



Full wwPDB EM Validation Report ⓘ

Apr 14, 2025 – 12:32 PM JST

PDB ID : 8Z7N / pdb_00008z7n
EMDB ID : EMD-39820
Title : Structure of HIV-1 CH119 SOSIP.664 trimer in complex with CD4 molecules
Authors : Li, D.; Wang, T.
Deposited on : 2024-04-20
Resolution : 3.58 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.dev117
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.42

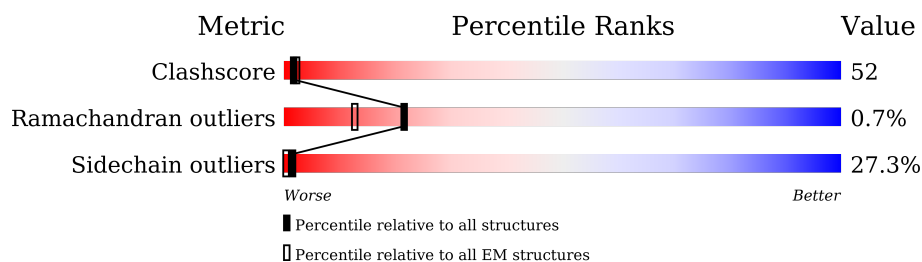
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.58 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	A	518	
1	D	518	
1	G	518	
2	B	164	
2	E	164	
2	H	164	
3	C	401	
3	F	401	

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Mol	Chain	Length	Quality of chain
3	I	401	<div><div><div></div><div></div><div></div><div></div></div><div><div>5%</div><div>11%</div><div>27%</div><div>6%</div><div>56%</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16641 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 Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	386	Total	C	N	O	S	0	0
			3019	1895	525	574	25		
1	D	386	Total	C	N	O	S	0	0
			3019	1895	525	574	25		
1	G	386	Total	C	N	O	S	0	0
			3019	1895	525	574	25		

There are 123 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A1EAH4
A	2	ASP	-	expression tag	UNP A1EAH4
A	3	ALA	-	expression tag	UNP A1EAH4
A	4	MET	-	expression tag	UNP A1EAH4
A	5	LYS	-	expression tag	UNP A1EAH4
A	6	ARG	-	expression tag	UNP A1EAH4
A	7	GLY	-	expression tag	UNP A1EAH4
A	8	LEU	-	expression tag	UNP A1EAH4
A	9	CYS	-	expression tag	UNP A1EAH4
A	10	CYS	-	expression tag	UNP A1EAH4
A	11	VAL	-	expression tag	UNP A1EAH4
A	12	LEU	-	expression tag	UNP A1EAH4
A	13	LEU	-	expression tag	UNP A1EAH4
A	14	LEU	-	expression tag	UNP A1EAH4
A	15	CYS	-	expression tag	UNP A1EAH4
A	16	GLY	-	expression tag	UNP A1EAH4
A	17	ALA	-	expression tag	UNP A1EAH4
A	18	VAL	-	expression tag	UNP A1EAH4
A	19	PHE	-	expression tag	UNP A1EAH4
A	20	VAL	-	expression tag	UNP A1EAH4
A	21	SER	-	expression tag	UNP A1EAH4
A	22	PRO	-	expression tag	UNP A1EAH4
A	23	SER	-	expression tag	UNP A1EAH4
A	24	GLN	-	expression tag	UNP A1EAH4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLU	-	expression tag	UNP A1EAH4
A	26	ILE	-	expression tag	UNP A1EAH4
A	27	HIS	-	expression tag	UNP A1EAH4
A	28	ALA	-	expression tag	UNP A1EAH4
A	29	ARG	-	expression tag	UNP A1EAH4
A	30	PHE	-	expression tag	UNP A1EAH4
A	31	ARG	-	expression tag	UNP A1EAH4
A	32	ARG	-	expression tag	UNP A1EAH4
A	33	GLY	-	expression tag	UNP A1EAH4
A	34	ALA	-	expression tag	UNP A1EAH4
A	35	ARG	-	expression tag	UNP A1EAH4
A	507	CYS	ALA	engineered mutation	UNP A1EAH4
A	515	ARG	-	expression tag	UNP A1EAH4
A	516	ARG	-	expression tag	UNP A1EAH4
A	517	ARG	-	expression tag	UNP A1EAH4
A	518	ARG	-	expression tag	UNP A1EAH4
A	519	ARG	-	expression tag	UNP A1EAH4
D	1	MET	-	initiating methionine	UNP A1EAH4
D	2	ASP	-	expression tag	UNP A1EAH4
D	3	ALA	-	expression tag	UNP A1EAH4
D	4	MET	-	expression tag	UNP A1EAH4
D	5	LYS	-	expression tag	UNP A1EAH4
D	6	ARG	-	expression tag	UNP A1EAH4
D	7	GLY	-	expression tag	UNP A1EAH4
D	8	LEU	-	expression tag	UNP A1EAH4
D	9	CYS	-	expression tag	UNP A1EAH4
D	10	CYS	-	expression tag	UNP A1EAH4
D	11	VAL	-	expression tag	UNP A1EAH4
D	12	LEU	-	expression tag	UNP A1EAH4
D	13	LEU	-	expression tag	UNP A1EAH4
D	14	LEU	-	expression tag	UNP A1EAH4
D	15	CYS	-	expression tag	UNP A1EAH4
D	16	GLY	-	expression tag	UNP A1EAH4
D	17	ALA	-	expression tag	UNP A1EAH4
D	18	VAL	-	expression tag	UNP A1EAH4
D	19	PHE	-	expression tag	UNP A1EAH4
D	20	VAL	-	expression tag	UNP A1EAH4
D	21	SER	-	expression tag	UNP A1EAH4
D	22	PRO	-	expression tag	UNP A1EAH4
D	23	SER	-	expression tag	UNP A1EAH4
D	24	GLN	-	expression tag	UNP A1EAH4
D	25	GLU	-	expression tag	UNP A1EAH4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	26	ILE	-	expression tag	UNP A1EAH4
D	27	HIS	-	expression tag	UNP A1EAH4
D	28	ALA	-	expression tag	UNP A1EAH4
D	29	ARG	-	expression tag	UNP A1EAH4
D	30	PHE	-	expression tag	UNP A1EAH4
D	31	ARG	-	expression tag	UNP A1EAH4
D	32	ARG	-	expression tag	UNP A1EAH4
D	33	GLY	-	expression tag	UNP A1EAH4
D	34	ALA	-	expression tag	UNP A1EAH4
D	35	ARG	-	expression tag	UNP A1EAH4
D	507	CYS	ALA	engineered mutation	UNP A1EAH4
D	515	ARG	-	expression tag	UNP A1EAH4
D	516	ARG	-	expression tag	UNP A1EAH4
D	517	ARG	-	expression tag	UNP A1EAH4
D	518	ARG	-	expression tag	UNP A1EAH4
D	519	ARG	-	expression tag	UNP A1EAH4
G	1	MET	-	initiating methionine	UNP A1EAH4
G	2	ASP	-	expression tag	UNP A1EAH4
G	3	ALA	-	expression tag	UNP A1EAH4
G	4	MET	-	expression tag	UNP A1EAH4
G	5	LYS	-	expression tag	UNP A1EAH4
G	6	ARG	-	expression tag	UNP A1EAH4
G	7	GLY	-	expression tag	UNP A1EAH4
G	8	LEU	-	expression tag	UNP A1EAH4
G	9	CYS	-	expression tag	UNP A1EAH4
G	10	CYS	-	expression tag	UNP A1EAH4
G	11	VAL	-	expression tag	UNP A1EAH4
G	12	LEU	-	expression tag	UNP A1EAH4
G	13	LEU	-	expression tag	UNP A1EAH4
G	14	LEU	-	expression tag	UNP A1EAH4
G	15	CYS	-	expression tag	UNP A1EAH4
G	16	GLY	-	expression tag	UNP A1EAH4
G	17	ALA	-	expression tag	UNP A1EAH4
G	18	VAL	-	expression tag	UNP A1EAH4
G	19	PHE	-	expression tag	UNP A1EAH4
G	20	VAL	-	expression tag	UNP A1EAH4
G	21	SER	-	expression tag	UNP A1EAH4
G	22	PRO	-	expression tag	UNP A1EAH4
G	23	SER	-	expression tag	UNP A1EAH4
G	24	GLN	-	expression tag	UNP A1EAH4
G	25	GLU	-	expression tag	UNP A1EAH4
G	26	ILE	-	expression tag	UNP A1EAH4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	27	HIS	-	expression tag	UNP A1EAH4
G	28	ALA	-	expression tag	UNP A1EAH4
G	29	ARG	-	expression tag	UNP A1EAH4
G	30	PHE	-	expression tag	UNP A1EAH4
G	31	ARG	-	expression tag	UNP A1EAH4
G	32	ARG	-	expression tag	UNP A1EAH4
G	33	GLY	-	expression tag	UNP A1EAH4
G	34	ALA	-	expression tag	UNP A1EAH4
G	35	ARG	-	expression tag	UNP A1EAH4
G	507	CYS	ALA	engineered mutation	UNP A1EAH4
G	515	ARG	-	expression tag	UNP A1EAH4
G	516	ARG	-	expression tag	UNP A1EAH4
G	517	ARG	-	expression tag	UNP A1EAH4
G	518	ARG	-	expression tag	UNP A1EAH4
G	519	ARG	-	expression tag	UNP A1EAH4

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	135	Total	C	N	O	S	0	0
			1070	680	181	202	7		
2	E	135	Total	C	N	O	S	0	0
			1070	680	181	202	7		
2	H	135	Total	C	N	O	S	0	0
			1070	680	181	202	7		

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	566	PRO	ILE	engineered mutation	UNP A1EAH4
B	612	CYS	THR	engineered mutation	UNP A1EAH4
B	672	GLY	-	expression tag	UNP A1EAH4
B	673	GLY	-	expression tag	UNP A1EAH4
B	674	GLY	-	expression tag	UNP A1EAH4
B	675	GLY	-	expression tag	UNP A1EAH4
B	676	GLY	-	expression tag	UNP A1EAH4
B	677	HIS	-	expression tag	UNP A1EAH4
B	678	HIS	-	expression tag	UNP A1EAH4
B	679	HIS	-	expression tag	UNP A1EAH4
B	680	HIS	-	expression tag	UNP A1EAH4
B	681	HIS	-	expression tag	UNP A1EAH4
B	682	HIS	-	expression tag	UNP A1EAH4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	566	PRO	ILE	engineered mutation	UNP A1EAH4
E	612	CYS	THR	engineered mutation	UNP A1EAH4
E	672	GLY	-	expression tag	UNP A1EAH4
E	673	GLY	-	expression tag	UNP A1EAH4
E	674	GLY	-	expression tag	UNP A1EAH4
E	675	GLY	-	expression tag	UNP A1EAH4
E	676	GLY	-	expression tag	UNP A1EAH4
E	677	HIS	-	expression tag	UNP A1EAH4
E	678	HIS	-	expression tag	UNP A1EAH4
E	679	HIS	-	expression tag	UNP A1EAH4
E	680	HIS	-	expression tag	UNP A1EAH4
E	681	HIS	-	expression tag	UNP A1EAH4
E	682	HIS	-	expression tag	UNP A1EAH4
H	566	PRO	ILE	engineered mutation	UNP A1EAH4
H	612	CYS	THR	engineered mutation	UNP A1EAH4
H	672	GLY	-	expression tag	UNP A1EAH4
H	673	GLY	-	expression tag	UNP A1EAH4
H	674	GLY	-	expression tag	UNP A1EAH4
H	675	GLY	-	expression tag	UNP A1EAH4
H	676	GLY	-	expression tag	UNP A1EAH4
H	677	HIS	-	expression tag	UNP A1EAH4
H	678	HIS	-	expression tag	UNP A1EAH4
H	679	HIS	-	expression tag	UNP A1EAH4
H	680	HIS	-	expression tag	UNP A1EAH4
H	681	HIS	-	expression tag	UNP A1EAH4
H	682	HIS	-	expression tag	UNP A1EAH4

- Molecule 3 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	177	Total	C	N	O	S	0	0
			1374	858	241	271	4		
3	F	177	Total	C	N	O	S	0	0
			1374	858	241	271	4		
3	I	177	Total	C	N	O	S	0	0
			1374	858	241	271	4		

There are 27 discrepancies between the modelled and reference sequences:

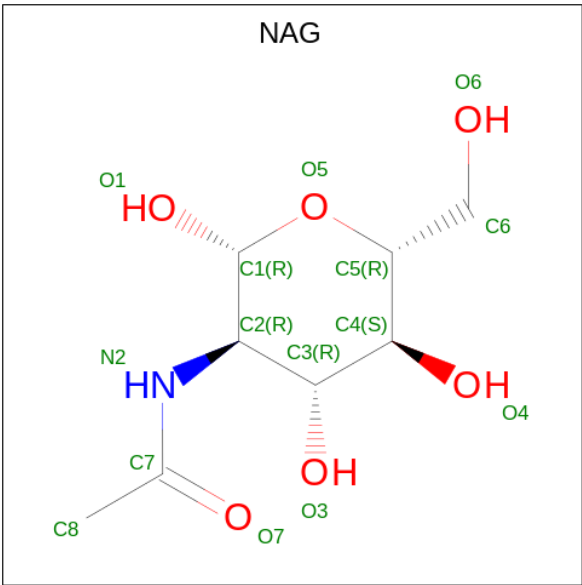
Chain	Residue	Modelled	Actual	Comment	Reference
C	370	GLY	-	expression tag	UNP P01730
C	371	SER	-	expression tag	UNP P01730

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Chain	Residue	Modelled	Actual	Comment	Reference
C	372	GLY	-	expression tag	UNP P01730
C	373	HIS	-	expression tag	UNP P01730
C	374	HIS	-	expression tag	UNP P01730
C	375	HIS	-	expression tag	UNP P01730
C	376	HIS	-	expression tag	UNP P01730
C	377	HIS	-	expression tag	UNP P01730
C	378	HIS	-	expression tag	UNP P01730
F	370	GLY	-	expression tag	UNP P01730
F	371	SER	-	expression tag	UNP P01730
F	372	GLY	-	expression tag	UNP P01730
F	373	HIS	-	expression tag	UNP P01730
F	374	HIS	-	expression tag	UNP P01730
F	375	HIS	-	expression tag	UNP P01730
F	376	HIS	-	expression tag	UNP P01730
F	377	HIS	-	expression tag	UNP P01730
F	378	HIS	-	expression tag	UNP P01730
I	370	GLY	-	expression tag	UNP P01730
I	371	SER	-	expression tag	UNP P01730
I	372	GLY	-	expression tag	UNP P01730
I	373	HIS	-	expression tag	UNP P01730
I	374	HIS	-	expression tag	UNP P01730
I	375	HIS	-	expression tag	UNP P01730
I	376	HIS	-	expression tag	UNP P01730
I	377	HIS	-	expression tag	UNP P01730
I	378	HIS	-	expression tag	UNP P01730

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

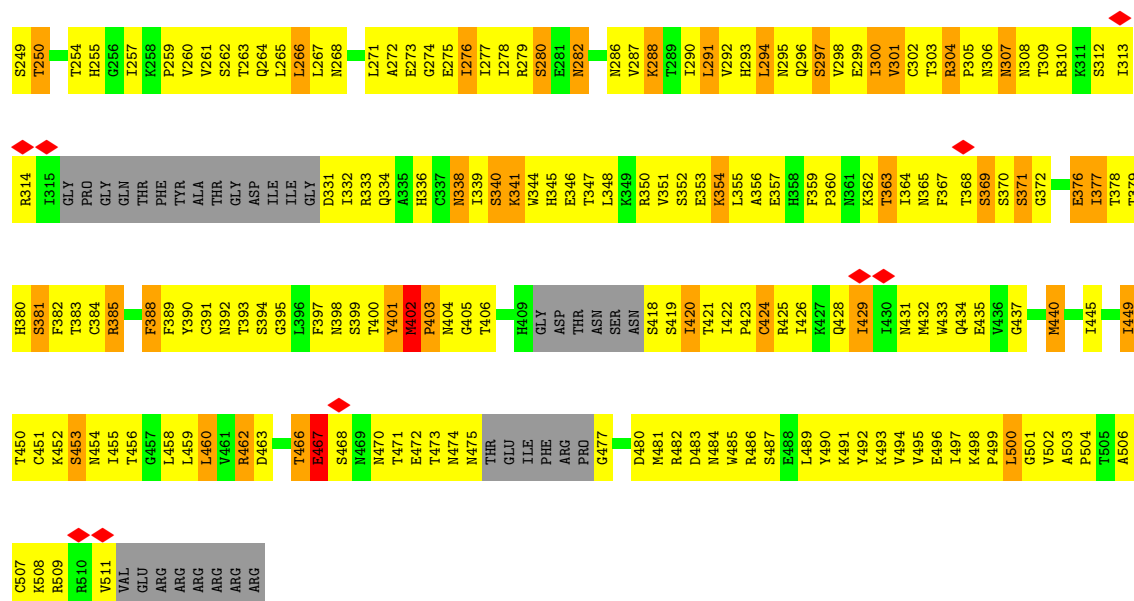


Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4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

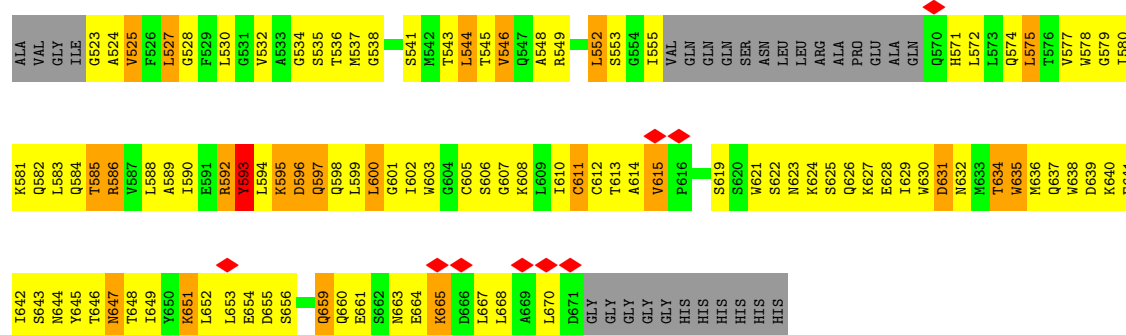
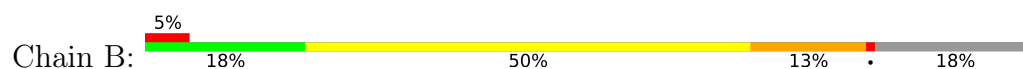
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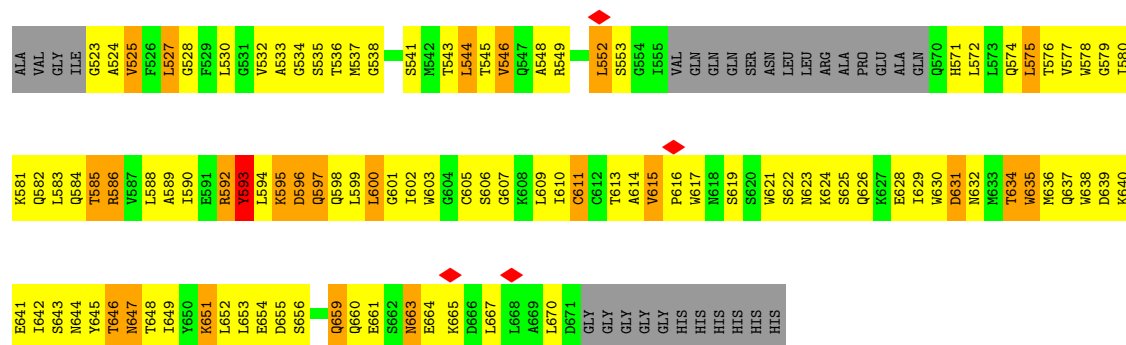
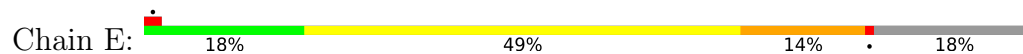
Mol	Chain	Residues	Atoms				AltConf
4	H	1	Total	C	N	O	0
			14	8	1	5	
4	H	1	Total	C	N	O	0
			14	8	1	5	
4	H	1	Total	C	N	O	0
			14	8	1	5	
4	H	1	Total	C	N	O	0
			14	8	1	5	



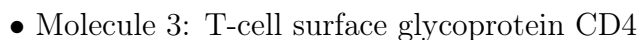
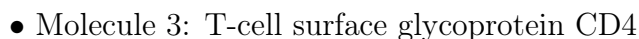
• Molecule 2: Envelope glycoprotein gp160



• Molecule 2: Envelope glycoprotein gp160



• Molecule 2: Envelope glycoprotein gp160



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1045667	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.521	Depositor
Minimum map value	-1.179	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.049	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	A	0.53	0/3082	0.74	3/4192 (0.1%)
1	D	0.53	0/3082	0.74	3/4192 (0.1%)
1	G	0.53	0/3082	0.74	3/4192 (0.1%)
2	B	0.51	1/1089 (0.1%)	0.74	2/1474 (0.1%)
2	E	0.51	1/1089 (0.1%)	0.74	2/1474 (0.1%)
2	H	0.51	1/1089 (0.1%)	0.74	2/1474 (0.1%)
3	C	0.39	0/1393	0.65	0/1878
3	F	0.39	0/1393	0.65	0/1878
3	I	0.39	0/1393	0.65	0/1878
All	All	0.49	3/16692 (0.0%)	0.72	15/22632 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	D	0	3
1	G	0	3
2	B	0	2
2	E	0	2
2	H	0	2
3	C	0	1
3	F	0	1
3	I	0	1
All	All	0	18

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	593	TYR	CD1-CE1	-5.74	1.30	1.39
2	B	593	TYR	CD1-CE1	-5.73	1.30	1.39
2	H	593	TYR	CD1-CE1	-5.66	1.30	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	552	LEU	CA-CB-CG	7.21	131.88	115.30
2	E	552	LEU	CA-CB-CG	7.20	131.86	115.30
2	B	552	LEU	CA-CB-CG	7.19	131.84	115.30
1	A	402	MET	N-CA-C	-6.41	93.70	111.00
1	D	402	MET	N-CA-C	-6.40	93.71	111.00
1	G	402	MET	N-CA-C	-6.40	93.73	111.00
1	G	211	CYS	CA-CB-SG	5.87	124.56	114.00
1	D	211	CYS	CA-CB-SG	5.86	124.54	114.00
1	A	211	CYS	CA-CB-SG	5.83	124.49	114.00
2	E	635	TRP	CA-CB-CG	5.36	123.88	113.70
2	H	635	TRP	CA-CB-CG	5.36	123.88	113.70
2	B	635	TRP	CA-CB-CG	5.33	123.83	113.70
1	A	467	GLU	CA-CB-CG	5.27	125.00	113.40
1	G	467	GLU	CA-CB-CG	5.27	124.99	113.40
1	D	467	GLU	CA-CB-CG	5.25	124.94	113.40

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	401	TYR	Peptide
1	A	402	MET	Peptide
1	A	82	PRO	Peptide
2	B	611	CYS	Peptide
2	B	634	THR	Peptide
3	C	173	LYS	Peptide
1	D	401	TYR	Peptide
1	D	402	MET	Peptide
1	D	82	PRO	Peptide
2	E	611	CYS	Peptide
2	E	634	THR	Peptide
3	F	173	LYS	Peptide
1	G	401	TYR	Peptide
1	G	402	MET	Peptide
1	G	82	PRO	Peptide

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Mol	Chain	Res	Type	Group
2	H	611	CYS	Peptide
2	H	634	THR	Peptide
3	I	173	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3019	0	2956	333	0
1	D	3019	0	2957	423	0
1	G	3019	0	2956	339	0
2	B	1070	0	1059	135	0
2	E	1070	0	1060	196	0
2	H	1070	0	1059	138	0
3	C	1374	0	1396	107	0
3	F	1374	0	1396	144	0
3	I	1374	0	1396	108	0
4	A	28	0	26	2	0
4	B	56	0	52	1	0
4	D	28	0	26	1	0
4	E	56	0	52	1	0
4	G	28	0	26	0	0
4	H	56	0	52	1	0
All	All	16641	0	16469	1718	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 52.

All (1718) 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:593:TYR:O	2:B:597:GLN:HB3	1.34	1.25
2:H:593:TYR:O	2:H:597:GLN:HB3	1.34	1.20
2:E:593:TYR:O	2:E:597:GLN:HB3	1.34	1.20
1:D:90:LEU:HB2	2:E:532:VAL:HG23	1.27	1.14
1:D:49:PRO:O	2:E:635:TRP:HB2	1.53	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:ASN:HB3	3:F:3:LYS:HD2	1.31	1.09
1:A:131:LEU:O	1:A:202:CYS:HA	1.59	1.03
1:G:131:LEU:O	1:G:202:CYS:HA	1.59	1.02
1:D:131:LEU:O	1:D:202:CYS:HA	1.59	1.02
2:E:594:LEU:O	2:E:598:GLN:N	1.95	1.00
2:H:594:LEU:O	2:H:598:GLN:N	1.95	1.00
2:E:598:GLN:HG3	2:E:599:LEU:HD22	1.43	0.98
2:B:594:LEU:O	2:B:598:GLN:N	1.95	0.98
1:A:276:ILE:HD12	1:A:354:LYS:HG2	1.46	0.98
1:D:97:GLU:OE2	2:E:640:LYS:NZ	1.95	0.98
1:D:282:ASN:H	3:F:92:LYS:H	1.09	0.98
1:G:276:ILE:HD12	1:G:354:LYS:HG2	1.46	0.97
2:B:598:GLN:HG3	2:B:599:LEU:HD22	1.43	0.97
2:H:598:GLN:HG3	2:H:599:LEU:HD22	1.43	0.97
2:H:600:LEU:HB2	2:H:606:SER:HA	1.46	0.96
2:E:600:LEU:HB2	2:E:606:SER:HA	1.46	0.96
1:D:276:ILE:HD12	1:D:354:LYS:HG2	1.46	0.95
2:B:600:LEU:HB2	2:B:606:SER:HA	1.46	0.95
1:G:40:LEU:HD11	2:H:626:GLN:HE22	1.30	0.94
1:G:276:ILE:HG22	1:G:294:LEU:HA	1.49	0.94
1:D:96:THR:OG1	2:E:637:GLN:OE1	1.85	0.94
1:G:223:TYR:N	1:G:254:THR:OG1	2.00	0.94
1:A:276:ILE:HG22	1:A:294:LEU:HA	1.49	0.93
1:D:223:TYR:N	1:D:254:THR:OG1	2.00	0.93
1:A:223:TYR:N	1:A:254:THR:OG1	2.00	0.93
1:D:276:ILE:HG22	1:D:294:LEU:HA	1.49	0.93
1:D:369:SER:O	1:D:475:ASN:ND2	2.04	0.91
1:D:90:LEU:HB2	2:E:532:VAL:CG2	2.01	0.90
1:D:402:MET:O	1:D:404:ASN:N	2.04	0.90
1:A:369:SER:O	1:A:475:ASN:ND2	2.04	0.90
1:G:402:MET:O	1:G:404:ASN:N	2.04	0.90
1:G:369:SER:O	1:G:475:ASN:ND2	2.04	0.89
1:A:402:MET:O	1:A:404:ASN:N	2.04	0.89
2:B:593:TYR:O	2:B:597:GLN:CB	2.21	0.89
2:E:593:TYR:O	2:E:597:GLN:CB	2.21	0.88
1:D:81:VAL:HG11	2:E:581:LYS:HD3	1.56	0.87
1:G:331:ASP:OD2	1:G:425:ARG:NH2	2.07	0.87
2:E:593:TYR:OH	2:H:598:GLN:OE1	1.92	0.87
1:D:235:ASN:ND2	1:D:247:ASN:O	2.08	0.87
2:H:593:TYR:O	2:H:597:GLN:CB	2.21	0.87
1:A:331:ASP:OD2	1:A:425:ARG:NH2	2.07	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:467:GLU:OE2	1:D:467:GLU:N	2.08	0.86
1:A:235:ASN:ND2	1:A:247:ASN:O	2.08	0.86
1:D:331:ASP:OD2	1:D:425:ARG:NH2	2.07	0.86
1:G:235:ASN:ND2	1:G:247:ASN:O	2.08	0.86
1:D:92:LEU:HD13	1:D:95:VAL:HG21	1.58	0.86
1:G:92:LEU:HD13	1:G:95:VAL:HG21	1.58	0.86
1:D:41:TRP:HA	2:E:616:PRO:HA	1.57	0.86
1:D:228:GLY:HA3	2:E:592:ARG:HH21	1.40	0.85
3:C:27:GLN:HA	3:C:41:ASN:HD22	1.42	0.85
3:F:120:LEU:HB3	3:F:144:LYS:HD2	1.59	0.85
1:A:467:GLU:OE2	1:A:467:GLU:N	2.08	0.85
1:G:97:GLU:OE2	1:G:493:LYS:NZ	2.10	0.85
3:C:120:LEU:HB3	3:C:144:LYS:HD2	1.59	0.85
1:A:92:LEU:HD13	1:A:95:VAL:HG21	1.58	0.84
3:I:120:LEU:HB3	3:I:144:LYS:HD2	1.59	0.84
1:A:97:GLU:OE2	1:A:493:LYS:NZ	2.10	0.84
1:A:223:TYR:H	1:A:254:THR:HG1	1.24	0.84
1:A:238:THR:O	1:A:279:ARG:NH1	2.11	0.84
1:D:97:GLU:OE2	1:D:493:LYS:NZ	2.10	0.84
1:G:467:GLU:OE2	1:G:467:GLU:N	2.08	0.84
2:B:530:LEU:HD23	2:B:544:LEU:HB2	1.59	0.84
2:E:530:LEU:HD23	2:E:544:LEU:HB2	1.59	0.84
2:H:530:LEU:HD23	2:H:544:LEU:HB2	1.59	0.84
1:A:255:HIS:HD1	1:A:492:TYR:HH	1.17	0.83
1:D:223:TYR:H	1:D:254:THR:HG1	1.26	0.83
1:A:499:PRO:HD3	2:B:592:ARG:HH22	1.41	0.83
1:D:238:THR:O	1:D:279:ARG:NH1	2.11	0.83
1:G:267:LEU:HA	1:G:453:SER:HB2	1.61	0.82
1:G:238:THR:O	1:G:279:ARG:NH1	2.11	0.82
1:A:267:LEU:HA	1:A:453:SER:HB2	1.61	0.82
3:I:30:TRP:N	3:I:39:LEU:O	2.12	0.82
3:F:27:GLN:HA	3:F:41:ASN:HD22	1.42	0.82
3:I:115:SER:HA	3:I:151:LEU:HD13	1.62	0.82
2:B:615:VAL:HG11	2:B:652:LEU:HB3	1.62	0.81
3:I:27:GLN:HA	3:I:41:ASN:HD22	1.42	0.81
1:A:272:ALA:HB3	1:A:295:ASN:HA	1.63	0.81
2:B:665:LYS:NZ	1:G:506:ALA:O	2.10	0.81
3:F:30:TRP:N	3:F:39:LEU:O	2.12	0.81
2:H:615:VAL:HG11	2:H:652:LEU:HB3	1.62	0.81
1:G:272:ALA:HB3	1:G:295:ASN:HA	1.63	0.81
3:C:30:TRP:N	3:C:39:LEU:O	2.12	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:115:SER:HA	3:F:151:LEU:HD13	1.62	0.81
3:F:159:TRP:HB2	3:F:174:ILE:HB	1.63	0.81
2:E:537:MET:HB2	2:E:630:TRP:HA	1.62	0.81
3:C:115:SER:HA	3:C:151:LEU:HD13	1.62	0.80
1:D:267:LEU:HA	1:D:453:SER:HB2	1.61	0.80
2:H:537:MET:HB2	2:H:630:TRP:HA	1.62	0.80
2:E:615:VAL:HG11	2:E:652:LEU:HB3	1.62	0.80
1:G:98:ASN:O	1:G:100:ASN:N	2.15	0.80
2:B:537:MET:HB2	2:B:630:TRP:HA	1.62	0.80
1:D:42:VAL:N	2:E:615:VAL:O	2.15	0.79
1:A:98:ASN:O	1:A:100:ASN:N	2.15	0.79
2:B:665:LYS:HZ3	1:G:506:ALA:HB1	1.48	0.79
1:A:294:LEU:N	1:A:456:THR:O	2.15	0.79
3:C:159:TRP:HB2	3:C:174:ILE:HB	1.63	0.79
1:G:294:LEU:N	1:G:456:THR:O	2.15	0.79
1:A:130:PRO:HB2	3:C:62:SER:HB3	1.65	0.79
1:G:275:GLU:HA	1:G:295:ASN:HD22	1.48	0.79
1:D:294:LEU:N	1:D:456:THR:O	2.15	0.79
1:D:502:VAL:HG12	2:E:617:TRP:HZ3	1.48	0.79
3:C:63:LEU:HD23	3:C:68:ASN:HB3	1.65	0.79
1:D:285:ASN:OD1	3:F:4:LYS:HB3	1.82	0.79
1:D:98:ASN:O	1:D:100:ASN:N	2.15	0.78
1:D:275:GLU:HA	1:D:295:ASN:HD22	1.48	0.78
1:D:285:ASN:ND2	3:F:94:GLU:O	2.16	0.78
3:I:159:TRP:HB2	3:I:174:ILE:HB	1.63	0.78
2:B:635:TRP:O	2:B:638:TRP:N	2.14	0.78
1:D:53:GLU:OE2	2:E:640:LYS:NZ	2.15	0.78
3:I:63:LEU:HD23	3:I:68:ASN:HB3	1.65	0.78
1:D:272:ALA:HB3	1:D:295:ASN:HA	1.63	0.78
3:F:76:LEU:HD22	3:F:99:VAL:HG11	1.66	0.78
3:I:76:LEU:HD22	3:I:99:VAL:HG11	1.66	0.78
1:A:218:PRO:HB3	1:A:259:PRO:HD2	1.66	0.78
2:E:635:TRP:O	2:E:638:TRP:N	2.14	0.77
3:F:63:LEU:HD23	3:F:68:ASN:HB3	1.65	0.77
2:B:665:LYS:NZ	1:G:506:ALA:HB1	1.99	0.77
2:H:635:TRP:O	2:H:638:TRP:N	2.14	0.77
1:D:288:LYS:HD2	3:F:94:GLU:OE1	1.84	0.77
1:A:339:ILE:HG22	1:A:340:SER:HB3	1.67	0.77
3:I:148:VAL:HG12	3:I:150:GLN:H	1.49	0.77
1:G:218:PRO:HB3	1:G:259:PRO:HD2	1.66	0.77
1:G:339:ILE:HG22	1:G:340:SER:HB3	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:83:THR:OG1	3:F:94:GLU:OE2	2.03	0.76
1:D:339:ILE:HG22	1:D:340:SER:HB3	1.67	0.76
3:F:148:VAL:HG12	3:F:150:GLN:H	1.49	0.76
2:B:608:LYS:HA	2:E:598:GLN:HE22	1.50	0.76
1:D:428:GLN:HG3	1:D:429:ILE:HG13	1.67	0.76
3:C:76:LEU:HD22	3:C:99:VAL:HG11	1.66	0.76
1:G:223:TYR:H	1:G:254:THR:HG1	1.32	0.76
1:A:275:GLU:HA	1:A:295:ASN:HD22	1.48	0.76
1:D:81:VAL:HB	2:E:578:TRP:CE3	2.19	0.76
1:D:218:PRO:HB3	1:D:259:PRO:HD2	1.66	0.76
1:D:340:SER:OG	1:D:341:LYS:N	2.17	0.76
1:G:428:GLN:HG3	1:G:429:ILE:HG13	1.67	0.75
2:E:589:ALA:O	2:E:593:TYR:HB2	1.87	0.75
1:D:228:GLY:H	2:E:527:LEU:HD21	1.52	0.75
3:C:148:VAL:HG12	3:C:150:GLN:H	1.49	0.75
3:I:83:THR:OG1	3:I:94:GLU:OE2	2.03	0.75
1:A:428:GLN:HG3	1:A:429:ILE:HG13	1.67	0.75
1:G:340:SER:OG	1:G:341:LYS:N	2.17	0.75
1:D:255:HIS:ND1	1:D:492:TYR:OH	2.13	0.75
1:D:504:PRO:HG3	2:E:617:TRP:CE2	2.21	0.75
2:H:589:ALA:O	2:H:593:TYR:HB2	1.87	0.75
1:A:97:GLU:HB3	1:A:99:PHE:HE1	1.53	0.74
3:C:83:THR:OG1	3:C:94:GLU:OE2	2.03	0.74
2:B:635:TRP:HA	2:B:638:TRP:HB3	1.69	0.74
1:A:340:SER:OG	1:A:341:LYS:N	2.17	0.74
1:G:255:HIS:HD1	1:G:492:TYR:HH	1.15	0.74
2:H:577:VAL:HA	2:H:580:ILE:HD12	1.70	0.74
1:D:93:GLU:HB2	2:E:534:GLY:O	1.86	0.74
2:E:635:TRP:HA	2:E:638:TRP:HB3	1.69	0.74
1:A:261:VAL:HG12	1:A:485:TRP:HZ2	1.53	0.73
2:B:577:VAL:HA	2:B:580:ILE:HD12	1.70	0.73
2:B:589:ALA:O	2:B:593:TYR:HB2	1.87	0.73
1:G:97:GLU:HB3	1:G:99:PHE:HE1	1.52	0.73
1:D:97:GLU:HB3	1:D:99:PHE:HE1	1.53	0.73
1:G:261:VAL:HG12	1:G:485:TRP:HZ2	1.53	0.73
1:D:261:VAL:HG12	1:D:485:TRP:HZ2	1.53	0.73
1:D:228:GLY:CA	2:E:592:ARG:HH21	2.02	0.73
1:A:98:ASN:N	1:A:98:ASN:OD1	2.21	0.73
1:D:98:ASN:N	1:D:98:ASN:OD1	2.21	0.73
2:H:635:TRP:HA	2:H:638:TRP:HB3	1.69	0.73
1:D:92:LEU:HA	2:E:533:ALA:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:SER:OG	1:D:288:LYS:O	2.07	0.72
1:G:98:ASN:N	1:G:98:ASN:OD1	2.21	0.72
1:A:249:SER:OG	1:A:250:THR:N	2.21	0.72
1:A:113:ASP:O	1:A:116:SER:OG	2.08	0.72
1:D:113:ASP:O	1:D:116:SER:OG	2.08	0.72
1:A:280:SER:OG	1:A:288:LYS:O	2.07	0.72
1:A:381:SER:HB3	1:A:390:TYR:HE1	1.55	0.72
1:D:249:SER:OG	1:D:250:THR:N	2.21	0.72
1:D:249:SER:OG	2:E:533:ALA:HB3	1.90	0.72
2:H:593:TYR:HE1	2:H:597:GLN:NE2	1.88	0.72
1:G:280:SER:OG	1:G:288:LYS:O	2.07	0.72
1:G:381:SER:HB3	1:G:390:TYR:HE1	1.55	0.72
2:E:577:VAL:HA	2:E:580:ILE:HD12	1.70	0.72
1:G:113:ASP:O	1:G:116:SER:OG	2.08	0.72
1:A:402:MET:HG3	1:A:403:PRO:HD3	1.71	0.72
1:D:50:VAL:HG22	2:E:635:TRP:HB3	1.72	0.72
2:E:593:TYR:HE1	2:E:597:GLN:NE2	1.88	0.72
3:C:128:PRO:HA	3:C:164:LEU:O	1.90	0.71
1:G:76:ALA:HB2	1:G:219:ILE:HD12	1.73	0.71
1:D:402:MET:HG3	1:D:403:PRO:HD3	1.71	0.71
1:G:503:ALA:HB2	2:H:635:TRP:HH2	1.55	0.71
1:A:120:GLN:OE1	1:A:120:GLN:N	2.23	0.71
3:I:128:PRO:HA	3:I:164:LEU:O	1.90	0.71
1:D:76:ALA:HB2	1:D:219:ILE:HD12	1.72	0.71
3:F:128:PRO:HA	3:F:164:LEU:O	1.90	0.71
1:D:381:SER:HB3	1:D:390:TYR:HE1	1.55	0.70
3:F:76:LEU:HB3	3:F:99:VAL:HG21	1.73	0.70
1:A:76:ALA:HB2	1:A:219:ILE:HD12	1.72	0.70
1:A:264:GLN:HA	1:A:459:LEU:HB2	1.74	0.70
2:B:593:TYR:HE1	2:B:597:GLN:NE2	1.88	0.70
1:G:293:HIS:ND1	1:G:487:SER:OG	2.25	0.70
2:E:586:ARG:NH2	2:H:591:GLU:OE1	2.24	0.70
3:F:28:PHE:H	3:F:41:ASN:HB3	1.56	0.70
1:D:293:HIS:ND1	1:D:487:SER:OG	2.25	0.70
1:A:234:CYS:O	1:A:491:LYS:NZ	2.22	0.70
1:G:264:GLN:HA	1:G:459:LEU:HB2	1.74	0.70
1:G:120:GLN:N	1:G:120:GLN:OE1	2.23	0.70
1:G:402:MET:HG3	1:G:403:PRO:HD3	1.71	0.70
1:D:264:GLN:HA	1:D:459:LEU:HB2	1.74	0.70
1:A:293:HIS:ND1	1:A:487:SER:OG	2.25	0.69
1:A:379:THR:HG21	1:A:390:TYR:HA	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:76:LEU:HD21	3:C:97:LEU:HD21	1.74	0.69
3:C:76:LEU:HB3	3:C:99:VAL:HG21	1.73	0.69
1:D:95:VAL:HG12	2:E:634:THR:OG1	1.91	0.69
1:D:120:GLN:OE1	1:D:120:GLN:N	2.23	0.69
1:D:41:TRP:HA	2:E:617:TRP:H	1.56	0.69
1:D:228:GLY:O	1:D:497:ILE:N	2.26	0.69
1:A:90:LEU:HD11	2:B:524:ALA:HA	1.72	0.69
3:C:28:PHE:H	3:C:41:ASN:HB3	1.56	0.69
2:H:602:ILE:HG13	2:H:654:GLU:HG2	1.75	0.69
3:I:76:LEU:HB3	3:I:99:VAL:HG21	1.73	0.69
1:D:44:VAL:H	2:E:613:THR:HG23	1.57	0.69
3:I:76:LEU:HD21	3:I:97:LEU:HD21	1.74	0.69
1:A:239:PHE:HE2	1:A:490:TYR:HB2	1.57	0.68
1:A:277:ILE:HG22	1:A:278:ILE:H	1.58	0.68
1:D:49:PRO:O	2:E:635:TRP:CB	2.37	0.68
1:G:237:LYS:O	1:G:279:ARG:NH2	2.26	0.68
1:D:42:VAL:HG22	2:E:617:TRP:HA	1.75	0.68
1:D:232:LEU:HD11	2:E:636:MET:SD	2.33	0.68
1:A:44:VAL:O	2:B:611:CYS:HB2	1.93	0.68
1:G:228:GLY:O	1:G:497:ILE:N	2.26	0.68
1:G:379:THR:HG21	1:G:390:TYR:HA	1.74	0.68
1:D:239:PHE:HE2	1:D:490:TYR:HB2	1.57	0.68
2:E:602:ILE:HG13	2:E:654:GLU:HG2	1.75	0.68
1:A:237:LYS:O	1:A:279:ARG:NH2	2.26	0.68
1:D:277:ILE:HG22	1:D:278:ILE:H	1.58	0.68
3:I:28:PHE:H	3:I:41:ASN:HB3	1.56	0.68
1:D:101:MET:O	1:D:486:ARG:HD3	1.94	0.68
1:G:277:ILE:HG22	1:G:278:ILE:H	1.58	0.68
1:D:379:THR:HG21	1:D:390:TYR:HA	1.74	0.68
1:D:278:ILE:HG22	1:D:292:VAL:HG12	1.75	0.68
1:D:338:ASN:N	1:D:338:ASN:OD1	2.26	0.68
1:A:228:GLY:O	1:A:497:ILE:N	2.26	0.68
1:G:239:PHE:HE2	1:G:490:TYR:HB2	1.57	0.67
3:I:134:SER:HB3	3:I:138:LYS:H	1.59	0.67
1:G:278:ILE:HG22	1:G:292:VAL:HG12	1.75	0.67
1:G:338:ASN:N	1:G:338:ASN:OD1	2.26	0.67
1:D:285:ASN:ND2	3:F:4:LYS:O	2.27	0.67
3:F:76:LEU:HD21	3:F:97:LEU:HD21	1.74	0.67
3:F:134:SER:HB3	3:F:138:LYS:H	1.59	0.67
1:A:278:ILE:HG22	1:A:292:VAL:HG12	1.75	0.67
1:D:237:LYS:O	1:D:279:ARG:NH2	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:47:THR:O	3:F:47:THR:OG1	2.13	0.67
2:H:594:LEU:O	2:H:596:ASP:N	2.28	0.67
2:B:584:GLN:O	2:B:588:LEU:HG	1.95	0.67
1:A:338:ASN:OD1	1:A:338:ASN:N	2.26	0.67
2:E:594:LEU:O	2:E:596:ASP:N	2.28	0.67
2:B:594:LEU:O	2:B:596:ASP:N	2.28	0.67
3:C:134:SER:HB3	3:C:138:LYS:H	1.59	0.67
1:D:431:ASN:OD1	1:D:432:MET:N	2.27	0.67
1:G:431:ASN:OD1	1:G:432:MET:N	2.27	0.67
2:B:602:ILE:HG13	2:B:654:GLU:HG2	1.75	0.67
1:D:228:GLY:N	2:E:527:LEU:HD21	2.10	0.67
1:D:463:ASP:OD2	1:D:475:ASN:ND2	2.22	0.67
1:G:40:LEU:HD11	2:H:626:GLN:NE2	2.08	0.67
1:G:101:MET:O	1:G:486:ARG:HD3	1.94	0.67
3:I:47:THR:O	3:I:47:THR:OG1	2.13	0.67
3:C:102:LEU:HD12	3:C:120:LEU:HB2	1.77	0.67
1:D:288:LYS:HG3	3:F:85:ILE:HD11	1.77	0.66
3:I:51:SER:N	3:I:54:ASN:OD1	2.26	0.66
1:A:101:MET:O	1:A:486:ARG:HD3	1.94	0.66
1:A:431:ASN:OD1	1:A:432:MET:N	2.27	0.66
1:D:50:VAL:CG2	2:E:635:TRP:HB3	2.26	0.66
1:D:42:VAL:HG13	2:E:617:TRP:HE3	1.61	0.66
3:F:102:LEU:HD12	3:F:120:LEU:HB2	1.77	0.66
2:H:584:GLN:O	2:H:588:LEU:HG	1.95	0.66
3:C:47:THR:O	3:C:47:THR:OG1	2.13	0.66
2:E:584:GLN:O	2:E:588:LEU:HG	1.95	0.66
3:F:78:ILE:HG22	3:F:123:PRO:HB3	1.78	0.66
1:D:281:GLU:HB2	3:F:92:LYS:HD2	1.78	0.66
1:A:255:HIS:ND1	1:A:492:TYR:OH	2.13	0.66
2:B:592:ARG:HA	2:B:595:LYS:HB3	1.78	0.66
1:D:509:ARG:HG2	2:E:614:ALA:HB1	1.76	0.65
2:H:592:ARG:HA	2:H:595:LYS:HB3	1.78	0.65
1:A:132:CYS:HB3	1:A:202:CYS:N	2.11	0.65
3:C:113:GLY:N	3:C:151:LEU:O	2.25	0.65
2:E:592:ARG:HA	2:E:595:LYS:HB3	1.78	0.65
1:G:101:MET:HE1	1:G:279:ARG:HD2	1.78	0.65
3:I:78:ILE:HG22	3:I:123:PRO:HB3	1.78	0.65
1:D:229:TYR:CD1	1:D:496:GLU:HA	2.32	0.65
1:D:234:CYS:O	1:D:491:LYS:NZ	2.22	0.65
1:G:132:CYS:HB3	1:G:202:CYS:N	2.12	0.65
1:A:344:TRP:O	1:A:347:THR:OG1	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:229:TYR:CD1	1:G:496:GLU:HA	2.32	0.65
1:D:132:CYS:HB3	1:D:202:CYS:N	2.11	0.65
1:D:242:THR:O	1:D:242:THR:OG1	2.09	0.65
1:D:308:ASN:ND2	1:D:331:ASP:O	2.30	0.65
4:A:601:NAG:H82	2:B:536:THR:HG23	1.79	0.65
3:C:51:SER:N	3:C:54:ASN:OD1	2.26	0.65
1:D:235:ASN:H	1:D:248:VAL:HB	1.62	0.65
1:G:275:GLU:HA	1:G:295:ASN:ND2	2.12	0.65
1:G:344:TRP:O	1:G:347:THR:OG1	2.13	0.65
1:A:263:THR:OG1	1:A:381:SER:OG	2.11	0.65
2:B:579:GLY:O	2:B:583:LEU:HG	1.97	0.64
1:D:93:GLU:H	2:E:534:GLY:HA3	1.61	0.64
1:A:229:TYR:CD1	1:A:496:GLU:HA	2.32	0.64
1:A:432:MET:HB3	1:A:434:GLN:HG3	1.80	0.64
3:C:78:ILE:HG22	3:C:123:PRO:HB3	1.78	0.64
1:D:511:VAL:O	2:E:663:ASN:ND2	2.30	0.64
1:A:497:ILE:HB	2:B:592:ARG:NH2	2.12	0.64
1:D:101:MET:HE1	1:D:279:ARG:HD2	1.78	0.64
1:G:369:SER:OG	1:G:463:ASP:OD2	2.14	0.64
3:I:102:LEU:HD12	3:I:120:LEU:HB2	1.77	0.64
1:D:232:LEU:HG	2:E:636:MET:CE	2.27	0.64
2:E:579:GLY:O	2:E:583:LEU:HG	1.97	0.64
1:D:92:LEU:N	1:D:248:VAL:O	2.18	0.64
1:D:237:LYS:HE2	1:D:274:GLY:H	1.63	0.64
1:G:237:LYS:HE2	1:G:274:GLY:H	1.63	0.64
1:D:275:GLU:HA	1:D:295:ASN:ND2	2.12	0.64
2:E:590:ILE:HD13	2:H:594:LEU:HD12	1.80	0.64
3:F:31:LYS:HA	3:F:38:ILE:HG13	1.80	0.64
1:G:92:LEU:N	1:G:248:VAL:O	2.18	0.64
1:A:363:THR:HG23	1:A:471:THR:HA	1.80	0.64
1:D:363:THR:HG23	1:D:471:THR:HA	1.80	0.64
1:D:92:LEU:HA	2:E:534:GLY:HA3	1.80	0.64
1:G:308:ASN:ND2	1:G:331:ASP:O	2.30	0.64
2:H:579:GLY:O	2:H:583:LEU:HG	1.97	0.64
1:A:369:SER:OG	1:A:463:ASP:OD2	2.14	0.63
1:G:363:THR:HG23	1:G:471:THR:HA	1.80	0.63
1:D:48:VAL:HB	2:E:635:TRP:CZ2	2.33	0.63
1:D:281:GLU:HB3	3:F:92:LYS:N	2.14	0.63
1:D:344:TRP:O	1:D:347:THR:OG1	2.13	0.63
1:D:369:SER:OG	1:D:463:ASP:OD2	2.14	0.63
2:E:600:LEU:HB2	2:E:606:SER:CA	2.26	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:SER:O	1:A:484:ASN:ND2	2.31	0.63
1:D:92:LEU:N	1:D:249:SER:HB2	2.13	0.63
1:A:235:ASN:H	1:A:248:VAL:HB	1.62	0.63
1:G:235:ASN:H	1:G:248:VAL:HB	1.62	0.63
1:A:499:PRO:CD	2:B:592:ARG:HH22	2.08	0.63
1:G:92:LEU:N	1:G:249:SER:HB2	2.13	0.63
1:A:275:GLU:HA	1:A:295:ASN:ND2	2.12	0.63
1:D:262:SER:O	1:D:484:ASN:ND2	2.31	0.63
1:G:262:SER:O	1:G:484:ASN:ND2	2.31	0.63
1:G:463:ASP:OD2	1:G:475:ASN:ND2	2.22	0.63
2:H:590:ILE:O	2:H:593:TYR:HB3	1.99	0.63
3:I:31:LYS:HA	3:I:38:ILE:HG13	1.80	0.63
1:A:92:LEU:N	1:A:249:SER:HB2	2.13	0.63
1:A:399:SER:HA	1:A:406:THR:HB	1.81	0.63
1:A:242:THR:O	1:A:242:THR:OG1	2.09	0.63
1:G:399:SER:HA	1:G:406:THR:HB	1.81	0.63
1:G:432:MET:HB3	1:G:434:GLN:HG3	1.80	0.63
3:F:84:TYR:HB2	3:F:95:VAL:HG22	1.82	0.62
1:G:268:ASN:H	1:G:453:SER:HB2	1.65	0.62
1:A:234:CYS:N	1:A:491:LYS:HB3	2.15	0.62
2:B:590:ILE:O	2:B:593:TYR:HB3	1.99	0.62
1:A:308:ASN:ND2	1:A:331:ASP:O	2.30	0.62
1:D:432:MET:HB3	1:D:434:GLN:HG3	1.80	0.62
1:D:509:ARG:HG2	2:E:614:ALA:CB	2.29	0.62
1:G:242:THR:O	1:G:242:THR:OG1	2.09	0.62
3:I:84:TYR:HB2	3:I:95:VAL:HG22	1.82	0.62
1:A:237:LYS:HE2	1:A:274:GLY:H	1.63	0.62
3:C:31:LYS:HA	3:C:38:ILE:HG13	1.80	0.62
1:D:92:LEU:CA	2:E:534:GLY:HA3	2.29	0.62
1:D:228:GLY:HA3	2:E:592:ARG:NH2	2.12	0.62
1:G:104:ASN:O	1:G:107:VAL:HG12	2.00	0.62
1:D:268:ASN:H	1:D:453:SER:HB2	1.65	0.62
1:D:285:ASN:HB3	3:F:3:LYS:CD	2.19	0.62
2:H:600:LEU:HB2	2:H:606:SER:CA	2.26	0.62
3:F:113:GLY:N	3:F:151:LEU:O	2.25	0.62
1:D:234:CYS:N	1:D:491:LYS:HB3	2.15	0.62
1:D:399:SER:HA	1:D:406:THR:HB	1.81	0.62
1:G:255:HIS:ND1	1:G:492:TYR:OH	2.13	0.62
1:A:104:ASN:O	1:A:107:VAL:HG12	1.99	0.61
1:D:263:THR:OG1	1:D:381:SER:OG	2.11	0.61
1:D:504:PRO:HG3	2:E:617:TRP:CD2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:PHE:CE2	1:A:490:TYR:HB2	2.35	0.61
2:E:590:ILE:O	2:E:593:TYR:HB3	1.99	0.61
2:E:622:SER:O	2:E:624:LYS:NZ	2.30	0.61
2:B:634:THR:HG23	2:B:637:GLN:HE21	1.65	0.61
1:D:498:LYS:NZ	2:E:646:THR:HG21	2.15	0.61
2:E:634:THR:HG23	2:E:637:GLN:HE21	1.65	0.61
1:D:104:ASN:O	1:D:107:VAL:HG12	2.00	0.61
1:D:239:PHE:CE2	1:D:490:TYR:HB2	2.35	0.61
1:G:46:TYR:O	2:H:530:LEU:HD13	2.00	0.61
1:A:63:ASP:HB2	1:A:83:THR:HG23	1.83	0.61
1:A:90:LEU:HD11	2:B:524:ALA:CA	2.30	0.61
1:A:304:ARG:O	1:A:304:ARG:HG2	2.01	0.61
1:G:52:LYS:HE3	2:H:640:LYS:HE2	1.82	0.61
1:G:234:CYS:N	1:G:491:LYS:HB3	2.14	0.61
2:E:536:THR:HG22	2:E:634:THR:HG22	1.82	0.61
2:E:576:THR:HG22	2:H:580:ILE:HD13	1.82	0.61
3:C:84:TYR:HB2	3:C:95:VAL:HG22	1.81	0.61
1:G:117:LEU:O	1:G:121:SER:OG	2.10	0.61
1:G:239:PHE:CE2	1:G:490:TYR:HB2	2.35	0.61
1:A:101:MET:HG3	1:A:490:TYR:HA	1.83	0.61
2:B:536:THR:HG22	2:B:634:THR:HG22	1.82	0.61
1:A:57:THR:HG22	1:A:109:GLN:HE22	1.66	0.61
1:A:225:THR:OG1	1:A:229:TYR:O	2.19	0.61
1:D:90:LEU:HD12	2:E:532:VAL:HG23	1.81	0.61
1:G:63:ASP:HB2	1:G:83:THR:HG23	1.83	0.60
1:G:249:SER:OG	1:G:250:THR:N	2.21	0.60
2:B:600:LEU:HB2	2:B:606:SER:CA	2.26	0.60
1:D:285:ASN:HB2	3:F:94:GLU:O	2.01	0.60
1:D:288:LYS:NZ	3:F:94:GLU:HB2	2.16	0.60
1:A:268:ASN:H	1:A:453:SER:HB2	1.65	0.60
1:G:266:LEU:HD11	1:G:456:THR:HG22	1.83	0.60
2:H:634:THR:HG23	2:H:637:GLN:HE21	1.65	0.60
3:I:113:GLY:N	3:I:151:LEU:O	2.25	0.60
2:B:622:SER:O	2:B:624:LYS:NZ	2.30	0.60
1:D:304:ARG:O	1:D:304:ARG:HG2	2.01	0.60
1:D:481:MET:HA	1:D:484:ASN:HB3	1.83	0.60
2:H:622:SER:O	2:H:624:LYS:NZ	2.30	0.60
1:A:481:MET:HA	1:A:484:ASN:HB3	1.83	0.60
1:D:57:THR:HG22	1:D:109:GLN:HE22	1.66	0.60
1:G:72:HIS:HB3	1:G:219:ILE:HD13	1.84	0.60
2:H:536:THR:HG22	2:H:634:THR:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:GLN:NE2	1:A:377:ILE:O	2.35	0.60
1:D:44:VAL:HG21	2:E:649:ILE:HG12	1.83	0.60
1:D:255:HIS:H	1:D:492:TYR:HH	1.50	0.60
1:G:390:TYR:N	1:G:425:ARG:O	2.23	0.60
1:A:266:LEU:HD11	1:A:456:THR:HG22	1.83	0.60
2:B:593:TYR:C	2:B:597:GLN:HB3	2.20	0.60
1:G:302:CYS:HB3	1:G:304:ARG:HH22	1.67	0.60
1:G:264:GLN:NE2	1:G:377:ILE:O	2.35	0.59
1:G:304:ARG:O	1:G:304:ARG:HG2	2.01	0.59
2:H:544:LEU:HG	2:H:545:THR:N	2.16	0.59
1:D:92:LEU:HD22	1:D:95:VAL:HG11	1.84	0.59
1:D:101:MET:HG3	1:D:490:TYR:HA	1.83	0.59
1:D:281:GLU:HG2	3:F:90:ASP:O	2.02	0.59
1:A:72:HIS:HB3	1:A:219:ILE:HD13	1.84	0.59
2:B:544:LEU:HG	2:B:545:THR:N	2.16	0.59
2:H:597:GLN:NE2	2:H:607:GLY:O	2.35	0.59
3:I:29:HIS:HA	3:I:40:GLY:HA2	1.84	0.59
1:A:123:LYS:HD3	1:A:212:PRO:HD2	1.84	0.59
1:A:508:LYS:HA	2:B:614:ALA:HA	1.85	0.59
2:E:544:LEU:HG	2:E:545:THR:N	2.16	0.59
1:D:63:ASP:HB2	1:D:83:THR:HG23	1.83	0.59
1:G:92:LEU:HD22	1:G:95:VAL:HG11	1.84	0.59
1:G:111:HIS:HE1	1:G:433:TRP:CZ3	2.21	0.59
1:G:234:CYS:O	1:G:491:LYS:NZ	2.22	0.59
1:G:499:PRO:HG3	2:H:527:LEU:HD11	1.84	0.59
1:A:262:SER:HB3	1:A:266:LEU:HA	1.85	0.59
1:D:48:VAL:HB	2:E:635:TRP:CE2	2.38	0.59
1:D:111:HIS:HE1	1:D:433:TRP:CZ3	2.21	0.59
2:E:597:GLN:NE2	2:E:607:GLY:O	2.35	0.59
1:G:45:TYR:HB3	2:H:610:ILE:HA	1.83	0.59
1:G:101:MET:HG3	1:G:490:TYR:HA	1.83	0.59
1:A:111:HIS:HE1	1:A:433:TRP:CZ3	2.21	0.59
1:D:262:SER:HB3	1:D:266:LEU:HA	1.85	0.59
1:D:385:ARG:HD3	1:D:445:ILE:HD13	1.84	0.59
1:G:123:LYS:HD3	1:G:212:PRO:HD2	1.84	0.59
1:A:348:LEU:O	1:A:351:VAL:HB	2.03	0.59
1:A:482:ARG:O	1:A:486:ARG:NE	2.35	0.59
3:C:7:LEU:HD13	3:C:168:LYS:HB3	1.85	0.59
1:D:264:GLN:NE2	1:D:377:ILE:O	2.35	0.59
1:A:214:VAL:HG13	1:A:215:SER:H	1.68	0.59
2:B:523:GLY:HA3	2:B:528:GLY:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:523:GLY:HA3	2:E:528:GLY:O	2.03	0.59
1:G:57:THR:HG22	1:G:109:GLN:HE22	1.66	0.59
1:A:302:CYS:HB3	1:A:304:ARG:HH22	1.67	0.59
2:B:532:VAL:HG13	2:B:535:SER:HB3	1.85	0.58
3:C:120:LEU:HD23	3:C:144:LYS:NZ	2.18	0.58
2:E:545:THR:O	2:E:549:ARG:NH1	2.36	0.58
1:G:237:LYS:HZ3	1:G:274:GLY:N	2.02	0.58
1:G:262:SER:HB3	1:G:266:LEU:HA	1.85	0.58
1:G:385:ARG:HD3	1:G:445:ILE:HD13	1.84	0.58
1:G:398:ASN:OD1	1:G:399:SER:N	2.36	0.58
1:G:481:MET:HA	1:G:484:ASN:HB3	1.83	0.58
1:A:92:LEU:HD22	1:A:95:VAL:HG11	1.84	0.58
2:B:545:THR:O	2:B:549:ARG:NH1	2.36	0.58
1:D:123:LYS:HD3	1:D:212:PRO:HD2	1.84	0.58
1:D:214:VAL:HG13	1:D:215:SER:H	1.68	0.58
1:D:225:THR:OG1	1:D:229:TYR:O	2.19	0.58
3:I:7:LEU:HD13	3:I:168:LYS:HB3	1.85	0.58
2:B:597:GLN:NE2	2:B:607:GLY:O	2.35	0.58
1:D:282:ASN:OD1	3:F:93:GLU:HG3	2.03	0.58
1:D:462:ARG:HA	1:D:474:ASN:HA	1.85	0.58
1:A:385:ARG:HD3	1:A:445:ILE:HD13	1.85	0.58
1:D:302:CYS:HB3	1:D:304:ARG:HH22	1.67	0.58
3:F:120:LEU:HD23	3:F:144:LYS:NZ	2.18	0.58
1:D:111:HIS:CE1	1:D:433:TRP:HZ3	2.22	0.58
1:D:266:LEU:HD11	1:D:456:THR:HG22	1.83	0.58
2:E:549:ARG:HH22	2:H:602:ILE:HG12	1.67	0.58
2:H:532:VAL:HG13	2:H:535:SER:HB3	1.85	0.58
2:H:545:THR:O	2:H:549:ARG:NH1	2.36	0.58
1:A:111:HIS:CE1	1:A:433:TRP:HZ3	2.22	0.58
1:A:254:THR:HB	1:A:492:TYR:CZ	2.39	0.58
3:C:29:HIS:HA	3:C:40:GLY:HA2	1.84	0.58
1:D:72:HIS:HB3	1:D:219:ILE:HD13	1.84	0.58
1:D:254:THR:HB	1:D:492:TYR:CZ	2.39	0.58
1:G:348:LEU:O	1:G:351:VAL:HB	2.03	0.58
2:H:523:GLY:HA3	2:H:528:GLY:O	2.03	0.58
3:I:164:LEU:HB2	3:I:169:LYS:HE3	1.86	0.58
3:I:120:LEU:HD23	3:I:144:LYS:NZ	2.18	0.58
1:A:390:TYR:N	1:A:425:ARG:O	2.23	0.58
2:E:532:VAL:HG13	2:E:535:SER:HB3	1.85	0.58
2:E:538:GLY:HA2	2:E:630:TRP:HE3	1.69	0.58
1:G:239:PHE:C	1:G:241:GLY:H	2.08	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:ILE:O	1:A:401:TYR:N	2.37	0.57
1:A:497:ILE:HB	2:B:592:ARG:HH21	1.69	0.57
2:B:538:GLY:HA2	2:B:630:TRP:HE3	1.69	0.57
1:D:41:TRP:CA	2:E:617:TRP:H	2.16	0.57
1:D:93:GLU:N	2:E:534:GLY:HA3	2.18	0.57
3:F:29:HIS:HA	3:F:40:GLY:HA2	1.84	0.57
3:F:164:LEU:HB2	3:F:169:LYS:HE3	1.86	0.57
1:G:291:LEU:HD22	1:G:487:SER:HB2	1.86	0.57
1:A:110:MET:O	1:A:114:VAL:HG23	2.04	0.57
1:A:291:LEU:HD22	1:A:487:SER:HB2	1.86	0.57
1:A:398:ASN:OD1	1:A:399:SER:N	2.36	0.57
1:D:232:LEU:HG	2:E:636:MET:HE3	1.86	0.57
1:D:348:LEU:O	1:D:351:VAL:HB	2.03	0.57
3:F:7:LEU:HD13	3:F:168:LYS:HB3	1.85	0.57
1:G:364:ILE:O	1:G:401:TYR:N	2.37	0.57
1:D:93:GLU:H	2:E:534:GLY:CA	2.16	0.57
1:D:117:LEU:HD23	1:D:121:SER:OG	2.05	0.57
1:D:282:ASN:HB2	3:F:93:GLU:N	2.18	0.57
1:D:291:LEU:HD22	1:D:487:SER:HB2	1.86	0.57
1:D:364:ILE:O	1:D:401:TYR:N	2.37	0.57
1:D:398:ASN:OD1	1:D:399:SER:N	2.36	0.57
2:H:593:TYR:C	2:H:597:GLN:HB3	2.20	0.57
1:A:278:ILE:HA	1:A:291:LEU:O	2.04	0.57
1:A:237:LYS:HZ3	1:A:274:GLY:N	2.03	0.57
1:A:463:ASP:OD2	1:A:475:ASN:ND2	2.22	0.57
1:G:111:HIS:CE1	1:G:433:TRP:HZ3	2.22	0.57
1:G:117:LEU:HD23	1:G:121:SER:OG	2.04	0.57
1:G:214:VAL:HG13	1:G:215:SER:H	1.68	0.57
1:A:391:CYS:HB3	1:A:424:CYS:HA	1.86	0.57
2:B:586:ARG:HH12	2:E:584:GLN:CD	2.08	0.57
1:D:232:LEU:O	1:D:492:TYR:HA	2.05	0.57
1:D:278:ILE:HA	1:D:291:LEU:O	2.04	0.57
1:G:254:THR:HB	1:G:492:TYR:CZ	2.39	0.57
1:G:263:THR:OG1	1:G:381:SER:OG	2.11	0.57
1:G:462:ARG:HA	1:G:474:ASN:HA	1.85	0.57
2:H:538:GLY:HA2	2:H:630:TRP:HE3	1.69	0.57
1:A:462:ARG:HA	1:A:474:ASN:HA	1.85	0.57
1:D:44:VAL:N	2:E:613:THR:HG23	2.19	0.57
3:I:16:LEU:HB3	3:I:95:VAL:HG11	1.87	0.57
1:G:110:MET:O	1:G:114:VAL:HG23	2.04	0.57
1:G:378:THR:OG1	1:G:379:THR:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:104:ALA:HB1	3:I:116:LEU:HD21	1.87	0.57
1:A:223:TYR:O	1:A:254:THR:HG23	2.05	0.57
1:G:502:VAL:O	2:H:635:TRP:HZ3	1.88	0.57
1:A:388:PHE:O	1:A:426:ILE:HG22	2.05	0.57
1:D:223:TYR:O	1:D:254:THR:HG23	2.05	0.57
1:D:388:PHE:O	1:D:426:ILE:HG22	2.05	0.57
1:D:391:CYS:HB3	1:D:424:CYS:HA	1.87	0.57
3:C:164:LEU:HB2	3:C:169:LYS:HE3	1.86	0.56
1:G:223:TYR:O	1:G:254:THR:HG23	2.05	0.56
1:G:238:THR:HG22	1:G:277:ILE:HG12	1.87	0.56
3:I:28:PHE:CD1	3:I:41:ASN:HB2	2.40	0.56
1:A:92:LEU:N	1:A:248:VAL:O	2.18	0.56
3:C:27:GLN:HG2	3:C:41:ASN:O	2.05	0.56
3:F:28:PHE:O	3:F:41:ASN:N	2.38	0.56
3:F:28:PHE:CD1	3:F:41:ASN:HB2	2.40	0.56
1:G:232:LEU:O	1:G:492:TYR:HA	2.05	0.56
1:A:117:LEU:HD23	1:A:121:SER:OG	2.05	0.56
1:A:117:LEU:O	1:A:121:SER:OG	2.10	0.56
1:A:232:LEU:O	1:A:492:TYR:HA	2.05	0.56
1:A:291:LEU:CD2	1:A:487:SER:HB2	2.36	0.56
3:C:16:LEU:HB3	3:C:95:VAL:HG11	1.87	0.56
1:D:90:LEU:CB	2:E:532:VAL:HG23	2.19	0.56
1:D:93:GLU:H	2:E:534:GLY:C	2.08	0.56
1:D:234:CYS:N	1:D:248:VAL:HG21	2.21	0.56
1:D:238:THR:HG22	1:D:277:ILE:HG12	1.87	0.56
1:D:239:PHE:C	1:D:241:GLY:H	2.08	0.56
1:D:482:ARG:O	1:D:486:ARG:NE	2.35	0.56
2:E:593:TYR:C	2:E:597:GLN:HB3	2.20	0.56
3:F:27:GLN:HG2	3:F:41:ASN:O	2.05	0.56
3:I:13:THR:HG22	3:I:14:VAL:H	1.71	0.56
3:F:51:SER:N	3:F:54:ASN:OD1	2.26	0.56
3:F:115:SER:OG	3:F:148:VAL:O	2.23	0.56
1:G:234:CYS:N	1:G:248:VAL:HG21	2.21	0.56
1:G:388:PHE:O	1:G:426:ILE:HG22	2.05	0.56
1:A:238:THR:HG22	1:A:277:ILE:HG12	1.87	0.56
3:C:153:LEU:HD11	3:C:178:VAL:HG11	1.88	0.56
1:D:291:LEU:CD2	1:D:487:SER:HB2	2.36	0.56
1:G:278:ILE:HA	1:G:291:LEU:O	2.05	0.56
3:I:30:TRP:CG	3:I:71:LEU:HD22	2.41	0.56
3:C:28:PHE:CD1	3:C:41:ASN:HB2	2.40	0.56
1:D:110:MET:O	1:D:114:VAL:HG23	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:104:ALA:HB1	3:F:116:LEU:HD21	1.87	0.56
1:A:229:TYR:HA	1:A:495:VAL:O	2.06	0.56
3:C:28:PHE:O	3:C:41:ASN:N	2.38	0.56
3:C:104:ALA:HB1	3:C:116:LEU:HD21	1.87	0.56
1:D:41:TRP:HD1	1:D:506:ALA:HA	1.71	0.56
1:D:115:ILE:HG22	1:D:433:TRP:CZ3	2.41	0.56
1:D:229:TYR:HA	1:D:495:VAL:O	2.06	0.56
1:A:237:LYS:HZ3	1:A:274:GLY:H	1.54	0.56
3:C:30:TRP:CG	3:C:71:LEU:HD22	2.41	0.56
1:G:300:ILE:HA	1:G:339:ILE:HG23	1.88	0.56
1:A:383:THR:HG22	1:A:388:PHE:HE1	1.70	0.56
1:G:291:LEU:CD2	1:G:487:SER:HB2	2.36	0.56
1:A:41:TRP:HD1	1:A:506:ALA:HA	1.71	0.56
1:D:378:THR:OG1	1:D:379:THR:N	2.38	0.56
3:I:27:GLN:HG2	3:I:41:ASN:O	2.05	0.56
1:A:45:TYR:HH	2:B:635:TRP:HH2	1.50	0.55
1:A:239:PHE:C	1:A:241:GLY:H	2.08	0.55
1:A:404:ASN:OD1	1:A:405:GLY:N	2.39	0.55
3:C:13:THR:HG22	3:C:14:VAL:H	1.70	0.55
1:G:383:THR:HG22	1:G:388:PHE:HE1	1.70	0.55
3:I:28:PHE:O	3:I:41:ASN:N	2.38	0.55
1:D:300:ILE:HA	1:D:339:ILE:HG23	1.88	0.55
1:D:404:ASN:OD1	1:D:405:GLY:N	2.39	0.55
1:G:41:TRP:HD1	1:G:506:ALA:HA	1.71	0.55
1:G:391:CYS:HB3	1:G:424:CYS:HA	1.87	0.55
1:A:378:THR:OG1	1:A:379:THR:N	2.38	0.55
2:B:583:LEU:O	2:B:586:ARG:HG3	2.06	0.55
1:D:237:LYS:HZ3	1:D:274:GLY:N	2.03	0.55
1:D:383:THR:HG22	1:D:388:PHE:HE1	1.70	0.55
2:E:583:LEU:O	2:E:586:ARG:HG3	2.06	0.55
3:F:153:LEU:HD11	3:F:178:VAL:HG11	1.88	0.55
3:I:29:HIS:CD2	3:I:40:GLY:HA3	2.42	0.55
1:A:90:LEU:HD11	2:B:524:ALA:N	2.21	0.55
1:A:257:ILE:HD11	1:A:492:TYR:HE2	1.72	0.55
2:B:596:ASP:O	2:B:600:LEU:N	2.40	0.55
3:C:9:LYS:HE2	3:C:172:PHE:CD1	2.42	0.55
3:F:30:TRP:CG	3:F:71:LEU:HD22	2.41	0.55
1:G:118:TRP:CE3	1:G:122:LEU:HD13	2.42	0.55
1:A:115:ILE:HG22	1:A:433:TRP:CZ3	2.41	0.55
1:D:118:TRP:CE3	1:D:122:LEU:HD13	2.42	0.55
1:G:115:ILE:HG22	1:G:433:TRP:CZ3	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:404:ASN:OD1	1:G:405:GLY:N	2.39	0.55
1:A:234:CYS:N	1:A:248:VAL:HG21	2.21	0.55
1:A:300:ILE:HA	1:A:339:ILE:HG23	1.88	0.55
3:F:9:LYS:HE2	3:F:172:PHE:CD1	2.42	0.55
3:F:13:THR:HG22	3:F:14:VAL:H	1.70	0.55
1:G:229:TYR:HA	1:G:495:VAL:O	2.06	0.55
1:A:118:TRP:CE3	1:A:122:LEU:HD13	2.42	0.55
3:C:115:SER:OG	3:C:148:VAL:O	2.23	0.55
2:E:596:ASP:O	2:E:600:LEU:N	2.40	0.55
1:A:239:PHE:C	1:A:241:GLY:N	2.61	0.55
1:A:333:ARG:NH2	1:A:428:GLN:OE1	2.40	0.55
3:C:112:GLN:HG3	3:C:152:GLU:HA	1.89	0.55
3:F:16:LEU:HB3	3:F:95:VAL:HG11	1.87	0.55
3:F:29:HIS:CD2	3:F:40:GLY:HA3	2.42	0.55
1:A:364:ILE:HB	1:A:401:TYR:HB3	1.89	0.55
3:F:112:GLN:HG3	3:F:152:GLU:HA	1.89	0.55
1:G:237:LYS:HZ3	1:G:274:GLY:H	1.53	0.55
1:G:257:ILE:HD11	1:G:492:TYR:HE2	1.72	0.55
1:A:265:LEU:O	1:A:380:HIS:NE2	2.37	0.54
3:C:29:HIS:CD2	3:C:40:GLY:HA3	2.42	0.54
1:D:333:ARG:NH2	1:D:428:GLN:OE1	2.40	0.54
1:G:111:HIS:HE1	1:G:433:TRP:HZ3	1.55	0.54
1:A:276:ILE:CG2	1:A:294:LEU:HA	2.31	0.54
1:D:239:PHE:C	1:D:241:GLY:N	2.61	0.54
1:G:420:ILE:HG22	1:G:421:THR:HG22	1.90	0.54
3:I:153:LEU:HD11	3:I:178:VAL:HG11	1.88	0.54
1:G:239:PHE:C	1:G:241:GLY:N	2.61	0.54
2:H:549:ARG:HA	2:H:552:LEU:HG	1.90	0.54
3:I:9:LYS:HE2	3:I:172:PHE:CD1	2.42	0.54
1:A:236:ASP:HB2	1:A:245:CYS:HB3	1.90	0.54
1:G:231:ILE:HG21	1:G:254:THR:HG22	1.90	0.54
2:H:583:LEU:O	2:H:586:ARG:HG3	2.06	0.54
3:I:112:GLN:HG3	3:I:152:GLU:HA	1.89	0.54
1:D:282:ASN:HB2	3:F:92:LYS:C	2.28	0.54
2:E:584:GLN:HB3	2:E:588:LEU:HD11	1.89	0.54
3:F:16:LEU:HD22	3:F:95:VAL:HG21	1.90	0.54
1:G:51:TRP:HB2	2:H:636:MET:HE3	1.89	0.54
1:G:364:ILE:HB	1:G:401:TYR:HB3	1.89	0.54
3:I:16:LEU:HD22	3:I:95:VAL:HG21	1.90	0.54
1:A:72:HIS:CD2	1:A:218:PRO:HA	2.43	0.54
1:G:333:ARG:NH2	1:G:428:GLN:OE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:LYS:O	1:A:211:CYS:HB2	2.07	0.54
1:D:391:CYS:HB3	1:D:423:PRO:O	2.08	0.54
3:I:131:GLN:HE22	3:I:141:GLN:HG2	1.73	0.54
1:D:44:VAL:HB	2:E:613:THR:HG21	1.88	0.54
1:D:123:LYS:O	1:D:211:CYS:HB2	2.07	0.54
1:D:231:ILE:HG21	1:D:254:THR:HG22	1.90	0.54
1:D:282:ASN:H	3:F:92:LYS:N	1.92	0.54
1:G:123:LYS:O	1:G:211:CYS:HB2	2.07	0.54
1:G:276:ILE:CG2	1:G:294:LEU:HA	2.31	0.54
2:H:584:GLN:HB3	2:H:588:LEU:HD11	1.89	0.54
2:H:648:THR:O	2:H:651:LYS:HB3	2.08	0.54
1:A:391:CYS:HB3	1:A:423:PRO:O	2.08	0.54
3:F:133:ARG:O	3:F:159:TRP:HB3	2.08	0.54
3:I:115:SER:OG	3:I:148:VAL:O	2.23	0.54
3:C:131:GLN:HE22	3:C:141:GLN:HG2	1.73	0.54
1:G:46:TYR:HB3	2:H:609:LEU:HD12	1.90	0.54
1:G:72:HIS:CD2	1:G:218:PRO:HA	2.43	0.54
1:G:237:LYS:CE	1:G:274:GLY:H	2.21	0.54
1:D:72:HIS:CD2	1:D:218:PRO:HA	2.43	0.53
1:D:264:GLN:HE21	1:D:477:GLY:HA2	1.72	0.53
1:D:288:LYS:HZ3	3:F:94:GLU:CB	2.21	0.53
1:G:62:SER:OG	1:G:76:ALA:HB1	2.09	0.53
1:G:391:CYS:HB3	1:G:423:PRO:O	2.08	0.53
1:D:237:LYS:CE	1:D:274:GLY:H	2.21	0.53
1:D:257:ILE:HD11	1:D:492:TYR:HE2	1.72	0.53
1:D:367:PHE:O	1:D:368:THR:HG22	2.08	0.53
2:E:648:THR:O	2:E:651:LYS:HB3	2.08	0.53
1:G:481:MET:O	1:G:484:ASN:N	2.41	0.53
1:D:42:VAL:HG22	2:E:617:TRP:CA	2.38	0.53
2:E:549:ARG:HA	2:E:552:LEU:HG	1.90	0.53
1:G:255:HIS:H	1:G:492:TYR:HH	1.56	0.53
3:C:133:ARG:O	3:C:159:TRP:HB3	2.08	0.53
1:G:264:GLN:HE21	1:G:477:GLY:HA2	1.72	0.53
1:A:42:VAL:HB	2:B:613:THR:OG1	2.09	0.53
1:A:62:SER:OG	1:A:76:ALA:HB1	2.09	0.53
1:A:367:PHE:O	1:A:368:THR:HG22	2.08	0.53
1:D:420:ILE:HG22	1:D:421:THR:HG22	1.90	0.53
2:E:543:THR:HA	2:E:546:VAL:HG23	1.91	0.53
3:F:120:LEU:HD21	3:F:163:VAL:HG21	1.91	0.53
3:I:133:ARG:O	3:I:159:TRP:HB3	2.08	0.53
2:B:608:LYS:HA	2:E:598:GLN:NE2	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:ASP:N	1:D:68:ASP:OD1	2.41	0.53
1:G:68:ASP:OD1	1:G:68:ASP:N	2.41	0.53
1:D:281:GLU:CB	3:F:92:LYS:HB2	2.39	0.53
2:E:656:SER:HA	2:E:659:GLN:HB3	1.91	0.53
3:F:131:GLN:HE22	3:F:141:GLN:HG2	1.73	0.53
2:H:596:ASP:O	2:H:600:LEU:N	2.40	0.53
1:A:286:ASN:HB3	1:A:462:ARG:CZ	2.39	0.53
1:A:420:ILE:HG22	1:A:421:THR:HG22	1.89	0.53
1:A:481:MET:O	1:A:484:ASN:N	2.41	0.53
1:D:236:ASP:HB2	1:D:245:CYS:HB3	1.90	0.53
1:D:364:ILE:HB	1:D:401:TYR:HB3	1.90	0.53
2:E:552:LEU:HD13	2:H:650:TYR:CD2	2.43	0.53
3:F:110:LEU:HD11	3:F:116:LEU:HD12	1.91	0.53
1:G:483:ASP:OD1	1:G:486:ARG:NE	2.42	0.53
2:H:574:GLN:O	2:H:577:VAL:HG22	2.09	0.53
2:B:656:SER:HA	2:B:659:GLN:HB3	1.91	0.53
3:C:120:LEU:HD21	3:C:163:VAL:HG21	1.91	0.53
1:D:50:VAL:HG11	2:E:639:ASP:CB	2.39	0.53
1:D:251:VAL:O	2:E:524:ALA:HB1	2.09	0.53
2:H:543:THR:HA	2:H:546:VAL:HG23	1.91	0.53
1:A:483:ASP:OD1	1:A:486:ARG:NE	2.42	0.53
3:C:64:TRP:CD1	3:C:69:PHE:HD1	2.27	0.53
1:D:62:SER:OG	1:D:76:ALA:HB1	2.09	0.53
1:D:302:CYS:HB3	1:D:304:ARG:NH2	2.24	0.53
1:D:506:ALA:H	2:H:665:LYS:NZ	2.06	0.53
2:E:574:GLN:O	2:E:577:VAL:HG22	2.09	0.53
1:G:46:TYR:C	2:H:530:LEU:HD13	2.29	0.53
1:G:367:PHE:O	1:G:368:THR:HG22	2.08	0.53
1:G:482:ARG:O	1:G:486:ARG:NE	2.35	0.53
3:I:110:LEU:HD11	3:I:116:LEU:HD12	1.91	0.53
1:A:264:GLN:HE21	1:A:477:GLY:HA2	1.72	0.52
1:A:302:CYS:HB3	1:A:304:ARG:NH2	2.24	0.52
2:B:543:THR:HA	2:B:546:VAL:HG23	1.91	0.52
2:B:584:GLN:HB3	2:B:588:LEU:HD11	1.89	0.52
2:E:635:TRP:HE3	2:E:638:TRP:CD1	2.28	0.52
1:G:264:GLN:HG2	1:G:477:GLY:N	2.24	0.52
2:H:593:TYR:HE1	2:H:597:GLN:HE21	1.57	0.52
3:I:28:PHE:CE1	3:I:41:ASN:HB2	2.44	0.52
1:A:467:GLU:H	1:A:467:GLU:CD	2.08	0.52
2:B:648:THR:O	2:B:651:LYS:HB3	2.08	0.52
3:C:16:LEU:HD22	3:C:95:VAL:HG21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:88:VAL:HG13	3:C:89:GLU:H	1.74	0.52
1:D:233:LYS:O	1:D:248:VAL:HG11	2.09	0.52
1:D:250:THR:CG2	2:E:524:ALA:HB2	2.40	0.52
1:D:264:GLN:HG2	1:D:477:GLY:N	2.24	0.52
1:D:502:VAL:HG12	2:E:617:TRP:CZ3	2.36	0.52
3:F:28:PHE:CE1	3:F:41:ASN:HB2	2.45	0.52
1:G:225:THR:OG1	1:G:229:TYR:O	2.19	0.52
1:G:480:ASP:OD1	3:I:43:GLY:HA3	2.09	0.52
3:I:86:CYS:N	3:I:93:GLU:O	2.42	0.52
1:D:117:LEU:O	1:D:121:SER:OG	2.10	0.52
1:D:353:GLU:O	1:D:357:GLU:HG3	2.09	0.52
1:D:481:MET:O	1:D:484:ASN:N	2.41	0.52
1:G:277:ILE:O	1:G:292:VAL:HA	2.10	0.52
2:H:548:ALA:HB3	2:H:549:ARG:NH1	2.24	0.52
2:H:600:LEU:HA	2:H:603:TRP:CE3	2.45	0.52
1:A:233:LYS:O	1:A:248:VAL:HG11	2.09	0.52
1:A:353:GLU:O	1:A:357:GLU:HG3	2.09	0.52
2:B:574:GLN:O	2:B:577:VAL:HG22	2.09	0.52
1:D:483:ASP:OD1	1:D:486:ARG:NE	2.42	0.52
1:A:231:ILE:HG21	1:A:254:THR:HG22	1.90	0.52
1:A:264:GLN:HG2	1:A:477:GLY:N	2.24	0.52
1:D:41:TRP:HA	2:E:617:TRP:N	2.23	0.52
1:D:308:ASN:ND2	1:D:334:GLN:OE1	2.43	0.52
1:G:301:VAL:HA	1:G:451:CYS:O	2.09	0.52
1:G:353:GLU:O	1:G:357:GLU:HG3	2.09	0.52
1:G:503:ALA:HB2	2:H:635:TRP:CH2	2.39	0.52
2:B:548:ALA:HB3	2:B:549:ARG:NH1	2.24	0.52
2:B:549:ARG:HA	2:B:552:LEU:HG	1.90	0.52
2:E:593:TYR:HE1	2:E:597:GLN:HE21	1.57	0.52
3:F:88:VAL:HG13	3:F:89:GLU:H	1.74	0.52
1:G:265:LEU:O	1:G:380:HIS:NE2	2.37	0.52
1:G:286:ASN:HB3	1:G:462:ARG:CZ	2.39	0.52
1:D:277:ILE:O	1:D:292:VAL:HA	2.10	0.52
2:E:548:ALA:HB3	2:E:549:ARG:NH1	2.24	0.52
2:E:598:GLN:O	2:E:601:GLY:N	2.41	0.52
1:G:233:LYS:O	1:G:248:VAL:HG11	2.09	0.52
1:G:236:ASP:HB2	1:G:245:CYS:HB3	1.90	0.52
3:I:64:TRP:CD1	3:I:69:PHE:HD1	2.27	0.52
1:A:64:ALA:HB2	1:A:76:ALA:HB3	1.91	0.52
1:A:301:VAL:HA	1:A:451:CYS:O	2.09	0.52
3:C:110:LEU:HD11	3:C:116:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:ASN:HB3	1:D:462:ARG:CZ	2.39	0.52
1:D:265:LEU:O	1:D:380:HIS:NE2	2.37	0.52
1:G:111:HIS:O	1:G:115:ILE:HG23	2.10	0.52
1:G:483:ASP:O	1:G:486:ARG:N	2.39	0.52
2:H:656:SER:HA	2:H:659:GLN:HB3	1.91	0.52
3:I:88:VAL:HG13	3:I:89:GLU:H	1.74	0.52
1:A:308:ASN:ND2	1:A:334:GLN:OE1	2.43	0.52
2:B:598:GLN:O	2:B:601:GLY:N	2.41	0.52
1:D:64:ALA:HB3	1:D:77:THR:HG23	1.92	0.52
2:E:525:VAL:HG23	2:E:527:LEU:O	2.10	0.52
3:F:52:LYS:HG3	3:F:53:LEU:HG	1.92	0.52
3:F:64:TRP:CD1	3:F:69:PHE:HD1	2.27	0.52
1:G:46:TYR:OH	2:H:527:LEU:HD13	2.09	0.52
2:H:634:THR:O	2:H:636:MET:N	2.43	0.52
1:A:73:ASN:HA	1:A:76:ALA:HB3	1.92	0.51
1:A:237:LYS:CE	1:A:274:GLY:H	2.21	0.51
1:D:46:TYR:HB3	2:E:609:LEU:O	2.10	0.51
1:D:95:VAL:CG1	2:E:534:GLY:HA2	2.40	0.51
1:D:111:HIS:O	1:D:115:ILE:HG23	2.10	0.51
1:D:281:GLU:HG2	3:F:91:GLN:HA	1.93	0.51
1:D:467:GLU:H	1:D:467:GLU:CD	2.08	0.51
2:E:600:LEU:HA	2:E:603:TRP:CE3	2.45	0.51
1:G:112:GLU:O	1:G:115:ILE:HG12	2.10	0.51
1:A:68:ASP:N	1:A:68:ASP:OD1	2.41	0.51
1:A:225:THR:OG1	1:A:226:PRO:O	2.29	0.51
1:A:228:GLY:O	1:A:497:ILE:HG12	2.10	0.51
1:A:376:GLU:HG2	3:C:45:PHE:HZ	1.75	0.51
1:D:42:VAL:HG13	2:E:617:TRP:CE3	2.44	0.51
1:D:248:VAL:HG22	1:D:249:SER:N	2.26	0.51
1:D:276:ILE:CG2	1:D:294:LEU:HA	2.31	0.51
1:D:301:VAL:HA	1:D:451:CYS:O	2.09	0.51
1:G:46:TYR:HB3	2:H:609:LEU:CD1	2.41	0.51
1:A:277:ILE:O	1:A:292:VAL:HA	2.10	0.51
2:B:634:THR:O	2:B:636:MET:N	2.43	0.51
3:C:28:PHE:CE1	3:C:41:ASN:HB2	2.45	0.51
1:D:64:ALA:HB2	1:D:76:ALA:HB3	1.91	0.51
1:D:225:THR:OG1	1:D:226:PRO:O	2.29	0.51
1:D:355:LEU:O	1:D:359:PHE:N	2.41	0.51
1:G:302:CYS:HB3	1:G:304:ARG:NH2	2.24	0.51
1:G:504:PRO:HG2	2:H:629:ILE:CD1	2.41	0.51
3:I:120:LEU:HD21	3:I:163:VAL:HG21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:ASP:O	1:A:486:ARG:N	2.39	0.51
1:G:225:THR:OG1	1:G:226:PRO:O	2.29	0.51
1:G:228:GLY:O	1:G:497:ILE:HG12	2.10	0.51
1:G:308:ASN:ND2	1:G:334:GLN:OE1	2.43	0.51
2:H:635:TRP:HE3	2:H:638:TRP:CD1	2.28	0.51
1:A:111:HIS:O	1:A:115:ILE:HG23	2.10	0.51
1:A:248:VAL:HG22	1:A:249:SER:N	2.26	0.51
2:B:600:LEU:HA	2:B:603:TRP:CE3	2.45	0.51
2:E:549:ARG:NH2	2:H:654:GLU:HB3	2.26	0.51
1:G:64:ALA:HB2	1:G:76:ALA:HB3	1.91	0.51
1:G:248:VAL:HG22	1:G:249:SER:N	2.26	0.51
2:B:635:TRP:HE3	2:B:638:TRP:CD1	2.28	0.51
2:B:668:LEU:HD13	1:G:508:LYS:HG3	1.92	0.51
3:C:52:LYS:HG3	3:C:53:LEU:HG	1.91	0.51
1:D:390:TYR:N	1:D:425:ARG:O	2.23	0.51
2:E:634:THR:O	2:E:636:MET:N	2.43	0.51
2:E:634:THR:H	2:E:637:GLN:HE21	1.58	0.51
2:H:525:VAL:HG23	2:H:527:LEU:O	2.10	0.51
1:A:112:GLU:O	1:A:115:ILE:HG12	2.11	0.51
2:B:525:VAL:HG23	2:B:527:LEU:O	2.10	0.51
2:B:544:LEU:HD11	2:B:610:ILE:HD11	1.93	0.51
1:D:73:ASN:HA	1:D:76:ALA:HB3	1.92	0.51
1:D:112:GLU:O	1:D:115:ILE:HG12	2.11	0.51
1:A:376:GLU:HG2	3:C:45:PHE:CZ	2.46	0.51
1:D:82:PRO:O	2:E:578:TRP:CE2	2.64	0.51
1:D:228:GLY:O	1:D:497:ILE:HG12	2.10	0.51
1:D:480:ASP:OD1	1:D:482:ARG:NH1	2.44	0.51
1:G:381:SER:HB3	1:G:390:TYR:CE1	2.40	0.51
3:I:37:LYS:O	3:I:49:GLY:HA3	2.11	0.51
3:I:52:LYS:HG3	3:I:53:LEU:HG	1.92	0.51
3:C:37:LYS:O	3:C:49:GLY:HA3	2.11	0.51
1:D:90:LEU:CD1	2:E:532:VAL:HG23	2.41	0.51
1:D:226:PRO:O	1:D:229:TYR:HB2	2.11	0.51
1:D:384:CYS:HB2	1:D:389:PHE:HE1	1.76	0.51
2:E:576:THR:HG22	2:H:580:ILE:CD1	2.40	0.51
1:G:64:ALA:HB3	1:G:77:THR:HG23	1.92	0.51
1:G:73:ASN:HA	1:G:76:ALA:HB3	1.93	0.51
2:H:634:THR:H	2:H:637:GLN:HE21	1.58	0.51
1:A:226:PRO:O	1:A:229:TYR:HB2	2.11	0.51
1:A:359:PHE:HE2	1:A:474:ASN:OD1	1.94	0.51
2:B:668:LEU:HD22	1:G:508:LYS:HE2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:634:THR:H	2:B:637:GLN:HE21	1.58	0.50
2:B:639:ASP:OD1	2:B:642:ILE:HG13	2.11	0.50
1:D:296:GLN:HG2	1:D:297:SER:H	1.76	0.50
1:G:359:PHE:HE2	1:G:474:ASN:OD1	1.95	0.50
2:H:639:ASP:OD1	2:H:642:ILE:HG13	2.11	0.50
1:A:233:LYS:HB3	1:A:248:VAL:CG2	2.41	0.50
1:G:233:LYS:HB3	1:G:248:VAL:CG2	2.41	0.50
1:G:384:CYS:HB2	1:G:389:PHE:HE1	1.76	0.50
2:H:598:GLN:O	2:H:606:SER:HB2	2.11	0.50
3:I:9:LYS:N	3:I:12:ASP:OD2	2.44	0.50
1:A:480:ASP:OD1	1:A:482:ARG:NH1	2.44	0.50
1:D:233:LYS:HB3	1:D:248:VAL:CG2	2.41	0.50
1:D:359:PHE:HE2	1:D:474:ASN:OD1	1.95	0.50
3:F:37:LYS:O	3:F:49:GLY:HA3	2.11	0.50
2:H:598:GLN:O	2:H:601:GLY:N	2.41	0.50
1:A:45:TYR:OH	2:B:635:TRP:HH2	1.93	0.50
1:A:296:GLN:HG2	1:A:297:SER:H	1.76	0.50
3:C:36:ILE:N	3:C:36:ILE:HD12	2.26	0.50
2:E:544:LEU:HD11	2:E:610:ILE:HD11	1.93	0.50
1:A:239:PHE:HB2	1:A:241:GLY:H	1.77	0.50
2:B:598:GLN:CG	2:B:599:LEU:HD22	2.30	0.50
1:D:307:ASN:HD22	1:D:336:HIS:HE1	1.60	0.50
2:E:639:ASP:OD1	2:E:642:ILE:HG13	2.11	0.50
3:F:25:SER:O	3:F:25:SER:OG	2.30	0.50
3:I:18:CYS:HB3	3:I:69:PHE:HB2	1.93	0.50
1:A:262:SER:OG	1:A:382:PHE:HB3	2.12	0.50
1:A:333:ARG:HB2	1:A:425:ARG:NH2	2.27	0.50
3:C:86:CYS:N	3:C:93:GLU:O	2.42	0.50
1:D:383:THR:HG22	1:D:388:PHE:CE1	2.46	0.50
2:E:598:GLN:O	2:E:606:SER:HB2	2.11	0.50
1:G:307:ASN:HD22	1:G:336:HIS:HE1	1.60	0.50
1:G:480:ASP:OD1	1:G:482:ARG:NH1	2.44	0.50
1:G:504:PRO:HG2	2:H:629:ILE:HD13	1.94	0.50
1:D:262:SER:OG	1:D:382:PHE:HB3	2.12	0.50
3:F:36:ILE:HD12	3:F:36:ILE:N	2.26	0.50
1:G:131:LEU:HD23	1:G:132:CYS:N	2.27	0.50
1:G:226:PRO:O	1:G:229:TYR:HB2	2.11	0.50
1:G:333:ARG:HB2	1:G:425:ARG:NH2	2.27	0.50
1:A:93:GLU:HB2	2:B:534:GLY:HA3	1.93	0.50
2:B:598:GLN:O	2:B:606:SER:HB2	2.11	0.50
3:C:9:LYS:N	3:C:12:ASP:OD2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:483:ASP:O	1:D:486:ARG:N	2.39	0.50
3:F:9:LYS:N	3:F:12:ASP:OD2	2.44	0.50
1:G:50:VAL:O	1:G:498:LYS:N	2.42	0.50
1:G:338:ASN:HB2	1:G:419:SER:HB2	1.94	0.50
1:G:344:TRP:O	1:G:348:LEU:HD12	2.12	0.50
1:G:355:LEU:O	1:G:359:PHE:N	2.41	0.50
3:I:39:LEU:HD22	3:I:46:LEU:HD11	1.94	0.50
1:A:53:GLU:N	1:A:53:GLU:OE1	2.45	0.50
1:A:307:ASN:HD22	1:A:336:HIS:HE1	1.60	0.50
1:D:263:THR:HG21	1:D:376:GLU:O	2.11	0.50
2:E:593:TYR:C	2:E:593:TYR:HD1	2.15	0.50
1:G:263:THR:HG21	1:G:376:GLU:O	2.11	0.50
1:A:135:LEU:H	1:A:200:ILE:HG23	1.77	0.49
1:A:381:SER:HB3	1:A:390:TYR:CE1	2.40	0.49
1:D:111:HIS:HE1	1:D:433:TRP:HZ3	1.55	0.49
1:D:237:LYS:HZ3	1:D:274:GLY:H	1.58	0.49
2:E:622:SER:HB3	2:E:624:LYS:HE2	1.94	0.49
1:G:262:SER:OG	1:G:382:PHE:HB3	2.12	0.49
2:H:544:LEU:HD11	2:H:610:ILE:HD11	1.93	0.49
3:I:23:LYS:HA	3:I:67:GLY:HA3	1.94	0.49
3:C:81:SER:O	3:C:81:SER:OG	2.30	0.49
1:D:333:ARG:HB2	1:D:425:ARG:NH2	2.27	0.49
3:F:39:LEU:HD22	3:F:46:LEU:HD11	1.93	0.49
1:G:44:VAL:HA	1:G:501:GLY:O	2.12	0.49
3:I:36:ILE:HD12	3:I:36:ILE:N	2.26	0.49
3:I:134:SER:HB2	3:I:159:TRP:CZ3	2.48	0.49
1:A:45:TYR:OH	2:B:635:TRP:CH2	2.65	0.49
1:A:57:THR:HA	1:A:109:GLN:HE22	1.78	0.49
1:A:64:ALA:HB3	1:A:77:THR:HG23	1.92	0.49
1:A:263:THR:HG21	1:A:376:GLU:O	2.11	0.49
1:A:302:CYS:CB	1:A:304:ARG:HH22	2.25	0.49
1:D:50:VAL:CG1	2:E:639:ASP:CB	2.90	0.49
1:D:508:LYS:O	2:H:668:LEU:HD22	2.12	0.49
3:C:39:LEU:HD22	3:C:46:LEU:HD11	1.93	0.49
1:D:53:GLU:N	1:D:53:GLU:OE1	2.45	0.49
3:F:134:SER:HB2	3:F:159:TRP:CZ3	2.48	0.49
2:H:651:LYS:HE2	2:H:652:LEU:HG	1.94	0.49
1:A:131:LEU:HD23	1:A:132:CYS:N	2.27	0.49
1:A:234:CYS:HB2	1:A:491:LYS:HA	1.95	0.49
4:A:601:NAG:H83	2:B:535:SER:HA	1.95	0.49
2:B:593:TYR:C	2:B:593:TYR:HD1	2.15	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:18:CYS:HB3	3:C:69:PHE:HB2	1.93	0.49
1:D:449:ILE:N	1:D:449:ILE:HD12	2.28	0.49
2:E:597:GLN:O	2:E:600:LEU:HD12	2.13	0.49
3:F:87:GLU:HA	3:F:91:GLN:O	2.13	0.49
1:G:51:TRP:O	2:H:636:MET:HE3	2.12	0.49
1:G:367:PHE:CZ	1:G:397:PHE:HD2	2.31	0.49
1:A:86:SER:O	1:A:86:SER:OG	2.29	0.49
1:A:255:HIS:H	1:A:492:TYR:HH	1.55	0.49
1:A:393:THR:O	1:A:393:THR:OG1	2.28	0.49
2:B:555:ILE:CD1	1:D:54:ALA:HB2	2.43	0.49
2:B:593:TYR:HE1	2:B:597:GLN:HE21	1.57	0.49
1:D:282:ASN:N	3:F:92:LYS:H	1.92	0.49
1:D:288:LYS:HZ3	3:F:94:GLU:HB2	1.78	0.49
1:D:381:SER:HB3	1:D:390:TYR:CE1	2.40	0.49
1:G:109:GLN:O	1:G:112:GLU:HG3	2.12	0.49
1:G:239:PHE:HB2	1:G:241:GLY:H	1.77	0.49
1:G:460:LEU:O	1:G:460:LEU:HG	2.13	0.49
2:H:597:GLN:O	2:H:600:LEU:HD12	2.13	0.49
1:A:44:VAL:HA	1:A:501:GLY:O	2.12	0.49
1:A:344:TRP:O	1:A:348:LEU:HD12	2.12	0.49
3:C:23:LYS:HA	3:C:67:GLY:HA3	1.94	0.49
3:C:38:ILE:O	3:C:39:LEU:HD23	2.13	0.49
1:D:50:VAL:HG12	1:D:498:LYS:HB2	1.94	0.49
1:D:131:LEU:HD23	1:D:132:CYS:N	2.27	0.49
1:D:135:LEU:H	1:D:200:ILE:HG23	1.78	0.49
1:D:228:GLY:H	2:E:527:LEU:CD2	2.24	0.49
1:D:239:PHE:HB2	1:D:241:GLY:H	1.77	0.49
1:D:460:LEU:O	1:D:460:LEU:HG	2.13	0.49
1:G:102:TRP:HA	1:G:486:ARG:NH1	2.28	0.49
1:G:296:GLN:HG2	1:G:297:SER:H	1.76	0.49
1:G:449:ILE:N	1:G:449:ILE:HD12	2.28	0.49
3:I:38:ILE:O	3:I:39:LEU:HD23	2.13	0.49
1:A:62:SER:HB2	1:A:221:ILE:HG23	1.95	0.49
3:C:134:SER:HB2	3:C:159:TRP:CZ3	2.48	0.49
1:D:44:VAL:HB	2:E:613:THR:CG2	2.43	0.49
1:D:338:ASN:HB2	1:D:419:SER:HB2	1.94	0.49
1:D:344:TRP:O	1:D:348:LEU:HD12	2.12	0.49
1:D:502:VAL:HG21	2:E:649:ILE:HG21	1.94	0.49
3:F:18:CYS:HB3	3:F:69:PHE:HB2	1.93	0.49
3:F:23:LYS:HA	3:F:67:GLY:HA3	1.94	0.49
3:F:34:ASN:OD1	3:F:34:ASN:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:PHE:CZ	1:A:397:PHE:HD2	2.31	0.49
1:A:383:THR:HG22	1:A:388:PHE:CE1	2.46	0.49
1:A:384:CYS:HB2	1:A:389:PHE:HE1	1.76	0.49
2:B:593:TYR:C	2:B:593:TYR:CD1	2.86	0.49
2:B:597:GLN:O	2:B:600:LEU:HD12	2.13	0.49
1:D:41:TRP:CD1	1:D:506:ALA:HA	2.48	0.49
1:D:44:VAL:HA	1:D:501:GLY:O	2.12	0.49
1:D:367:PHE:CZ	1:D:397:PHE:HD2	2.31	0.49
1:G:53:GLU:OE1	1:G:53:GLU:N	2.45	0.49
1:G:135:LEU:H	1:G:200:ILE:HG23	1.77	0.49
1:G:260:VAL:HG11	1:G:267:LEU:O	2.13	0.49
3:I:87:GLU:HA	3:I:91:GLN:O	2.13	0.49
1:A:44:VAL:HG22	1:A:502:VAL:HA	1.95	0.49
1:A:70:GLU:OE1	1:A:215:SER:OG	2.20	0.49
1:D:109:GLN:O	1:D:112:GLU:HG3	2.12	0.49
1:G:393:THR:O	1:G:393:THR:OG1	2.28	0.49
1:A:449:ILE:N	1:A:449:ILE:HD12	2.28	0.48
1:D:302:CYS:CB	1:D:304:ARG:HH22	2.25	0.48
3:F:38:ILE:O	3:F:39:LEU:HD23	2.12	0.48
2:H:635:TRP:C	2:H:638:TRP:H	2.11	0.48
1:A:338:ASN:HB2	1:A:419:SER:HB2	1.94	0.48
1:D:92:LEU:HG	1:D:249:SER:HA	1.95	0.48
1:G:57:THR:HA	1:G:109:GLN:HE22	1.78	0.48
3:I:34:ASN:OD1	3:I:34:ASN:N	2.46	0.48
1:A:50:VAL:HG12	1:A:498:LYS:HB2	1.94	0.48
1:A:102:TRP:HA	1:A:486:ARG:NH1	2.28	0.48
1:A:109:GLN:O	1:A:112:GLU:HG3	2.12	0.48
1:A:372:GLY:O	3:C:48:LYS:HB2	2.12	0.48
3:C:56:ARG:HH22	3:C:77:LYS:HG3	1.78	0.48
1:D:62:SER:HB2	1:D:221:ILE:HG23	1.95	0.48
2:E:600:LEU:HD12	2:E:606:SER:HA	1.96	0.48
2:E:651:LYS:HE2	2:E:652:LEU:HG	1.94	0.48
1:G:50:VAL:HG12	1:G:498:LYS:HB2	1.94	0.48
1:G:383:THR:HG22	1:G:388:PHE:CE1	2.46	0.48
2:H:593:TYR:C	2:H:593:TYR:HD1	2.15	0.48
1:A:41:TRP:CD1	1:A:506:ALA:HA	2.48	0.48
3:C:34:ASN:OD1	3:C:34:ASN:N	2.46	0.48
3:C:165:GLN:NE2	3:C:166:ASN:OD1	2.47	0.48
3:I:56:ARG:HH22	3:I:77:LYS:HG3	1.78	0.48
1:A:234:CYS:HA	1:A:248:VAL:HG11	1.96	0.48
2:B:651:LYS:HE2	2:B:652:LEU:HG	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:506:ALA:H	2:H:665:LYS:HZ3	1.61	0.48
3:C:87:GLU:HA	3:C:91:GLN:O	2.13	0.48
1:D:57:THR:HA	1:D:109:GLN:HE22	1.77	0.48
1:D:369:SER:O	1:D:369:SER:OG	2.32	0.48
1:G:62:SER:HB2	1:G:221:ILE:HG23	1.95	0.48
1:G:132:CYS:HB3	1:G:201:ASN:C	2.34	0.48
1:G:233:LYS:HB3	1:G:248:VAL:HG21	1.95	0.48
1:G:369:SER:O	1:G:369:SER:OG	2.32	0.48
2:H:622:SER:HB3	2:H:624:LYS:HE2	1.94	0.48
1:D:102:TRP:HA	1:D:486:ARG:NH1	2.28	0.48
1:D:132:CYS:HB3	1:D:201:ASN:C	2.34	0.48
1:G:92:LEU:HG	1:G:249:SER:HA	1.95	0.48
1:G:234:CYS:HA	1:G:248:VAL:HG11	1.96	0.48
1:A:67:TYR:HD1	1:A:67:TYR:O	1.97	0.48
1:A:231:ILE:HG21	1:A:254:THR:CG2	2.44	0.48
1:A:460:LEU:HG	1:A:460:LEU:O	2.13	0.48
2:B:622:SER:HB3	2:B:624:LYS:HE2	1.94	0.48
1:D:42:VAL:HB	2:E:615:VAL:HG23	1.95	0.48
1:D:44:VAL:HG22	1:D:502:VAL:HA	1.95	0.48
1:G:234:CYS:HB2	1:G:491:LYS:HA	1.95	0.48
1:A:257:ILE:HG21	1:A:489:LEU:HD11	1.96	0.48
1:A:260:VAL:HG11	1:A:267:LEU:O	2.13	0.48
3:C:61:ARG:HG3	3:C:64:TRP:CH2	2.49	0.48
1:D:231:ILE:HG21	1:D:254:THR:CG2	2.44	0.48
1:D:234:CYS:HB2	1:D:491:LYS:HA	1.95	0.48
1:D:285:ASN:HB2	3:F:94:GLU:HB3	1.95	0.48
1:D:391:CYS:N	1:D:424:CYS:SG	2.87	0.48
2:E:548:ALA:HA	2:H:599:LEU:HG	1.95	0.48
2:E:644:ASN:HB3	4:E:704:NAG:O5	2.13	0.48
3:F:56:ARG:HH22	3:F:77:LYS:HG3	1.78	0.48
3:F:86:CYS:N	3:F:93:GLU:O	2.42	0.48
1:A:92:LEU:HG	1:A:249:SER:HA	1.95	0.48
1:D:239:PHE:CE2	1:D:490:TYR:HD2	2.32	0.48
1:G:231:ILE:HG21	1:G:254:THR:CG2	2.44	0.48
1:G:302:CYS:CB	1:G:304:ARG:HH22	2.25	0.48
3:I:103:THR:OG1	3:I:104:ALA:N	2.47	0.48
1:A:355:LEU:O	1:A:359:PHE:N	2.41	0.47
3:C:32:ASN:HB3	3:C:38:ILE:HD11	1.95	0.47
3:C:140:ILE:HG22	3:C:146:LEU:HD22	1.96	0.47
1:D:67:TYR:HD1	1:D:67:TYR:O	1.97	0.47
1:D:260:VAL:HG11	1:D:267:LEU:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:239:PHE:CE2	1:G:490:TYR:HD2	2.32	0.47
1:G:257:ILE:HG21	1:G:489:LEU:HD11	1.96	0.47
1:G:502:VAL:O	2:H:635:TRP:CZ3	2.66	0.47
3:C:164:LEU:HA	3:C:168:LYS:O	2.15	0.47
2:E:593:TYR:C	2:E:593:TYR:CD1	2.86	0.47
1:G:391:CYS:N	1:G:424:CYS:SG	2.87	0.47
2:H:598:GLN:CG	2:H:599:LEU:HD22	2.30	0.47
3:I:32:ASN:HB3	3:I:38:ILE:HD11	1.95	0.47
1:A:350:ARG:HA	1:A:353:GLU:HG3	1.96	0.47
1:D:350:ARG:HA	1:D:353:GLU:HG3	1.97	0.47
2:E:594:LEU:HD23	2:E:594:LEU:HA	1.65	0.47
3:F:165:GLN:NE2	3:F:166:ASN:OD1	2.47	0.47
3:I:61:ARG:HG3	3:I:64:TRP:CH2	2.49	0.47
1:A:58:LEU:HD12	1:A:223:TYR:HD2	1.79	0.47
1:A:369:SER:O	1:A:369:SER:OG	2.31	0.47
3:C:4:LYS:HZ3	3:C:95:VAL:HG12	1.79	0.47
3:C:103:THR:OG1	3:C:104:ALA:N	2.47	0.47
3:F:164:LEU:HA	3:F:168:LYS:O	2.14	0.47
1:G:125:CYS:HB2	1:G:440:MET:O	2.14	0.47
2:H:593:TYR:C	2:H:593:TYR:CD1	2.86	0.47
2:H:600:LEU:HD12	2:H:606:SER:HA	1.96	0.47
1:D:233:LYS:HB3	1:D:248:VAL:HG21	1.96	0.47
1:G:67:TYR:O	1:G:67:TYR:HD1	1.97	0.47
1:D:50:VAL:HG11	2:E:639:ASP:HB2	1.96	0.47
1:D:234:CYS:HA	1:D:248:VAL:HG11	1.96	0.47
3:F:32:ASN:HB3	3:F:38:ILE:HD11	1.95	0.47
3:F:140:ILE:HG22	3:F:146:LEU:HD22	1.96	0.47
1:G:481:MET:HA	1:G:484:ASN:CB	2.45	0.47
3:I:164:LEU:HA	3:I:168:LYS:O	2.15	0.47
1:A:64:ALA:HB1	1:A:73:ASN:HB3	1.97	0.47
1:A:125:CYS:HB2	1:A:440:MET:O	2.14	0.47
1:A:391:CYS:N	1:A:424:CYS:SG	2.87	0.47
3:C:159:TRP:NE1	3:C:176:ILE:HG13	2.29	0.47
1:D:58:LEU:HD12	1:D:223:TYR:HD2	1.79	0.47
1:D:64:ALA:HB1	1:D:73:ASN:HB3	1.97	0.47
1:D:99:PHE:N	1:D:99:PHE:HD1	2.13	0.47
1:D:481:MET:HA	1:D:484:ASN:CB	2.45	0.47
2:E:599:LEU:C	2:E:601:GLY:N	2.68	0.47
2:E:645:TYR:O	2:E:649:ILE:HG22	2.15	0.47
3:F:107:ASP:OD2	3:F:108:THR:OG1	2.23	0.47
1:G:41:TRP:CD1	1:G:506:ALA:HA	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:44:VAL:HG22	1:G:502:VAL:HA	1.95	0.47
1:G:51:TRP:O	2:H:636:MET:CE	2.63	0.47
3:I:165:GLN:NE2	3:I:166:ASN:OD1	2.47	0.47
1:A:126:VAL:HG12	1:A:208:THR:HG23	1.96	0.47
1:A:132:CYS:HB3	1:A:201:ASN:C	2.34	0.47
1:A:239:PHE:CE2	1:A:490:TYR:HD2	2.32	0.47
1:D:276:ILE:HA	1:D:293:HIS:O	2.15	0.47
1:D:498:LYS:HZ3	2:E:646:THR:HG21	1.80	0.47
2:E:545:THR:HB	2:E:549:ARG:CZ	2.45	0.47
3:F:159:TRP:NE1	3:F:176:ILE:HG13	2.29	0.47
1:G:97:GLU:HB3	1:G:99:PHE:CE1	2.43	0.47
2:H:545:THR:HB	2:H:549:ARG:CZ	2.45	0.47
2:B:600:LEU:HD12	2:B:606:SER:HA	1.96	0.47
1:D:125:CYS:HB2	1:D:440:MET:O	2.14	0.47
1:D:285:ASN:HA	3:F:3:LYS:HB2	1.96	0.47
1:D:285:ASN:CG	3:F:94:GLU:O	2.52	0.47
3:F:117:THR:OG1	3:F:118:LEU:N	2.48	0.47
1:G:286:ASN:HB3	1:G:462:ARG:CD	2.45	0.47
2:H:645:TYR:O	2:H:649:ILE:HG22	2.15	0.47
1:A:101:MET:HB2	1:A:101:MET:HE2	1.77	0.47
1:A:276:ILE:HA	1:A:293:HIS:O	2.15	0.47
2:E:635:TRP:C	2:E:638:TRP:H	2.11	0.47
3:F:61:ARG:HG3	3:F:64:TRP:CH2	2.49	0.47
3:F:103:THR:OG1	3:F:104:ALA:N	2.47	0.47
1:G:58:LEU:HD12	1:G:223:TYR:HD2	1.79	0.47
1:G:275:GLU:HA	1:G:295:ASN:HB3	1.97	0.47
1:G:276:ILE:HA	1:G:293:HIS:O	2.14	0.47
1:G:340:SER:O	1:G:341:LYS:HB2	2.15	0.47
3:I:140:ILE:HG22	3:I:146:LEU:HD22	1.96	0.47
1:A:233:LYS:HB3	1:A:248:VAL:HG21	1.96	0.46
3:C:173:LYS:HB3	3:C:175:ASP:OD1	2.15	0.46
1:D:99:PHE:N	1:D:99:PHE:CD1	2.84	0.46
1:D:286:ASN:HB3	1:D:462:ARG:CD	2.45	0.46
2:E:580:ILE:HA	2:E:583:LEU:CD1	2.45	0.46
1:G:99:PHE:N	1:G:99:PHE:CD1	2.84	0.46
1:A:99:PHE:N	1:A:99:PHE:HD1	2.13	0.46
1:A:268:ASN:H	1:A:453:SER:HA	1.80	0.46
1:A:275:GLU:HA	1:A:295:ASN:HB3	1.97	0.46
1:A:376:GLU:HB2	3:C:45:PHE:CZ	2.51	0.46
1:D:81:VAL:HG21	2:E:578:TRP:CZ3	2.50	0.46
1:D:306:ASN:O	1:D:308:ASN:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:99:PHE:N	1:G:99:PHE:HD1	2.13	0.46
1:A:72:HIS:HE1	1:A:216:PHE:CG	2.34	0.46
1:A:286:ASN:HB3	1:A:462:ARG:CD	2.45	0.46
1:A:354:LYS:HD3	1:A:354:LYS:HA	1.61	0.46
2:B:552:LEU:HD12	2:B:553:SER:N	2.31	0.46
3:C:40:GLY:O	3:C:47:THR:HG23	2.16	0.46
1:D:257:ILE:HG21	1:D:489:LEU:HD11	1.96	0.46
1:D:275:GLU:HA	1:D:295:ASN:HB3	1.97	0.46
1:D:285:ASN:CB	3:F:94:GLU:O	2.63	0.46
3:I:159:TRP:NE1	3:I:176:ILE:HG13	2.29	0.46
1:A:50:VAL:O	1:A:498:LYS:N	2.42	0.46
2:B:545:THR:HB	2:B:549:ARG:CZ	2.45	0.46
1:D:50:VAL:O	1:D:498:LYS:N	2.42	0.46
1:D:232:LEU:CD1	2:E:636:MET:SD	3.03	0.46
1:D:271:LEU:HD21	1:D:454:ASN:HB3	1.98	0.46
1:A:290:ILE:HB	1:A:460:LEU:O	2.16	0.46
1:D:72:HIS:HE1	1:D:216:PHE:CG	2.34	0.46
2:E:585:THR:OG1	2:E:586:ARG:N	2.49	0.46
1:G:47:GLY:N	1:G:499:PRO:O	2.49	0.46
1:G:306:ASN:O	1:G:308:ASN:N	2.48	0.46
2:H:580:ILE:HA	2:H:583:LEU:CD1	2.45	0.46
1:A:271:LEU:HD21	1:A:454:ASN:HB3	1.98	0.46
1:A:507:CYS:HB3	2:B:612:CYS:HB3	1.32	0.46
2:B:545:THR:O	2:B:548:ALA:HB3	2.16	0.46
3:C:117:THR:OG1	3:C:118:LEU:N	2.48	0.46
1:D:47:GLY:N	1:D:499:PRO:O	2.49	0.46
3:F:131:GLN:NE2	3:F:141:GLN:HG2	2.31	0.46
3:F:173:LYS:HB3	3:F:175:ASP:OD1	2.15	0.46
1:G:126:VAL:HG12	1:G:208:THR:HG23	1.96	0.46
1:G:268:ASN:H	1:G:453:SER:HA	1.80	0.46
1:G:290:ILE:HB	1:G:460:LEU:O	2.16	0.46
2:H:545:THR:O	2:H:548:ALA:HB3	2.16	0.46
3:I:117:THR:OG1	3:I:118:LEU:N	2.48	0.46
3:I:173:LYS:HB3	3:I:175:ASP:OD1	2.15	0.46
1:A:76:ALA:HA	1:A:80:CYS:HB2	1.98	0.46
1:A:99:PHE:N	1:A:99:PHE:CD1	2.83	0.46
1:D:498:LYS:HZ2	2:E:646:THR:HG21	1.79	0.46
1:G:239:PHE:O	1:G:240:ASN:HB3	2.16	0.46
1:G:271:LEU:HD21	1:G:454:ASN:HB3	1.98	0.46
1:A:306:ASN:O	1:A:308:ASN:N	2.49	0.46
2:B:580:ILE:HA	2:B:583:LEU:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:585:THR:OG1	2:B:586:ARG:N	2.49	0.46
1:D:50:VAL:CG1	2:E:639:ASP:HB2	2.46	0.46
3:F:15:GLU:OE1	3:F:16:LEU:N	2.49	0.46
1:G:76:ALA:HA	1:G:80:CYS:HB2	1.98	0.46
3:I:81:SER:O	3:I:81:SER:OG	2.30	0.46
1:A:66:ALA:HB2	1:A:77:THR:HG21	1.98	0.46
3:C:25:SER:O	3:C:25:SER:OG	2.30	0.46
1:D:44:VAL:HG21	2:E:649:ILE:CG1	2.46	0.46
1:D:76:ALA:HA	1:D:80:CYS:HB2	1.98	0.46
1:D:268:ASN:H	1:D:453:SER:HA	1.80	0.46
2:E:545:THR:O	2:E:548:ALA:HB3	2.16	0.46
1:G:255:HIS:CG	1:G:492:TYR:HH	2.31	0.46
3:I:40:GLY:O	3:I:47:THR:HG23	2.16	0.46
1:A:40:LEU:HD12	1:A:40:LEU:HA	1.77	0.46
2:B:668:LEU:HD13	1:G:508:LYS:CG	2.46	0.46
1:D:340:SER:O	1:D:341:LYS:HB2	2.15	0.46
1:G:372:GLY:HA2	1:G:378:THR:HG21	1.98	0.46
2:H:599:LEU:C	2:H:601:GLY:N	2.68	0.46
3:I:131:GLN:NE2	3:I:141:GLN:HG2	2.31	0.46
1:A:453:SER:OG	1:A:454:ASN:N	2.49	0.45
2:B:645:TYR:O	2:B:649:ILE:HG22	2.15	0.45
3:C:117:THR:O	3:C:118:LEU:HD23	2.16	0.45
1:D:126:VAL:HG12	1:D:208:THR:HG23	1.96	0.45
1:D:500:LEU:HD13	1:D:500:LEU:HA	1.78	0.45
2:E:641:GLU:OE1	2:E:642:ILE:HG23	2.16	0.45
1:G:350:ARG:HA	1:G:353:GLU:HG3	1.97	0.45
1:A:239:PHE:O	1:A:240:ASN:HB3	2.16	0.45
2:B:583:LEU:O	2:B:584:GLN:C	2.54	0.45
2:E:635:TRP:CA	2:E:638:TRP:HB3	2.43	0.45
1:A:228:GLY:C	1:A:497:ILE:HG12	2.37	0.45
1:A:340:SER:O	1:A:341:LYS:HB2	2.15	0.45
1:D:228:GLY:C	1:D:497:ILE:HG12	2.37	0.45
2:E:552:LEU:HD12	2:E:553:SER:N	2.31	0.45
1:G:64:ALA:HB1	1:G:73:ASN:HB3	1.97	0.45
1:G:72:HIS:HE1	1:G:216:PHE:CG	2.34	0.45
2:H:641:GLU:OE1	2:H:642:ILE:HG23	2.16	0.45
3:C:39:LEU:HD12	3:C:71:LEU:HD13	1.99	0.45
3:C:140:ILE:HD11	3:C:159:TRP:HZ3	1.82	0.45
1:D:290:ILE:HB	1:D:460:LEU:O	2.16	0.45
1:D:372:GLY:HA2	1:D:378:THR:HG21	1.99	0.45
2:E:552:LEU:HD13	2:H:650:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:552:LEU:HD12	2:H:553:SER:N	2.31	0.45
1:A:372:GLY:HA2	1:A:378:THR:HG21	1.98	0.45
1:A:373:GLY:HA2	3:C:48:LYS:HD2	1.98	0.45
2:B:599:LEU:C	2:B:601:GLY:N	2.68	0.45
3:C:131:GLN:NE2	3:C:141:GLN:HG2	2.31	0.45
1:D:66:ALA:HB2	1:D:77:THR:HG21	1.98	0.45
1:D:73:ASN:O	1:D:77:THR:OG1	2.35	0.45
2:H:583:LEU:O	2:H:584:GLN:C	2.54	0.45
2:H:585:THR:OG1	2:H:586:ARG:N	2.49	0.45
1:A:420:ILE:HG22	1:A:421:THR:N	2.32	0.45
1:A:432:MET:HG2	1:A:437:GLY:O	2.17	0.45
2:B:582:GLN:OE1	2:B:586:ARG:HD2	2.17	0.45
2:B:641:GLU:OE1	2:B:642:ILE:HG23	2.16	0.45
1:D:42:VAL:HG23	2:E:615:VAL:C	2.36	0.45
1:D:239:PHE:O	1:D:240:ASN:HB3	2.16	0.45
1:D:282:ASN:CG	3:F:93:GLU:HG3	2.36	0.45
1:D:354:LYS:HD3	1:D:354:LYS:HA	1.61	0.45
3:F:40:GLY:O	3:F:47:THR:HG23	2.16	0.45
3:F:117:THR:O	3:F:118:LEU:HD23	2.16	0.45
1:G:47:GLY:H	1:G:499:PRO:HB2	1.82	0.45
1:G:265:LEU:HA	1:G:265:LEU:HD23	1.70	0.45
1:G:287:VAL:HA	3:I:37:LYS:NZ	2.32	0.45
1:G:432:MET:HG2	1:G:437:GLY:O	2.17	0.45
3:I:107:ASP:OD2	3:I:108:THR:OG1	2.23	0.45
1:A:47:GLY:N	1:A:499:PRO:O	2.49	0.45
1:D:47:GLY:HA2	1:D:499:PRO:HB2	1.99	0.45
1:D:338:ASN:HA	1:D:421:THR:HA	1.98	0.45
2:E:589:ALA:O	2:E:593:TYR:CB	2.62	0.45
1:G:73:ASN:O	1:G:77:THR:OG1	2.35	0.45
1:A:47:GLY:HA2	1:A:499:PRO:HB2	1.99	0.45
1:A:70:GLU:OE2	1:A:72:HIS:ND1	2.46	0.45
1:A:85:PRO:HD3	2:B:578:TRP:HE1	1.82	0.45
1:A:239:PHE:HB3	1:A:243:GLY:N	2.32	0.45
1:A:338:ASN:HA	1:A:421:THR:HA	1.98	0.45
1:A:481:MET:HA	1:A:484:ASN:CB	2.45	0.45
2:B:532:VAL:O	2:B:535:SER:OG	2.20	0.45
1:D:340:SER:O	1:D:341:LYS:HD3	2.16	0.45
1:A:72:HIS:CE1	1:A:217:GLU:H	2.35	0.45
1:A:130:PRO:CB	3:C:62:SER:HB3	2.43	0.45
1:D:86:SER:O	1:D:86:SER:OG	2.29	0.45
1:D:482:ARG:O	1:D:486:ARG:NH2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:128:PRO:CA	3:F:164:LEU:O	2.64	0.45
1:G:225:THR:HG22	1:G:231:ILE:HG13	1.99	0.45
1:G:228:GLY:C	1:G:497:ILE:HG12	2.37	0.45
1:G:233:LYS:HG3	1:G:492:TYR:CE1	2.52	0.45
1:A:225:THR:HG22	1:A:231:ILE:HG13	1.99	0.45
1:A:233:LYS:HG3	1:A:492:TYR:CE1	2.52	0.45
1:A:356:ALA:O	1:A:360:PRO:HA	2.17	0.45
3:C:35:GLN:HA	3:C:35:GLN:HE21	1.82	0.45
1:D:420:ILE:HG22	1:D:421:THR:N	2.32	0.45
1:D:432:MET:HG2	1:D:437:GLY:O	2.17	0.45
3:F:39:LEU:HD12	3:F:71:LEU:HD13	1.99	0.45
1:D:47:GLY:H	1:D:499:PRO:HB2	1.82	0.44
1:D:281:GLU:HB3	3:F:92:LYS:HB2	1.99	0.44
3:F:140:ILE:HD11	3:F:159:TRP:HZ3	1.82	0.44
1:G:66:ALA:HB2	1:G:77:THR:HG21	1.98	0.44
1:G:214:VAL:HG13	1:G:215:SER:N	2.32	0.44
3:I:117:THR:O	3:I:118:LEU:HD23	2.16	0.44
1:A:47:GLY:H	1:A:499:PRO:HB2	1.82	0.44
1:D:281:GLU:HB2	3:F:92:LYS:HB2	1.99	0.44
1:D:288:LYS:NZ	3:F:94:GLU:CB	2.79	0.44
2:E:594:LEU:O	2:E:597:GLN:N	2.50	0.44
1:G:72:HIS:CE1	1:G:217:GLU:H	2.35	0.44
1:G:338:ASN:HA	1:G:421:THR:HA	1.98	0.44
3:I:39:LEU:HD12	3:I:71:LEU:HD13	1.99	0.44
3:I:140:ILE:HD11	3:I:159:TRP:HZ3	1.82	0.44
2:B:635:TRP:C	2:B:638:TRP:H	2.11	0.44
1:D:281:GLU:CG	3:F:91:GLN:HA	2.47	0.44
1:D:351:VAL:O	1:D:355:LEU:HG	2.17	0.44
2:E:582:GLN:OE1	2:E:586:ARG:HD2	2.17	0.44
1:G:237:LYS:NZ	1:G:274:GLY:H	2.15	0.44
1:G:239:PHE:HB3	1:G:243:GLY:N	2.32	0.44
2:H:582:GLN:OE1	2:H:586:ARG:HD2	2.17	0.44
3:I:35:GLN:HA	3:I:35:GLN:HE21	1.82	0.44
1:A:340:SER:O	1:A:341:LYS:HD3	2.16	0.44
2:B:594:LEU:O	2:B:597:GLN:N	2.50	0.44
2:B:665:LYS:CE	1:G:506:ALA:HB1	2.47	0.44
1:D:362:LYS:HD3	1:D:470:ASN:OD1	2.17	0.44
1:G:420:ILE:HG22	1:G:421:THR:N	2.32	0.44
1:A:44:VAL:HG22	1:A:502:VAL:HG22	2.00	0.44
1:A:286:ASN:O	1:A:462:ARG:NH1	2.51	0.44
1:D:225:THR:HG22	1:D:231:ILE:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:ASN:OD1	3:F:91:GLN:C	2.56	0.44
1:G:50:VAL:HG22	2:H:635:TRP:CB	2.47	0.44
3:C:15:GLU:OE1	3:C:16:LEU:N	2.49	0.44
3:C:116:LEU:CB	3:C:151:LEU:HD21	2.48	0.44
1:D:72:HIS:CE1	1:D:217:GLU:H	2.35	0.44
1:D:286:ASN:O	1:D:462:ARG:NH1	2.51	0.44
1:D:356:ALA:O	1:D:360:PRO:HA	2.17	0.44
3:F:20:ALA:HB2	3:F:88:VAL:HG21	2.00	0.44
1:G:286:ASN:O	1:G:462:ARG:NH1	2.51	0.44
2:H:634:THR:HG23	2:H:637:GLN:NE2	2.30	0.44
1:A:395:GLY:O	1:A:397:PHE:HD1	2.01	0.44
2:B:602:ILE:HG23	2:B:603:TRP:CD1	2.53	0.44
3:C:30:TRP:HB2	3:C:39:LEU:HB2	1.99	0.44
1:D:237:LYS:NZ	1:D:274:GLY:H	2.15	0.44
1:D:239:PHE:HB3	1:D:243:GLY:N	2.32	0.44
2:E:583:LEU:O	2:E:584:GLN:C	2.54	0.44
1:G:47:GLY:HA2	1:G:499:PRO:HB2	1.99	0.44
1:G:340:SER:O	1:G:341:LYS:HD3	2.16	0.44
1:G:351:VAL:O	1:G:355:LEU:HG	2.17	0.44
1:A:51:TRP:HB3	1:A:495:VAL:CG2	2.48	0.44
1:A:362:LYS:HD3	1:A:470:ASN:OD1	2.17	0.44
1:D:288:LYS:NZ	3:F:94:GLU:N	2.65	0.44
1:D:395:GLY:O	1:D:397:PHE:HD1	2.01	0.44
2:E:586:ARG:O	2:E:589:ALA:HB3	2.17	0.44
3:F:3:LYS:HZ2	3:F:96:GLN:HB2	1.83	0.44
1:G:72:HIS:HE1	1:G:216:PHE:CD2	2.36	0.44
1:G:356:ALA:O	1:G:360:PRO:HA	2.17	0.44
1:G:466:THR:N	1:G:467:GLU:OE2	2.51	0.44
3:I:20:ALA:HB2	3:I:88:VAL:HG21	2.00	0.44
3:I:128:PRO:CA	3:I:164:LEU:O	2.64	0.44
1:A:111:HIS:CE1	1:A:433:TRP:CZ3	3.01	0.44
1:A:351:VAL:O	1:A:355:LEU:HG	2.17	0.44
1:A:509:ARG:HG2	2:B:614:ALA:HB2	1.99	0.44
1:D:44:VAL:HG22	1:D:502:VAL:HG22	2.00	0.44
1:G:51:TRP:HB3	1:G:495:VAL:CG2	2.48	0.44
1:G:86:SER:O	1:G:86:SER:OG	2.29	0.44
2:H:602:ILE:HG23	2:H:603:TRP:CD1	2.53	0.44
1:A:482:ARG:O	1:A:486:ARG:NH2	2.47	0.43
1:D:214:VAL:HG13	1:D:215:SER:N	2.32	0.43
2:E:602:ILE:HG23	2:E:603:TRP:CD1	2.53	0.43
3:F:35:GLN:HA	3:F:35:GLN:HE21	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:504:PRO:HB2	2:H:626:GLN:OE1	2.17	0.43
2:H:586:ARG:O	2:H:589:ALA:HB3	2.17	0.43
1:A:73:ASN:O	1:A:77:THR:OG1	2.35	0.43
1:A:461:VAL:O	1:A:475:ASN:N	2.45	0.43
1:D:235:ASN:N	1:D:248:VAL:HB	2.32	0.43
1:D:466:THR:HG1	3:F:3:LYS:N	2.16	0.43
2:E:603:TRP:HB3	2:E:653:LEU:HD21	2.00	0.43
3:F:102:LEU:HB2	3:F:120:LEU:HD12	2.00	0.43
1:G:231:ILE:O	1:G:231:ILE:HG22	2.18	0.43
1:G:362:LYS:HD3	1:G:470:ASN:OD1	2.17	0.43
1:G:392:ASN:HD21	1:G:394:SER:HB3	1.84	0.43
3:I:15:GLU:OE1	3:I:16:LEU:N	2.49	0.43
3:I:30:TRP:HB2	3:I:39:LEU:HB2	1.99	0.43
1:A:255:HIS:CG	1:A:492:TYR:HH	2.31	0.43
1:D:92:LEU:HD23	2:E:533:ALA:C	2.39	0.43
1:D:233:LYS:HG3	1:D:492:TYR:CE1	2.52	0.43
1:G:395:GLY:O	1:G:397:PHE:HD1	2.01	0.43
2:H:594:LEU:O	2:H:597:GLN:N	2.50	0.43
1:A:48:VAL:O	1:A:50:VAL:HG23	2.18	0.43
1:A:239:PHE:CD1	1:A:239:PHE:N	2.85	0.43
2:B:541:SER:O	2:B:544:LEU:HB3	2.18	0.43
2:B:599:LEU:C	2:B:601:GLY:H	2.21	0.43
3:C:76:LEU:CB	3:C:99:VAL:HG21	2.46	0.43
3:C:102:LEU:HB2	3:C:120:LEU:HD12	2.00	0.43
1:D:367:PHE:CE2	1:D:370:SER:HB2	2.54	0.43
1:D:453:SER:OG	1:D:454:ASN:N	2.49	0.43
1:A:41:TRP:HB2	1:A:507:CYS:H	1.83	0.43
2:B:586:ARG:O	2:B:589:ALA:HB3	2.17	0.43
1:D:302:CYS:O	1:D:450:THR:HA	2.18	0.43
3:F:30:TRP:HB2	3:F:39:LEU:HB2	1.99	0.43
3:F:140:ILE:HG21	3:F:146:LEU:HB3	2.01	0.43
1:G:41:TRP:HB2	1:G:507:CYS:H	1.83	0.43
1:G:228:GLY:HA2	1:G:497:ILE:HG12	2.00	0.43
1:G:250:THR:HG21	2:H:524:ALA:CB	2.47	0.43
1:G:453:SER:OG	1:G:454:ASN:N	2.49	0.43
2:H:541:SER:O	2:H:544:LEU:HB3	2.18	0.43
2:H:599:LEU:C	2:H:601:GLY:H	2.21	0.43
3:I:4:LYS:HZ3	3:I:95:VAL:HG12	1.82	0.43
1:A:237:LYS:NZ	1:A:274:GLY:H	2.15	0.43
2:B:603:TRP:HB3	2:B:653:LEU:HD21	1.99	0.43
1:D:51:TRP:HB3	1:D:495:VAL:CG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:264:GLN:NE2	1:G:378:THR:O	2.42	0.43
1:A:72:HIS:HE1	1:A:216:PHE:CD2	2.36	0.43
1:A:214:VAL:HG13	1:A:215:SER:N	2.32	0.43
1:A:231:ILE:O	1:A:231:ILE:HG22	2.17	0.43
1:A:466:THR:N	1:A:467:GLU:OE2	2.51	0.43
3:C:140:ILE:HG21	3:C:146:LEU:HB3	2.01	0.43
3:C:144:LYS:HA	3:C:144:LYS:HD3	1.81	0.43
1:D:50:VAL:C	1:D:51:TRP:CD1	2.92	0.43
1:D:466:THR:N	1:D:467:GLU:OE2	2.51	0.43
1:D:483:ASP:OD1	1:D:486:ARG:CZ	2.67	0.43
2:E:571:HIS:HB3	2:E:575:LEU:HD22	2.01	0.43
3:F:4:LYS:HZ3	3:F:95:VAL:HG12	1.84	0.43
3:F:116:LEU:CB	3:F:151:LEU:HD21	2.48	0.43
1:G:302:CYS:O	1:G:450:THR:HA	2.19	0.43
2:H:538:GLY:HA2	2:H:630:TRP:CE3	2.53	0.43
2:H:647:ASN:OD1	2:H:647:ASN:N	2.51	0.43
1:A:367:PHE:CE2	1:A:370:SER:HB2	2.54	0.43
1:D:72:HIS:HE1	1:D:216:PHE:CD2	2.36	0.43
1:D:255:HIS:CG	1:D:492:TYR:HH	2.34	0.43
1:D:282:ASN:OD1	3:F:93:GLU:N	2.50	0.43
2:E:549:ARG:HH22	2:H:602:ILE:CG1	2.30	0.43
2:E:621:TRP:HA	2:E:645:TYR:CZ	2.54	0.43
3:F:64:TRP:C	3:F:66:GLN:H	2.22	0.43
1:G:48:VAL:O	1:G:50:VAL:HG23	2.19	0.43
2:H:536:THR:HA	2:H:634:THR:HA	2.01	0.43
1:A:65:LYS:HB2	1:A:68:ASP:OD1	2.18	0.43
1:A:97:GLU:HB3	1:A:99:PHE:CE1	2.43	0.43
2:B:624:LYS:HE3	2:B:638:TRP:HZ3	1.84	0.43
3:C:64:TRP:C	3:C:66:GLN:H	2.22	0.43
2:E:548:ALA:HB2	2:H:599:LEU:HD12	2.00	0.43
2:E:634:THR:HG23	2:E:637:GLN:NE2	2.30	0.43
2:E:647:ASN:OD1	2:E:647:ASN:N	2.51	0.43
1:G:239:PHE:N	1:G:239:PHE:CD1	2.85	0.43
1:G:367:PHE:CE2	1:G:370:SER:HB2	2.54	0.43
2:H:603:TRP:HB3	2:H:653:LEU:HD21	1.99	0.43
1:A:50:VAL:C	1:A:51:TRP:CD1	2.92	0.43
1:A:483:ASP:HA	1:A:486:ARG:CB	2.49	0.43
2:B:647:ASN:OD1	2:B:647:ASN:N	2.51	0.43
1:D:92:LEU:HB3	2:E:534:GLY:HA3	2.00	0.43
1:D:228:GLY:HA2	1:D:497:ILE:HG12	2.00	0.43
1:D:235:ASN:OD1	1:D:248:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:300:ILE:O	1:D:452:LYS:HA	2.19	0.43
1:G:65:LYS:HB2	1:G:68:ASP:OD1	2.18	0.43
1:G:354:LYS:HD3	1:G:354:LYS:HA	1.61	0.43
3:I:19:THR:O	3:I:88:VAL:HG11	2.19	0.43
1:A:235:ASN:OD1	1:A:248:VAL:HG23	2.19	0.42
1:D:41:TRP:O	2:E:617:TRP:HB2	2.19	0.42
1:D:65:LYS:HB2	1:D:68:ASP:OD1	2.19	0.42
1:G:287:VAL:HA	3:I:37:LYS:HZ2	1.84	0.42
3:I:84:TYR:HB2	3:I:95:VAL:CG2	2.49	0.42
1:A:235:ASN:N	1:A:248:VAL:HB	2.32	0.42
1:A:483:ASP:OD1	1:A:486:ARG:CZ	2.67	0.42
2:B:594:LEU:HA	2:B:594:LEU:HD23	1.65	0.42
1:D:42:VAL:HG23	2:E:615:VAL:O	2.18	0.42
1:D:48:VAL:O	1:D:50:VAL:HG23	2.18	0.42
1:D:266:LEU:H	1:D:266:LEU:HD23	1.84	0.42
1:D:278:ILE:C	1:D:279:ARG:HG2	2.39	0.42
1:D:392:ASN:HD21	1:D:394:SER:HB3	1.84	0.42
2:E:541:SER:O	2:E:544:LEU:HB3	2.18	0.42
1:G:371:SER:HB3	3:I:54:ASN:ND2	2.34	0.42
1:G:483:ASP:OD1	1:G:486:ARG:CZ	2.67	0.42
2:H:588:LEU:HG	2:H:588:LEU:H	1.58	0.42
2:H:631:ASP:OD1	2:H:631:ASP:N	2.53	0.42
2:B:619:SER:O	2:B:623:ASN:HB2	2.19	0.42
2:B:631:ASP:N	2:B:631:ASP:OD1	2.53	0.42
2:B:634:THR:N	2:B:637:GLN:HE21	2.18	0.42
3:C:59:SER:OG	3:C:70:PRO:O	2.34	0.42
1:D:267:LEU:HD13	1:D:382:PHE:CD2	2.55	0.42
1:G:45:TYR:CB	2:H:609:LEU:O	2.67	0.42
1:G:266:LEU:HD23	1:G:266:LEU:H	1.84	0.42
1:G:341:LYS:HG3	1:G:344:TRP:CE3	2.54	0.42
3:I:102:LEU:HB2	3:I:120:LEU:HD12	2.00	0.42
3:I:105:ASN:OD1	3:I:116:LEU:HG	2.19	0.42
1:D:41:TRP:HB2	1:D:507:CYS:H	1.83	0.42
1:D:134:THR:HA	1:D:200:ILE:HG23	2.01	0.42
1:D:265:LEU:HD22	1:D:455:ILE:HG12	2.01	0.42
1:D:341:LYS:HG3	1:D:344:TRP:CE3	2.54	0.42
2:E:619:SER:O	2:E:623:ASN:HB2	2.19	0.42
3:F:77:LYS:O	3:F:79:GLU:N	2.53	0.42
1:G:44:VAL:HG22	1:G:502:VAL:HG22	2.00	0.42
1:G:50:VAL:C	1:G:51:TRP:CD1	2.92	0.42
1:G:278:ILE:C	1:G:279:ARG:HG2	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:350:ARG:O	1:G:353:GLU:HG3	2.20	0.42
1:G:388:PHE:HB2	1:G:390:TYR:CZ	2.55	0.42
2:H:619:SER:O	2:H:623:ASN:HB2	2.19	0.42
2:H:621:TRP:HA	2:H:645:TYR:CZ	2.54	0.42
3:I:116:LEU:CB	3:I:151:LEU:HD21	2.48	0.42
1:A:134:THR:HA	1:A:200:ILE:HG23	2.01	0.42
1:A:228:GLY:HA2	1:A:497:ILE:HG12	2.00	0.42
1:A:266:LEU:HD23	1:A:266:LEU:H	1.84	0.42
1:A:350:ARG:HA	1:A:353:GLU:CG	2.50	0.42
1:A:350:ARG:O	1:A:353:GLU:HG3	2.20	0.42
1:A:388:PHE:HB2	1:A:390:TYR:CZ	2.55	0.42
2:B:571:HIS:HB3	2:B:575:LEU:HD22	2.01	0.42
1:D:261:VAL:HG12	1:D:485:TRP:CZ2	2.43	0.42
3:F:5:VAL:HG12	3:F:6:VAL:O	2.20	0.42
3:F:105:ASN:OD1	3:F:116:LEU:HG	2.19	0.42
1:G:233:LYS:C	1:G:248:VAL:HG21	2.40	0.42
1:G:462:ARG:H	1:G:462:ARG:HG3	1.14	0.42
1:G:483:ASP:HA	1:G:486:ARG:CB	2.50	0.42
2:H:536:THR:HG21	2:H:631:ASP:O	2.19	0.42
1:A:265:LEU:HD23	1:A:265:LEU:HA	1.70	0.42
1:A:341:LYS:HG3	1:A:344:TRP:CE3	2.54	0.42
1:A:392:ASN:HD21	1:A:394:SER:HB3	1.84	0.42
2:B:621:TRP:HA	2:B:645:TYR:CZ	2.54	0.42
2:B:627:LYS:O	4:B:703:NAG:H82	2.20	0.42
2:B:634:THR:HG23	2:B:637:GLN:NE2	2.30	0.42
3:C:5:VAL:HG12	3:C:6:VAL:O	2.20	0.42
3:C:105:ASN:OD1	3:C:116:LEU:HG	2.19	0.42
1:D:461:VAL:O	1:D:475:ASN:N	2.45	0.42
2:E:624:LYS:HE3	2:E:638:TRP:HZ3	1.84	0.42
3:F:135:PRO:HD3	3:F:159:TRP:CD1	2.55	0.42
1:G:134:THR:HA	1:G:200:ILE:HG23	2.01	0.42
1:A:302:CYS:O	1:A:450:THR:HA	2.19	0.42
3:C:77:LYS:O	3:C:79:GLU:N	2.53	0.42
1:D:40:LEU:HD12	1:D:40:LEU:HA	1.77	0.42
1:D:239:PHE:N	1:D:239:PHE:CD1	2.85	0.42
1:D:288:LYS:HZ2	3:F:94:GLU:N	2.17	0.42
2:E:586:ARG:HG3	2:E:586:ARG:H	1.53	0.42
3:F:76:LEU:CB	3:F:99:VAL:HG21	2.46	0.42
1:G:300:ILE:O	1:G:452:LYS:HA	2.19	0.42
2:H:596:ASP:HA	2:H:599:LEU:H	1.85	0.42
3:I:144:LYS:HD3	3:I:144:LYS:HA	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:ARG:CZ	3:C:61:ARG:HH12	2.33	0.42
3:C:36:ILE:N	3:C:36:ILE:CD1	2.83	0.42
2:E:552:LEU:HD12	2:E:553:SER:H	1.85	0.42
2:E:631:ASP:OD1	2:E:631:ASP:N	2.53	0.42
3:I:5:VAL:HG12	3:I:6:VAL:O	2.20	0.42
3:I:120:LEU:HD23	3:I:144:LYS:HZ1	1.84	0.42
3:I:140:ILE:HG21	3:I:146:LEU:HB3	2.01	0.42
2:B:634:THR:O	2:B:634:THR:OG1	2.28	0.42
1:D:233:LYS:C	1:D:248:VAL:HG21	2.40	0.42
1:D:350:ARG:HA	1:D:353:GLU:CG	2.50	0.42
1:D:395:GLY:O	1:D:397:PHE:N	2.53	0.42
2:E:536:THR:HA	2:E:634:THR:HA	2.01	0.42
1:G:235:ASN:OD1	1:G:248:VAL:HG23	2.19	0.42
2:H:571:HIS:HB3	2:H:575:LEU:HD22	2.01	0.42
2:H:589:ALA:O	2:H:593:TYR:CB	2.63	0.42
1:A:267:LEU:HD13	1:A:382:PHE:CD2	2.55	0.42
2:B:536:THR:HA	2:B:634:THR:HA	2.01	0.42
3:C:19:THR:O	3:C:88:VAL:HG11	2.19	0.42
3:C:20:ALA:HB2	3:C:88:VAL:HG21	2.00	0.42
3:C:31:LYS:HE2	3:C:37:LYS:HG2	2.02	0.42
3:C:128:PRO:CA	3:C:164:LEU:O	2.64	0.42
1:D:231:ILE:HG22	1:D:231:ILE:O	2.18	0.42
1:D:388:PHE:HB2	1:D:390:TYR:CZ	2.55	0.42
2:E:536:THR:HG21	2:E:631:ASP:O	2.19	0.42
1:G:265:LEU:HD22	1:G:455:ILE:HG12	2.01	0.42
2:H:596:ASP:O	2:H:599:LEU:N	2.53	0.42
2:H:624:LYS:HE3	2:H:638:TRP:HZ3	1.84	0.42
1:A:81:VAL:HG21	2:B:581:LYS:NZ	2.35	0.41
1:A:93:GLU:O	1:A:95:VAL:N	2.53	0.41
1:A:265:LEU:HD22	1:A:455:ILE:HG12	2.01	0.41
1:A:278:ILE:C	1:A:279:ARG:HG2	2.39	0.41
1:A:395:GLY:O	1:A:397:PHE:N	2.53	0.41
3:F:81:SER:O	3:F:81:SER:OG	2.30	0.41
1:G:267:LEU:HD13	1:G:382:PHE:CD2	2.55	0.41
1:G:482:ARG:O	1:G:486:ARG:NH2	2.47	0.41
3:I:64:TRP:C	3:I:66:GLN:H	2.22	0.41
1:A:112:GLU:HA	1:A:115:ILE:HG12	2.02	0.41
1:A:261:VAL:HG12	1:A:485:TRP:CZ2	2.43	0.41
2:B:536:THR:HG21	2:B:631:ASP:O	2.19	0.41
2:B:596:ASP:O	2:B:599:LEU:N	2.53	0.41
2:B:596:ASP:HA	2:B:599:LEU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:84:TYR:HB2	3:C:95:VAL:CG2	2.48	0.41
3:C:116:LEU:HB3	3:C:151:LEU:HD21	2.02	0.41
1:D:483:ASP:HA	1:D:486:ARG:CB	2.49	0.41
2:E:644:ASN:OD1	2:E:645:TYR:N	2.53	0.41
1:G:219:ILE:H	1:G:219:ILE:HG12	1.69	0.41
3:I:36:ILE:N	3:I:36:ILE:CD1	2.83	0.41
1:A:135:LEU:O	1:A:200:ILE:HG12	2.20	0.41
1:A:418:SER:HB2	1:A:419:SER:H	1.60	0.41
2:B:599:LEU:HD13	2:B:599:LEU:HA	1.92	0.41
2:B:601:GLY:N	2:B:606:SER:HB2	2.35	0.41
1:D:41:TRP:HA	2:E:616:PRO:CA	2.41	0.41
1:D:112:GLU:HA	1:D:115:ILE:HG12	2.02	0.41
1:D:495:VAL:HG21	2:E:636:MET:CE	2.50	0.41
2:E:601:GLY:N	2:E:606:SER:HB2	2.35	0.41
2:E:634:THR:N	2:E:637:GLN:HE21	2.18	0.41
3:F:19:THR:O	3:F:88:VAL:HG11	2.19	0.41
3:F:36:ILE:N	3:F:36:ILE:CD1	2.83	0.41
3:F:149:SER:O	3:F:149:SER:OG	2.38	0.41
2:H:634:THR:N	2:H:637:GLN:HE21	2.18	0.41
1:A:106:MET:CE	1:A:494:VAL:HG23	2.50	0.41
1:A:233:LYS:C	1:A:248:VAL:HG21	2.40	0.41
1:A:300:ILE:O	1:A:452:LYS:HA	2.19	0.41
2:B:552:LEU:HD12	2:B:553:SER:H	1.85	0.41
1:D:44:VAL:O	2:E:611:CYS:HB2	2.21	0.41
2:E:596:ASP:O	2:E:599:LEU:N	2.53	0.41
2:E:598:GLN:CG	2:E:599:LEU:HD22	2.30	0.41
2:E:625:SER:O	2:E:629:ILE:HG13	2.21	0.41
3:F:31:LYS:HE2	3:F:37:LYS:HG2	2.02	0.41
3:F:150:GLN:O	3:F:151:LEU:HD12	2.20	0.41
1:G:114:VAL:HG11	1:G:485:TRP:CH2	2.56	0.41
1:G:350:ARG:HA	1:G:353:GLU:CG	2.50	0.41
1:G:500:LEU:HA	1:G:500:LEU:HD13	1.78	0.41
2:H:635:TRP:O	2:H:638:TRP:HB3	2.21	0.41
3:I:77:LYS:O	3:I:79:GLU:N	2.53	0.41
3:I:79:GLU:C	3:I:81:SER:H	2.24	0.41
1:A:264:GLN:NE2	1:A:378:THR:O	2.42	0.41
1:D:106:MET:CE	1:D:494:VAL:HG23	2.50	0.41
1:D:298:VAL:HB	1:D:455:ILE:HD13	2.03	0.41
1:D:350:ARG:O	1:D:353:GLU:HG3	2.20	0.41
3:F:144:LYS:HA	3:F:144:LYS:HD3	1.81	0.41
2:H:635:TRP:CA	2:H:638:TRP:HB3	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:150:GLN:O	3:I:151:LEU:HD12	2.20	0.41
1:A:97:GLU:OE2	2:B:640:LYS:NZ	2.54	0.41
2:B:628:GLU:HG2	2:B:632:ASN:HD22	1.85	0.41
1:D:56:THR:HG1	1:D:229:TYR:HE2	1.64	0.41
1:D:282:ASN:OD1	3:F:92:LYS:N	2.54	0.41
1:D:286:ASN:HA	1:D:288:LYS:HE2	2.02	0.41
2:E:628:GLU:HG2	2:E:632:ASN:HD22	1.85	0.41
1:G:106:MET:CE	1:G:494:VAL:HG23	2.50	0.41
1:G:135:LEU:O	1:G:200:ILE:HG12	2.20	0.41
3:I:97:LEU:HD11	3:I:99:VAL:HB	2.03	0.41
1:A:307:ASN:HD22	1:A:336:HIS:CE1	2.38	0.41
2:B:589:ALA:O	2:B:593:TYR:CB	2.62	0.41
2:B:598:GLN:HE21	2:B:598:GLN:C	2.24	0.41
3:C:135:PRO:HD3	3:C:159:TRP:CD1	2.55	0.41
1:D:41:TRP:HB2	1:D:507:CYS:N	2.35	0.41
1:D:115:ILE:HG22	1:D:433:TRP:CH2	2.56	0.41
1:D:250:THR:HG21	2:E:524:ALA:HB2	2.01	0.41
4:D:601:NAG:O7	4:D:601:NAG:O3	2.30	0.41
2:E:599:LEU:C	2:E:601:GLY:H	2.21	0.41
3:F:97:LEU:HD11	3:F:99:VAL:HB	2.03	0.41
3:F:116:LEU:HB3	3:F:151:LEU:HD21	2.02	0.41
2:H:601:GLY:N	2:H:606:SER:HB2	2.35	0.41
1:A:41:TRP:HB2	1:A:507:CYS:N	2.35	0.41
1:A:75:TRP:CD2	1:A:117:LEU:HG	2.56	0.41
2:B:538:GLY:HA2	2:B:630:TRP:CE3	2.53	0.41
2:B:625:SER:O	2:B:629:ILE:HG13	2.21	0.41
2:B:644:ASN:OD1	2:B:645:TYR:N	2.53	0.41
3:C:149:SER:O	3:C:149:SER:OG	2.38	0.41
1:D:70:GLU:OE2	1:D:72:HIS:ND1	2.46	0.41
1:D:135:LEU:O	1:D:200:ILE:HG12	2.20	0.41
1:D:283:LEU:HA	1:D:286:ASN:OD1	2.21	0.41
1:G:261:VAL:HG12	1:G:485:TRP:CZ2	2.43	0.41
3:I:31:LYS:HE2	3:I:37:LYS:HG2	2.02	0.41
3:I:116:LEU:HB3	3:I:151:LEU:HD21	2.02	0.41
1:A:114:VAL:HG11	1:A:485:TRP:CH2	2.56	0.41
1:A:257:ILE:HD11	1:A:492:TYR:CE2	2.53	0.41
1:D:93:GLU:HG3	2:E:535:SER:HA	2.02	0.41
1:D:114:VAL:HG11	1:D:485:TRP:CH2	2.56	0.41
3:F:39:LEU:HD13	3:F:46:LEU:HD11	2.03	0.41
1:G:41:TRP:HB2	1:G:507:CYS:N	2.35	0.41
1:G:58:LEU:HD11	1:G:494:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:62:SER:OG	1:G:62:SER:O	2.39	0.41
1:G:75:TRP:CD2	1:G:117:LEU:HG	2.56	0.41
1:G:112:GLU:HA	1:G:115:ILE:HG12	2.02	0.41
1:G:128:LEU:HD12	1:G:128:LEU:HA	1.92	0.41
1:G:257:ILE:HD11	1:G:492:TYR:CE2	2.53	0.41
1:G:304:ARG:CZ	1:G:304:ARG:HB3	2.30	0.41
1:G:395:GLY:O	1:G:397:PHE:N	2.53	0.41
1:G:467:GLU:H	1:G:467:GLU:CD	2.07	0.41
2:H:625:SER:O	2:H:629:ILE:HG13	2.21	0.41
2:H:634:THR:O	2:H:634:THR:OG1	2.28	0.41
3:I:135:PRO:HD3	3:I:159:TRP:CD1	2.55	0.41
1:A:304:ARG:CZ	1:A:304:ARG:HB3	2.30	0.41
1:A:500:LEU:HD13	1:A:500:LEU:HA	1.78	0.41
2:B:635:TRP:CA	2:B:638:TRP:HB3	2.43	0.41
1:D:58:LEU:HD11	1:D:494:VAL:HG21	2.03	0.41
1:D:93:GLU:O	1:D:95:VAL:N	2.53	0.41
1:D:111:HIS:CE1	1:D:433:TRP:CZ3	3.01	0.41
1:D:282:ASN:CG	3:F:91:GLN:HB3	2.42	0.41
2:E:598:GLN:HE21	2:E:598:GLN:C	2.24	0.41
2:E:635:TRP:O	2:E:638:TRP:HB3	2.21	0.41
3:F:63:LEU:HB3	3:F:68:ASN:O	2.21	0.41
3:F:79:GLU:C	3:F:81:SER:H	2.24	0.41
1:G:115:ILE:HG22	1:G:433:TRP:CH2	2.56	0.41
1:G:307:ASN:HD22	1:G:336:HIS:CE1	2.38	0.41
2:H:628:GLU:HG2	2:H:632:ASN:HD22	1.85	0.41
3:I:12:ASP:OD1	3:I:76:LEU:HD12	2.21	0.41
3:I:78:ILE:H	3:I:78:ILE:HG13	1.46	0.41
1:A:286:ASN:HA	1:A:288:LYS:HE2	2.03	0.40
3:C:39:LEU:HD13	3:C:46:LEU:HD11	2.03	0.40
3:C:79:GLU:C	3:C:81:SER:H	2.24	0.40
1:G:235:ASN:N	1:G:248:VAL:HB	2.32	0.40
3:I:63:LEU:HB3	3:I:68:ASN:O	2.21	0.40
1:A:283:LEU:HA	1:A:286:ASN:OD1	2.21	0.40
1:D:63:ASP:HA	1:D:82:PRO:HA	2.03	0.40
1:D:119:ASP:OD1	1:D:119:ASP:N	2.55	0.40
1:D:265:LEU:HA	1:D:265:LEU:HD23	1.70	0.40
1:D:367:PHE:CE1	1:D:475:ASN:HA	2.57	0.40
2:E:596:ASP:HA	2:E:599:LEU:H	1.85	0.40
3:F:84:TYR:HB2	3:F:95:VAL:CG2	2.48	0.40
1:G:56:THR:HG1	1:G:229:TYR:HE2	1.65	0.40
1:G:63:ASP:HA	1:G:82:PRO:HA	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:298:VAL:HB	1:G:455:ILE:HD13	2.03	0.40
1:G:507:CYS:HB3	2:H:612:CYS:HB3	1.17	0.40
2:H:644:ASN:OD1	2:H:645:TYR:N	2.53	0.40
1:A:62:SER:OG	1:A:62:SER:O	2.39	0.40
1:A:282:ASN:O	1:A:288:LYS:HE2	2.22	0.40
1:G:134:THR:OG1	3:I:66:GLN:NE2	2.54	0.40
1:G:282:ASN:O	1:G:288:LYS:HE2	2.22	0.40
1:A:63:ASP:HA	1:A:82:PRO:HA	2.03	0.40
1:A:108:ASN:O	1:A:112:GLU:HG2	2.22	0.40
2:B:555:ILE:HD11	1:D:54:ALA:HB2	2.02	0.40
2:B:597:GLN:HA	2:B:600:LEU:CD1	2.52	0.40
2:E:597:GLN:HA	2:E:600:LEU:CD1	2.52	0.40
3:F:134:SER:HB2	3:F:159:TRP:CE3	2.57	0.40
1:G:51:TRP:CD1	1:G:497:ILE:HD12	2.57	0.40
1:G:119:ASP:OD1	1:G:119:ASP:N	2.55	0.40
2:H:552:LEU:HD12	2:H:553:SER:H	1.85	0.40
2:H:598:GLN:HE21	2:H:598:GLN:C	2.24	0.40
3:I:149:SER:O	3:I:149:SER:OG	2.38	0.40
1:A:45:TYR:HB3	2:B:610:ILE:HA	2.04	0.40
1:A:119:ASP:OD1	1:A:119:ASP:N	2.55	0.40
1:A:221:ILE:HG22	1:A:222:HIS:N	2.37	0.40
1:A:228:GLY:C	1:A:229:TYR:HD1	2.25	0.40
1:A:333:ARG:HA	1:A:426:ILE:HD11	2.04	0.40
2:B:602:ILE:HG12	2:H:549:ARG:HH22	1.86	0.40
1:D:75:TRP:CD2	1:D:117:LEU:HG	2.56	0.40
1:D:221:ILE:HG22	1:D:222:HIS:N	2.37	0.40
3:F:12:ASP:OD1	3:F:76:LEU:HD12	2.21	0.40
3:F:120:LEU:HD23	3:F:144:LYS:HZ3	1.84	0.40
1:G:255:HIS:N	1:G:492:TYR:OH	2.35	0.40
1:G:420:ILE:O	1:G:421:THR:HB	2.22	0.40
2:H:644:ASN:HB3	4:H:704:NAG:O5	2.21	0.40
3:I:39:LEU:HD13	3:I:46:LEU:HD11	2.03	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	A	374/518 (72%)	280 (75%)	90 (24%)	4 (1%)	12	45
1	D	374/518 (72%)	279 (75%)	91 (24%)	4 (1%)	12	45
1	G	374/518 (72%)	279 (75%)	91 (24%)	4 (1%)	12	45
2	B	131/164 (80%)	101 (77%)	29 (22%)	1 (1%)	16	51
2	E	131/164 (80%)	101 (77%)	29 (22%)	1 (1%)	16	51
2	H	131/164 (80%)	101 (77%)	29 (22%)	1 (1%)	16	51
3	C	175/401 (44%)	141 (81%)	34 (19%)	0	100	100
3	F	175/401 (44%)	141 (81%)	34 (19%)	0	100	100
3	I	175/401 (44%)	141 (81%)	34 (19%)	0	100	100
All	All	2040/3249 (63%)	1564 (77%)	461 (23%)	15 (1%)	21	53

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	ASN
1	A	305	PRO
1	A	307	ASN
1	D	282	ASN
1	D	305	PRO
1	D	307	ASN
1	G	282	ASN
1	G	305	PRO
1	G	307	ASN
1	A	403	PRO
2	B	595	LYS
1	D	403	PRO
1	G	403	PRO
2	H	595	LYS
2	E	595	LYS

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	A	347/462 (75%)	254 (73%)	93 (27%)	0	3
1	D	347/462 (75%)	254 (73%)	93 (27%)	0	3
1	G	347/462 (75%)	254 (73%)	93 (27%)	0	3
2	B	117/137 (85%)	87 (74%)	30 (26%)	0	3
2	E	117/137 (85%)	87 (74%)	30 (26%)	0	3
2	H	117/137 (85%)	87 (74%)	30 (26%)	0	3
3	C	160/355 (45%)	113 (71%)	47 (29%)	0	2
3	F	160/355 (45%)	113 (71%)	47 (29%)	0	2
3	I	160/355 (45%)	112 (70%)	48 (30%)	0	2
All	All	1872/2862 (65%)	1361 (73%)	511 (27%)	1	2

All (511) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	TYR
1	A	48	VAL
1	A	52	LYS
1	A	57	THR
1	A	59	PHE
1	A	62	SER
1	A	67	TYR
1	A	69	THR
1	A	71	VAL
1	A	77	THR
1	A	80	CYS
1	A	83	THR
1	A	86	SER
1	A	90	LEU
1	A	94	ASN
1	A	98	ASN
1	A	112	GLU
1	A	119	ASP
1	A	123	LYS
1	A	128	LEU
1	A	131	LEU
1	A	132	CYS
1	A	133	VAL

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Mol	Chain	Res	Type
1	A	136	GLU
1	A	137	CYS
1	A	199	LEU
1	A	200	ILE
1	A	204	THR
1	A	205	SER
1	A	211	CYS
1	A	219	ILE
1	A	225	THR
1	A	232	LEU
1	A	242	THR
1	A	245	CYS
1	A	247	ASN
1	A	250	THR
1	A	266	LEU
1	A	273	GLU
1	A	276	ILE
1	A	280	SER
1	A	288	LYS
1	A	291	LEU
1	A	294	LEU
1	A	297	SER
1	A	299	GLU
1	A	300	ILE
1	A	301	VAL
1	A	303	THR
1	A	304	ARG
1	A	309	THR
1	A	310	ARG
1	A	312	SER
1	A	313	ILE
1	A	314	ARG
1	A	332	ILE
1	A	338	ASN
1	A	340	SER
1	A	341	LYS
1	A	345	HIS
1	A	346	GLU
1	A	352	SER
1	A	354	LYS
1	A	363	THR
1	A	365	ASN

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Mol	Chain	Res	Type
1	A	369	SER
1	A	371	SER
1	A	376	GLU
1	A	377	ILE
1	A	381	SER
1	A	385	ARG
1	A	388	PHE
1	A	400	THR
1	A	418	SER
1	A	420	ILE
1	A	422	ILE
1	A	424	CYS
1	A	429	ILE
1	A	435	GLU
1	A	440	MET
1	A	449	ILE
1	A	453	SER
1	A	458	LEU
1	A	460	LEU
1	A	462	ARG
1	A	466	THR
1	A	467	GLU
1	A	468	SER
1	A	472	GLU
1	A	473	THR
1	A	500	LEU
1	A	509	ARG
1	A	511	VAL
2	B	525	VAL
2	B	527	LEU
2	B	544	LEU
2	B	546	VAL
2	B	572	LEU
2	B	575	LEU
2	B	585	THR
2	B	586	ARG
2	B	592	ARG
2	B	593	TYR
2	B	596	ASP
2	B	597	GLN
2	B	600	LEU
2	B	605	CYS

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Mol	Chain	Res	Type
2	B	615	VAL
2	B	626	GLN
2	B	631	ASP
2	B	643	SER
2	B	646	THR
2	B	647	ASN
2	B	651	LYS
2	B	655	ASP
2	B	659	GLN
2	B	660	GLN
2	B	661	GLU
2	B	663	ASN
2	B	664	GLU
2	B	665	LYS
2	B	667	LEU
2	B	670	LEU
3	C	10	LYS
3	C	17	THR
3	C	19	THR
3	C	21	SER
3	C	25	SER
3	C	26	ILE
3	C	27	GLN
3	C	29	HIS
3	C	33	SER
3	C	34	ASN
3	C	36	ILE
3	C	44	SER
3	C	45	PHE
3	C	47	THR
3	C	52	LYS
3	C	55	ASP
3	C	62	SER
3	C	63	LEU
3	C	77	LYS
3	C	78	ILE
3	C	81	SER
3	C	83	THR
3	C	87	GLU
3	C	100	PHE
3	C	103	THR
3	C	106	SER

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Mol	Chain	Res	Type
3	C	107	ASP
3	C	109	HIS
3	C	110	LEU
3	C	114	GLN
3	C	115	SER
3	C	119	THR
3	C	121	GLU
3	C	122	SER
3	C	129	SER
3	C	131	GLN
3	C	144	LYS
3	C	145	THR
3	C	147	SER
3	C	152	GLU
3	C	160	THR
3	C	162	THR
3	C	167	GLN
3	C	170	VAL
3	C	171	GLU
3	C	174	ILE
3	C	178	VAL
1	D	45	TYR
1	D	48	VAL
1	D	52	LYS
1	D	57	THR
1	D	59	PHE
1	D	62	SER
1	D	67	TYR
1	D	69	THR
1	D	71	VAL
1	D	77	THR
1	D	80	CYS
1	D	83	THR
1	D	86	SER
1	D	90	LEU
1	D	94	ASN
1	D	98	ASN
1	D	112	GLU
1	D	119	ASP
1	D	123	LYS
1	D	128	LEU
1	D	131	LEU

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Mol	Chain	Res	Type
1	D	132	CYS
1	D	133	VAL
1	D	136	GLU
1	D	137	CYS
1	D	199	LEU
1	D	200	ILE
1	D	204	THR
1	D	205	SER
1	D	211	CYS
1	D	219	ILE
1	D	225	THR
1	D	232	LEU
1	D	242	THR
1	D	245	CYS
1	D	247	ASN
1	D	250	THR
1	D	266	LEU
1	D	273	GLU
1	D	276	ILE
1	D	280	SER
1	D	288	LYS
1	D	291	LEU
1	D	294	LEU
1	D	297	SER
1	D	299	GLU
1	D	300	ILE
1	D	301	VAL
1	D	303	THR
1	D	304	ARG
1	D	309	THR
1	D	310	ARG
1	D	312	SER
1	D	313	ILE
1	D	314	ARG
1	D	332	ILE
1	D	338	ASN
1	D	340	SER
1	D	341	LYS
1	D	345	HIS
1	D	346	GLU
1	D	352	SER
1	D	354	LYS

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Mol	Chain	Res	Type
1	D	363	THR
1	D	365	ASN
1	D	369	SER
1	D	371	SER
1	D	376	GLU
1	D	377	ILE
1	D	381	SER
1	D	385	ARG
1	D	388	PHE
1	D	400	THR
1	D	418	SER
1	D	420	ILE
1	D	422	ILE
1	D	424	CYS
1	D	429	ILE
1	D	435	GLU
1	D	440	MET
1	D	449	ILE
1	D	453	SER
1	D	458	LEU
1	D	460	LEU
1	D	462	ARG
1	D	466	THR
1	D	467	GLU
1	D	468	SER
1	D	472	GLU
1	D	473	THR
1	D	500	LEU
1	D	509	ARG
1	D	511	VAL
2	E	525	VAL
2	E	527	LEU
2	E	544	LEU
2	E	546	VAL
2	E	572	LEU
2	E	575	LEU
2	E	585	THR
2	E	586	ARG
2	E	592	ARG
2	E	593	TYR
2	E	596	ASP
2	E	597	GLN

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Mol	Chain	Res	Type
2	E	600	LEU
2	E	605	CYS
2	E	615	VAL
2	E	626	GLN
2	E	631	ASP
2	E	643	SER
2	E	646	THR
2	E	647	ASN
2	E	651	LYS
2	E	655	ASP
2	E	659	GLN
2	E	660	GLN
2	E	661	GLU
2	E	663	ASN
2	E	664	GLU
2	E	665	LYS
2	E	667	LEU
2	E	670	LEU
3	F	10	LYS
3	F	17	THR
3	F	19	THR
3	F	21	SER
3	F	25	SER
3	F	26	ILE
3	F	27	GLN
3	F	29	HIS
3	F	33	SER
3	F	34	ASN
3	F	36	ILE
3	F	44	SER
3	F	45	PHE
3	F	47	THR
3	F	52	LYS
3	F	55	ASP
3	F	62	SER
3	F	63	LEU
3	F	77	LYS
3	F	78	ILE
3	F	81	SER
3	F	83	THR
3	F	87	GLU
3	F	100	PHE

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Mol	Chain	Res	Type
3	F	103	THR
3	F	106	SER
3	F	107	ASP
3	F	109	HIS
3	F	110	LEU
3	F	114	GLN
3	F	115	SER
3	F	119	THR
3	F	121	GLU
3	F	122	SER
3	F	129	SER
3	F	131	GLN
3	F	144	LYS
3	F	145	THR
3	F	147	SER
3	F	152	GLU
3	F	160	THR
3	F	162	THR
3	F	167	GLN
3	F	170	VAL
3	F	171	GLU
3	F	174	ILE
3	F	178	VAL
1	G	45	TYR
1	G	48	VAL
1	G	52	LYS
1	G	57	THR
1	G	59	PHE
1	G	62	SER
1	G	67	TYR
1	G	69	THR
1	G	71	VAL
1	G	77	THR
1	G	80	CYS
1	G	83	THR
1	G	86	SER
1	G	90	LEU
1	G	94	ASN
1	G	98	ASN
1	G	112	GLU
1	G	119	ASP
1	G	123	LYS

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Mol	Chain	Res	Type
1	G	128	LEU
1	G	131	LEU
1	G	132	CYS
1	G	133	VAL
1	G	136	GLU
1	G	137	CYS
1	G	199	LEU
1	G	200	ILE
1	G	204	THR
1	G	205	SER
1	G	211	CYS
1	G	219	ILE
1	G	225	THR
1	G	232	LEU
1	G	242	THR
1	G	245	CYS
1	G	247	ASN
1	G	250	THR
1	G	266	LEU
1	G	273	GLU
1	G	276	ILE
1	G	280	SER
1	G	288	LYS
1	G	291	LEU
1	G	294	LEU
1	G	297	SER
1	G	299	GLU
1	G	300	ILE
1	G	301	VAL
1	G	303	THR
1	G	304	ARG
1	G	309	THR
1	G	310	ARG
1	G	312	SER
1	G	313	ILE
1	G	314	ARG
1	G	332	ILE
1	G	338	ASN
1	G	340	SER
1	G	341	LYS
1	G	345	HIS
1	G	346	GLU

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Mol	Chain	Res	Type
1	G	352	SER
1	G	354	LYS
1	G	363	THR
1	G	365	ASN
1	G	369	SER
1	G	371	SER
1	G	376	GLU
1	G	377	ILE
1	G	381	SER
1	G	385	ARG
1	G	388	PHE
1	G	400	THR
1	G	418	SER
1	G	420	ILE
1	G	422	ILE
1	G	424	CYS
1	G	429	ILE
1	G	435	GLU
1	G	440	MET
1	G	449	ILE
1	G	453	SER
1	G	458	LEU
1	G	460	LEU
1	G	462	ARG
1	G	466	THR
1	G	467	GLU
1	G	468	SER
1	G	472	GLU
1	G	473	THR
1	G	500	LEU
1	G	509	ARG
1	G	511	VAL
2	H	525	VAL
2	H	527	LEU
2	H	544	LEU
2	H	546	VAL
2	H	572	LEU
2	H	575	LEU
2	H	585	THR
2	H	586	ARG
2	H	592	ARG
2	H	593	TYR

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Mol	Chain	Res	Type
2	H	596	ASP
2	H	597	GLN
2	H	600	LEU
2	H	605	CYS
2	H	615	VAL
2	H	626	GLN
2	H	631	ASP
2	H	643	SER
2	H	646	THR
2	H	647	ASN
2	H	651	LYS
2	H	655	ASP
2	H	659	GLN
2	H	660	GLN
2	H	661	GLU
2	H	663	ASN
2	H	664	GLU
2	H	665	LYS
2	H	667	LEU
2	H	670	LEU
3	I	7	LEU
3	I	10	LYS
3	I	17	THR
3	I	19	THR
3	I	21	SER
3	I	25	SER
3	I	26	ILE
3	I	27	GLN
3	I	29	HIS
3	I	33	SER
3	I	34	ASN
3	I	36	ILE
3	I	44	SER
3	I	45	PHE
3	I	47	THR
3	I	52	LYS
3	I	55	ASP
3	I	62	SER
3	I	63	LEU
3	I	77	LYS
3	I	78	ILE
3	I	81	SER

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Mol	Chain	Res	Type
3	I	83	THR
3	I	87	GLU
3	I	100	PHE
3	I	103	THR
3	I	106	SER
3	I	107	ASP
3	I	109	HIS
3	I	110	LEU
3	I	114	GLN
3	I	115	SER
3	I	119	THR
3	I	121	GLU
3	I	122	SER
3	I	129	SER
3	I	131	GLN
3	I	144	LYS
3	I	145	THR
3	I	147	SER
3	I	152	GLU
3	I	160	THR
3	I	162	THR
3	I	167	GLN
3	I	170	VAL
3	I	171	GLU
3	I	174	ILE
3	I	178	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN
1	A	111	HIS
1	A	296	GLN
1	A	307	ASN
2	B	550	GLN
2	B	637	GLN
2	B	658	ASN
3	C	41	ASN
3	C	131	GLN
1	D	109	GLN
1	D	111	HIS
1	D	296	GLN

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Mol	Chain	Res	Type
1	D	307	ASN
2	E	550	GLN
2	E	658	ASN
3	F	41	ASN
3	F	131	GLN
1	G	109	GLN
1	G	111	HIS
1	G	295	ASN
1	G	296	GLN
1	G	307	ASN
2	H	550	GLN
2	H	626	GLN
2	H	637	GLN
2	H	658	ASN
3	I	41	ASN
3	I	66	GLN
3	I	131	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

18 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	E	704	2	14,14,15	0.55	0	17,19,21	0.44	0
4	NAG	B	702	2	14,14,15	0.26	0	17,19,21	0.41	0
4	NAG	A	601	1	14,14,15	0.48	0	17,19,21	0.45	0
4	NAG	E	702	2	14,14,15	0.38	0	17,19,21	0.42	0
4	NAG	H	702	2	14,14,15	0.56	0	17,19,21	0.45	0
4	NAG	A	602	1	14,14,15	0.69	1 (7%)	17,19,21	0.38	0
4	NAG	D	602	1	14,14,15	0.36	0	17,19,21	0.73	1 (5%)
4	NAG	G	601	1	14,14,15	0.20	0	17,19,21	0.44	0
4	NAG	G	602	1	14,14,15	0.39	0	17,19,21	0.43	0
4	NAG	H	703	2	14,14,15	0.37	0	17,19,21	0.50	0
4	NAG	H	701	2	14,14,15	0.23	0	17,19,21	0.47	0
4	NAG	D	601	1	14,14,15	0.48	0	17,19,21	0.49	0
4	NAG	E	703	2	14,14,15	0.16	0	17,19,21	0.55	0
4	NAG	B	703	2	14,14,15	0.20	0	17,19,21	0.56	0
4	NAG	B	701	2	14,14,15	0.19	0	17,19,21	0.59	1 (5%)
4	NAG	H	704	2	14,14,15	0.40	0	17,19,21	0.47	0
4	NAG	E	701	2	14,14,15	0.43	0	17,19,21	0.52	0
4	NAG	B	704	2	14,14,15	0.45	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	E	704	2	-	4/6/23/26	0/1/1/1
4	NAG	B	702	2	-	1/6/23/26	0/1/1/1
4	NAG	A	601	1	-	3/6/23/26	0/1/1/1
4	NAG	E	702	2	-	1/6/23/26	0/1/1/1
4	NAG	H	702	2	-	1/6/23/26	0/1/1/1
4	NAG	A	602	1	-	0/6/23/26	0/1/1/1
4	NAG	D	602	1	-	1/6/23/26	0/1/1/1
4	NAG	G	601	1	-	2/6/23/26	0/1/1/1
4	NAG	G	602	1	-	2/6/23/26	0/1/1/1
4	NAG	H	703	2	-	4/6/23/26	0/1/1/1
4	NAG	H	701	2	-	2/6/23/26	0/1/1/1
4	NAG	D	601	1	-	3/6/23/26	0/1/1/1
4	NAG	E	703	2	-	2/6/23/26	0/1/1/1
4	NAG	B	703	2	-	2/6/23/26	0/1/1/1
4	NAG	B	701	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	H	704	2	-	3/6/23/26	0/1/1/1
4	NAG	E	701	2	-	2/6/23/26	0/1/1/1
4	NAG	B	704	2	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	NAG	O5-C1	-2.27	1.40	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602	NAG	C1-O5-C5	2.52	115.60	112.19
4	B	701	NAG	C1-O5-C5	2.02	114.93	112.19

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	701	NAG	O5-C5-C6-O6
4	B	701	NAG	O5-C5-C6-O6
4	G	601	NAG	O5-C5-C6-O6
4	H	703	NAG	O5-C5-C6-O6
4	B	701	NAG	C4-C5-C6-O6
4	H	701	NAG	C4-C5-C6-O6
4	E	703	NAG	O5-C5-C6-O6
4	D	601	NAG	C1-C2-N2-C7
4	E	701	NAG	O5-C5-C6-O6
4	A	601	NAG	C4-C5-C6-O6
4	E	703	NAG	C4-C5-C6-O6
4	B	703	NAG	O5-C5-C6-O6
4	G	601	NAG	C4-C5-C6-O6
4	B	703	NAG	C4-C5-C6-O6
4	E	704	NAG	O5-C5-C6-O6
4	A	601	NAG	O5-C5-C6-O6
4	H	703	NAG	C4-C5-C6-O6
4	E	701	NAG	C4-C5-C6-O6
4	B	702	NAG	O5-C5-C6-O6
4	B	704	NAG	C1-C2-N2-C7
4	E	704	NAG	C1-C2-N2-C7

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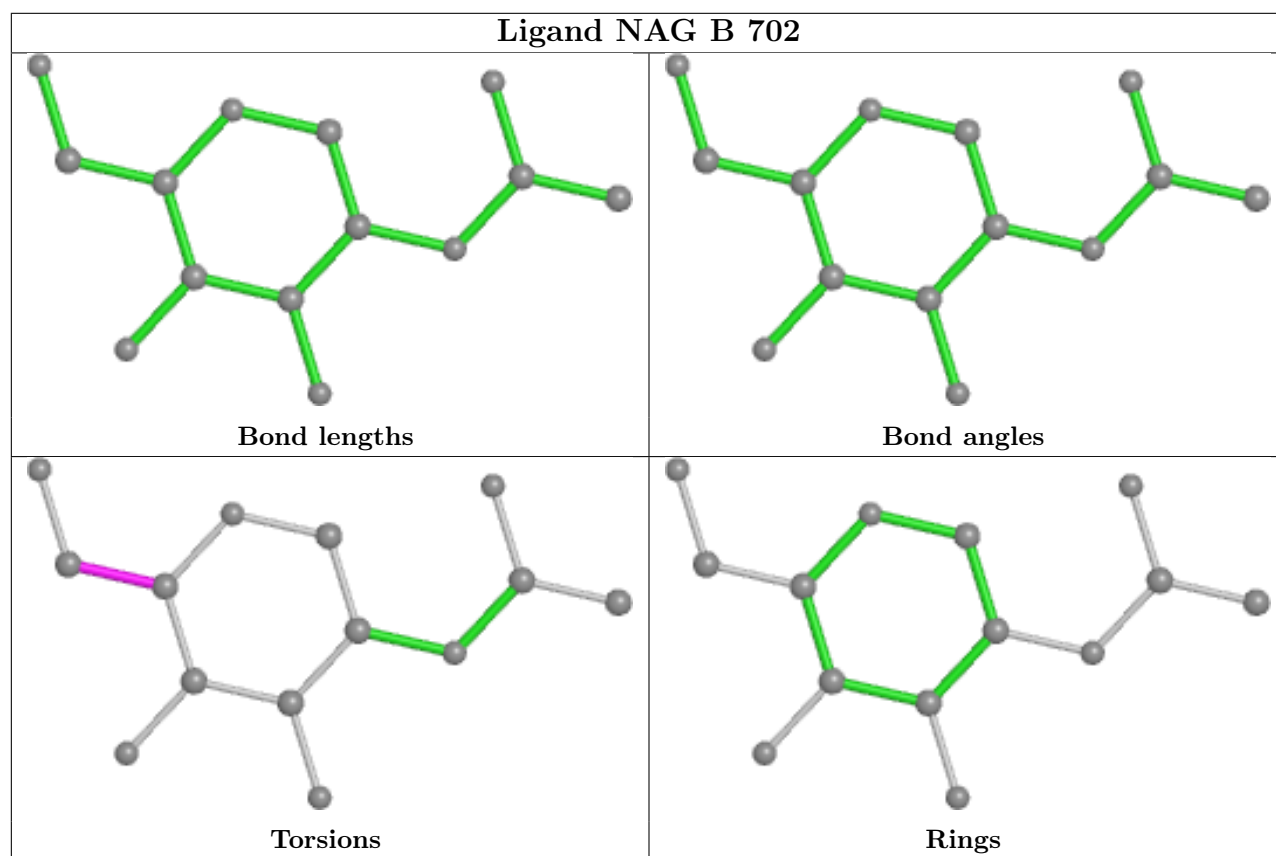
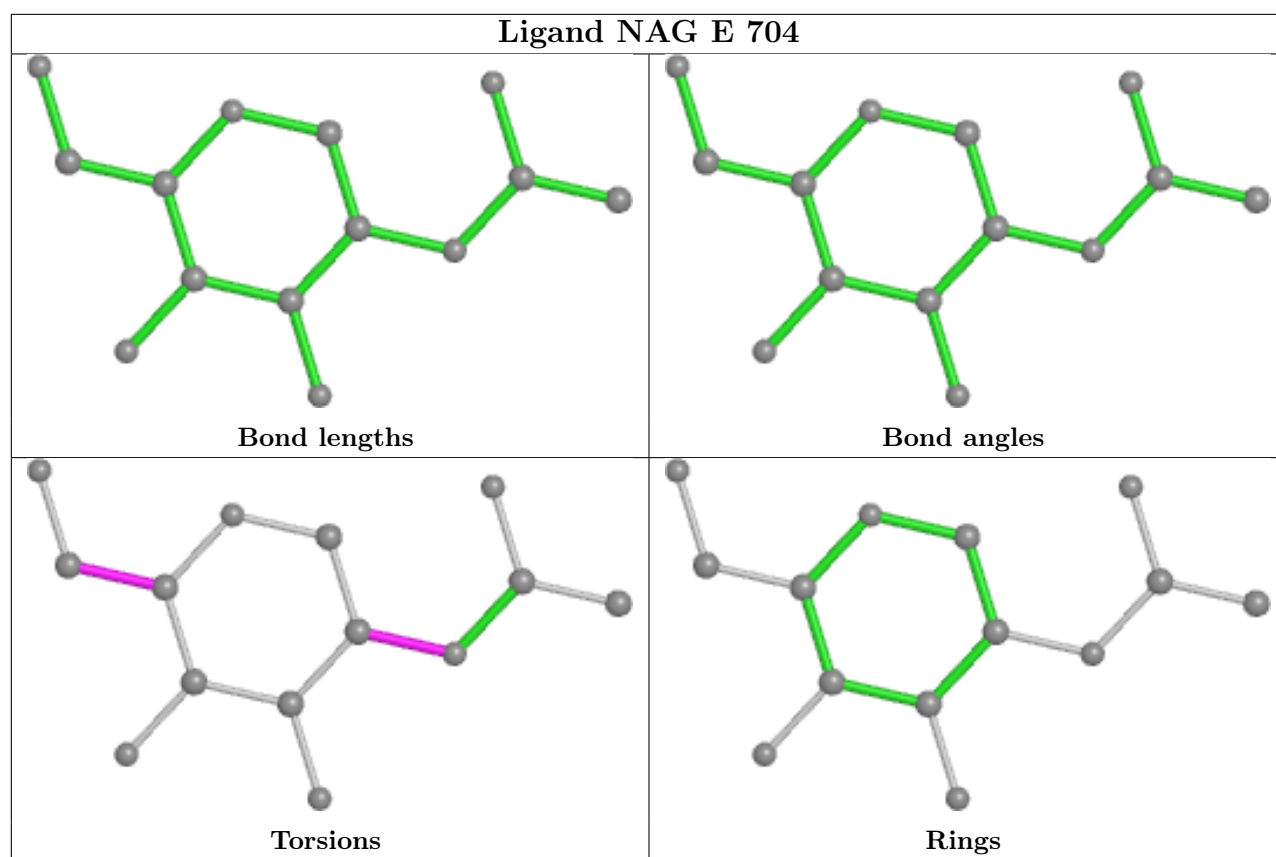
Mol	Chain	Res	Type	Atoms
4	H	704	NAG	C1-C2-N2-C7
4	B	704	NAG	O5-C5-C6-O6
4	H	702	NAG	O5-C5-C6-O6
4	E	702	NAG	O5-C5-C6-O6
4	H	704	NAG	O5-C5-C6-O6
4	D	601	NAG	O5-C5-C6-O6
4	G	602	NAG	C1-C2-N2-C7
4	H	703	NAG	C1-C2-N2-C7
4	A	601	NAG	C1-C2-N2-C7
4	B	704	NAG	C3-C2-N2-C7
4	E	704	NAG	C3-C2-N2-C7
4	E	704	NAG	C4-C5-C6-O6
4	D	602	NAG	C1-C2-N2-C7
4	D	601	NAG	C3-C2-N2-C7
4	G	602	NAG	C3-C2-N2-C7
4	H	703	NAG	C3-C2-N2-C7
4	H	704	NAG	C3-C2-N2-C7

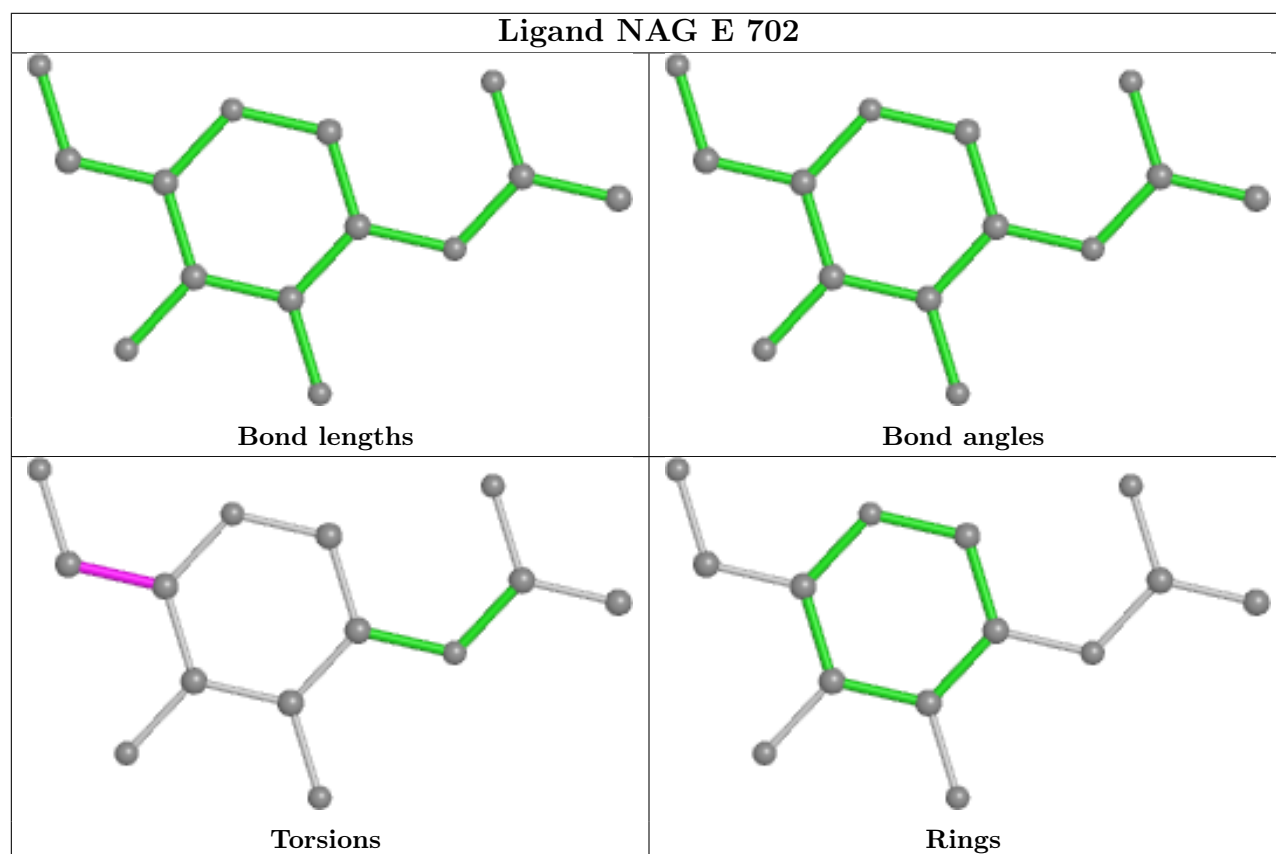
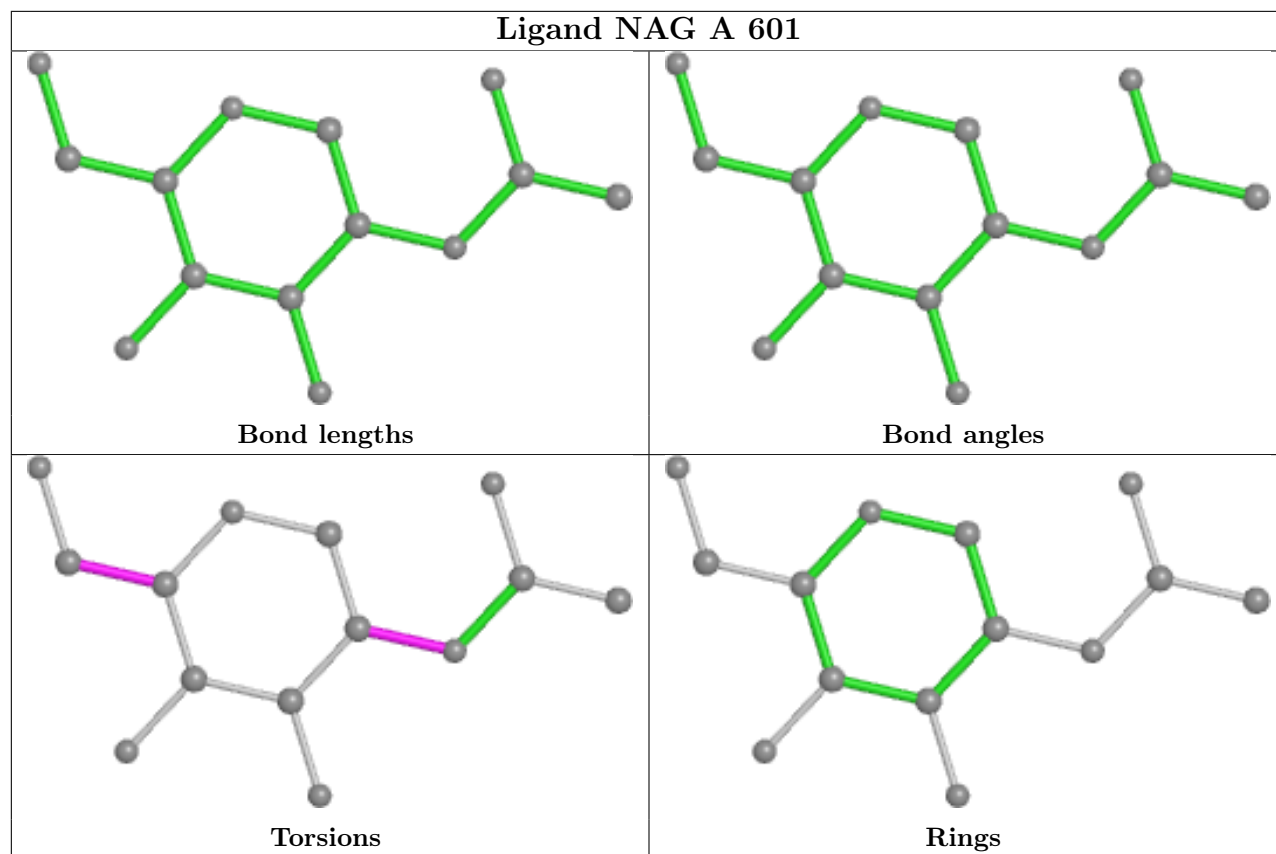
There are no ring outliers.

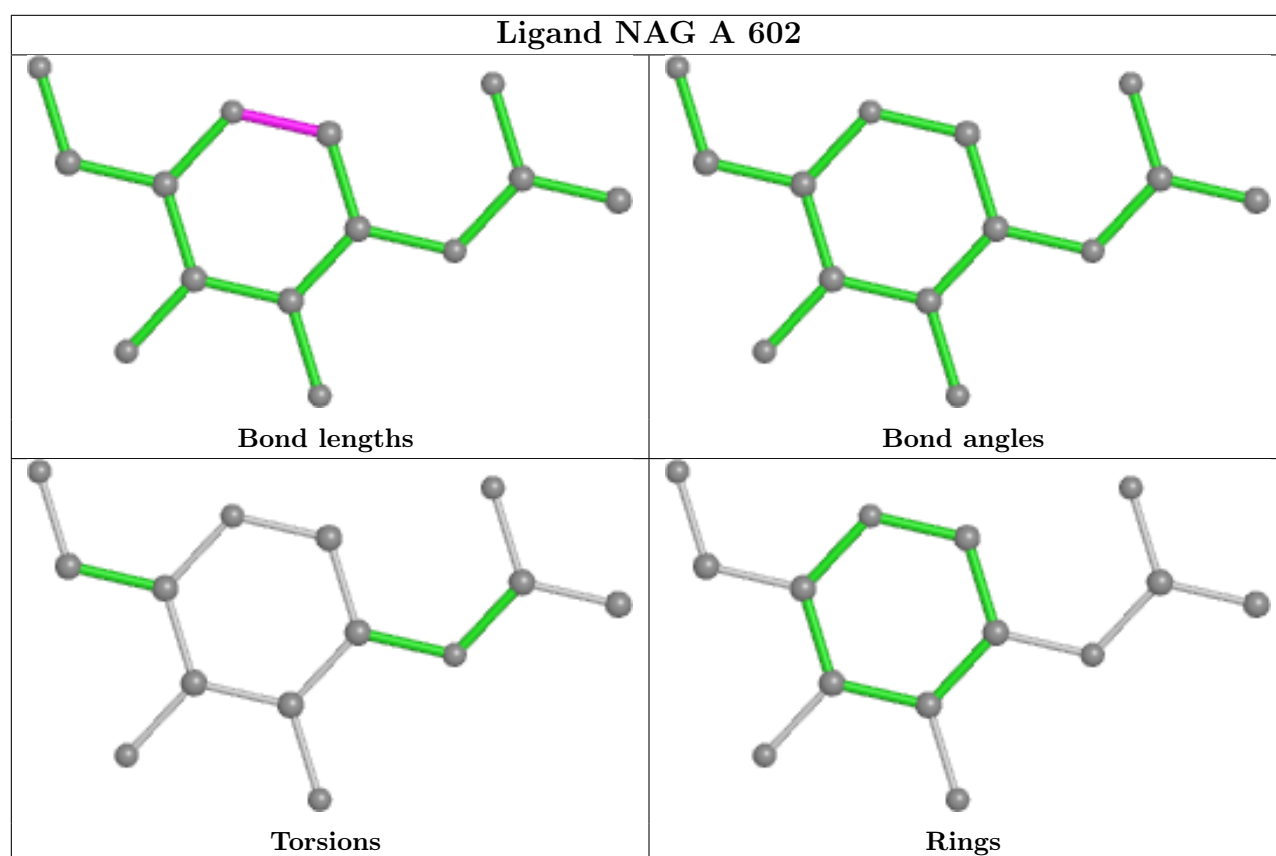
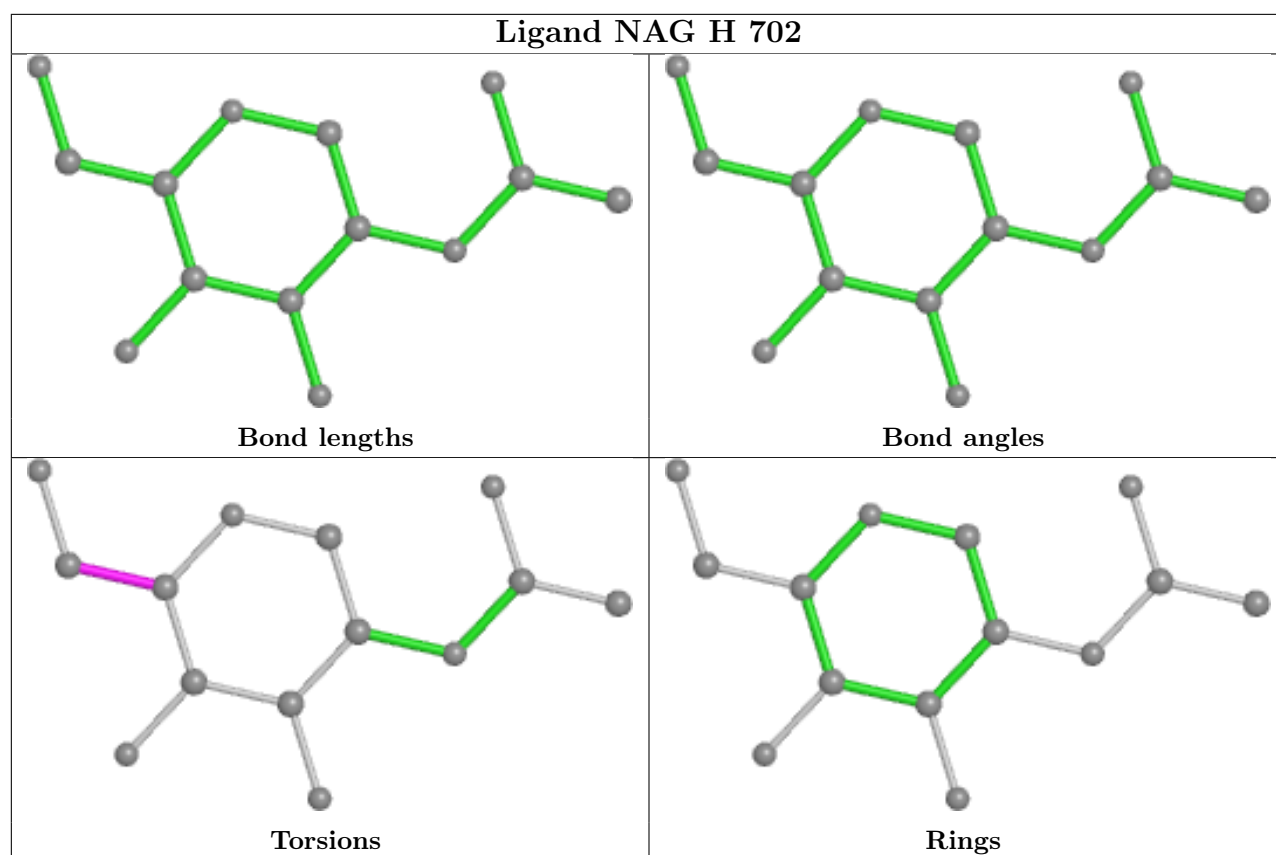
5 monomers are involved in 6 short contacts:

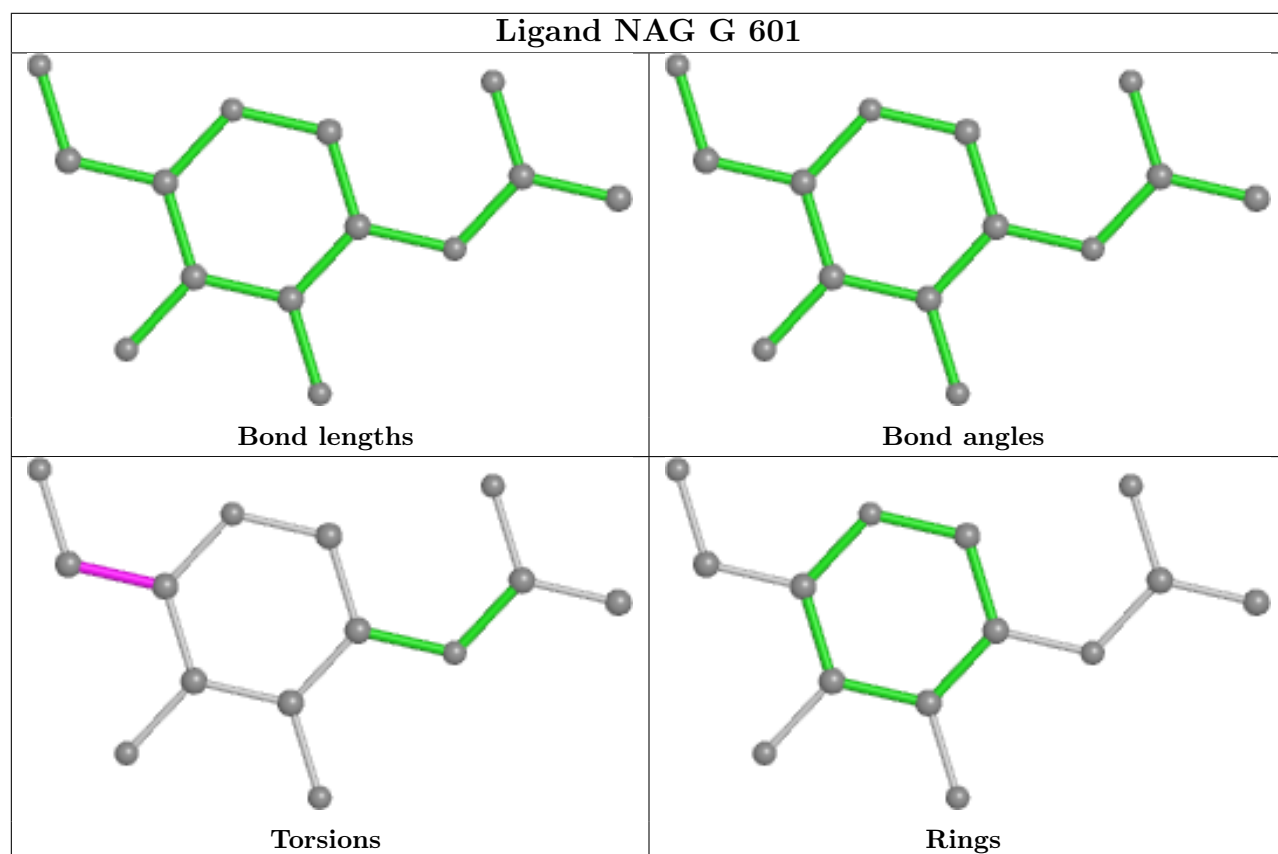
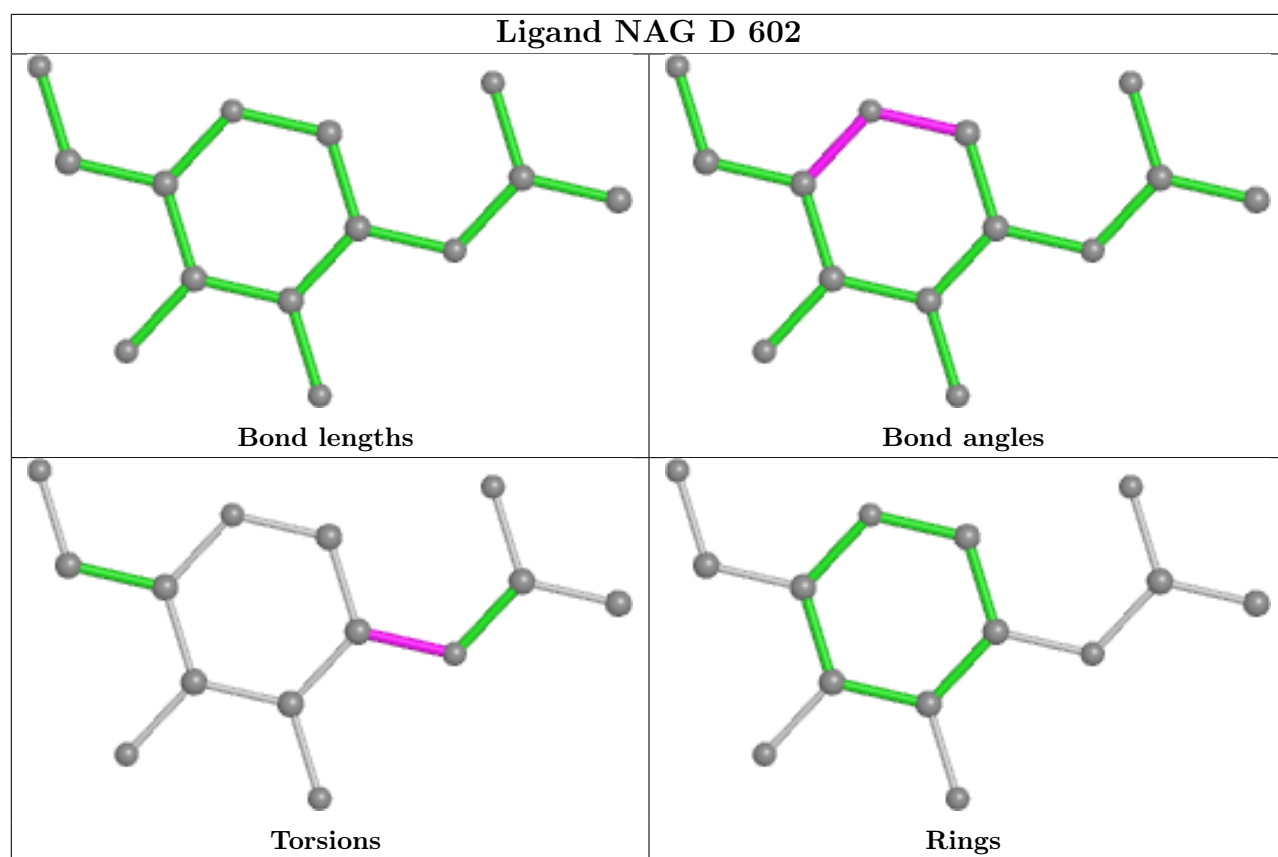
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	704	NAG	1	0
4	A	601	NAG	2	0
4	D	601	NAG	1	0
4	B	703	NAG	1	0
4	H	704	NAG	1	0

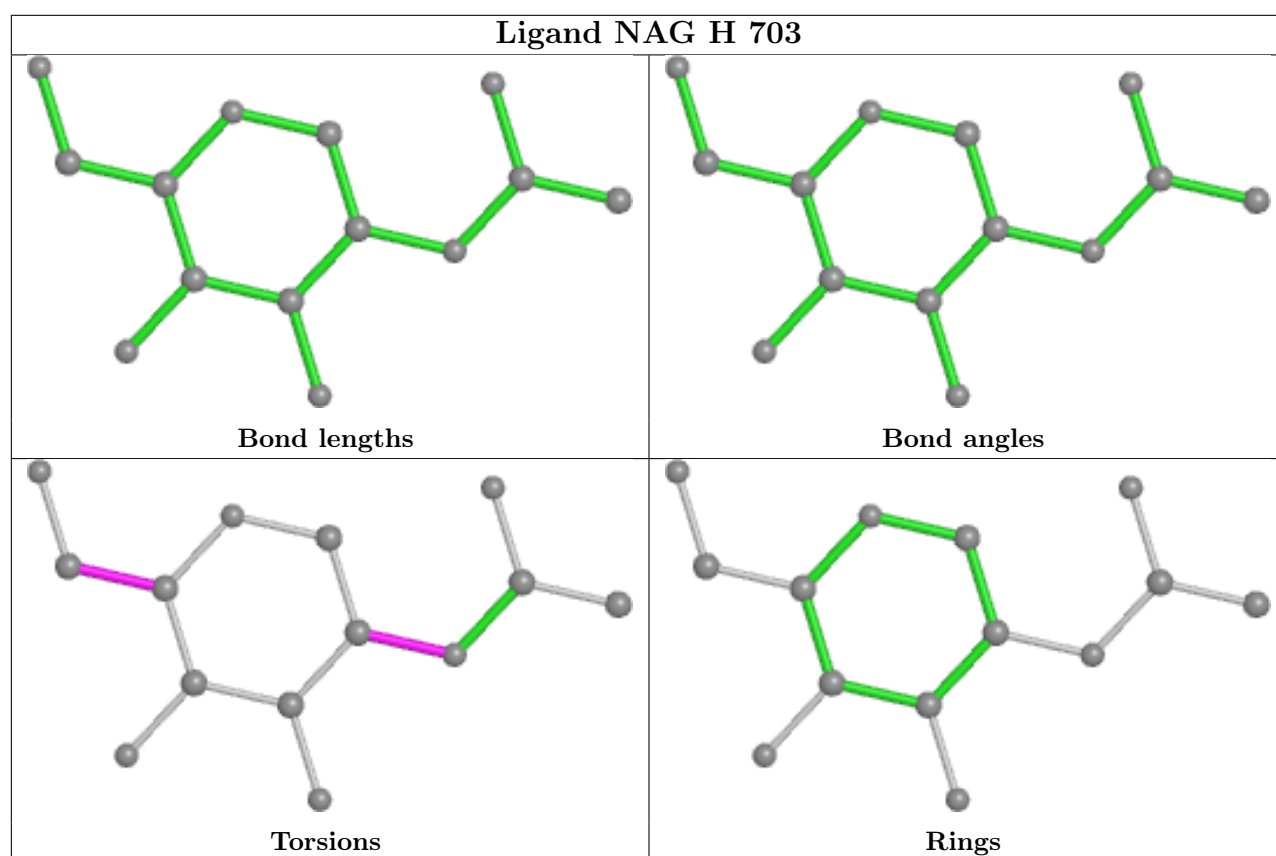
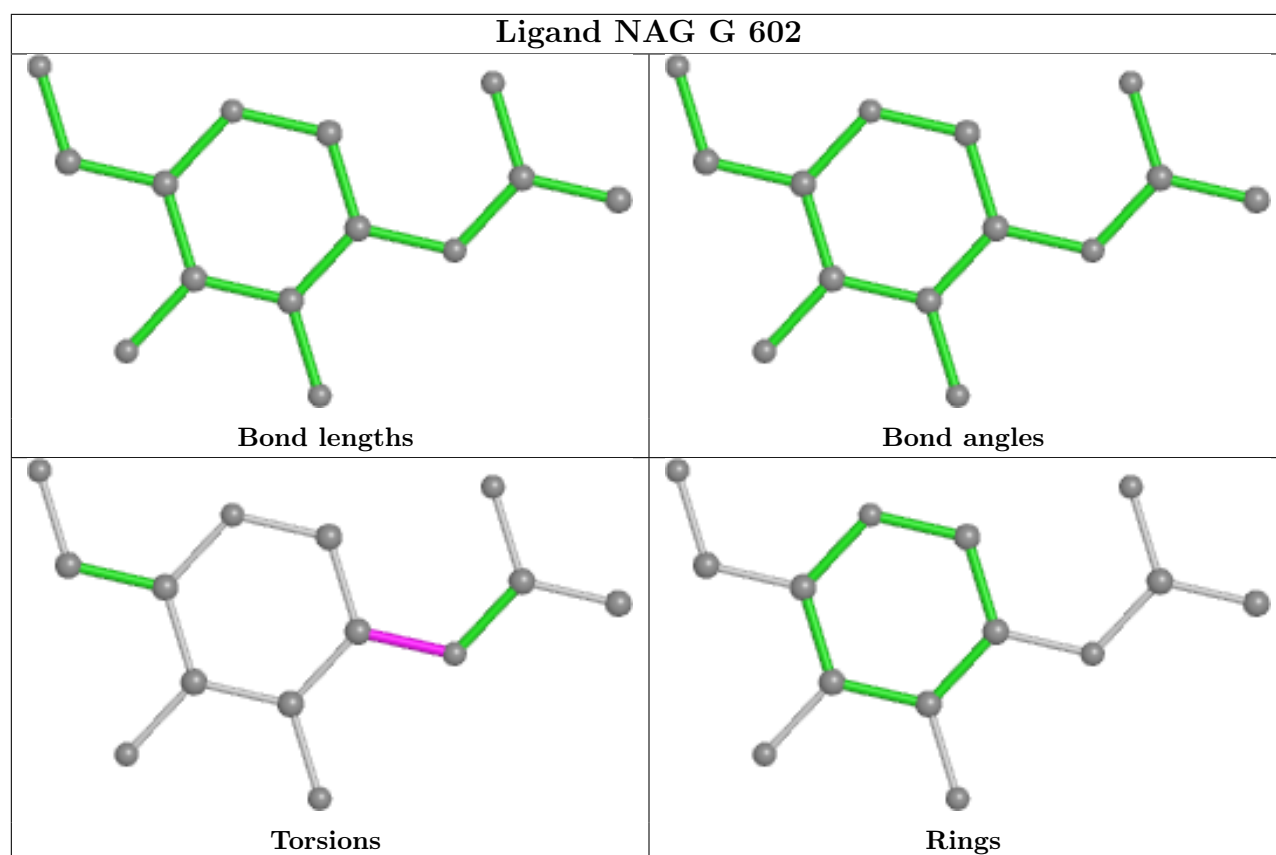
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

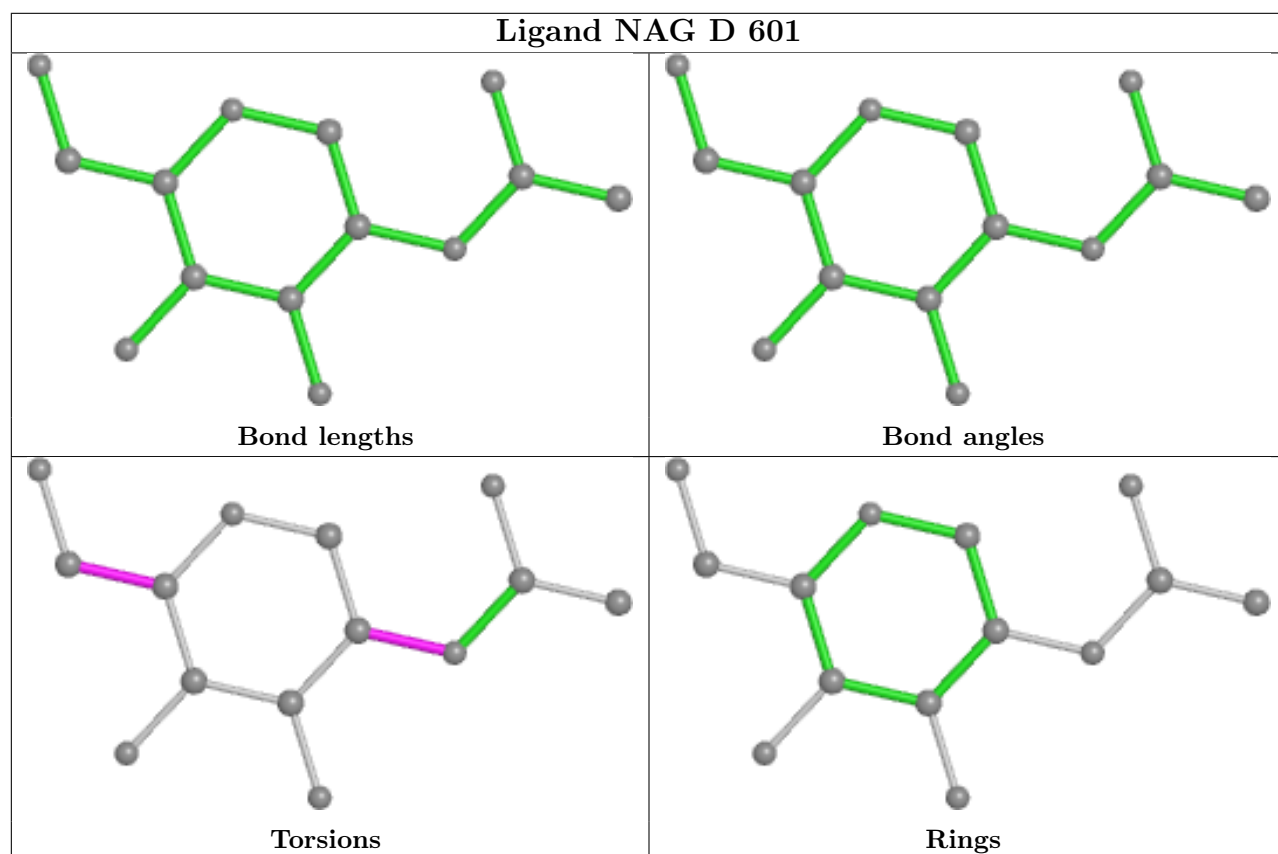
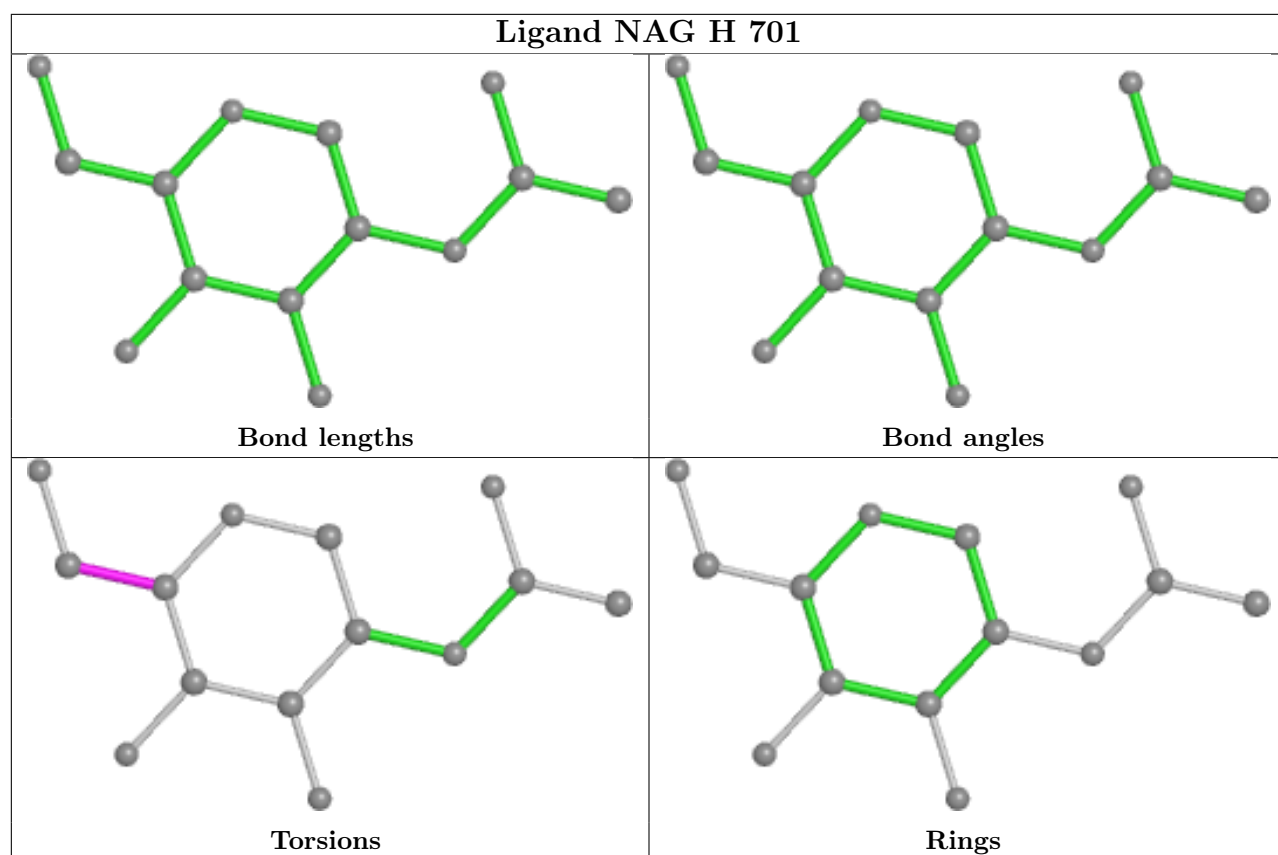


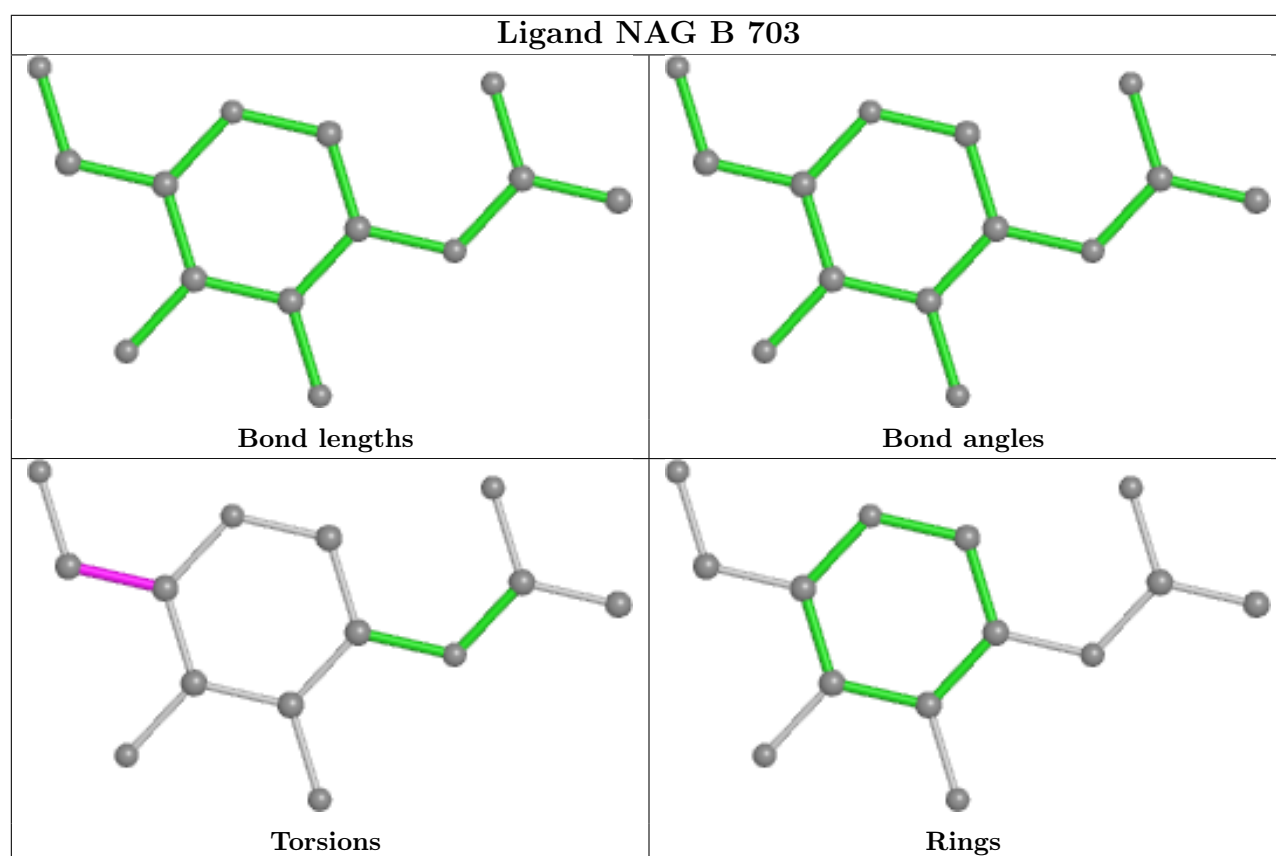
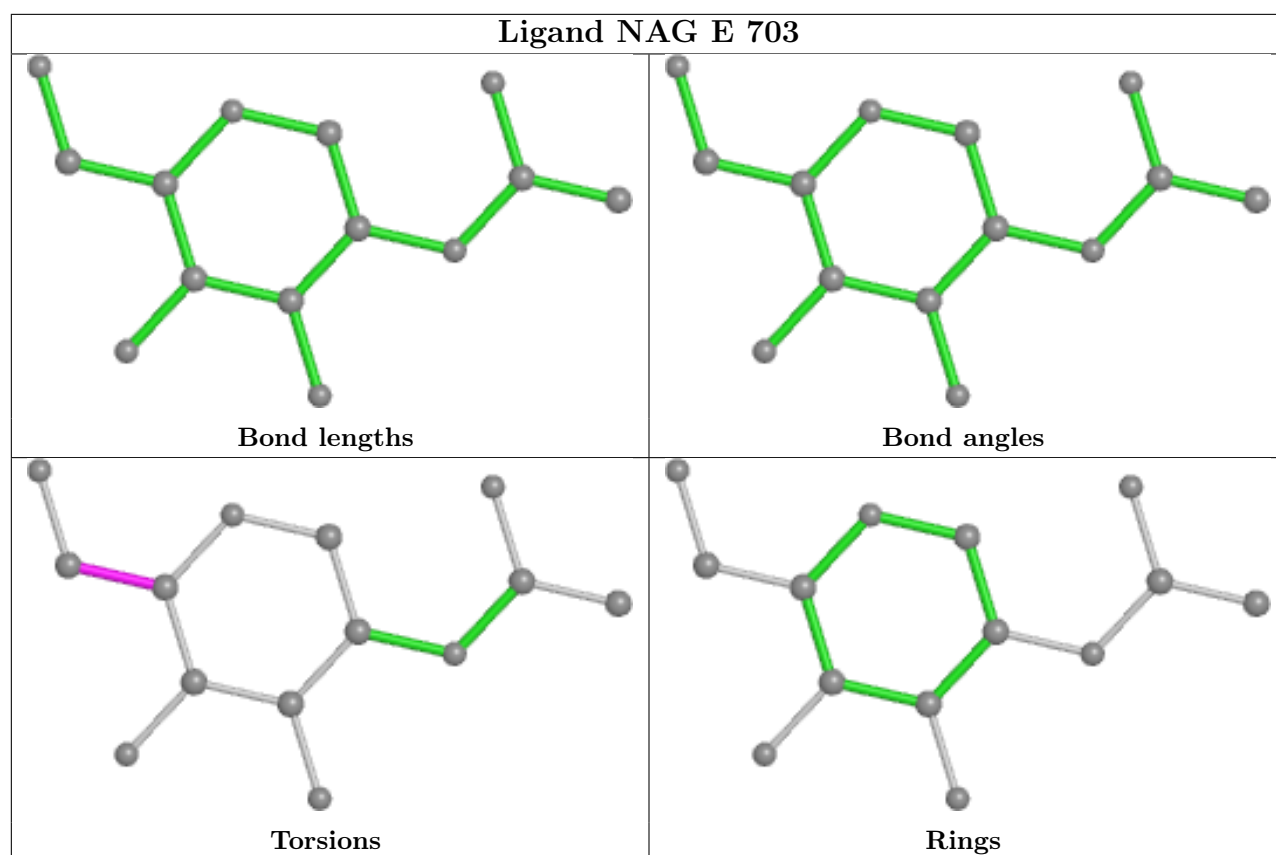


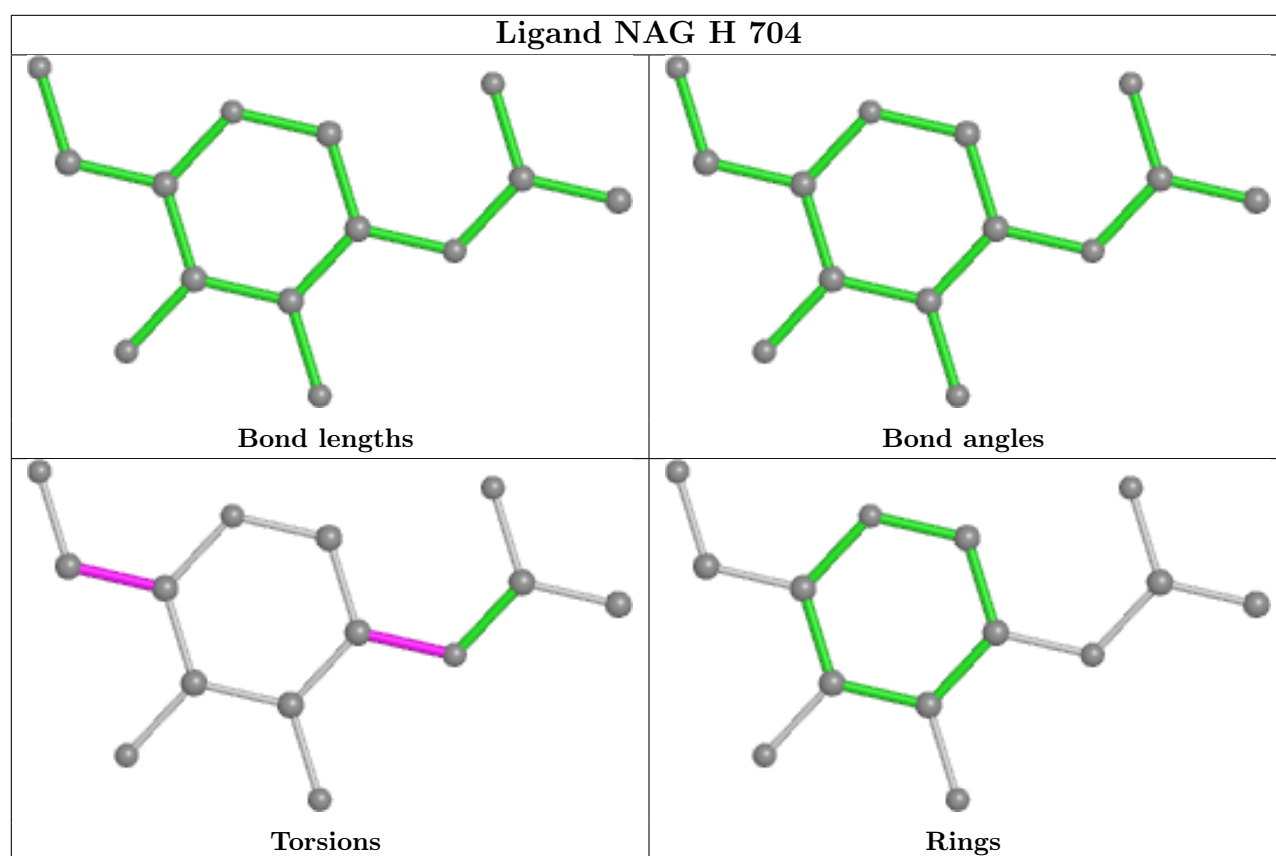
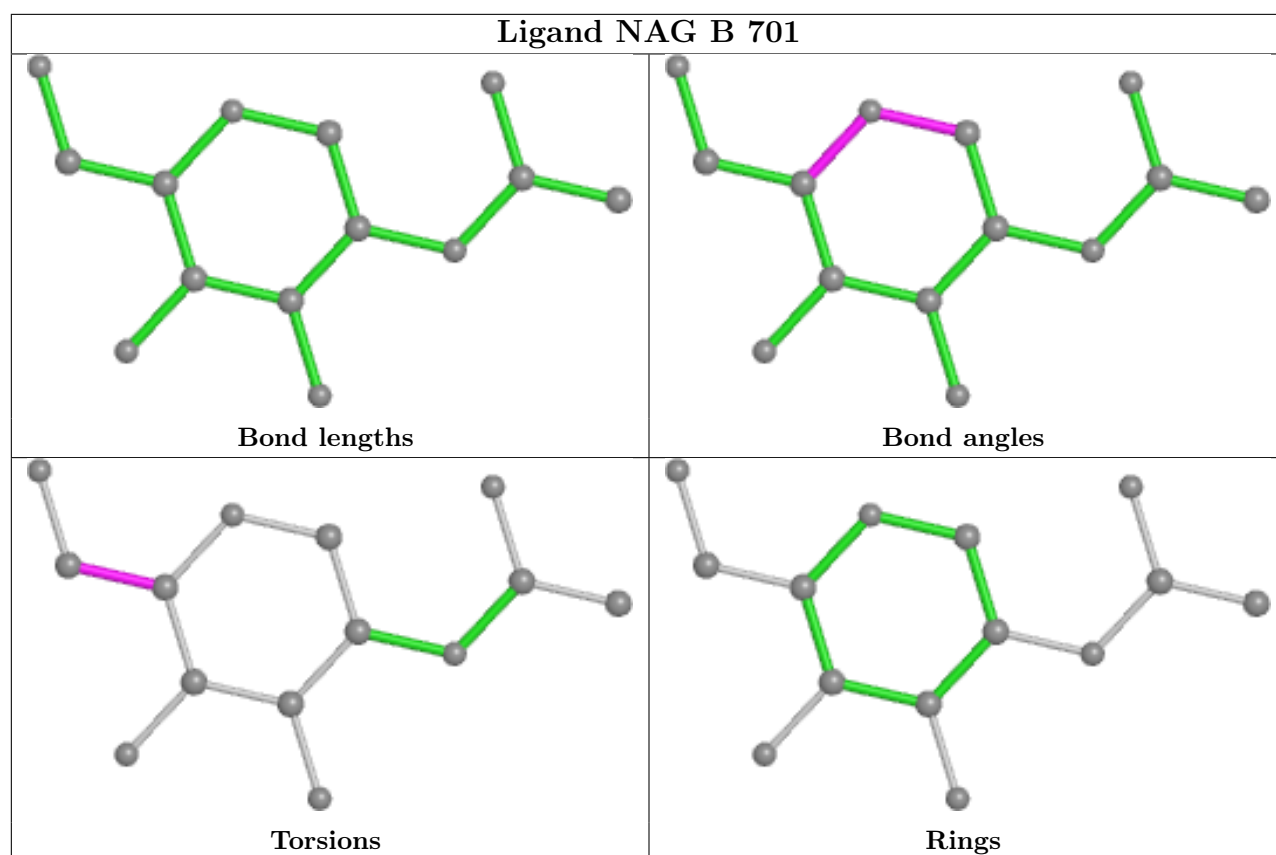


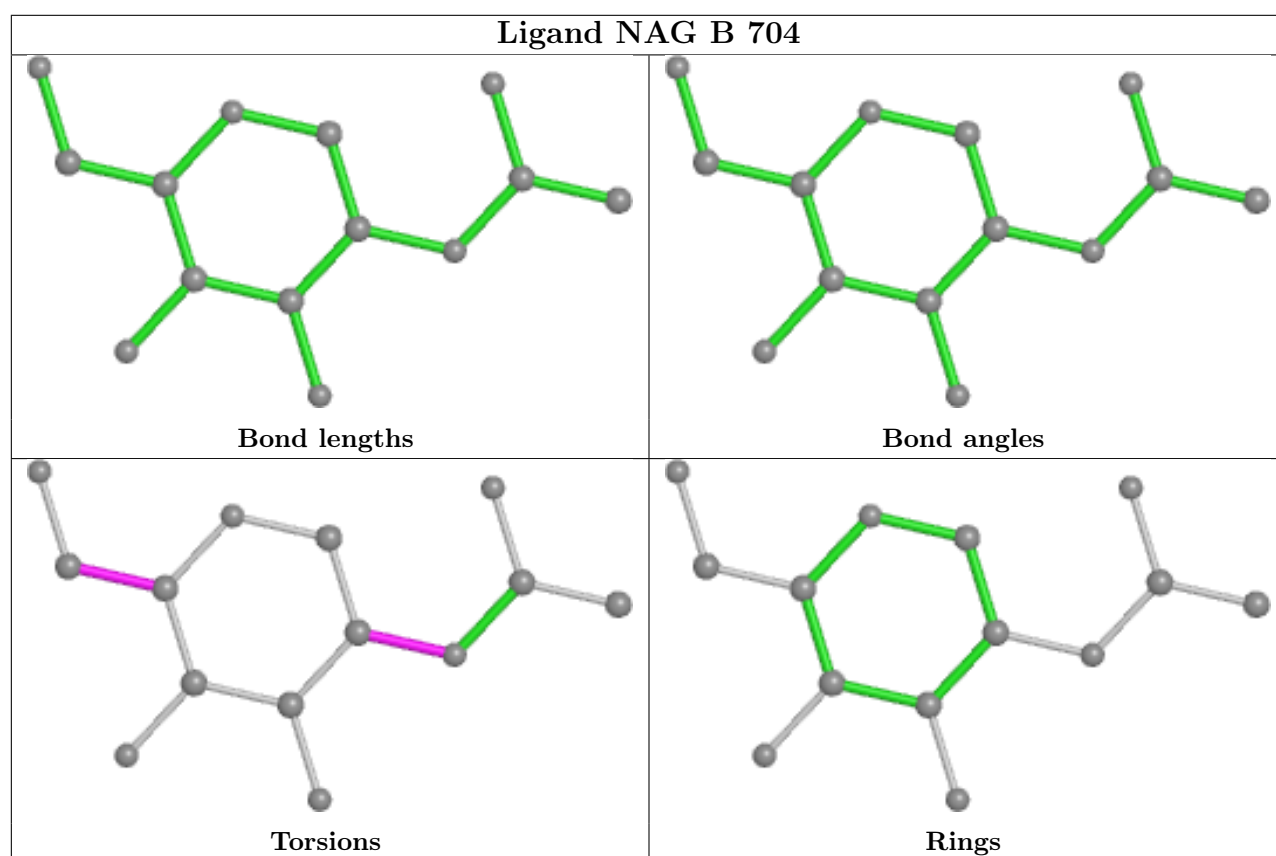
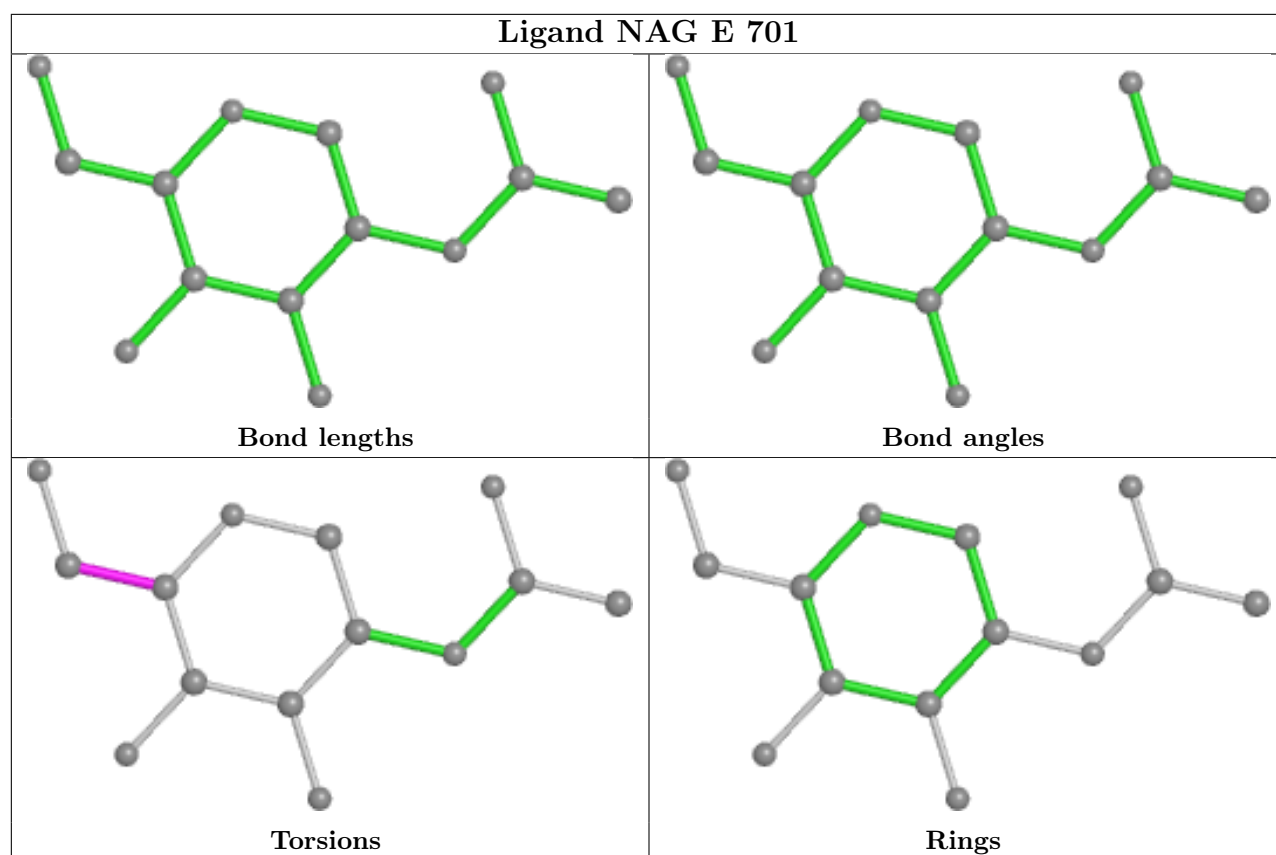












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	D	1
1	G	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	341:LYS	C	344:TRP	N	6.12
1	D	341:LYS	C	344:TRP	N	6.12
1	G	341:LYS	C	344:TRP	N	6.12

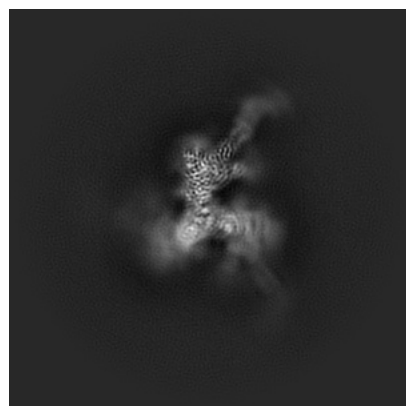
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39820. These allow visual inspection of the internal detail of the map and identification of artifacts.

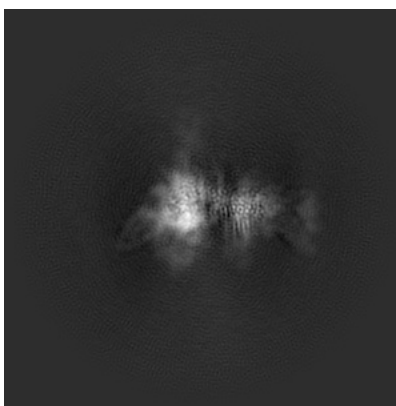
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

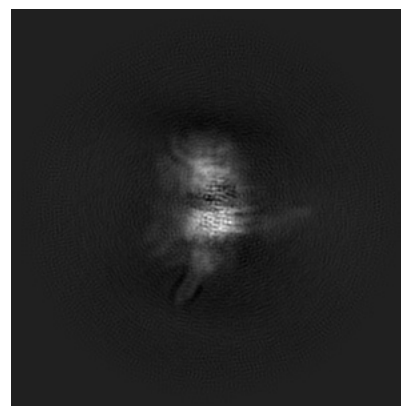
6.1.1 Primary map



X

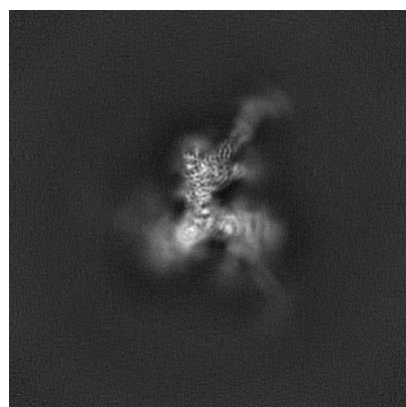


Y

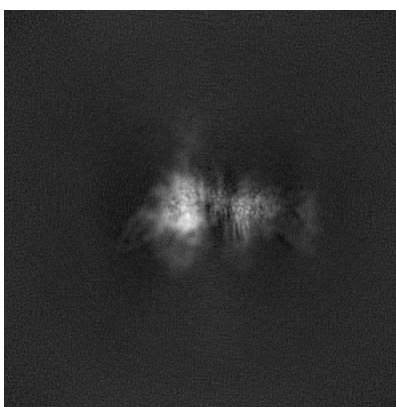


Z

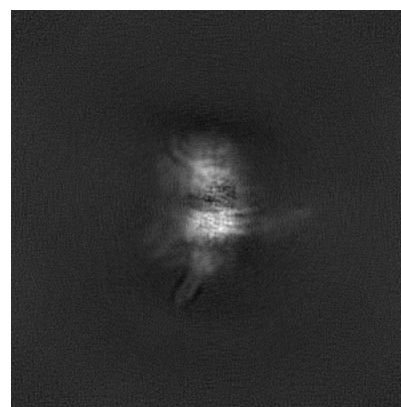
6.1.2 Raw map



X



Y

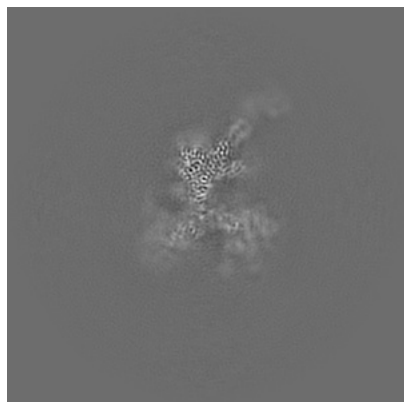


Z

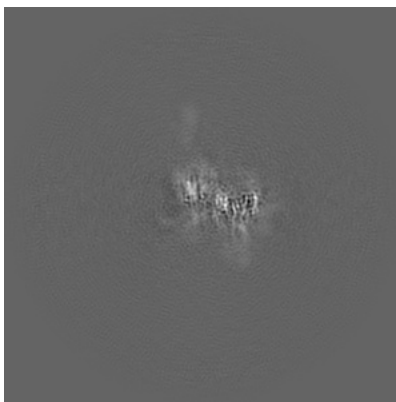
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

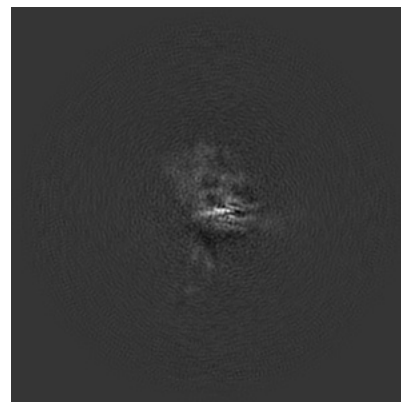
6.2.1 Primary map



X Index: 250

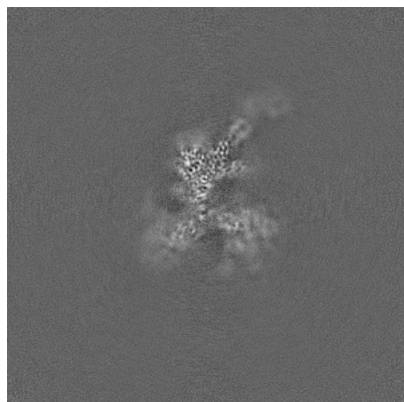


Y Index: 250



Z Index: 250

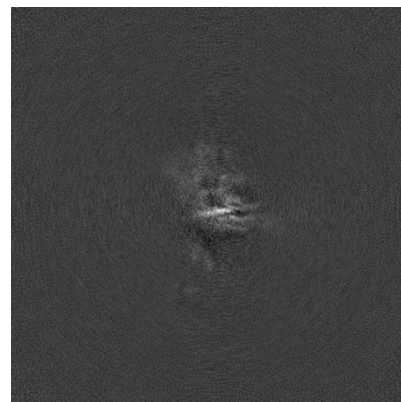
6.2.2 Raw map



X Index: 250



Y Index: 250

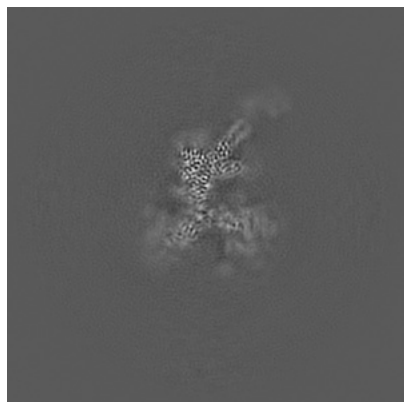


Z Index: 250

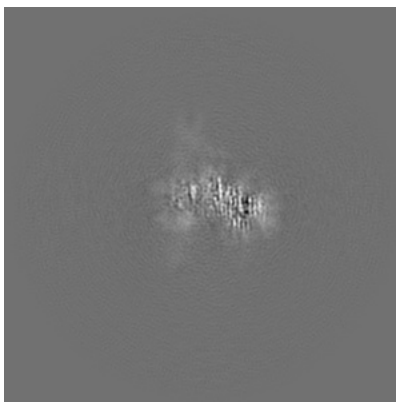
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

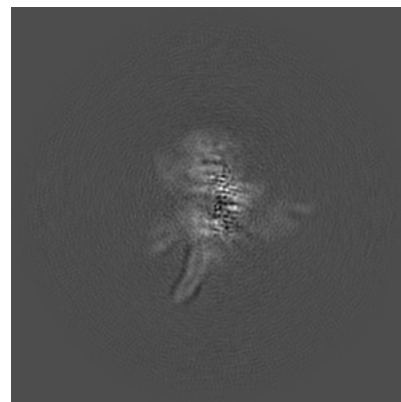
6.3.1 Primary map



X Index: 252

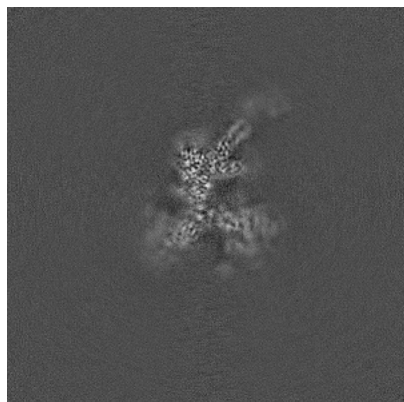


Y Index: 234

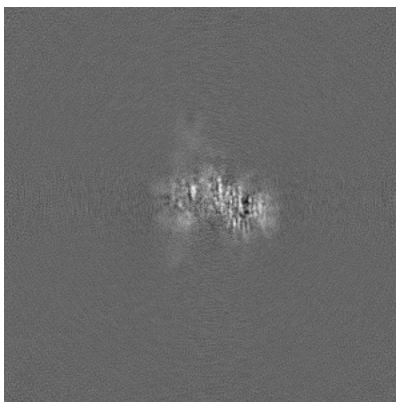


Z Index: 229

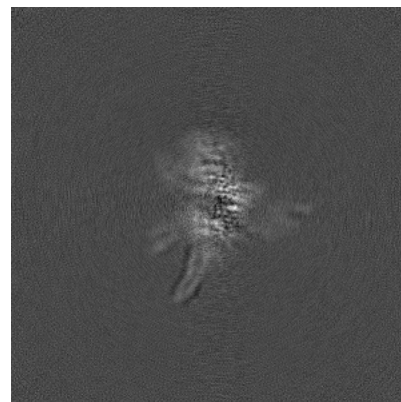
6.3.2 Raw map



X Index: 252



Y Index: 234

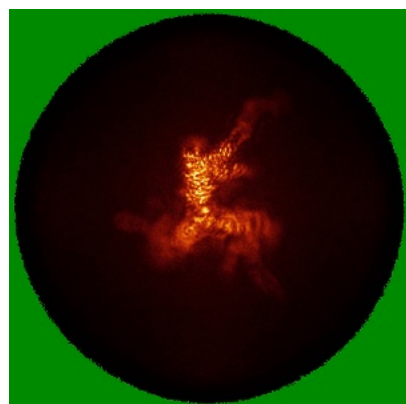


Z Index: 229

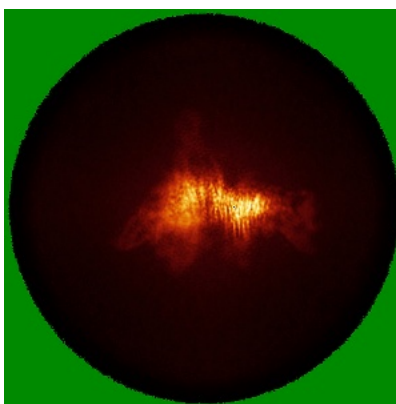
The images above show the largest variance slices of the map in three orthogonal directions.

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

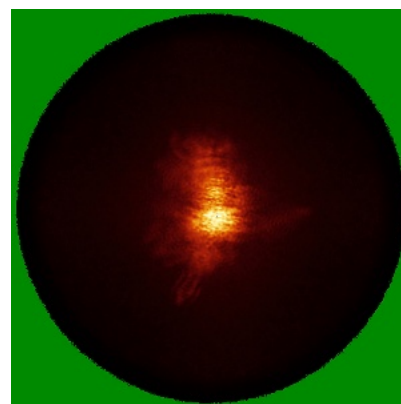
6.4.1 Primary map



X



Y

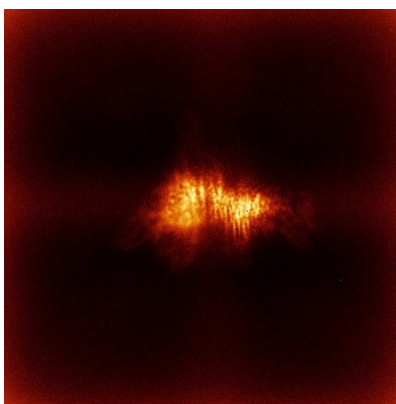


Z

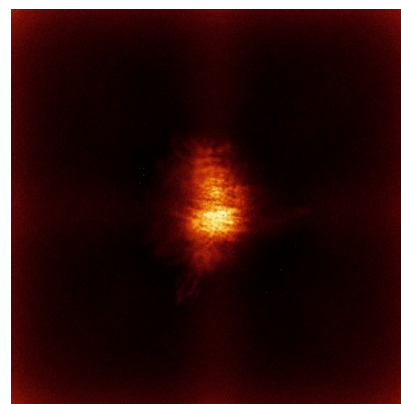
6.4.2 Raw map



X



Y

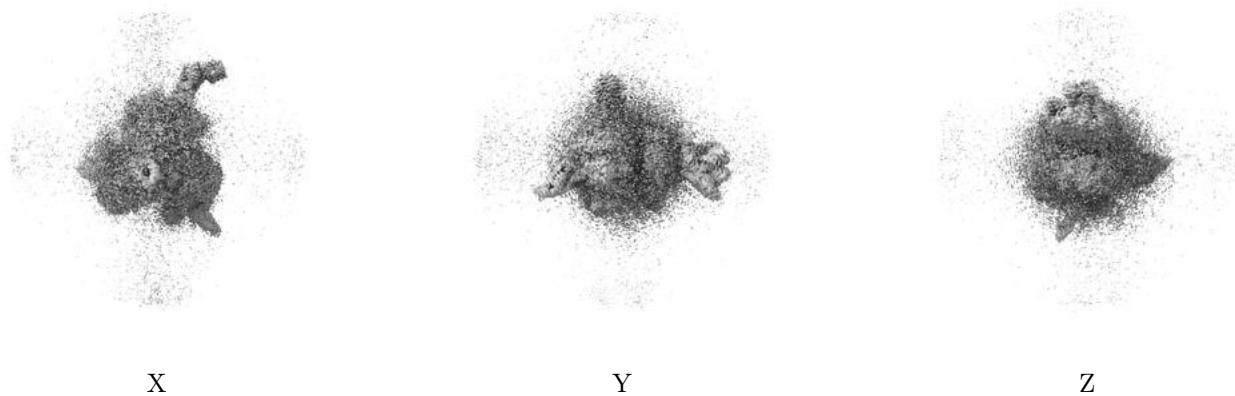


Z

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.

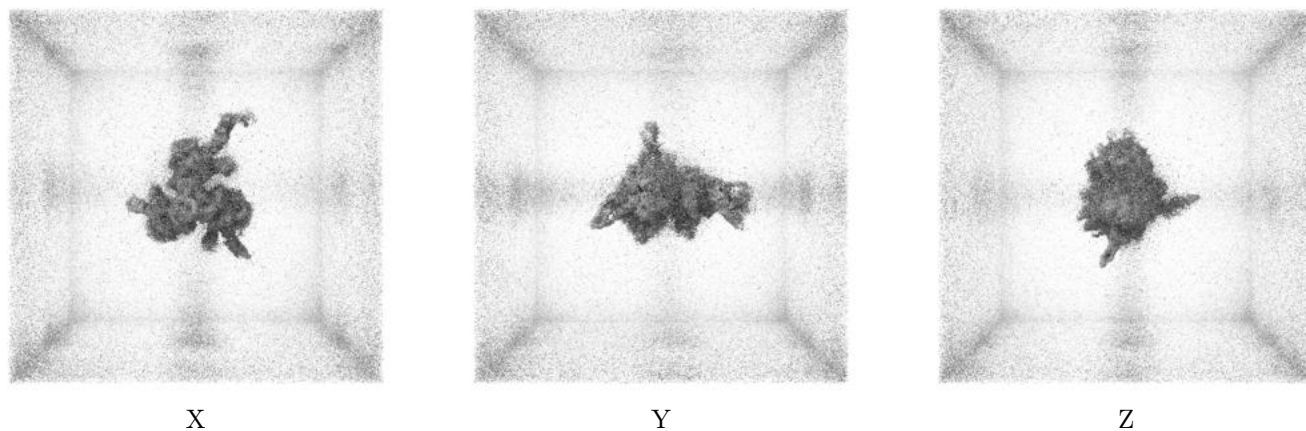
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.049. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

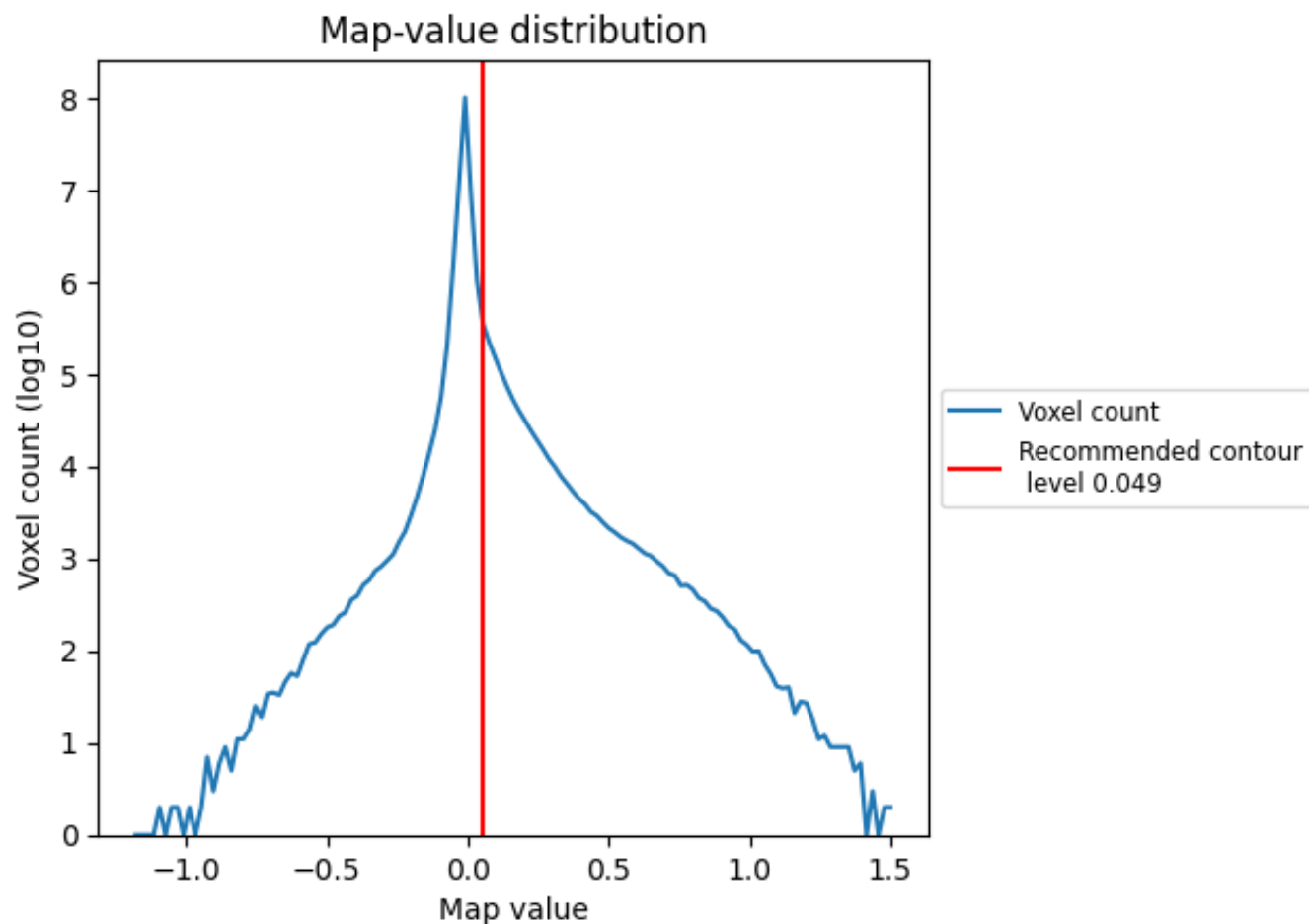
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

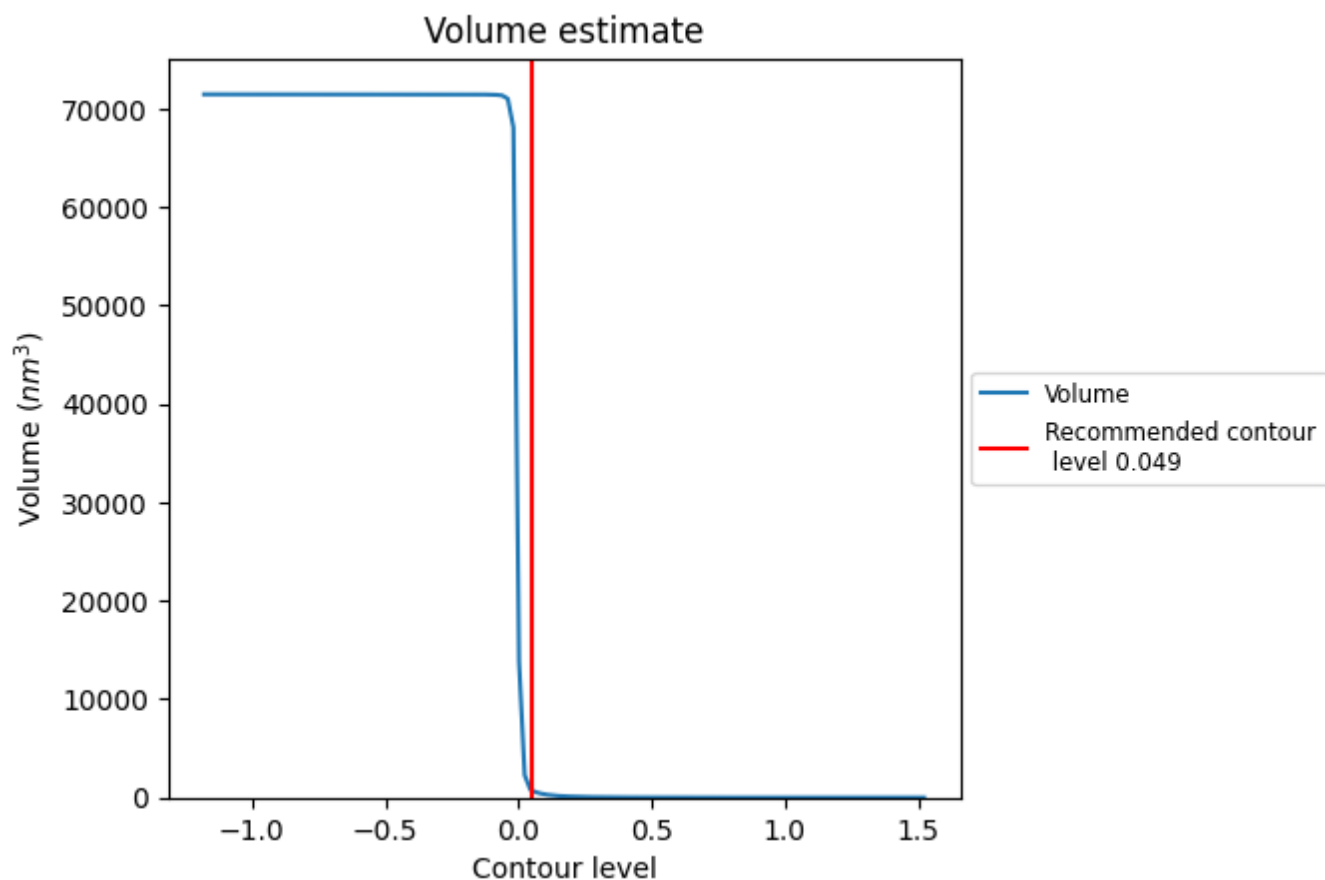
This section contains the results of statistical analysis of the map.

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.

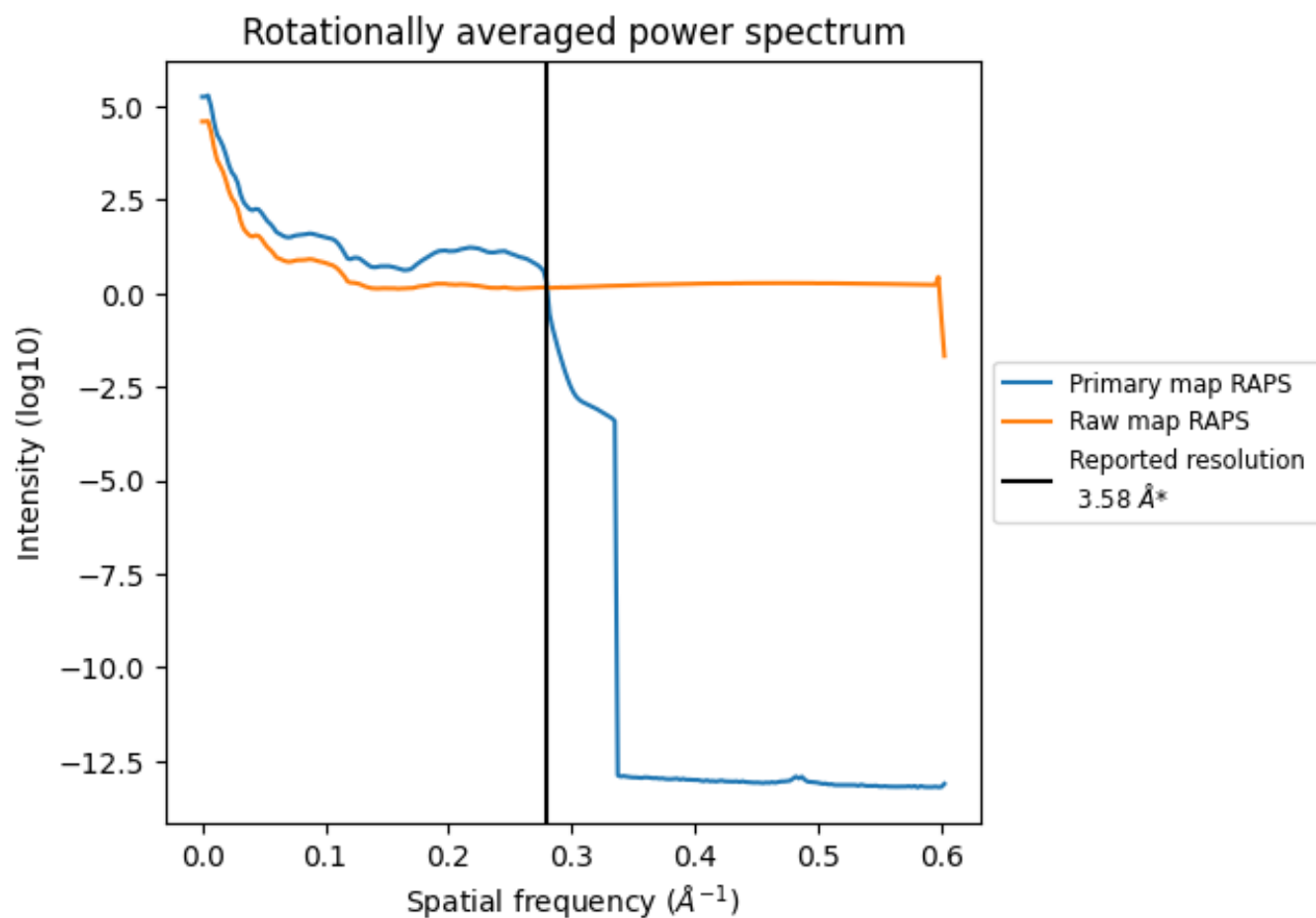
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 757 nm^3 ; this corresponds to an approximate mass of 684 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 ⓘ

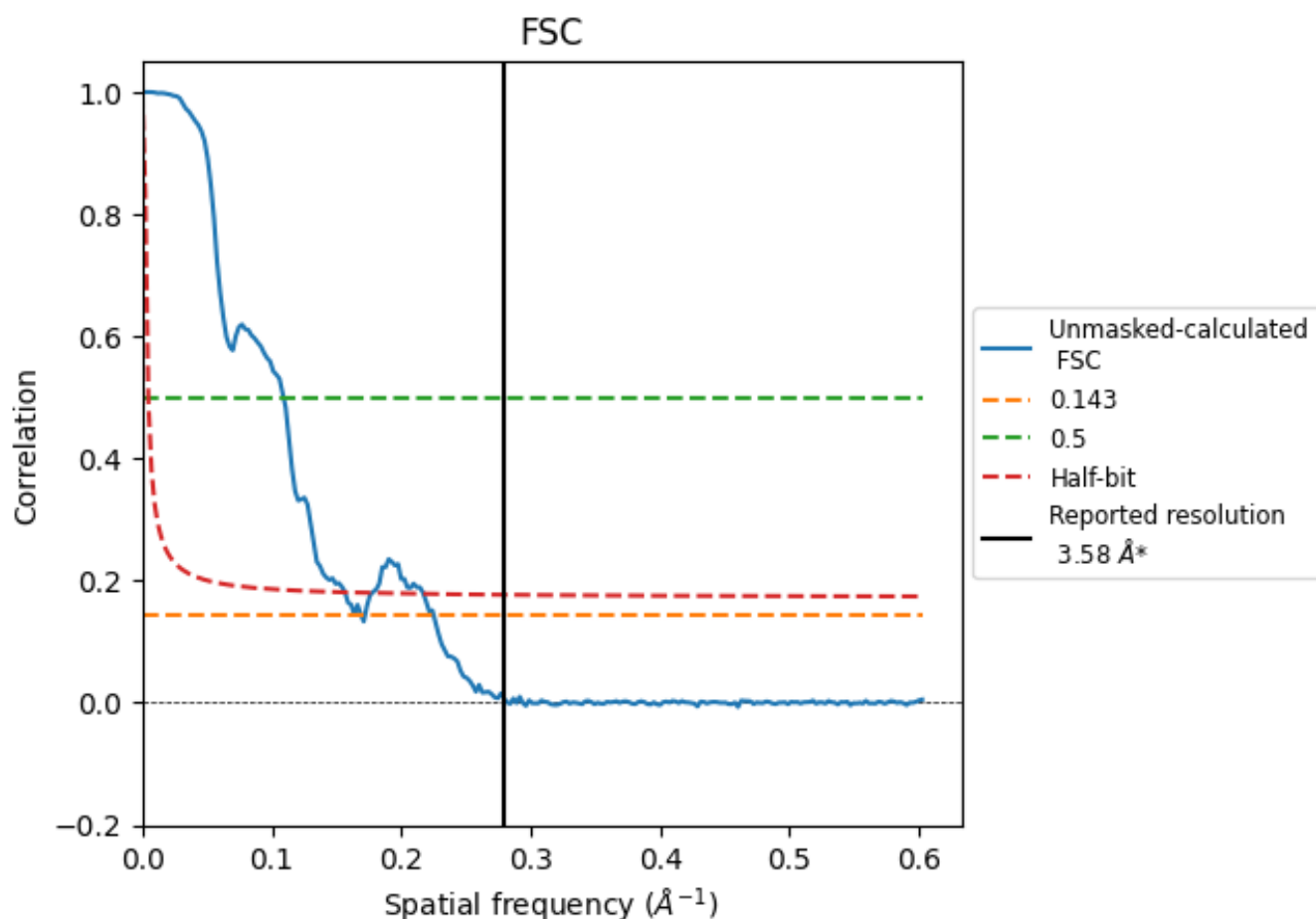


*Reported resolution corresponds to spatial frequency of 0.279 \AA^{-1}

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 0.279 Å⁻¹

8.2 Resolution estimates [i](#)

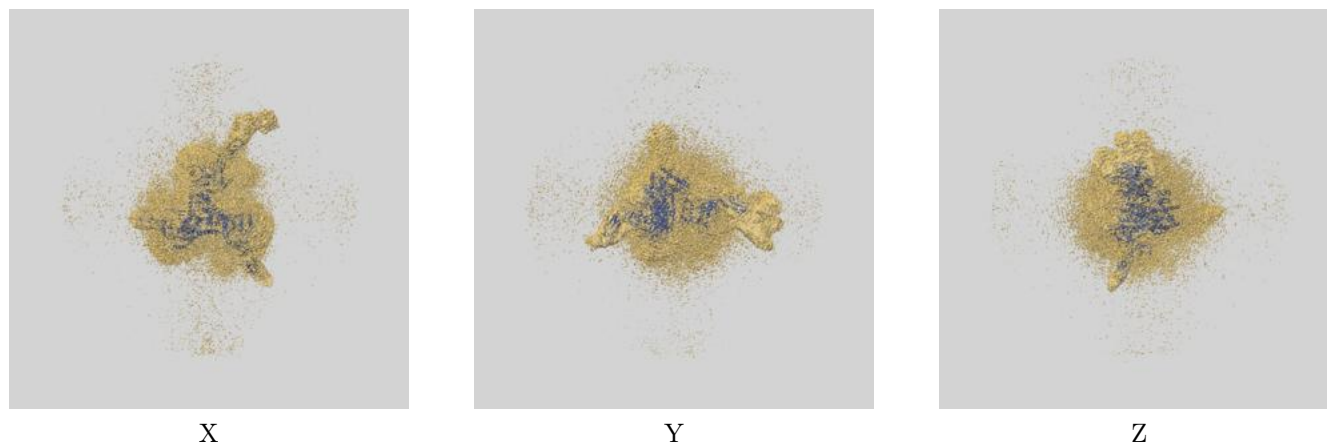
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.58	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.91	9.16	6.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.91 differs from the reported value 3.58 by more than 10 %

9 Map-model fit [i](#)

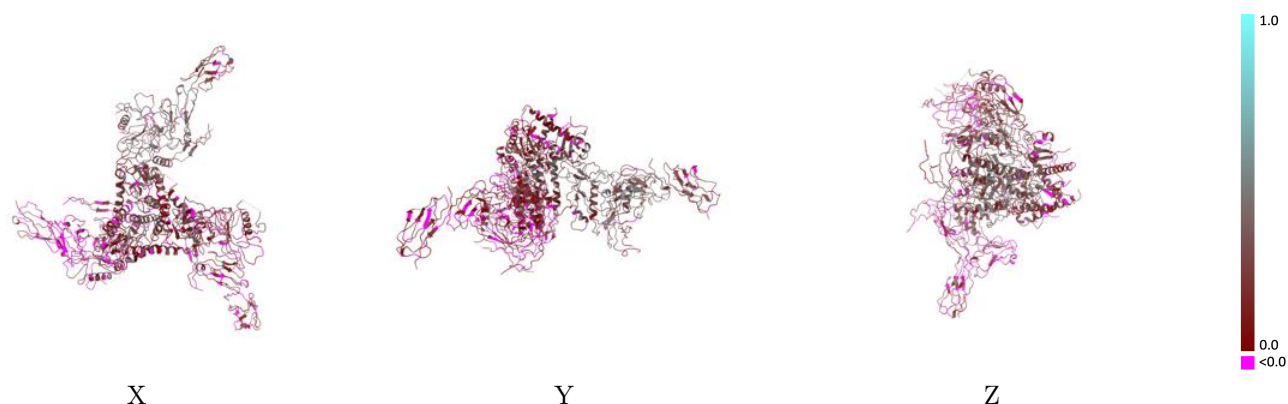
This section contains information regarding the fit between EMDB map EMD-39820 and PDB model 8Z7N. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.049 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](#)



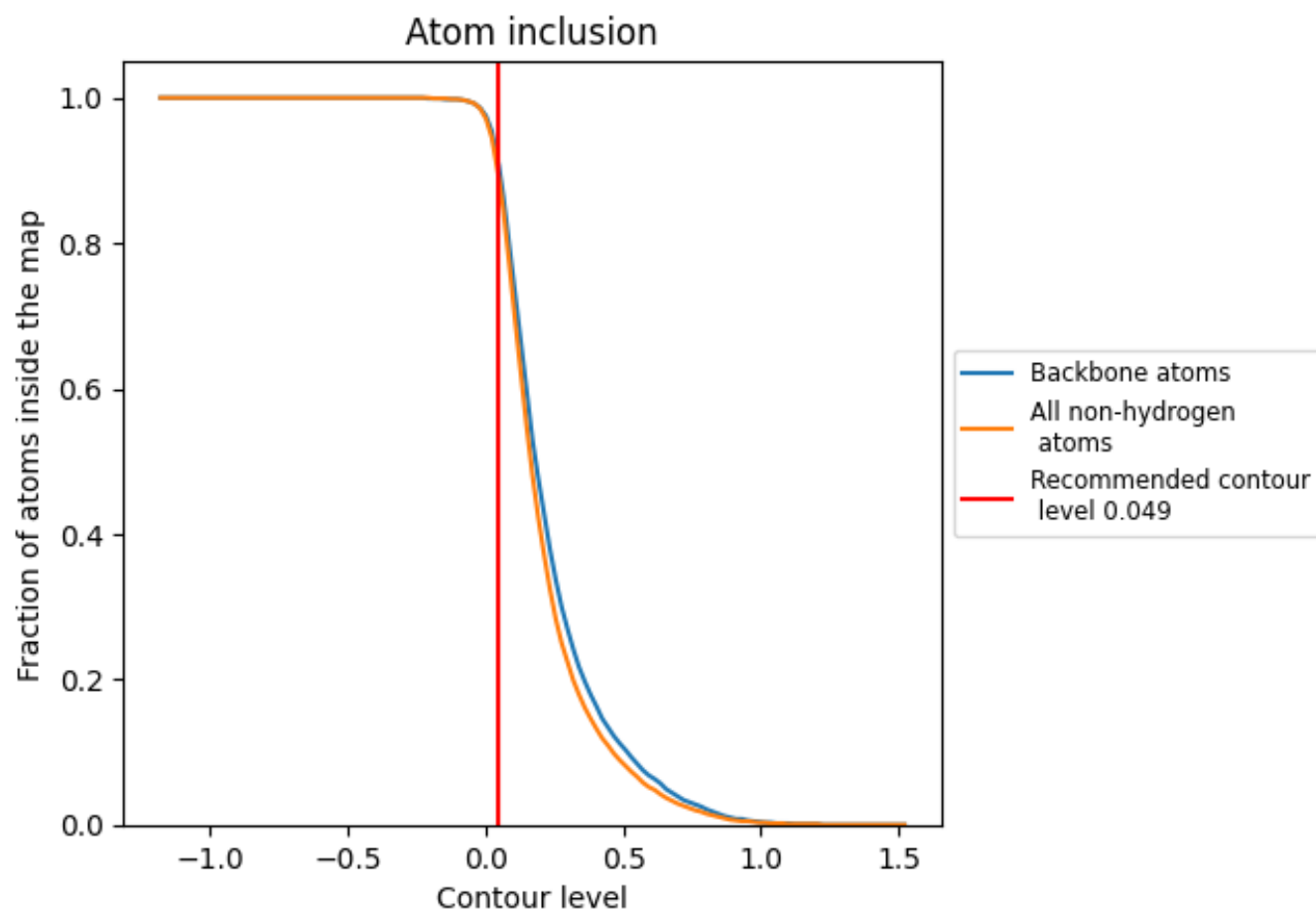
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.049).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.049) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8890</div>	<div><div></div>0.1820</div>
A	<div><div></div>0.9330</div>	<div><div></div>0.3200</div>
B	<div><div></div>0.8530</div>	<div><div></div>0.2260</div>
C	<div><div></div>0.9460</div>	<div><div></div>0.3170</div>
D	<div><div></div>0.8590</div>	<div><div></div>0.1230</div>
E	<div><div></div>0.8860</div>	<div><div></div>0.1930</div>
F	<div><div></div>0.8150</div>	<div><div></div>0.0190</div>
G	<div><div></div>0.9240</div>	<div><div></div>0.1320</div>
H	<div><div></div>0.9080</div>	<div><div></div>0.1840</div>
I	<div><div></div>0.8190</div>	<div><div></div>0.0950</div>

1.0

0.0

<0.0