index: 208



Y Index: 208



Z Index: 208

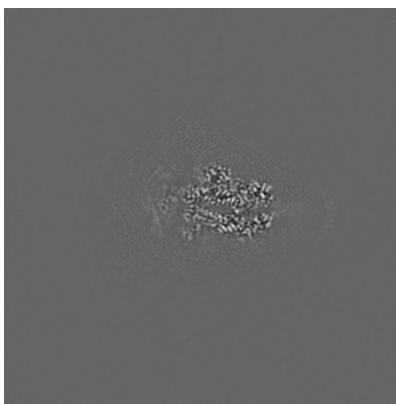
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

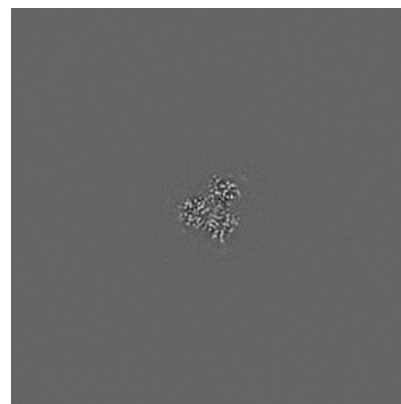
6.3.1 Primary map



X Index: 219



Y Index: 198

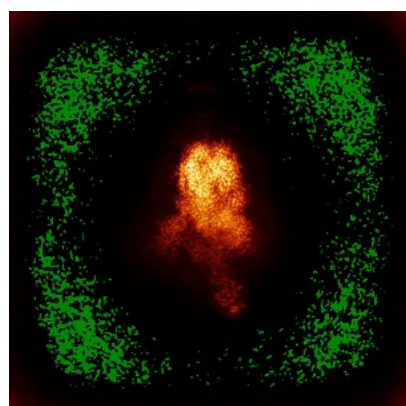


Z Index: 246

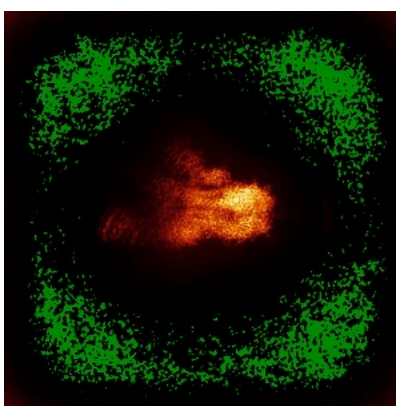
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

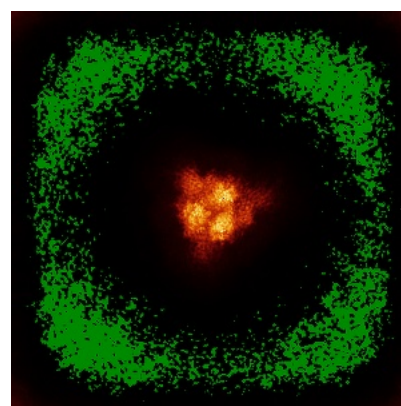
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

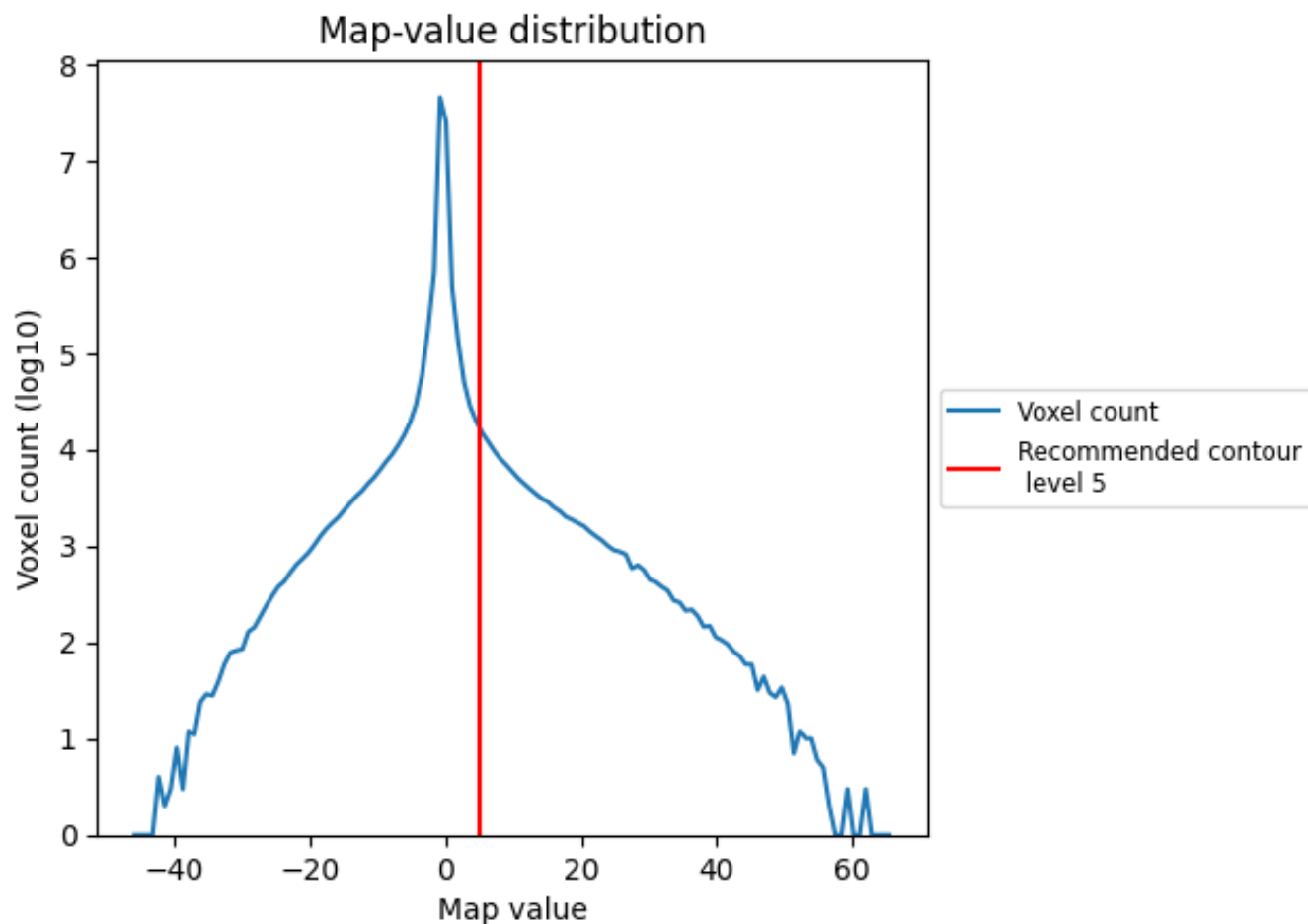
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

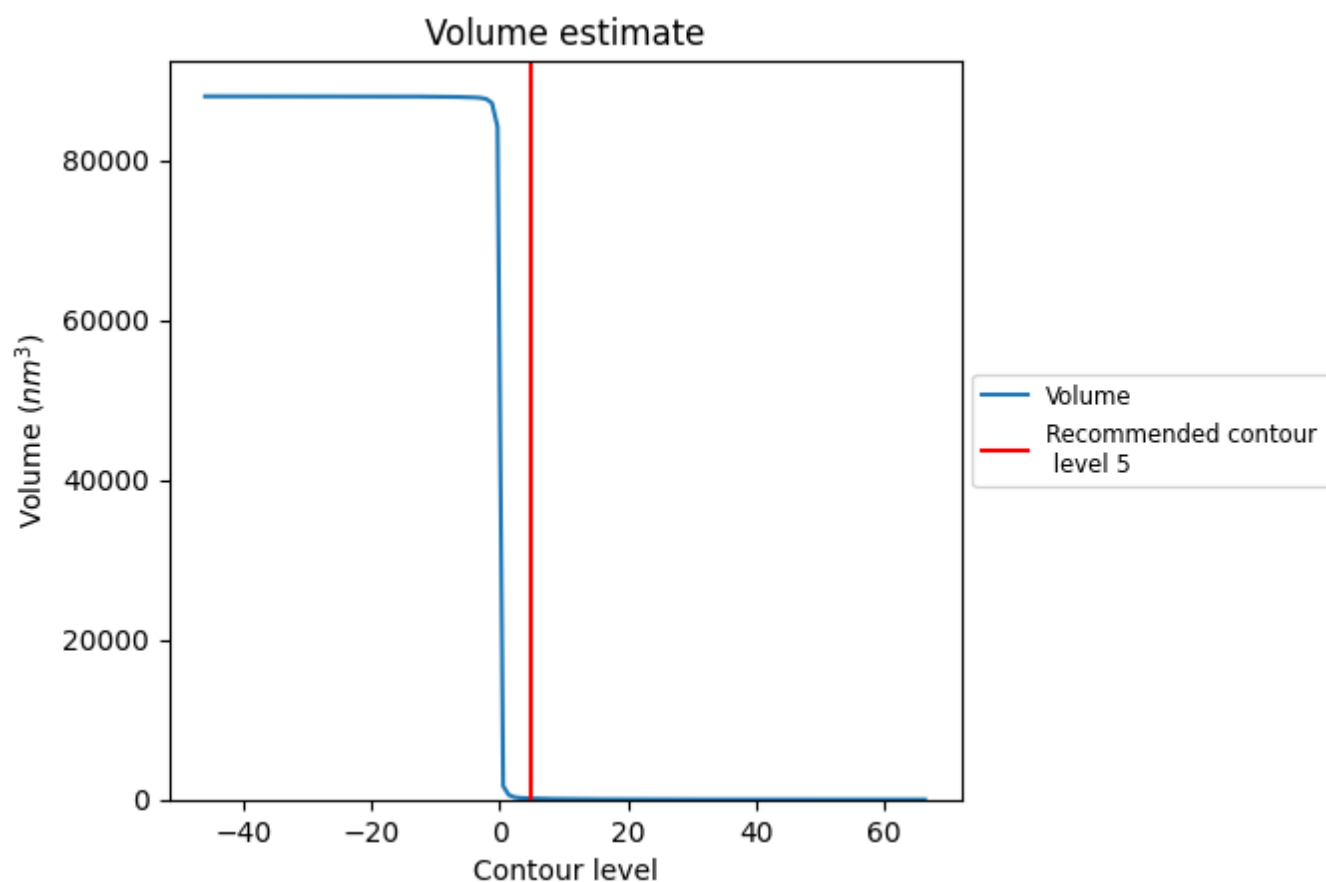
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

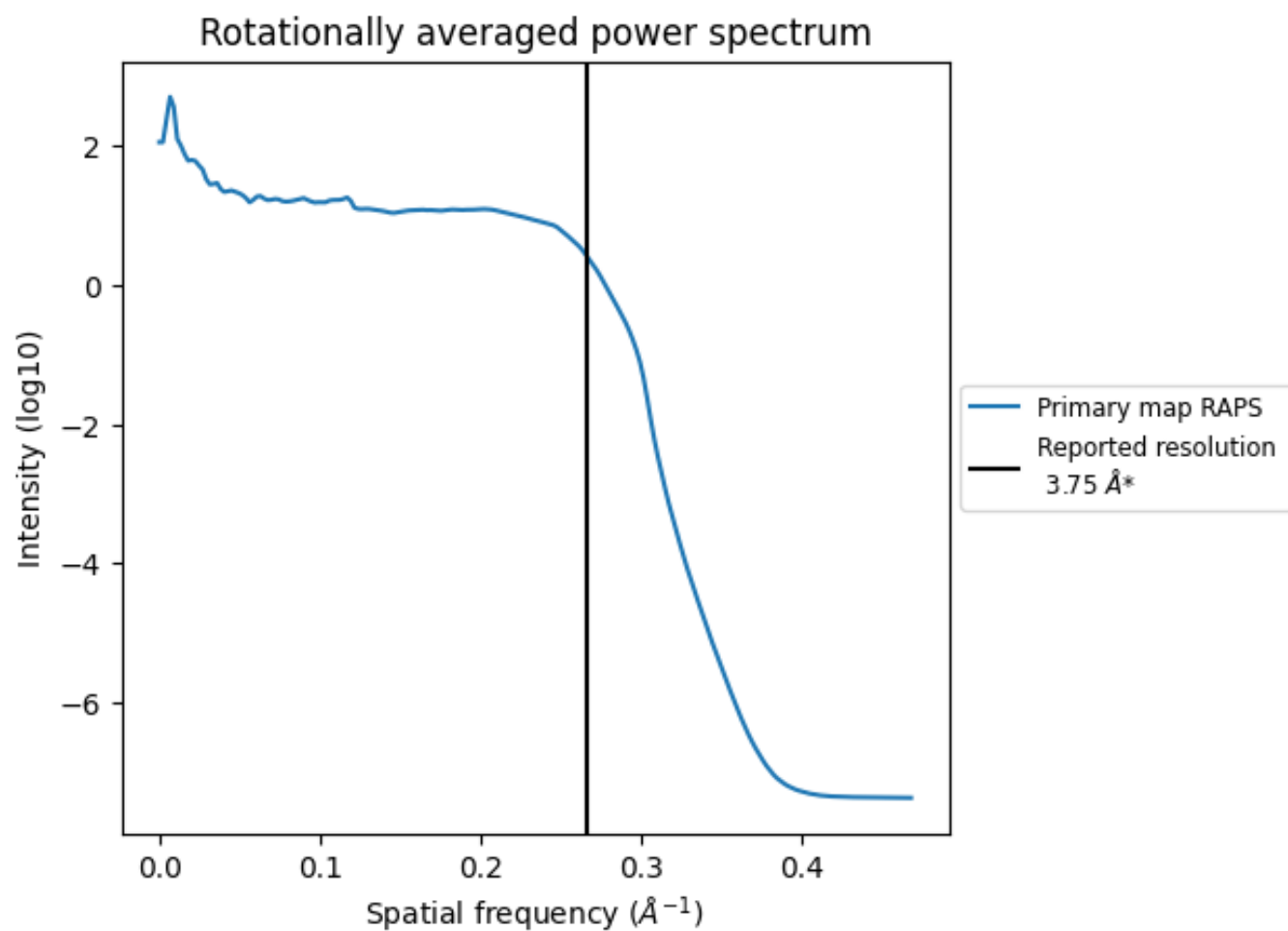
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 138 nm³; this corresponds to an approximate mass of 125 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

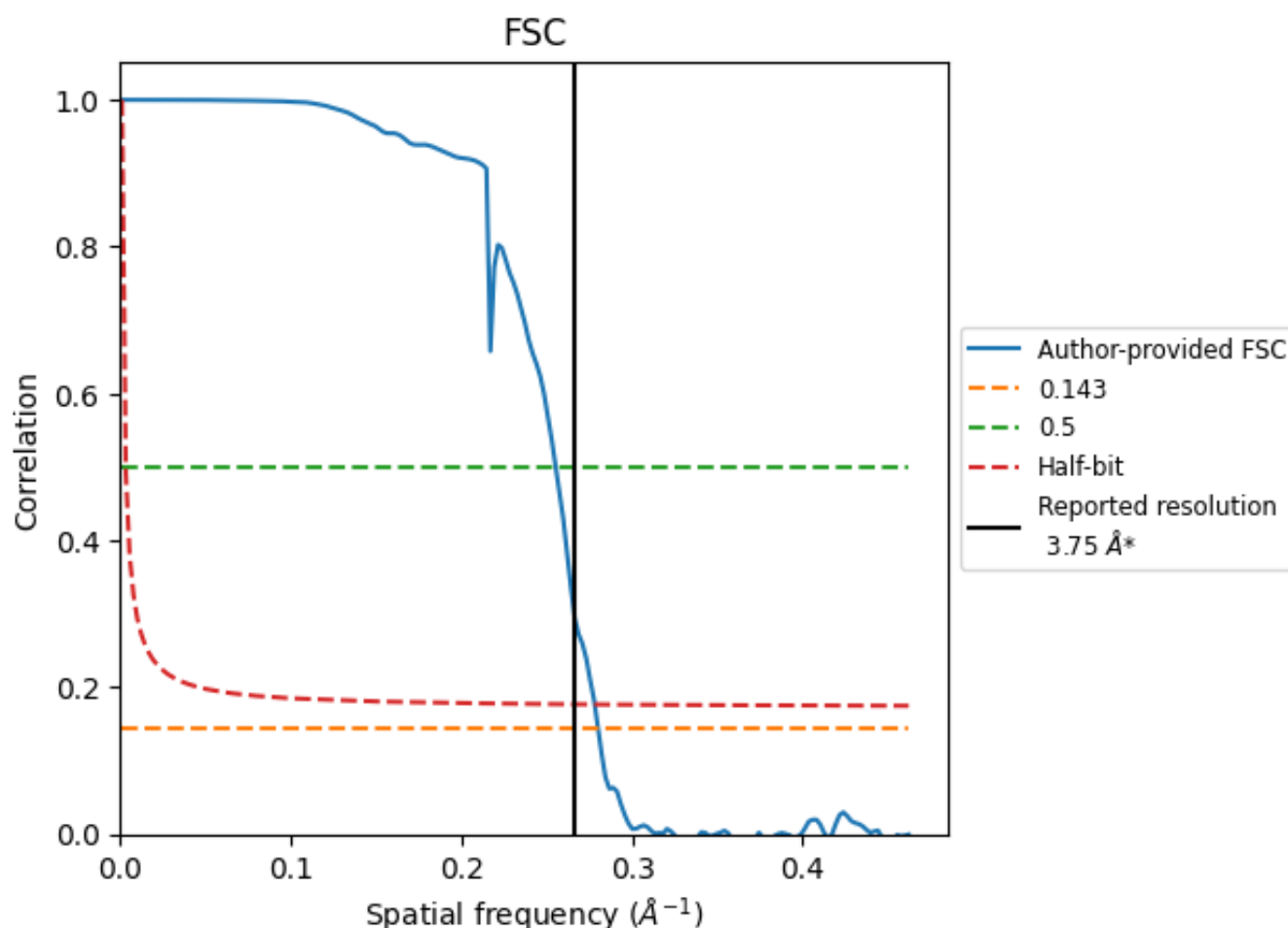


*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

8.2 Resolution estimates [i](#)

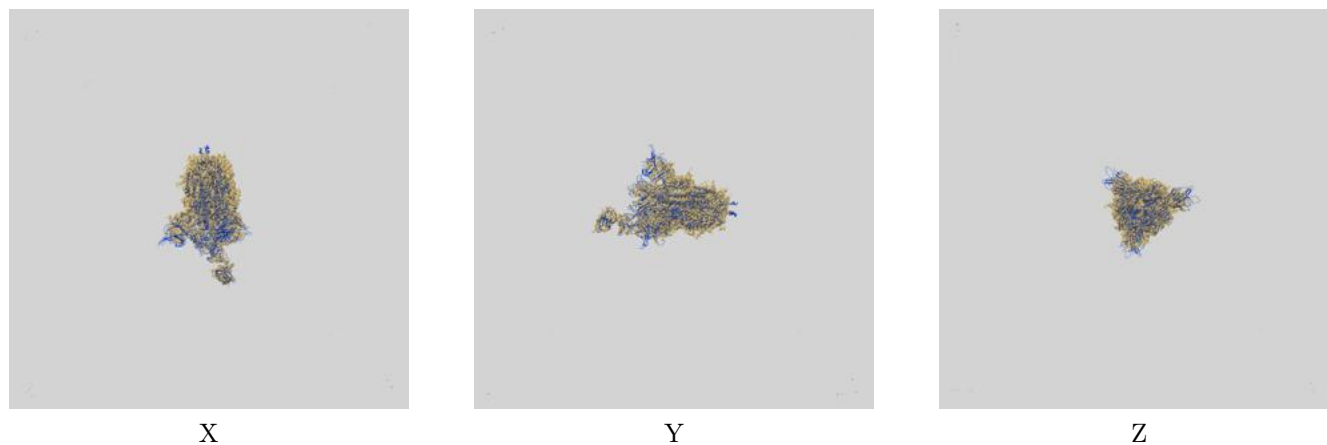
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	3.75	-
Author-provided FSC curve	3.57	3.92	3.60
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

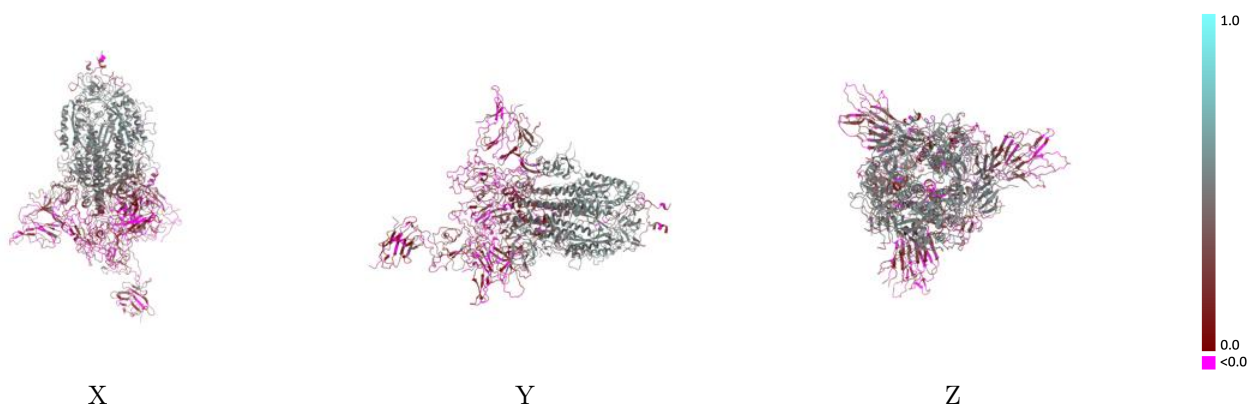
This section contains information regarding the fit between EMDB map EMD-28688 and PDB model 8EYH. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



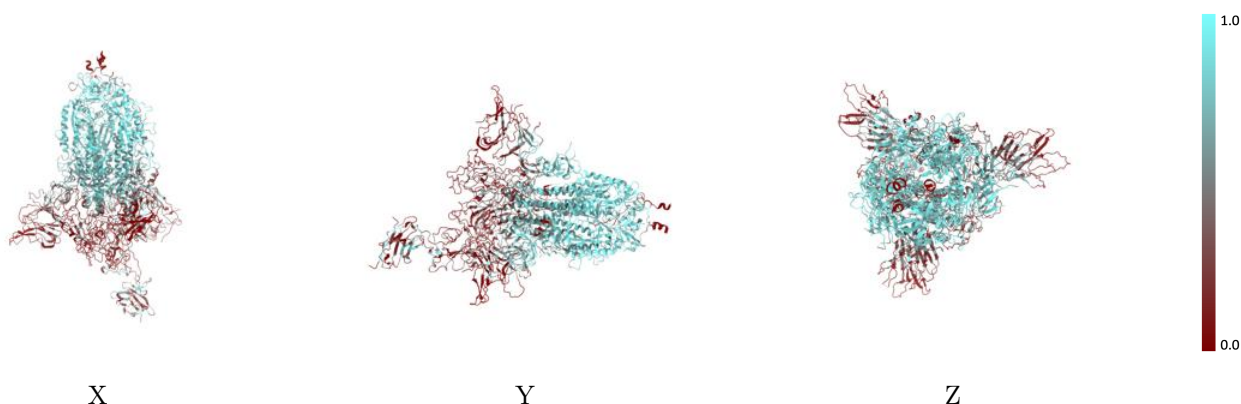
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



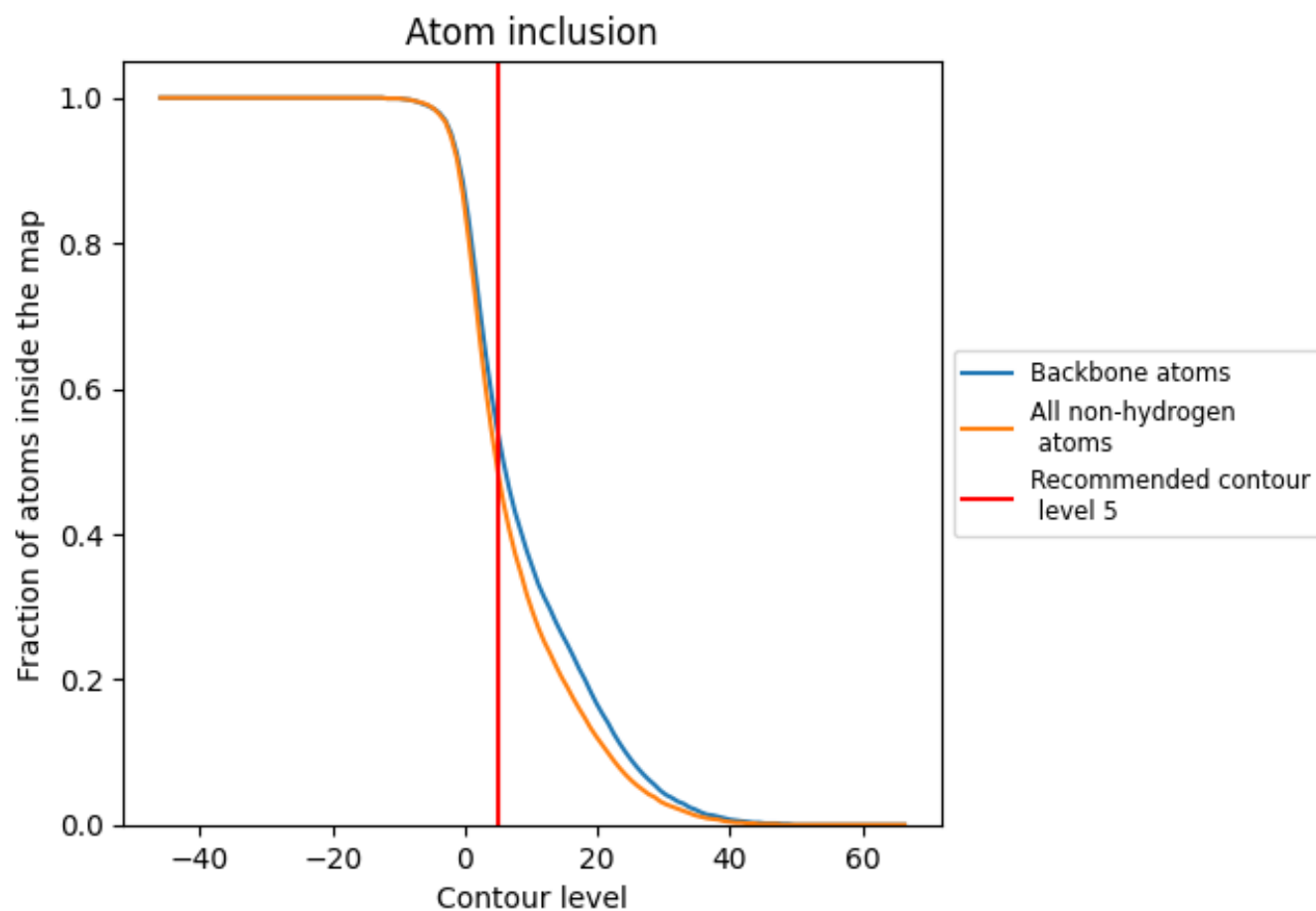
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4850	<div></div> 0.2870
A	<div></div> 0.4980	<div></div> 0.3080
B	<div></div> 0.5100	<div></div> 0.3000
C	<div></div> 0.4630	<div></div> 0.2720
D	<div></div> 0.3500	<div></div> 0.1460
E	<div></div> 0.3210	<div></div> 0.1470
F	<div></div> 0.1790	<div></div> 0.0860
G	<div></div> 0.3570	<div></div> 0.1290
H	<div></div> 0.2140	<div></div> 0.0730
I	<div></div> 0.0710	<div></div> -0.0470

1.0

0.0

<0.0