



Full wwPDB EM Validation Report ⓘ

Sep 29, 2025 – 12:16 PM EDT

PDB ID : 9NMN / pdb_00009nmn
EMDB ID : EMD-49534
Title : Structure of mouse RyR1 (Ca²⁺/CFF/ATP dataset; open pore)
Authors : Weninger, G.; Marks, A.R.
Deposited on : 2025-03-04
Resolution : 3.09 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.dev129
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

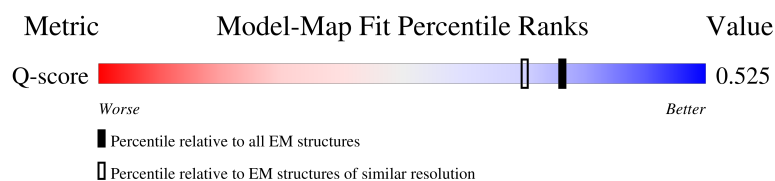
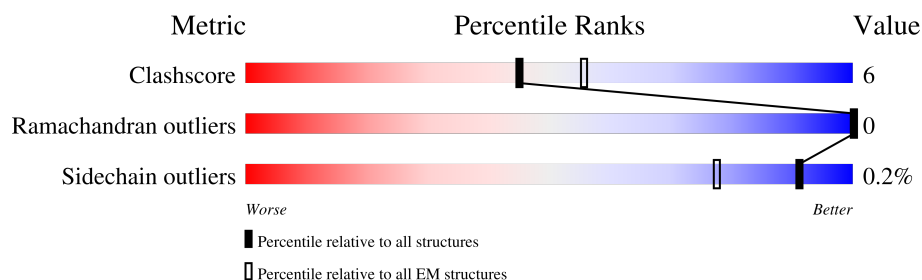
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	14003 (2.59 - 3.59)

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	5035	
1	B	5035	
1	C	5035	
1	D	5035	

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Mol	Chain	Length	Quality of chain
2	E	108	<div><div></div><div>87%</div><div>12%</div><div></div></div>
2	F	108	<div><div></div><div>88%</div><div>11%</div><div></div></div>
2	G	108	<div><div></div><div>89%</div><div>10%</div><div></div></div>
2	H	108	<div><div></div><div>89%</div><div>10%</div><div></div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 143248 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4373	Total	C	N	O	S	0	0
			34797	22132	5983	6445	237		
1	B	4373	Total	C	N	O	S	0	0
			34797	22132	5983	6445	237		
1	C	4373	Total	C	N	O	S	0	0
			34797	22132	5983	6445	237		
1	D	4373	Total	C	N	O	S	0	0
			34797	22132	5983	6445	237		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

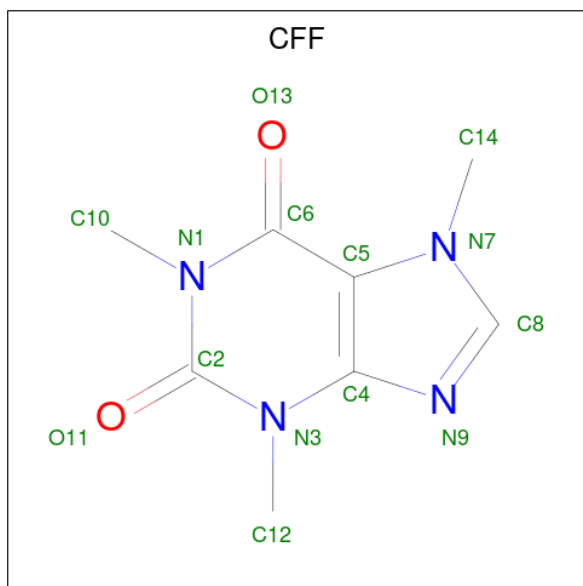
Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	107	Total	C	N	O	S	0	0
			829	526	145	155	3		
2	F	107	Total	C	N	O	S	0	0
			829	526	145	155	3		
2	G	107	Total	C	N	O	S	0	0
			829	526	145	155	3		
2	H	107	Total	C	N	O	S	0	0
			829	526	145	155	3		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	

- Molecule 4 is CAFFEINE (CCD ID: CFF) (formula: C₈H₁₀N₄O₂) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	4	2	
4	B	1	Total	C	N	O	0
			14	8	4	2	
4	C	1	Total	C	N	O	0
			14	8	4	2	
4	D	1	Total	C	N	O	0
			14	8	4	2	

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total 31	C 10	N 5	O 13	P 3	0
5	A	1	Total 31	C 10	N 5	O 13	P 3	0
5	B	1	Total 31	C 10	N 5	O 13	P 3	0
5	B	1	Total 31	C 10	N 5	O 13	P 3	0
5	C	1	Total 31	C 10	N 5	O 13	P 3	0
5	C	1	Total 31	C 10	N 5	O 13	P 3	0
5	D	1	Total 31	C 10	N 5	O 13	P 3	0
5	D	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

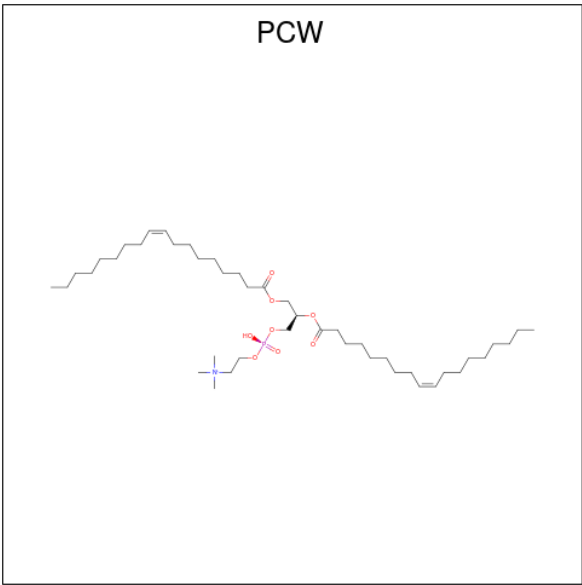
Mol	Chain	Residues	Atoms	AltConf
6	A	1	Total Ca 1 1	0
6	B	1	Total Ca 1 1	0
6	C	1	Total Ca 1 1	0

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Mol	Chain	Residues	Atoms		AltConf
6	D	1	Total	Ca	0
			1	1	

- Molecule 7 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).

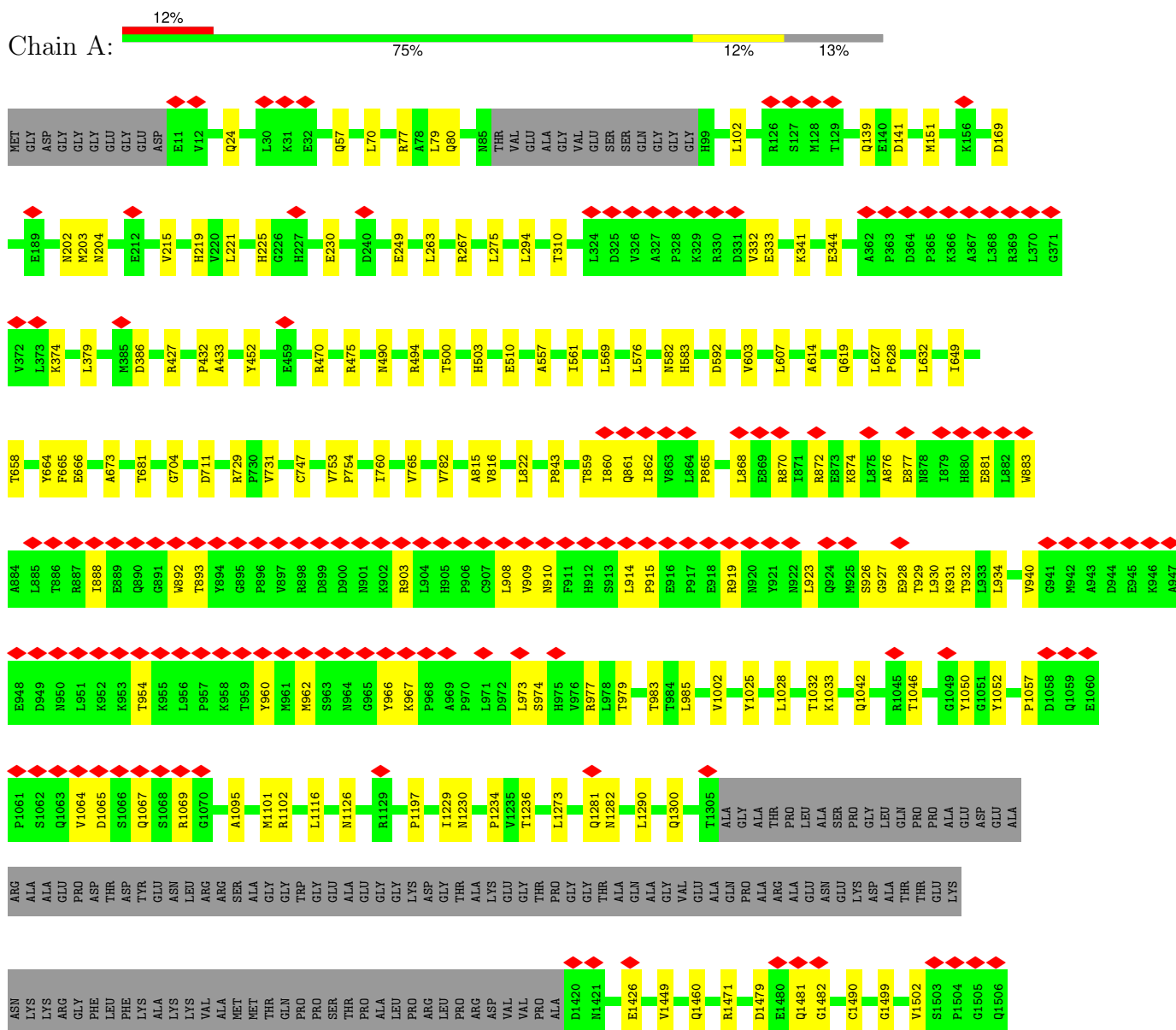


Mol	Chain	Residues	Atoms						AltConf
7	A	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	A	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	B	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	B	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	C	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	C	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	D	1	Total	C	N	O	P		0
			54	44	1	8	1		
7	D	1	Total	C	N	O	P		0
			54	44	1	8	1		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ryanodine receptor 1















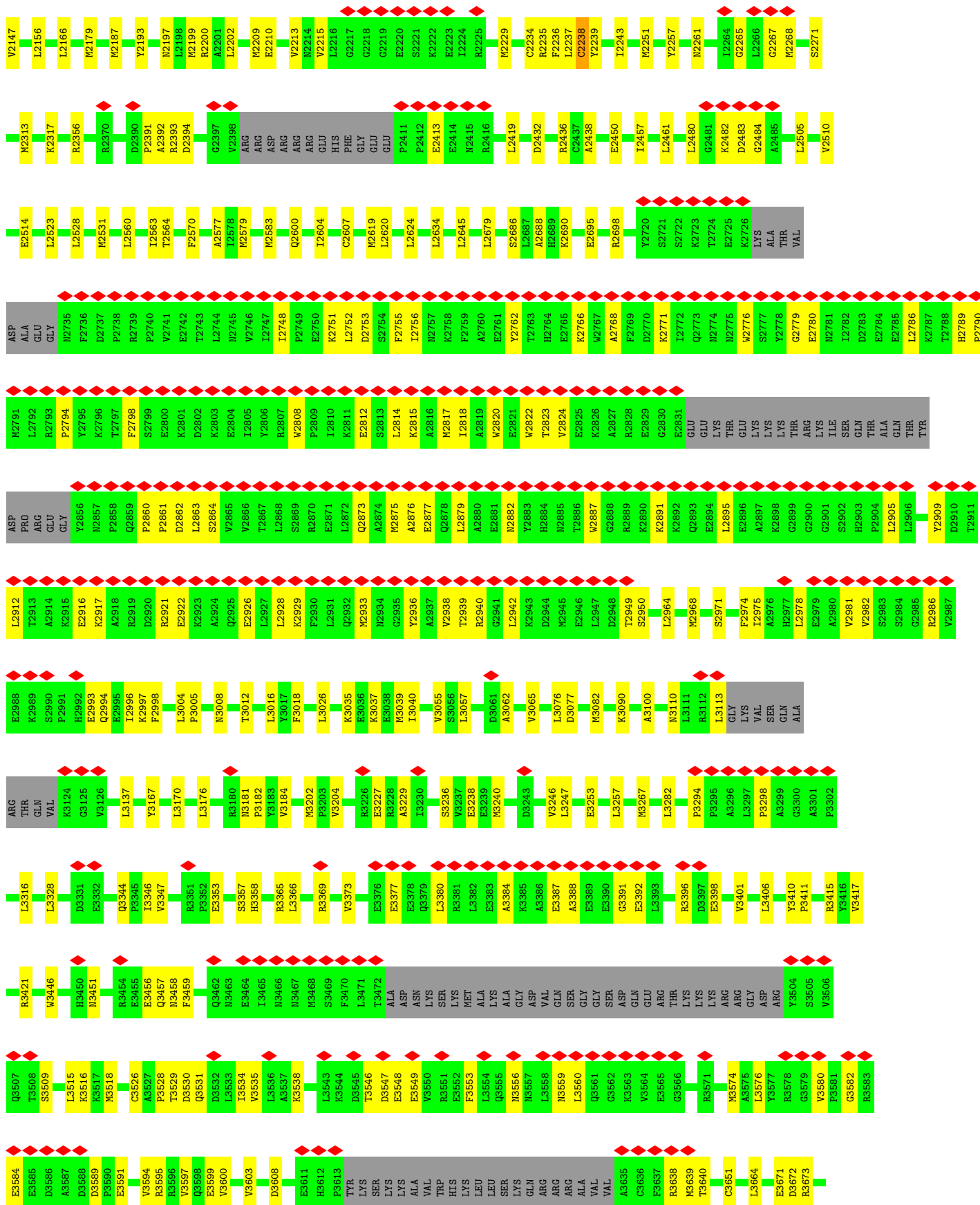





Figure 1: Schematic representation of the protein structure of the 12S OMT. The diagram shows a linear sequence of amino acids from MET to K156. Residues are color-coded: green for residues 1-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, 67-68, 69-70, 71-72, 73-74, 75-76, 77-78, 79-80, 81-82, 83-84, 85-86, 87-88, 89-90, 91-92, 93-94, 95-96, 97-98, 99-100, 101-102, 103-104, 105-106, 107-108, 109-110, 111-112, 113-114, 115-116, 117-118, 119-120, 121-122, 123-124, 125-126, 127-128, 129-130, 131-132, 133-134, 135-136, 137-138, 139-140, 141-142, 143-144, 145-146, 147-148, 149-150, 151-152, 153-154, 155-156. Red diamonds indicate specific residues: E11, V12, Q24, L30, X31, E32, Q57, L70, R77, A78, L79, Q80, R85, THR, VAL, GLU, ALA, GLY, VAL, GLU, SER, SER, GLN, GLY, GLY, H99, L102, L110, R126, S127, M128, T129, Q139, E140, D141, M151, K156. The sequence is divided into segments by vertical lines.





● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H:  89% 10% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26588	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.463	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	427.776, 427.776, 427.776	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8355, 0.8355, 0.8355	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, CA, CFF, PCW, ZN

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	0.20	0/35586	0.36	4/48203 (0.0%)
1	B	0.20	0/35586	0.36	4/48203 (0.0%)
1	C	0.20	0/35586	0.36	4/48203 (0.0%)
1	D	0.20	0/35586	0.36	4/48203 (0.0%)
2	E	0.17	0/847	0.34	0/1142
2	F	0.17	0/847	0.32	0/1142
2	G	0.18	0/847	0.33	0/1142
2	H	0.18	0/847	0.33	0/1142
All	All	0.20	0/145732	0.36	16/197380 (0.0%)

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	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2237	LEU	CA-C-N	8.49	134.18	120.60
1	C	2237	LEU	C-N-CA	8.49	134.18	120.60
1	A	2237	LEU	CA-C-N	8.48	134.16	120.60
1	A	2237	LEU	C-N-CA	8.48	134.16	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2237	LEU	CA-C-N	8.48	134.16	120.60
1	B	2237	LEU	C-N-CA	8.48	134.16	120.60
1	D	2237	LEU	CA-C-N	8.48	134.16	120.60
1	D	2237	LEU	C-N-CA	8.48	134.16	120.60
1	B	2238	CYS	CA-CB-SG	7.68	132.06	114.40
1	A	2238	CYS	CA-CB-SG	7.67	132.03	114.40
1	C	2238	CYS	CA-CB-SG	7.66	132.03	114.40
1	D	2238	CYS	CA-CB-SG	7.65	131.99	114.40
1	D	2238	CYS	N-CA-CB	-5.60	100.80	110.32
1	A	2238	CYS	N-CA-CB	-5.58	100.84	110.32
1	B	2238	CYS	N-CA-CB	-5.58	100.84	110.32
1	C	2238	CYS	N-CA-CB	-5.57	100.86	110.32

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	4701	ARG	Sidechain
1	A	4720	ARG	Sidechain
1	B	4701	ARG	Sidechain
1	B	4720	ARG	Sidechain
1	C	4701	ARG	Sidechain
1	C	4720	ARG	Sidechain
1	D	4701	ARG	Sidechain
1	D	4720	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34797	0	34384	428	0
1	B	34797	0	34384	432	0
1	C	34797	0	34384	425	0
1	D	34797	0	34384	427	0
2	E	829	0	826	11	0
2	F	829	0	826	11	0
2	G	829	0	826	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	829	0	826	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	14	0	10	0	0
4	B	14	0	10	0	0
4	C	14	0	10	0	0
4	D	14	0	10	0	0
5	A	62	0	24	1	0
5	B	62	0	24	1	0
5	C	62	0	24	1	0
5	D	62	0	24	2	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	108	0	168	0	0
7	B	108	0	168	0	0
7	C	108	0	168	1	0
7	D	108	0	168	1	0
All	All	143248	0	141648	1734	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 6.

All (1734) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2234:CYS:SG	1:D:2271:SER:OG	2.24	0.94
1:A:2234:CYS:SG	1:A:2271:SER:OG	2.24	0.94
1:B:2234:CYS:SG	1:B:2271:SER:OG	2.24	0.94
1:C:2234:CYS:SG	1:C:2271:SER:OG	2.24	0.94
1:C:2879:LEU:HD12	1:C:2928:LEU:HD21	1.55	0.88
1:A:893:THR:O	1:A:903:ARG:NH1	2.07	0.87
1:C:893:THR:O	1:C:903:ARG:NH1	2.07	0.87
1:B:2879:LEU:HD12	1:B:2928:LEU:HD21	1.55	0.87
1:B:2762:TYR:OH	1:B:2861:PRO:O	1.93	0.87
1:C:2762:TYR:OH	1:C:2861:PRO:O	1.93	0.87
1:B:893:THR:O	1:B:903:ARG:NH1	2.07	0.87
1:D:2762:TYR:OH	1:D:2861:PRO:O	1.93	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2879:LEU:HD12	1:D:2928:LEU:HD21	1.55	0.87
1:D:893:THR:O	1:D:903:ARG:NH1	2.07	0.86
1:A:2879:LEU:HD12	1:A:2928:LEU:HD21	1.55	0.86
1:A:2762:TYR:OH	1:A:2861:PRO:O	1.93	0.84
1:B:2912:LEU:O	1:B:2917:LYS:NZ	2.12	0.82
1:A:2912:LEU:O	1:A:2917:LYS:NZ	2.12	0.82
1:C:2912:LEU:O	1:C:2917:LYS:NZ	2.12	0.81
1:D:2912:LEU:O	1:D:2917:LYS:NZ	2.12	0.81
1:C:3082:MET:O	1:C:3090:LYS:NZ	2.15	0.80
1:A:3082:MET:O	1:A:3090:LYS:NZ	2.15	0.80
1:D:3082:MET:O	1:D:3090:LYS:NZ	2.15	0.79
1:B:2862:ASP:OD2	1:B:2864:SER:OG	2.01	0.79
1:B:3082:MET:O	1:B:3090:LYS:NZ	2.15	0.79
1:A:3714:LYS:NZ	1:A:3716:LYS:O	2.16	0.79
1:C:2862:ASP:OD2	1:C:2864:SER:OG	2.01	0.79
1:B:3456:GLU:OE2	1:B:3509:SER:OG	2.00	0.78
1:C:3456:GLU:OE2	1:C:3509:SER:OG	2.00	0.78
1:D:3456:GLU:OE2	1:D:3509:SER:OG	2.00	0.78
1:C:3714:LYS:NZ	1:C:3716:LYS:O	2.16	0.78
1:D:3236:SER:OG	1:D:3238:GLU:OE1	2.02	0.78
1:A:3236:SER:OG	1:A:3238:GLU:OE1	2.02	0.77
1:A:2197:ASN:OD1	1:A:2200:ARG:NH2	2.18	0.77
1:A:2862:ASP:OD2	1:A:2864:SER:OG	2.01	0.77
1:C:3236:SER:OG	1:C:3238:GLU:OE1	2.02	0.77
1:A:3456:GLU:OE2	1:A:3509:SER:OG	2.00	0.77
1:C:2197:ASN:OD1	1:C:2200:ARG:NH2	2.18	0.77
1:D:2197:ASN:OD1	1:D:2200:ARG:NH2	2.18	0.77
1:D:2862:ASP:OD2	1:D:2864:SER:OG	2.01	0.77
1:B:2197:ASN:OD1	1:B:2200:ARG:NH2	2.18	0.77
1:B:24:GLN:OE1	1:B:204:ASN:ND2	2.18	0.76
1:C:1236:THR:OG1	1:C:1703:ARG:NH1	2.19	0.76
1:B:3236:SER:OG	1:B:3238:GLU:OE1	2.02	0.76
1:C:24:GLN:OE1	1:C:204:ASN:ND2	2.18	0.76
1:B:1236:THR:OG1	1:B:1703:ARG:NH1	2.19	0.76
1:A:24:GLN:OE1	1:A:204:ASN:ND2	2.18	0.76
1:A:1236:THR:OG1	1:A:1703:ARG:NH1	2.19	0.75
1:D:1236:THR:OG1	1:D:1703:ARG:NH1	2.19	0.75
1:D:24:GLN:OE1	1:D:204:ASN:ND2	2.18	0.75
1:C:2187:MET:O	1:C:2193:TYR:OH	2.02	0.75
1:C:3531:GLN:O	1:C:3535:VAL:HG23	1.88	0.73
1:A:3531:GLN:O	1:A:3535:VAL:HG23	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:88:HIS:ND1	2:E:91:ILE:HD13	2.03	0.73
1:B:2993:GLU:HA	1:B:2996:ILE:HD12	1.70	0.73
1:D:3538:LYS:NZ	1:D:3608:ASP:OD2	2.15	0.73
1:D:3714:LYS:NZ	1:D:3716:LYS:O	2.16	0.73
1:A:865:PRO:HD2	1:A:868:LEU:HD12	1.70	0.73
1:A:2993:GLU:HA	1:A:2996:ILE:HD12	1.70	0.73
1:B:3531:GLN:O	1:B:3535:VAL:HG23	1.88	0.73
1:A:2523:LEU:HD21	1:A:2583:MET:SD	2.28	0.73
1:B:2523:LEU:HD21	1:B:2583:MET:SD	2.28	0.73
1:A:2187:MET:O	1:A:2193:TYR:OH	2.02	0.73
1:D:3531:GLN:O	1:D:3535:VAL:HG23	1.88	0.73
1:D:914:LEU:O	1:D:919:ARG:NH1	2.22	0.73
1:A:914:LEU:O	1:A:919:ARG:NH1	2.22	0.72
1:C:2523:LEU:HD21	1:C:2583:MET:SD	2.28	0.72
1:C:865:PRO:HD2	1:C:868:LEU:HD12	1.70	0.72
1:B:914:LEU:O	1:B:919:ARG:NH1	2.22	0.72
1:C:1793:ALA:O	1:C:1794:THR:OG1	2.06	0.72
1:D:865:PRO:HD2	1:D:868:LEU:HD12	1.70	0.72
1:D:2523:LEU:HD21	1:D:2583:MET:SD	2.28	0.72
1:C:914:LEU:O	1:C:919:ARG:NH1	2.22	0.72
1:D:2187:MET:O	1:D:2193:TYR:OH	2.02	0.71
1:B:865:PRO:HD2	1:B:868:LEU:HD12	1.70	0.71
1:B:1793:ALA:O	1:B:1794:THR:OG1	2.06	0.71
1:D:2993:GLU:HA	1:D:2996:ILE:HD12	1.70	0.71
1:C:2993:GLU:HA	1:C:2996:ILE:HD12	1.70	0.71
1:B:2187:MET:O	1:B:2193:TYR:OH	2.02	0.71
1:B:4908:GLU:O	1:B:4912:VAL:HG13	1.91	0.70
1:B:2823:THR:OG1	1:B:2939:THR:OG1	2.09	0.70
1:C:2823:THR:OG1	1:C:2939:THR:OG1	2.09	0.70
1:C:4908:GLU:O	1:C:4912:VAL:HG13	1.91	0.70
1:D:4009:ASP:OD2	1:D:4011:SER:OG	2.10	0.70
1:D:914:LEU:HD12	1:D:915:PRO:HD2	1.74	0.70
1:B:3714:LYS:NZ	1:B:3716:LYS:O	2.16	0.70
1:D:4908:GLU:O	1:D:4912:VAL:HG13	1.91	0.70
1:A:914:LEU:HD12	1:A:915:PRO:HD2	1.73	0.69
1:A:4009:ASP:OD2	1:A:4011:SER:OG	2.10	0.69
1:A:1793:ALA:O	1:A:1794:THR:OG1	2.06	0.69
1:C:914:LEU:HD12	1:C:915:PRO:HD2	1.74	0.69
1:D:2823:THR:OG1	1:D:2939:THR:OG1	2.09	0.69
1:A:2823:THR:OG1	1:A:2939:THR:OG1	2.09	0.69
1:A:4908:GLU:O	1:A:4912:VAL:HG13	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3369:ARG:NH2	1:A:3398:GLU:OE1	2.26	0.69
1:B:1042:GLN:O	1:B:1046:THR:HG23	1.93	0.69
1:B:3369:ARG:NH2	1:B:3398:GLU:OE1	2.26	0.69
1:A:1042:GLN:O	1:A:1046:THR:HG23	1.93	0.69
1:C:4009:ASP:OD2	1:C:4011:SER:OG	2.10	0.69
1:A:102:LEU:HB3	1:A:151:MET:HE1	1.75	0.69
2:E:41:ARG:NH2	2:E:103:GLU:OE1	2.25	0.69
1:D:3369:ARG:NH2	1:D:3398:GLU:OE1	2.26	0.69
1:D:2570:PHE:CE1	1:D:2583:MET:HE1	2.29	0.68
2:G:88:HIS:CD2	1:C:1788:LEU:HD21	2.28	0.68
1:B:102:LEU:HB3	1:B:151:MET:HE1	1.75	0.68
1:C:2560:LEU:O	1:C:2564:THR:HG23	1.94	0.68
1:D:2564:THR:HG22	1:D:2607:CYS:HA	1.75	0.68
2:H:88:HIS:ND1	2:H:91:ILE:HD13	2.09	0.68
1:C:1042:GLN:O	1:C:1046:THR:HG23	1.93	0.68
1:C:3538:LYS:NZ	1:C:3608:ASP:OD2	2.15	0.68
1:D:1042:GLN:O	1:D:1046:THR:HG23	1.93	0.68
1:C:2780:GLU:OE2	1:C:2786:LEU:HD12	1.94	0.68
1:C:3176:LEU:HD21	1:C:3184:VAL:HG13	1.76	0.68
1:B:914:LEU:HD12	1:B:915:PRO:HD2	1.74	0.68
1:C:2564:THR:HG22	1:C:2607:CYS:HA	1.75	0.68
1:A:3176:LEU:HD21	1:A:3184:VAL:HG13	1.76	0.68
1:D:102:LEU:HB3	1:D:151:MET:HE1	1.75	0.68
1:A:2560:LEU:O	1:A:2564:THR:HG23	1.94	0.68
1:A:4235:GLU:OE2	1:A:5015:ARG:NH2	2.27	0.68
1:B:2817:MET:HE2	1:B:2879:LEU:HD11	1.76	0.68
1:B:3176:LEU:HD21	1:B:3184:VAL:HG13	1.76	0.68
1:B:3538:LYS:NZ	1:B:3608:ASP:OD2	2.15	0.68
1:B:4009:ASP:OD2	1:B:4011:SER:OG	2.10	0.68
1:D:3176:LEU:HD21	1:D:3184:VAL:HG13	1.76	0.68
1:B:2780:GLU:OE2	1:B:2786:LEU:HD12	1.94	0.67
1:C:4235:GLU:OE2	1:C:5015:ARG:NH2	2.27	0.67
1:A:2570:PHE:CE1	1:A:2583:MET:HE1	2.29	0.67
1:C:3369:ARG:NH2	1:C:3398:GLU:OE1	2.26	0.67
1:D:2814:LEU:HD23	1:D:2817:MET:HE3	1.76	0.67
1:B:2570:PHE:CE1	1:B:2583:MET:HE1	2.29	0.67
1:C:2570:PHE:CE1	1:C:2583:MET:HE1	2.29	0.67
1:A:2780:GLU:OE2	1:A:2786:LEU:HD12	1.94	0.67
1:A:2814:LEU:HD23	1:A:2817:MET:HE3	1.76	0.67
1:B:1981:LEU:HD22	1:B:1995:ARG:HB3	1.77	0.67
1:B:2560:LEU:O	1:B:2564:THR:HG23	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2564:THR:HG22	1:B:2607:CYS:HA	1.75	0.67
1:D:4235:GLU:OE2	1:D:5015:ARG:NH2	2.27	0.67
1:C:102:LEU:HB3	1:C:151:MET:HE1	1.75	0.67
1:D:470:ARG:NE	1:D:3713:GLU:OE1	2.28	0.67
1:D:1793:ALA:O	1:D:1794:THR:OG1	2.06	0.67
1:D:2560:LEU:O	1:D:2564:THR:HG23	1.94	0.67
1:D:2817:MET:HE2	1:D:2879:LEU:HD11	1.76	0.67
1:B:1025:TYR:O	1:B:1033:LYS:NZ	2.28	0.67
1:C:3176:LEU:HD23	1:C:3176:LEU:O	1.95	0.67
1:D:3176:LEU:O	1:D:3176:LEU:HD23	1.95	0.67
1:D:1025:TYR:O	1:D:1033:LYS:NZ	2.28	0.67
1:A:470:ARG:NE	1:A:3713:GLU:OE1	2.28	0.66
1:A:2564:THR:HG22	1:A:2607:CYS:HA	1.75	0.66
1:C:2817:MET:HE2	1:C:2879:LEU:HD11	1.76	0.66
1:D:2780:GLU:OE2	1:D:2786:LEU:HD12	1.94	0.66
2:E:25:VAL:HG12	2:E:104:LEU:HA	1.77	0.66
1:A:1981:LEU:HD22	1:A:1995:ARG:HB3	1.77	0.66
1:B:470:ARG:NE	1:B:3713:GLU:OE1	2.28	0.66
1:B:2156:LEU:HD13	1:B:2199:MET:HE1	1.78	0.66
1:B:4235:GLU:OE2	1:B:5015:ARG:NH2	2.27	0.66
1:A:2817:MET:HE2	1:A:2879:LEU:HD11	1.76	0.66
1:A:1025:TYR:O	1:A:1033:LYS:NZ	2.28	0.66
2:F:88:HIS:ND1	2:F:91:ILE:HD13	2.09	0.66
1:B:3176:LEU:O	1:B:3176:LEU:HD23	1.95	0.66
1:C:2814:LEU:HD23	1:C:2817:MET:HE3	1.76	0.66
1:A:2755:PHE:CD2	1:A:2814:LEU:HD11	2.31	0.66
1:C:470:ARG:NE	1:C:3713:GLU:OE1	2.28	0.66
1:C:4550:LEU:HD12	1:C:4661:CYS:SG	2.36	0.66
1:A:3176:LEU:O	1:A:3176:LEU:HD23	1.95	0.66
1:B:4550:LEU:HD12	1:B:4661:CYS:SG	2.36	0.66
1:D:1981:LEU:HD22	1:D:1995:ARG:HB3	1.77	0.66
1:A:4550:LEU:HD12	1:A:4661:CYS:SG	2.36	0.65
1:B:3257:LEU:HD23	1:B:3267:MET:HE2	1.78	0.65
1:C:1981:LEU:HD22	1:C:1995:ARG:HB3	1.77	0.65
1:D:2755:PHE:CD2	1:D:2814:LEU:HD11	2.31	0.65
1:D:4550:LEU:HD12	1:D:4661:CYS:SG	2.36	0.65
1:A:3530:ASP:O	1:A:3534:ILE:HD12	1.97	0.65
1:B:2814:LEU:HD23	1:B:2817:MET:HE3	1.76	0.65
1:A:2968:MET:HA	1:A:2968:MET:HE3	1.79	0.65
1:A:3257:LEU:HD23	1:A:3267:MET:HE2	1.78	0.65
2:F:26:HIS:HD2	2:F:105:LEU:HD11	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:GLN:O	1:A:310:THR:HG23	1.97	0.65
1:A:2645:LEU:HD13	1:A:2679:LEU:HD21	1.78	0.65
1:C:57:GLN:O	1:C:310:THR:HG23	1.97	0.65
1:B:57:GLN:O	1:B:310:THR:HG23	1.97	0.65
1:C:2156:LEU:HD13	1:C:2199:MET:HE1	1.78	0.65
1:C:2755:PHE:CD2	1:C:2814:LEU:HD11	2.31	0.65
1:D:3530:ASP:O	1:D:3534:ILE:HD12	1.97	0.65
1:A:452:TYR:O	1:A:475:ARG:NH2	2.30	0.65
1:B:2755:PHE:CD2	1:B:2814:LEU:HD11	2.31	0.65
1:C:452:TYR:O	1:C:475:ARG:NH2	2.30	0.65
1:D:70:LEU:HD13	1:D:102:LEU:HD11	1.79	0.65
1:C:1025:TYR:O	1:C:1033:LYS:NZ	2.28	0.65
1:D:57:GLN:O	1:D:310:THR:HG23	1.97	0.65
1:D:2156:LEU:HD13	1:D:2199:MET:HE1	1.78	0.65
1:D:2968:MET:HE3	1:D:2968:MET:HA	1.79	0.65
1:C:2645:LEU:HD13	1:C:2679:LEU:HD21	1.78	0.65
1:A:3547:ASP:OD1	1:A:3548:GLU:N	2.31	0.64
1:A:4745:SER:O	1:A:4749:THR:HG23	1.97	0.64
2:G:88:HIS:ND1	2:G:91:ILE:HD13	2.11	0.64
1:B:70:LEU:HD13	1:B:102:LEU:HD11	1.79	0.64
1:C:3547:ASP:OD1	1:C:3548:GLU:N	2.31	0.64
1:B:2645:LEU:HD13	1:B:2679:LEU:HD21	1.78	0.64
1:B:3530:ASP:O	1:B:3534:ILE:HD12	1.97	0.64
1:A:2755:PHE:HD2	1:A:2814:LEU:HD11	1.63	0.64
1:B:452:TYR:O	1:B:475:ARG:NH2	2.30	0.64
1:C:2968:MET:HA	1:C:2968:MET:HE3	1.79	0.64
1:D:3257:LEU:HD23	1:D:3267:MET:HE2	1.78	0.64
1:D:4745:SER:O	1:D:4749:THR:HG23	1.98	0.64
1:C:3530:ASP:O	1:C:3534:ILE:HD12	1.97	0.64
1:D:452:TYR:O	1:D:475:ARG:NH2	2.30	0.64
1:C:70:LEU:HD13	1:C:102:LEU:HD11	1.79	0.64
1:C:2234:CYS:O	1:C:2235:ARG:C	2.41	0.64
1:A:2156:LEU:HD13	1:A:2199:MET:HE1	1.78	0.64
1:A:2234:CYS:O	1:A:2235:ARG:C	2.41	0.64
1:C:3576:LEU:O	1:C:3580:VAL:HG23	1.98	0.64
1:C:3860:GLY:O	1:C:3871:ARG:NH2	2.31	0.64
1:D:3576:LEU:O	1:D:3580:VAL:HG23	1.98	0.64
1:A:3538:LYS:NZ	1:A:3608:ASP:OD2	2.15	0.64
1:A:3576:LEU:O	1:A:3580:VAL:HG23	1.98	0.64
1:B:4745:SER:O	1:B:4749:THR:HG23	1.97	0.64
1:C:3257:LEU:HD23	1:C:3267:MET:HE2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2755:PHE:HD2	1:D:2814:LEU:HD11	1.63	0.64
1:A:70:LEU:HD13	1:A:102:LEU:HD11	1.79	0.64
1:D:3547:ASP:OD1	1:D:3548:GLU:N	2.31	0.64
1:A:3860:GLY:O	1:A:3871:ARG:NH2	2.31	0.63
1:B:2968:MET:HA	1:B:2968:MET:HE3	1.79	0.63
1:B:3860:GLY:O	1:B:3871:ARG:NH2	2.31	0.63
1:D:2645:LEU:HD13	1:D:2679:LEU:HD21	1.78	0.63
1:B:3576:LEU:O	1:B:3580:VAL:HG23	1.98	0.63
1:D:3559:ASN:OD1	1:D:3560:LEU:HD12	1.99	0.63
1:B:169:ASP:OD1	1:B:202:ASN:ND2	2.32	0.63
1:B:2695:GLU:OE1	1:B:2698:ARG:NH1	2.31	0.63
1:C:872:ARG:NH1	1:C:923:LEU:O	2.31	0.63
1:C:2695:GLU:OE1	1:C:2698:ARG:NH1	2.31	0.63
1:C:2755:PHE:HD2	1:C:2814:LEU:HD11	1.63	0.63
1:D:876:ALA:CB	1:D:923:LEU:HD23	2.29	0.63
1:D:2695:GLU:OE1	1:D:2698:ARG:NH1	2.31	0.63
1:A:3559:ASN:OD1	1:A:3560:LEU:HD12	1.99	0.63
1:B:2755:PHE:HD2	1:B:2814:LEU:HD11	1.63	0.63
1:D:3860:GLY:O	1:D:3871:ARG:NH2	2.31	0.63
1:B:876:ALA:CB	1:B:923:LEU:HD23	2.29	0.63
1:B:3547:ASP:OD1	1:B:3548:GLU:N	2.31	0.63
1:D:341:LYS:NZ	1:D:344:GLU:OE1	2.32	0.63
1:D:2234:CYS:O	1:D:2235:ARG:C	2.41	0.63
1:A:169:ASP:OD1	1:A:202:ASN:ND2	2.32	0.63
2:H:12:ASP:OD1	2:H:13:GLY:N	2.32	0.63
1:A:2695:GLU:OE1	1:A:2698:ARG:NH1	2.31	0.63
2:F:12:ASP:OD1	2:F:13:GLY:N	2.32	0.63
2:G:12:ASP:OD1	2:G:13:GLY:N	2.32	0.63
1:C:341:LYS:NZ	1:C:344:GLU:OE1	2.32	0.63
1:C:3559:ASN:OD1	1:C:3560:LEU:HD12	1.99	0.63
1:C:4745:SER:O	1:C:4749:THR:HG23	1.97	0.63
1:A:1978:TYR:OH	1:A:3639:MET:SD	2.49	0.62
1:B:1978:TYR:OH	1:B:3639:MET:SD	2.49	0.62
1:A:341:LYS:NZ	1:A:344:GLU:OE1	2.32	0.62
1:C:876:ALA:CB	1:C:923:LEU:HD23	2.29	0.62
1:B:872:ARG:NH1	1:B:923:LEU:O	2.31	0.62
1:B:929:THR:HG23	1:B:930:LEU:HD22	1.82	0.62
1:B:3559:ASN:OD1	1:B:3560:LEU:HD12	1.99	0.62
1:D:872:ARG:NH1	1:D:923:LEU:O	2.32	0.62
1:D:3672:ASP:OD1	1:D:3673:ARG:N	2.33	0.62
1:A:929:THR:HG23	1:A:930:LEU:HD22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3672:ASP:OD1	1:C:3673:ARG:N	2.33	0.62
1:D:4649:THR:OG1	1:D:4801:HIS:NE2	2.29	0.62
1:A:876:ALA:CB	1:A:923:LEU:HD23	2.29	0.62
1:C:2863:LEU:HD23	1:C:2933:MET:HE3	1.82	0.62
1:A:872:ARG:NH1	1:A:923:LEU:O	2.31	0.62
1:B:1974:GLN:NE2	1:B:2006:GLN:OE1	2.32	0.62
1:D:169:ASP:OD1	1:D:202:ASN:ND2	2.32	0.62
1:D:2863:LEU:HD23	1:D:2933:MET:HE3	1.82	0.62
1:A:1974:GLN:NE2	1:A:2006:GLN:OE1	2.32	0.62
1:C:169:ASP:OD1	1:C:202:ASN:ND2	2.32	0.62
1:D:1974:GLN:NE2	1:D:2006:GLN:OE1	2.32	0.62
1:B:4649:THR:OG1	1:B:4801:HIS:NE2	2.29	0.62
1:A:4222:PHE:HA	1:A:4948:VAL:HG21	1.82	0.61
2:G:80:ASP:OD1	2:G:81:TYR:N	2.33	0.61
1:B:3534:ILE:HG13	1:B:3597:VAL:HG23	1.81	0.61
1:C:929:THR:HG23	1:C:930:LEU:HD22	1.82	0.61
1:D:664:TYR:OH	1:D:666:GLU:OE2	2.18	0.61
1:D:929:THR:HG23	1:D:930:LEU:HD22	1.82	0.61
1:D:4222:PHE:HA	1:D:4948:VAL:HG21	1.82	0.61
1:A:3534:ILE:HG13	1:A:3597:VAL:HG23	1.81	0.61
1:B:341:LYS:NZ	1:B:344:GLU:OE1	2.32	0.61
1:C:1234:PRO:O	1:C:1703:ARG:NH2	2.34	0.61
1:C:1974:GLN:NE2	1:C:2006:GLN:OE1	2.32	0.61
1:A:3672:ASP:OD1	1:A:3673:ARG:N	2.33	0.61
1:B:2879:LEU:HD12	1:B:2928:LEU:CD2	2.29	0.61
1:B:3446:TRP:NE1	1:B:3456:GLU:OE1	2.33	0.61
1:B:3672:ASP:OD1	1:B:3673:ARG:N	2.33	0.61
1:D:1426:GLU:OE1	1:D:1426:GLU:N	2.34	0.61
2:E:26:HIS:ND1	2:E:105:LEU:HD11	2.16	0.61
1:B:876:ALA:HB1	1:B:923:LEU:HD23	1.83	0.61
1:C:2523:LEU:HD23	1:C:2579:MET:HE1	1.83	0.61
2:H:80:ASP:OD1	2:H:81:TYR:N	2.33	0.61
1:B:2234:CYS:O	1:B:2235:ARG:C	2.41	0.61
1:A:2022:CYS:O	1:A:2029:ARG:NH2	2.34	0.61
2:E:80:ASP:OD1	2:E:81:TYR:N	2.33	0.61
1:C:2022:CYS:O	1:C:2029:ARG:NH2	2.34	0.61
1:D:1978:TYR:OH	1:D:3639:MET:SD	2.49	0.61
1:D:2022:CYS:O	1:D:2029:ARG:NH2	2.34	0.61
1:D:3446:TRP:NE1	1:D:3456:GLU:OE1	2.33	0.61
1:D:3534:ILE:HG13	1:D:3597:VAL:HG23	1.81	0.61
1:D:1234:PRO:O	1:D:1703:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1234:PRO:O	1:A:1703:ARG:NH2	2.34	0.61
1:A:3446:TRP:NE1	1:A:3456:GLU:OE1	2.33	0.61
1:B:2863:LEU:HD23	1:B:2933:MET:HE3	1.82	0.61
1:D:876:ALA:HB1	1:D:923:LEU:HD23	1.82	0.61
1:D:2688:ALA:O	1:D:2994:GLN:NE2	2.34	0.61
1:A:2523:LEU:HD23	1:A:2579:MET:HE1	1.83	0.61
2:F:80:ASP:OD1	2:F:81:TYR:N	2.33	0.61
1:B:1234:PRO:O	1:B:1703:ARG:NH2	2.33	0.61
1:B:2688:ALA:O	1:B:2994:GLN:NE2	2.34	0.61
1:A:2688:ALA:O	1:A:2994:GLN:NE2	2.34	0.60
1:A:2863:LEU:HD23	1:A:2933:MET:HE3	1.82	0.60
1:B:2022:CYS:O	1:B:2029:ARG:NH2	2.34	0.60
1:B:2523:LEU:HD23	1:B:2579:MET:HE1	1.83	0.60
1:C:3534:ILE:HG13	1:C:3597:VAL:HG23	1.81	0.60
1:C:3972:ILE:HG21	1:C:3983:LEU:HD12	1.83	0.60
1:C:876:ALA:HB1	1:C:923:LEU:HD23	1.82	0.60
1:D:2213:VAL:HG12	1:D:2257:TYR:CE2	2.37	0.60
1:D:3972:ILE:HG21	1:D:3983:LEU:HD12	1.83	0.60
1:A:876:ALA:HB1	1:A:923:LEU:HD23	1.82	0.60
1:B:4222:PHE:HA	1:B:4948:VAL:HG21	1.82	0.60
1:D:2514:GLU:OE1	1:D:2514:GLU:N	2.35	0.60
1:C:2213:VAL:HG12	1:C:2257:TYR:CE2	2.37	0.60
1:C:2514:GLU:N	1:C:2514:GLU:OE1	2.35	0.60
1:C:2688:ALA:O	1:C:2994:GLN:NE2	2.34	0.60
1:C:4222:PHE:HA	1:C:4948:VAL:HG21	1.82	0.60
1:C:1426:GLU:N	1:C:1426:GLU:OE1	2.34	0.60
1:C:3446:TRP:NE1	1:C:3456:GLU:OE1	2.33	0.60
1:D:4974:GLU:OE1	1:D:4978:LEU:HD11	2.01	0.60
1:A:2514:GLU:OE1	1:A:2514:GLU:N	2.35	0.60
1:A:4974:GLU:OE1	1:A:4978:LEU:HD11	2.02	0.60
1:C:4649:THR:OG1	1:C:4801:HIS:NE2	2.29	0.60
1:D:2523:LEU:HD23	1:D:2579:MET:HE1	1.83	0.60
1:A:1555:VAL:HG21	1:A:1562:VAL:CG1	2.32	0.60
1:A:4649:THR:OG1	1:A:4801:HIS:NE2	2.29	0.60
1:B:1426:GLU:OE1	1:B:1426:GLU:N	2.34	0.60
1:B:2514:GLU:OE1	1:B:2514:GLU:N	2.35	0.60
1:B:4225:VAL:HB	1:B:4948:VAL:HG23	1.84	0.60
2:F:41:ARG:NH2	2:F:103:GLU:OE1	2.35	0.59
1:B:2213:VAL:HG12	1:B:2257:TYR:CE2	2.37	0.59
1:A:2879:LEU:HD12	1:A:2928:LEU:CD2	2.29	0.59
2:E:12:ASP:OD1	2:E:13:GLY:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1555:VAL:HG21	1:B:1562:VAL:CG1	2.32	0.59
1:B:1792:GLY:N	1:B:1795:GLU:OE2	2.35	0.59
1:C:2879:LEU:HD12	1:C:2928:LEU:CD2	2.29	0.59
1:D:1792:GLY:N	1:D:1795:GLU:OE2	2.35	0.59
1:D:2794:PRO:O	1:D:2798:PHE:N	2.35	0.59
1:A:2213:VAL:HG12	1:A:2257:TYR:CE2	2.37	0.59
1:A:2794:PRO:O	1:A:2798:PHE:N	2.35	0.59
1:C:1555:VAL:HG21	1:C:1562:VAL:CG1	2.32	0.59
1:C:4225:VAL:HB	1:C:4948:VAL:HG23	1.85	0.59
1:D:1555:VAL:HG21	1:D:1562:VAL:CG1	2.32	0.59
1:D:4225:VAL:HB	1:D:4948:VAL:HG23	1.85	0.59
1:A:954:THR:O	1:A:967:LYS:NZ	2.33	0.59
1:B:4974:GLU:OE1	1:B:4978:LEU:HD11	2.01	0.59
1:C:1978:TYR:OH	1:C:3639:MET:SD	2.49	0.59
1:A:1792:GLY:N	1:A:1795:GLU:OE2	2.35	0.58
1:A:4225:VAL:HB	1:A:4948:VAL:HG23	1.84	0.58
2:H:41:ARG:NH2	2:H:103:GLU:OE1	2.36	0.58
1:B:3972:ILE:HG21	1:B:3983:LEU:HD12	1.83	0.58
1:C:1792:GLY:N	1:C:1795:GLU:OE2	2.35	0.58
1:A:649:ILE:HG23	1:A:815:ALA:HB3	1.85	0.58
1:A:664:TYR:OH	1:A:666:GLU:OE2	2.18	0.58
1:B:582:ASN:OD1	1:B:583:HIS:N	2.36	0.58
1:C:4974:GLU:OE1	1:C:4978:LEU:HD11	2.02	0.58
1:D:649:ILE:HG23	1:D:815:ALA:HB3	1.85	0.58
1:D:954:THR:O	1:D:967:LYS:NZ	2.33	0.58
1:D:2875:MET:CE	1:D:2938:VAL:HG12	2.33	0.58
1:C:582:ASN:OD1	1:C:583:HIS:N	2.36	0.58
1:A:3328:LEU:HD23	1:A:3365:ARG:NH1	2.19	0.58
1:C:3328:LEU:HD23	1:C:3365:ARG:NH1	2.19	0.58
1:A:2875:MET:CE	1:A:2938:VAL:HG12	2.33	0.58
1:A:3972:ILE:HG21	1:A:3983:LEU:HD12	1.83	0.58
2:G:41:ARG:NH2	2:G:103:GLU:OE1	2.36	0.58
1:B:2394:ASP:OD1	1:B:2419:LEU:N	2.37	0.58
1:B:2875:MET:CE	1:B:2938:VAL:HG12	2.33	0.58
1:C:2394:ASP:OD1	1:C:2419:LEU:N	2.37	0.58
1:C:2794:PRO:O	1:C:2798:PHE:N	2.35	0.58
1:C:2875:MET:CE	1:C:2938:VAL:HG12	2.33	0.58
1:C:4837:MET:HE2	1:C:4837:MET:HA	1.86	0.58
1:B:3328:LEU:HD23	1:B:3365:ARG:NH1	2.19	0.58
1:D:582:ASN:OD1	1:D:583:HIS:N	2.36	0.58
1:B:664:TYR:OH	1:B:666:GLU:OE2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1426:GLU:OE1	1:A:1426:GLU:N	2.34	0.58
1:A:2394:ASP:OD1	1:A:2419:LEU:N	2.37	0.58
1:B:4837:MET:HA	1:B:4837:MET:HE2	1.86	0.57
1:A:582:ASN:OD1	1:A:583:HIS:N	2.36	0.57
1:C:649:ILE:HG23	1:C:815:ALA:HB3	1.85	0.57
1:C:2753:ASP:HA	1:C:2756:ILE:HD12	1.86	0.57
1:D:3328:LEU:HD23	1:D:3365:ARG:NH1	2.19	0.57
1:D:1869:GLU:OE1	1:D:1872:VAL:N	2.33	0.57
1:D:2879:LEU:HD12	1:D:2928:LEU:CD2	2.29	0.57
2:F:26:HIS:CD2	2:F:105:LEU:HD11	2.38	0.57
1:B:649:ILE:HG23	1:B:815:ALA:HB3	1.85	0.57
1:B:926:SER:O	1:B:929:THR:HG22	2.05	0.57
1:D:2394:ASP:OD1	1:D:2419:LEU:N	2.37	0.57
1:C:3387:GLU:OE1	1:C:3387:GLU:N	2.38	0.57
1:D:2753:ASP:HA	1:D:2756:ILE:HD12	1.86	0.57
1:C:614:ALA:HB2	1:C:1677:LEU:HD12	1.87	0.57
1:D:614:ALA:HB2	1:D:1677:LEU:HD12	1.87	0.57
1:D:658:THR:HG22	1:D:1002:VAL:HG21	1.87	0.57
1:A:1744:ARG:NE	1:A:1964:GLU:OE2	2.38	0.57
1:C:870:ARG:NH2	1:C:1052:TYR:OH	2.38	0.57
1:C:954:THR:O	1:C:967:LYS:NZ	2.33	0.57
1:D:870:ARG:NH2	1:D:1052:TYR:OH	2.38	0.57
1:D:4837:MET:HE2	1:D:4837:MET:HA	1.86	0.57
1:B:1744:ARG:NE	1:B:1964:GLU:OE2	2.38	0.56
1:B:4086:ASP:OD2	1:B:4088:ARG:N	2.38	0.56
1:C:4086:ASP:OD2	1:C:4088:ARG:N	2.38	0.56
1:C:658:THR:HG22	1:C:1002:VAL:HG21	1.87	0.56
1:C:926:SER:O	1:C:929:THR:HG22	2.05	0.56
1:D:926:SER:O	1:D:929:THR:HG22	2.05	0.56
1:A:2887:TRP:CG	1:A:2891:LYS:HZ1	2.22	0.56
1:A:4837:MET:HE2	1:A:4837:MET:HA	1.86	0.56
1:D:1744:ARG:NE	1:D:1964:GLU:OE2	2.38	0.56
1:A:2753:ASP:HA	1:A:2756:ILE:HD12	1.86	0.56
2:E:78:SER:OG	2:E:80:ASP:OD1	2.23	0.56
1:D:888:ILE:HD13	1:D:962:MET:HE1	1.88	0.56
1:A:926:SER:O	1:A:929:THR:HG22	2.05	0.56
1:B:870:ARG:NH2	1:B:1052:TYR:OH	2.38	0.56
1:B:2756:ILE:HG13	1:B:2814:LEU:HD12	1.88	0.56
1:C:888:ILE:HD13	1:C:962:MET:HE1	1.88	0.56
1:C:2756:ILE:HG13	1:C:2814:LEU:HD12	1.88	0.56
1:A:658:THR:HG22	1:A:1002:VAL:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:870:ARG:NH2	1:A:1052:TYR:OH	2.38	0.56
1:A:2213:VAL:HG12	1:A:2257:TYR:HE2	1.71	0.56
1:A:3387:GLU:OE1	1:A:3387:GLU:N	2.38	0.56
1:C:1744:ARG:NE	1:C:1964:GLU:OE2	2.38	0.56
1:C:1869:GLU:OE1	1:C:1872:VAL:N	2.33	0.56
1:C:2166:LEU:HB3	1:C:2179:MET:HE1	1.87	0.56
1:C:2863:LEU:HD23	1:C:2933:MET:CE	2.36	0.56
1:D:2213:VAL:HG12	1:D:2257:TYR:HE2	1.71	0.56
1:D:3387:GLU:OE1	1:D:3387:GLU:N	2.38	0.56
1:B:2166:LEU:HB3	1:B:2179:MET:HE1	1.87	0.56
1:B:2753:ASP:HA	1:B:2756:ILE:HD12	1.86	0.56
1:A:614:ALA:HB2	1:A:1677:LEU:HD12	1.87	0.56
1:A:3282:LEU:HD12	1:A:3316:LEU:HD22	1.88	0.56
1:B:658:THR:HG22	1:B:1002:VAL:HG21	1.87	0.56
1:D:2863:LEU:HD23	1:D:2933:MET:CE	2.36	0.56
1:A:1449:VAL:HG22	1:A:1555:VAL:HG23	1.88	0.56
1:A:1558:THR:O	1:A:1558:THR:HG22	2.05	0.56
1:B:614:ALA:HB2	1:B:1677:LEU:HD12	1.87	0.56
1:A:888:ILE:HD11	1:A:893:THR:HG22	1.88	0.56
1:A:2863:LEU:HD23	1:A:2933:MET:CE	2.36	0.56
1:B:888:ILE:HD13	1:B:962:MET:HE1	1.88	0.56
1:B:1558:THR:HG22	1:B:1558:THR:O	2.05	0.56
1:B:3387:GLU:N	1:B:3387:GLU:OE1	2.38	0.56
1:D:2887:TRP:CG	1:D:2891:LYS:HZ1	2.24	0.56
1:A:888:ILE:HD13	1:A:962:MET:HE1	1.88	0.55
1:B:1449:VAL:HG22	1:B:1555:VAL:HG23	1.88	0.55
1:D:1558:THR:HG22	1:D:1558:THR:O	2.05	0.55
1:B:658:THR:HG22	1:B:1002:VAL:CG2	2.36	0.55
1:B:888:ILE:HD11	1:B:893:THR:HG22	1.88	0.55
1:B:2209:MET:O	1:B:2213:VAL:HG13	2.07	0.55
1:A:2166:LEU:HB3	1:A:2179:MET:HE1	1.87	0.55
1:B:2794:PRO:O	1:B:2798:PHE:N	2.35	0.55
1:C:888:ILE:HD11	1:C:893:THR:HG22	1.88	0.55
1:C:1449:VAL:HG22	1:C:1555:VAL:HG23	1.88	0.55
1:D:888:ILE:HD11	1:D:893:THR:HG22	1.88	0.55
1:D:928:GLU:O	1:D:932:THR:HG23	2.07	0.55
1:D:1449:VAL:HG22	1:D:1555:VAL:HG23	1.88	0.55
1:D:3282:LEU:HD12	1:D:3316:LEU:HD22	1.88	0.55
1:A:928:GLU:O	1:A:932:THR:HG23	2.07	0.55
1:B:3282:LEU:HD12	1:B:3316:LEU:HD22	1.88	0.55
1:C:1558:THR:O	1:C:1558:THR:HG22	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2863:LEU:HD23	1:B:2933:MET:CE	2.36	0.55
1:C:2887:TRP:CG	1:C:2891:LYS:HZ1	2.25	0.55
1:A:658:THR:HG22	1:A:1002:VAL:CG2	2.36	0.55
1:C:892:TRP:CB	1:C:903:ARG:HE	2.20	0.55
1:D:2166:LEU:HB3	1:D:2179:MET:HE1	1.87	0.55
1:A:3347:VAL:HG11	1:A:3415:ARG:CB	2.37	0.55
1:C:3347:VAL:HG11	1:C:3415:ARG:CB	2.37	0.55
1:C:3828:GLU:OE1	1:C:3828:GLU:N	2.39	0.55
1:C:3862:VAL:HG12	1:C:3868:VAL:HG12	1.89	0.55
1:D:2239:TYR:CE2	1:D:2243:ILE:HD11	2.42	0.55
1:D:2756:ILE:HG13	1:D:2814:LEU:HD12	1.88	0.55
1:D:3862:VAL:HG12	1:D:3868:VAL:HG12	1.89	0.55
1:A:2756:ILE:HG13	1:A:2814:LEU:HD12	1.88	0.55
1:B:2887:TRP:CG	1:B:2891:LYS:HZ1	2.24	0.55
1:C:658:THR:HG22	1:C:1002:VAL:CG2	2.36	0.55
1:C:2213:VAL:HG12	1:C:2257:TYR:HE2	1.71	0.55
1:C:2239:TYR:CE2	1:C:2243:ILE:HD11	2.42	0.55
1:D:892:TRP:CB	1:D:903:ARG:HE	2.20	0.55
1:A:2239:TYR:CE2	1:A:2243:ILE:HD11	2.42	0.55
1:C:664:TYR:OH	1:C:666:GLU:OE2	2.18	0.55
1:C:1281:GLN:O	1:C:1282:ASN:OD1	2.25	0.55
1:A:892:TRP:CB	1:A:903:ARG:HE	2.20	0.54
1:A:2863:LEU:HD22	1:A:2929:LYS:HB3	1.90	0.54
1:C:928:GLU:O	1:C:932:THR:HG23	2.07	0.54
1:D:2978:LEU:HD22	1:D:3057:LEU:HD21	1.89	0.54
1:A:3752:VAL:HG22	1:A:3753:GLU:H	1.73	0.54
1:B:928:GLU:O	1:B:932:THR:HG23	2.07	0.54
1:B:2213:VAL:HG12	1:B:2257:TYR:HE2	1.71	0.54
1:C:2209:MET:O	1:C:2213:VAL:HG13	2.07	0.54
1:D:658:THR:HG22	1:D:1002:VAL:CG2	2.36	0.54
1:D:1281:GLN:O	1:D:1282:ASN:OD1	2.25	0.54
1:D:3347:VAL:HG11	1:D:3415:ARG:CB	2.37	0.54
1:A:1281:GLN:O	1:A:1282:ASN:OD1	2.25	0.54
1:A:2978:LEU:HD22	1:A:3057:LEU:HD21	1.89	0.54
1:A:1740:THR:HG22	1:A:2147:VAL:HG22	1.89	0.54
1:B:1281:GLN:O	1:B:1282:ASN:OD1	2.25	0.54
1:B:2863:LEU:HD22	1:B:2929:LYS:HB3	1.90	0.54
1:D:1758:GLY:N	1:D:1759:PRO:CD	2.71	0.54
1:D:2209:MET:O	1:D:2213:VAL:HG13	2.07	0.54
1:D:2905:LEU:HD12	1:D:2916:GLU:HG2	1.89	0.54
1:C:3282:LEU:HD12	1:C:3316:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3752:VAL:HG22	1:D:3753:GLU:H	1.73	0.54
1:A:2209:MET:O	1:A:2213:VAL:HG13	2.07	0.54
1:A:3862:VAL:HG12	1:A:3868:VAL:HG12	1.89	0.54
1:B:3752:VAL:HG22	1:B:3753:GLU:H	1.73	0.54
1:A:1758:GLY:N	1:A:1759:PRO:CD	2.71	0.54
1:A:2905:LEU:HD12	1:A:2916:GLU:HG2	1.89	0.54
2:H:26:HIS:ND1	2:H:105:LEU:HD11	2.22	0.54
1:B:1965:CYS:SG	1:B:1969:LYS:NZ	2.81	0.54
1:D:2863:LEU:HD22	1:D:2929:LYS:HB3	1.90	0.54
1:A:1869:GLU:OE1	1:A:1872:VAL:N	2.33	0.54
1:B:3347:VAL:HG11	1:B:3415:ARG:CB	2.37	0.54
1:B:3862:VAL:HG12	1:B:3868:VAL:HG12	1.89	0.54
1:C:1740:THR:HG22	1:C:2147:VAL:HG22	1.89	0.54
1:C:1758:GLY:N	1:C:1759:PRO:CD	2.71	0.54
1:C:4931:GLN:OE1	1:D:4928:ALA:HB2	2.08	0.54
1:A:4086:ASP:OD2	1:A:4088:ARG:N	2.38	0.54
1:B:892:TRP:CB	1:B:903:ARG:HE	2.20	0.54
1:B:2239:TYR:CE2	1:B:2243:ILE:HD11	2.42	0.54
1:C:2751:LYS:O	1:C:2936:TYR:OH	2.26	0.54
1:C:2863:LEU:HD22	1:C:2929:LYS:HB3	1.89	0.54
1:A:3828:GLU:OE1	1:A:3828:GLU:N	2.39	0.54
1:B:2978:LEU:HD22	1:B:3057:LEU:HD21	1.89	0.54
1:C:3227:GLU:O	1:C:3229:ALA:N	2.40	0.54
1:A:3227:GLU:O	1:A:3229:ALA:N	2.40	0.53
2:G:26:HIS:ND1	2:G:105:LEU:HD11	2.22	0.53
1:B:1758:GLY:N	1:B:1759:PRO:CD	2.71	0.53
1:B:2905:LEU:HD12	1:B:2916:GLU:HG2	1.90	0.53
1:A:4244:THR:HG22	1:A:4248:MET:HE3	1.90	0.53
1:B:4244:THR:HG22	1:B:4248:MET:HE3	1.90	0.53
1:B:4931:GLN:OE1	1:C:4928:ALA:HB2	2.08	0.53
1:D:1965:CYS:SG	1:D:1969:LYS:NZ	2.81	0.53
1:D:3828:GLU:OE1	1:D:3828:GLU:N	2.39	0.53
1:A:868:LEU:HD12	1:A:934:LEU:HD11	1.90	0.53
1:A:3770:GLN:OE1	1:A:3812:ASN:ND2	2.42	0.53
1:D:3357:SER:OG	1:D:3358:HIS:ND1	2.37	0.53
1:B:3770:GLN:OE1	1:B:3812:ASN:ND2	2.42	0.53
1:C:2905:LEU:HD12	1:C:2916:GLU:HG2	1.90	0.53
1:A:1965:CYS:SG	1:A:1969:LYS:NZ	2.81	0.53
1:A:2209:MET:CE	1:A:2251:MET:HE1	2.39	0.53
1:C:1965:CYS:SG	1:C:1969:LYS:NZ	2.81	0.53
2:G:78:SER:OG	2:G:80:ASP:OD1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:874:LYS:NZ	1:B:1050:TYR:OH	2.38	0.53
1:B:1102:ARG:NH1	1:B:1116:LEU:O	2.42	0.53
1:C:874:LYS:NZ	1:C:1050:TYR:OH	2.38	0.53
1:C:3752:VAL:HG22	1:C:3753:GLU:H	1.73	0.53
1:C:4720:ARG:HD2	1:C:4746:LEU:HD13	1.91	0.53
1:D:1740:THR:HG22	1:D:2147:VAL:HG22	1.89	0.53
1:A:3392:GLU:OE2	1:A:3396:ARG:NE	2.42	0.53
1:B:3227:GLU:O	1:B:3229:ALA:N	2.40	0.53
1:B:3392:GLU:OE2	1:B:3396:ARG:NE	2.42	0.53
1:C:1102:ARG:NH1	1:C:1116:LEU:O	2.42	0.53
1:C:2978:LEU:HD22	1:C:3057:LEU:HD21	1.89	0.53
1:D:432:PRO:O	1:D:433:ALA:HB3	2.09	0.53
1:D:3392:GLU:OE2	1:D:3396:ARG:NE	2.42	0.53
1:D:4244:THR:HG22	1:D:4248:MET:HE3	1.91	0.53
1:A:985:LEU:HD13	1:A:1057:PRO:HD2	1.91	0.53
1:C:2209:MET:CE	1:C:2251:MET:HE1	2.39	0.53
1:A:1102:ARG:NH1	1:A:1116:LEU:O	2.42	0.53
1:A:2751:LYS:O	1:A:2936:TYR:OH	2.26	0.53
2:H:78:SER:OG	2:H:80:ASP:OD1	2.24	0.53
1:B:432:PRO:O	1:B:433:ALA:HB3	2.09	0.53
1:B:2209:MET:CE	1:B:2251:MET:HE1	2.39	0.53
1:B:3253:GLU:O	1:B:3257:LEU:HD13	2.09	0.53
1:C:868:LEU:HD12	1:C:934:LEU:HD11	1.90	0.53
1:C:985:LEU:HD13	1:C:1057:PRO:HD2	1.91	0.53
1:D:877:GLU:O	1:D:881:GLU:HG2	2.09	0.53
1:B:1740:THR:HG22	1:B:2147:VAL:HG22	1.89	0.53
1:C:3392:GLU:OE2	1:C:3396:ARG:NE	2.42	0.53
1:C:432:PRO:O	1:C:433:ALA:HB3	2.09	0.52
1:C:3253:GLU:O	1:C:3257:LEU:HD13	2.09	0.52
1:C:3640:THR:O	1:C:3640:THR:HG23	2.10	0.52
1:D:2209:MET:CE	1:D:2251:MET:HE1	2.39	0.52
1:C:4148:VAL:HG22	1:C:4181:LEU:HD13	1.91	0.52
1:D:985:LEU:HD13	1:D:1057:PRO:HD2	1.91	0.52
1:D:2620:LEU:O	1:D:2624:LEU:HD23	2.10	0.52
1:D:3227:GLU:O	1:D:3229:ALA:N	2.40	0.52
1:D:4148:VAL:HG22	1:D:4181:LEU:HD13	1.91	0.52
1:A:1758:GLY:N	1:A:1759:PRO:HD2	2.25	0.52
1:A:4928:ALA:HB2	1:D:4931:GLN:OE1	2.09	0.52
1:B:985:LEU:HD13	1:B:1057:PRO:HD2	1.91	0.52
1:B:4148:VAL:HG22	1:B:4181:LEU:HD13	1.91	0.52
1:D:868:LEU:HD12	1:D:934:LEU:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2523:LEU:HD23	1:D:2579:MET:CE	2.40	0.52
1:D:3770:GLN:OE1	1:D:3812:ASN:ND2	2.42	0.52
1:A:3640:THR:HG23	1:A:3640:THR:O	2.10	0.52
1:B:868:LEU:HD12	1:B:934:LEU:HD11	1.90	0.52
1:B:877:GLU:O	1:B:881:GLU:HG2	2.09	0.52
1:A:3344:GLN:O	1:A:3347:VAL:HG12	2.10	0.52
1:B:2523:LEU:HD23	1:B:2579:MET:CE	2.40	0.52
1:B:2971:SER:HA	1:B:2974:PHE:CD1	2.45	0.52
1:C:877:GLU:O	1:C:881:GLU:HG2	2.09	0.52
1:C:2356:ARG:NH2	1:C:2450:GLU:OE2	2.43	0.52
1:D:1102:ARG:NH1	1:D:1116:LEU:O	2.42	0.52
1:D:1758:GLY:N	1:D:1759:PRO:HD2	2.25	0.52
1:A:2971:SER:HA	1:A:2974:PHE:CD1	2.45	0.52
1:A:4148:VAL:HG22	1:A:4181:LEU:HD13	1.91	0.52
1:C:4964:ASP:O	1:C:4968:THR:HG23	2.10	0.52
1:A:2949:THR:HG23	1:A:2950:SER:H	1.75	0.52
1:A:3366:LEU:HD13	1:A:3406:LEU:HD23	1.91	0.52
1:B:3640:THR:HG23	1:B:3640:THR:O	2.10	0.52
1:B:3714:LYS:HZ3	1:B:3718:ASP:CG	2.18	0.52
1:C:3344:GLN:O	1:C:3347:VAL:HG12	2.10	0.52
1:C:3770:GLN:OE1	1:C:3812:ASN:ND2	2.42	0.52
1:C:4244:THR:HG22	1:C:4248:MET:HE3	1.90	0.52
1:D:859:THR:OG1	1:D:928:GLU:OE1	2.26	0.52
1:D:2971:SER:HA	1:D:2974:PHE:CD1	2.45	0.52
1:D:3344:GLN:O	1:D:3347:VAL:HG12	2.10	0.52
1:B:1869:GLU:OE1	1:B:1872:VAL:N	2.33	0.52
1:D:2779:GLY:N	1:D:2789:HIS:O	2.42	0.52
1:A:877:GLU:O	1:A:881:GLU:HG2	2.09	0.52
1:A:1229:ILE:HG23	1:A:1230:ASN:N	2.25	0.52
1:A:2523:LEU:HD23	1:A:2579:MET:CE	2.40	0.52
1:B:4720:ARG:HD2	1:B:4746:LEU:HD13	1.91	0.52
1:C:1479:ASP:N	1:C:1482:GLY:O	2.41	0.52
1:C:2620:LEU:O	1:C:2624:LEU:HD23	2.10	0.52
1:C:2523:LEU:HD23	1:C:2579:MET:CE	2.40	0.52
1:C:2971:SER:HA	1:C:2974:PHE:CD1	2.45	0.52
1:D:4974:GLU:CD	1:D:4978:LEU:HD11	2.35	0.52
1:A:4964:ASP:O	1:A:4968:THR:HG23	2.10	0.51
1:B:1229:ILE:HG23	1:B:1230:ASN:N	2.25	0.51
1:B:3366:LEU:HD13	1:B:3406:LEU:HD23	1.91	0.51
1:B:4974:GLU:CD	1:B:4978:LEU:HD11	2.35	0.51
1:C:2756:ILE:CG1	1:C:2814:LEU:HD12	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2949:THR:HG23	1:C:2950:SER:H	1.75	0.51
1:D:1229:ILE:HG23	1:D:1230:ASN:N	2.25	0.51
1:D:2356:ARG:NH2	1:D:2450:GLU:OE2	2.43	0.51
1:A:4720:ARG:HD2	1:A:4746:LEU:HD13	1.91	0.51
1:A:4974:GLU:CD	1:A:4978:LEU:HD11	2.35	0.51
1:B:2949:THR:HG23	1:B:2950:SER:H	1.74	0.51
1:C:2000:ARG:O	1:C:3638:ARG:NH1	2.42	0.51
1:C:4974:GLU:CD	1:C:4978:LEU:HD11	2.35	0.51
1:D:3640:THR:HG23	1:D:3640:THR:O	2.10	0.51
1:A:2863:LEU:HD12	1:A:2926:GLU:OE1	2.11	0.51
1:B:1758:GLY:N	1:B:1759:PRO:HD2	2.25	0.51
1:D:3714:LYS:HZ3	1:D:3718:ASP:CG	2.19	0.51
1:A:874:LYS:NZ	1:A:1050:TYR:OH	2.38	0.51
1:A:3253:GLU:O	1:A:3257:LEU:HD13	2.09	0.51
1:B:2756:ILE:CG1	1:B:2814:LEU:HD12	2.40	0.51
1:B:2863:LEU:HD12	1:B:2926:GLU:OE1	2.11	0.51
1:D:3055:VAL:HG23	1:D:3062:ALA:HB1	1.93	0.51
1:A:2356:ARG:NH2	1:A:2450:GLU:OE2	2.43	0.51
1:A:3035:LYS:O	1:A:3039:MET:HG3	2.10	0.51
1:A:3457:GLN:OE1	1:A:3457:GLN:HA	2.11	0.51
1:C:4930:ILE:O	1:C:4934:ILE:HD12	2.11	0.51
1:D:3008:ASN:O	1:D:3012:THR:OG1	2.29	0.51
1:D:3035:LYS:O	1:D:3039:MET:HG3	2.10	0.51
1:D:3253:GLU:O	1:D:3257:LEU:HD13	2.09	0.51
1:A:2620:LEU:O	1:A:2624:LEU:HD23	2.10	0.51
1:A:3008:ASN:O	1:A:3012:THR:OG1	2.29	0.51
1:C:1229:ILE:HG23	1:C:1230:ASN:N	2.25	0.51
1:C:3055:VAL:HG23	1:C:3062:ALA:HB1	1.93	0.51
1:D:2949:THR:HG23	1:D:2950:SER:H	1.75	0.51
1:D:4086:ASP:OD2	1:D:4088:ARG:N	2.38	0.51
1:A:432:PRO:O	1:A:433:ALA:HB3	2.09	0.51
1:A:3417:VAL:O	1:A:3421:ARG:N	2.44	0.51
1:B:954:THR:O	1:B:967:LYS:NZ	2.33	0.51
1:B:974:SER:O	1:B:977:ARG:NH2	2.44	0.51
1:B:3457:GLN:HA	1:B:3457:GLN:OE1	2.11	0.51
1:B:3828:GLU:OE1	1:B:3828:GLU:N	2.39	0.51
1:B:4930:ILE:O	1:B:4934:ILE:HD12	2.11	0.51
1:B:4964:ASP:O	1:B:4968:THR:HG23	2.10	0.51
1:C:974:SER:O	1:C:977:ARG:NH2	2.44	0.51
1:D:4964:ASP:O	1:D:4968:THR:HG23	2.10	0.51
1:A:1479:ASP:N	1:A:1482:GLY:O	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2620:LEU:O	1:B:2624:LEU:HD23	2.10	0.51
1:B:3035:LYS:O	1:B:3039:MET:HG3	2.10	0.51
1:C:3457:GLN:OE1	1:C:3457:GLN:HA	2.11	0.51
2:F:78:SER:OG	2:F:80:ASP:OD1	2.26	0.51
1:B:2356:ARG:NH2	1:B:2450:GLU:OE2	2.43	0.51
1:B:3344:GLN:O	1:B:3347:VAL:HG12	2.10	0.51
1:C:3366:LEU:HD13	1:C:3406:LEU:HD23	1.91	0.51
1:A:2756:ILE:CG1	1:A:2814:LEU:HD12	2.40	0.51
1:A:2779:GLY:N	1:A:2789:HIS:O	2.42	0.51
1:A:2822:TRP:CE3	1:A:2875:MET:HE3	2.46	0.51
1:A:3055:VAL:HG23	1:A:3062:ALA:HB1	1.93	0.51
1:A:4930:ILE:O	1:A:4934:ILE:HD12	2.11	0.51
1:A:4931:GLN:OE1	1:B:4928:ALA:HB2	2.11	0.51
1:C:2234:CYS:O	1:C:2236:PHE:N	2.44	0.51
1:C:3035:LYS:O	1:C:3039:MET:HG3	2.10	0.51
1:D:3366:LEU:HD13	1:D:3406:LEU:HD23	1.91	0.51
1:D:4720:ARG:HD2	1:D:4746:LEU:HD13	1.91	0.51
1:C:3417:VAL:O	1:C:3421:ARG:N	2.44	0.50
1:D:883:TRP:CZ3	1:D:908:LEU:HD23	2.46	0.50
1:D:2756:ILE:CG1	1:D:2814:LEU:HD12	2.40	0.50
1:A:2313:MET:HE3	1:A:2317:LYS:HE2	1.93	0.50
1:B:883:TRP:CZ3	1:B:908:LEU:HD23	2.46	0.50
1:B:2234:CYS:O	1:B:2236:PHE:N	2.44	0.50
1:C:2863:LEU:HD12	1:C:2926:GLU:OE1	2.11	0.50
1:D:673:ALA:O	1:D:681:THR:OG1	2.29	0.50
1:A:2313:MET:HE3	1:A:2317:LYS:CE	2.42	0.50
1:B:2822:TRP:CE3	1:B:2875:MET:HE3	2.46	0.50
1:B:3004:LEU:HD11	1:B:3065:VAL:HG22	1.94	0.50
1:D:2313:MET:HE3	1:D:2317:LYS:CE	2.42	0.50
1:D:4930:ILE:O	1:D:4934:ILE:HD12	2.11	0.50
1:A:3004:LEU:HD11	1:A:3065:VAL:HG22	1.94	0.50
1:C:1758:GLY:N	1:C:1759:PRO:HD2	2.25	0.50
1:D:874:LYS:NZ	1:D:1050:TYR:OH	2.38	0.50
1:D:3457:GLN:OE1	1:D:3457:GLN:HA	2.11	0.50
1:A:883:TRP:CZ3	1:A:908:LEU:HD23	2.46	0.50
1:A:3730:MET:O	1:A:3733:SER:OG	2.28	0.50
1:B:2265:GLY:O	1:B:2267:GLY:N	2.42	0.50
1:D:2863:LEU:HD12	1:D:2926:GLU:OE1	2.11	0.50
1:D:3417:VAL:O	1:D:3421:ARG:N	2.44	0.50
1:B:2313:MET:HE3	1:B:2317:LYS:HE2	1.93	0.50
1:B:3055:VAL:HG23	1:B:3062:ALA:HB1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2313:MET:HE3	1:C:2317:LYS:CE	2.42	0.50
1:C:3240:MET:HA	1:C:3240:MET:HE3	1.94	0.50
1:D:3384:ALA:O	1:D:3388:ALA:N	2.40	0.50
1:A:974:SER:O	1:A:977:ARG:NH2	2.44	0.50
1:B:859:THR:OG1	1:B:928:GLU:OE1	2.26	0.50
1:C:883:TRP:CZ3	1:C:908:LEU:HD23	2.46	0.50
1:C:3004:LEU:HD11	1:C:3065:VAL:HG22	1.94	0.50
1:D:974:SER:O	1:D:977:ARG:NH2	2.44	0.50
1:D:3004:LEU:HD11	1:D:3065:VAL:HG22	1.94	0.50
1:A:859:THR:OG1	1:A:928:GLU:OE1	2.26	0.50
1:A:2234:CYS:O	1:A:2236:PHE:N	2.44	0.50
1:B:3417:VAL:O	1:B:3421:ARG:N	2.44	0.50
1:B:4686:ILE:HG23	1:B:4730:PHE:CD2	2.47	0.50
1:D:2045:ILE:HD11	1:D:2132:LEU:HB2	1.94	0.50
1:D:2156:LEU:CD1	1:D:2199:MET:HE1	2.42	0.50
1:D:2234:CYS:O	1:D:2236:PHE:N	2.44	0.50
1:B:2808:TRP:NE1	1:B:2812:GLU:OE2	2.45	0.49
1:C:4686:ILE:HG23	1:C:4730:PHE:CD2	2.47	0.49
1:D:3687:GLU:OE1	1:D:3695:LYS:NZ	2.45	0.49
1:A:3357:SER:OG	1:A:3358:HIS:ND1	2.37	0.49
1:A:4694:ASP:OD2	1:A:4697:GLY:N	2.44	0.49
1:C:2822:TRP:CE3	1:C:2875:MET:HE3	2.46	0.49
1:A:569:LEU:HD12	1:A:603:VAL:HG13	1.95	0.49
1:B:868:LEU:HD11	1:B:940:VAL:HG11	1.94	0.49
1:B:4981:HIS:O	5:B:8003:ATP:N6	2.45	0.49
1:C:2210:GLU:O	1:C:2213:VAL:HG22	2.12	0.49
1:C:4677:ARG:NH2	1:C:4713:TYR:OH	2.46	0.49
1:C:4694:ASP:OD2	1:C:4697:GLY:N	2.44	0.49
1:D:2265:GLY:O	1:D:2267:GLY:N	2.42	0.49
1:A:1959:LEU:HD23	1:A:2139:LEU:HD21	1.94	0.49
1:B:2971:SER:HA	1:B:2974:PHE:CE1	2.48	0.49
1:B:3008:ASN:O	1:B:3012:THR:OG1	2.29	0.49
1:D:4981:HIS:O	5:D:8003:ATP:N6	2.45	0.49
1:B:1959:LEU:HD23	1:B:2139:LEU:HD21	1.94	0.49
1:B:2313:MET:HE3	1:B:2317:LYS:CE	2.42	0.49
1:C:2808:TRP:NE1	1:C:2812:GLU:OE2	2.46	0.49
1:D:4148:VAL:HG22	1:D:4181:LEU:CD1	2.42	0.49
1:A:2156:LEU:CD1	1:A:2199:MET:HE1	2.42	0.49
1:A:3240:MET:HE3	1:A:3240:MET:HA	1.94	0.49
1:A:4686:ILE:HG23	1:A:4730:PHE:CD2	2.47	0.49
1:C:816:VAL:HG11	1:C:822:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:859:THR:OG1	1:C:928:GLU:OE1	2.26	0.49
1:C:4148:VAL:HG22	1:C:4181:LEU:CD1	2.43	0.49
1:A:2971:SER:HA	1:A:2974:PHE:CE1	2.48	0.49
1:D:569:LEU:HD12	1:D:603:VAL:HG13	1.95	0.49
1:A:2808:TRP:NE1	1:A:2812:GLU:OE2	2.45	0.49
1:A:4148:VAL:HG22	1:A:4181:LEU:CD1	2.43	0.49
1:D:2822:TRP:CE3	1:D:2875:MET:HE3	2.46	0.49
1:B:1479:ASP:N	1:B:1482:GLY:O	2.41	0.49
1:C:2779:GLY:N	1:C:2789:HIS:O	2.42	0.49
1:C:2971:SER:HA	1:C:2974:PHE:CE1	2.48	0.49
1:D:816:VAL:HG11	1:D:822:LEU:HB2	1.94	0.49
1:D:2313:MET:HE3	1:D:2317:LYS:HE2	1.93	0.49
1:A:868:LEU:CD1	1:A:934:LEU:HD11	2.43	0.49
1:B:3240:MET:HA	1:B:3240:MET:HE3	1.94	0.49
1:B:3687:GLU:OE1	1:B:3695:LYS:NZ	2.45	0.49
1:C:427:ARG:NH2	1:C:510:GLU:OE2	2.46	0.49
1:C:868:LEU:HD11	1:C:940:VAL:HG11	1.94	0.49
1:C:2766:LYS:HZ1	1:C:2860:PRO:HB2	1.78	0.49
1:D:1642:ILE:HD11	1:D:1649:MET:HE3	1.95	0.49
1:D:2971:SER:HA	1:D:2974:PHE:CE1	2.48	0.49
1:D:4686:ILE:HG23	1:D:4730:PHE:CD2	2.47	0.49
1:A:2265:GLY:O	1:A:2267:GLY:N	2.42	0.48
1:A:4677:ARG:NH2	1:A:4713:TYR:OH	2.46	0.48
1:B:569:LEU:HD12	1:B:603:VAL:HG13	1.95	0.48
1:B:2210:GLU:O	1:B:2213:VAL:HG22	2.12	0.48
1:C:2156:LEU:CD1	1:C:2199:MET:HE1	2.42	0.48
1:C:2438:ALA:HB2	1:C:2510:VAL:HG22	1.95	0.48
1:D:70:LEU:HD21	1:D:203:MET:HE1	1.95	0.48
1:D:1479:ASP:N	1:D:1482:GLY:O	2.41	0.48
1:A:1642:ILE:HD11	1:A:1649:MET:HE3	1.95	0.48
1:B:427:ARG:NH2	1:B:510:GLU:OE2	2.46	0.48
1:B:3730:MET:O	1:B:3733:SER:OG	2.28	0.48
1:B:4148:VAL:HG22	1:B:4181:LEU:CD1	2.43	0.48
1:C:1645:GLU:OE1	1:C:1647:ARG:NH2	2.46	0.48
1:C:1959:LEU:HD23	1:C:2139:LEU:HD21	1.94	0.48
1:C:2313:MET:HE3	1:C:2317:LYS:HE2	1.93	0.48
1:C:2997:LYS:O	1:C:2998:PHE:C	2.56	0.48
1:D:2210:GLU:O	1:D:2213:VAL:HG22	2.12	0.48
1:D:2808:TRP:NE1	1:D:2812:GLU:OE2	2.45	0.48
1:A:427:ARG:NH2	1:A:510:GLU:OE2	2.46	0.48
1:A:816:VAL:HG11	1:A:822:LEU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2045:ILE:HD11	1:A:2132:LEU:HB2	1.94	0.48
1:A:3687:GLU:OE1	1:A:3695:LYS:NZ	2.45	0.48
1:B:2045:ILE:HD11	1:B:2132:LEU:HB2	1.94	0.48
1:B:4677:ARG:NH2	1:B:4713:TYR:OH	2.46	0.48
1:B:4709:PHE:HB3	1:B:4710:PRO:HD3	1.96	0.48
1:B:4900:GLU:O	1:B:4911:ARG:NH2	2.44	0.48
1:C:2045:ILE:HD11	1:C:2132:LEU:HB2	1.94	0.48
1:C:2949:THR:HG23	1:C:2950:SER:N	2.28	0.48
1:D:427:ARG:NH2	1:D:510:GLU:OE2	2.46	0.48
1:A:3246:VAL:HG12	1:A:3247:LEU:N	2.28	0.48
1:C:70:LEU:HD21	1:C:203:MET:HE1	1.95	0.48
1:C:569:LEU:HD12	1:C:603:VAL:HG13	1.95	0.48
1:D:859:THR:HG21	1:D:932:THR:HG22	1.96	0.48
1:A:2875:MET:HE2	1:A:2938:VAL:HG12	1.95	0.48
1:B:3369:ARG:O	1:B:3373:VAL:HG23	2.14	0.48
1:A:2210:GLU:O	1:A:2213:VAL:HG22	2.12	0.48
1:A:2949:THR:HG23	1:A:2950:SER:N	2.28	0.48
1:A:4709:PHE:HB3	1:A:4710:PRO:HD3	1.96	0.48
1:B:2156:LEU:CD1	1:B:2199:MET:HE1	2.42	0.48
1:B:3246:VAL:HG12	1:B:3247:LEU:N	2.28	0.48
1:C:859:THR:HG21	1:C:932:THR:HG22	1.96	0.48
1:D:1273:LEU:HD22	1:D:1290:LEU:HD11	1.95	0.48
1:D:3240:MET:HE3	1:D:3240:MET:HA	1.94	0.48
1:D:4709:PHE:HB3	1:D:4710:PRO:HD3	1.96	0.48
1:B:816:VAL:HG11	1:B:822:LEU:HB2	1.95	0.48
1:B:2234:CYS:O	1:B:2238:CYS:CB	2.62	0.48
1:C:3170:LEU:C	1:C:3170:LEU:HD23	2.39	0.48
1:C:3246:VAL:HG12	1:C:3247:LEU:N	2.28	0.48
1:D:729:ARG:NH2	1:D:1490:CYS:SG	2.87	0.48
1:D:1959:LEU:HD23	1:D:2139:LEU:HD21	1.94	0.48
1:A:859:THR:HG21	1:A:932:THR:HG22	1.96	0.48
1:A:1645:GLU:OE1	1:A:1647:ARG:NH2	2.46	0.48
1:A:2974:PHE:CE2	1:A:2996:ILE:HG12	2.48	0.48
1:B:592:ASP:HA	1:B:632:LEU:HD21	1.95	0.48
1:B:1645:GLU:OE1	1:B:1647:ARG:NH2	2.46	0.48
1:B:2779:GLY:N	1:B:2789:HIS:O	2.42	0.48
1:B:2949:THR:HG23	1:B:2950:SER:N	2.28	0.48
1:B:2974:PHE:CE2	1:B:2996:ILE:HG12	2.48	0.48
1:C:2876:ALA:HB3	1:C:2921:ARG:NH1	2.29	0.48
1:C:2974:PHE:CE2	1:C:2996:ILE:HG12	2.48	0.48
1:C:3369:ARG:O	1:C:3373:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3714:LYS:HZ3	1:C:3718:ASP:CG	2.21	0.48
1:D:2234:CYS:C	1:D:2238:CYS:HB2	2.39	0.48
1:D:2876:ALA:HB3	1:D:2921:ARG:NH1	2.29	0.48
1:D:2974:PHE:CE2	1:D:2996:ILE:HG12	2.48	0.48
1:A:868:LEU:HD11	1:A:940:VAL:HG11	1.94	0.48
1:A:4900:GLU:O	1:A:4911:ARG:NH2	2.44	0.48
1:B:70:LEU:HD21	1:B:203:MET:HE1	1.95	0.48
1:B:868:LEU:CD1	1:B:934:LEU:HD11	2.43	0.48
1:B:2457:ILE:O	1:B:2461:LEU:HD13	2.14	0.48
1:B:2876:ALA:HB3	1:B:2921:ARG:NH1	2.29	0.48
1:B:3847:LEU:HD13	1:C:77:ARG:NH1	2.29	0.48
1:C:139:GLN:NE2	1:C:141:ASP:O	2.47	0.48
1:C:729:ARG:NH2	1:C:1490:CYS:SG	2.87	0.48
1:C:1642:ILE:HD11	1:C:1649:MET:HE3	1.95	0.48
1:D:868:LEU:HD11	1:D:940:VAL:HG11	1.94	0.48
1:D:2234:CYS:O	1:D:2238:CYS:CB	2.62	0.48
1:D:2949:THR:HG23	1:D:2950:SER:N	2.28	0.48
1:D:3246:VAL:HG12	1:D:3247:LEU:N	2.28	0.48
1:B:729:ARG:NH2	1:B:1490:CYS:SG	2.87	0.48
1:C:2257:TYR:CZ	1:C:2261:ASN:OD1	2.67	0.48
1:C:2875:MET:HE2	1:C:2938:VAL:HG12	1.95	0.48
1:D:868:LEU:CD1	1:D:934:LEU:HD11	2.43	0.48
1:D:1645:GLU:OE1	1:D:1647:ARG:NH2	2.46	0.48
1:D:4677:ARG:NH2	1:D:4713:TYR:OH	2.46	0.48
1:A:1273:LEU:HD22	1:A:1290:LEU:HD11	1.95	0.47
1:A:2457:ILE:O	1:A:2461:LEU:HD13	2.14	0.47
1:A:3170:LEU:HD23	1:A:3170:LEU:C	2.39	0.47
1:A:4981:HIS:O	5:A:8003:ATP:N6	2.45	0.47
1:B:139:GLN:NE2	1:B:141:ASP:O	2.47	0.47
1:B:2257:TYR:CZ	1:B:2261:ASN:OD1	2.67	0.47
1:B:2438:ALA:HB2	1:B:2510:VAL:HG22	1.95	0.47
1:B:3353:GLU:OE1	1:B:3353:GLU:N	2.44	0.47
1:C:868:LEU:HD22	1:C:930:LEU:HD12	1.96	0.47
1:C:3008:ASN:O	1:C:3012:THR:OG1	2.29	0.47
1:C:4709:PHE:HB3	1:C:4710:PRO:HD3	1.96	0.47
1:C:4902:PRO:HB3	1:C:4911:ARG:HG2	1.96	0.47
1:C:4981:HIS:O	5:C:8003:ATP:N6	2.45	0.47
1:D:2438:ALA:HB2	1:D:2510:VAL:HG22	1.95	0.47
1:A:70:LEU:HD21	1:A:203:MET:HE1	1.95	0.47
1:A:2257:TYR:CZ	1:A:2261:ASN:OD1	2.67	0.47
1:A:2432:ASP:OD2	1:A:2436:ARG:NE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2000:ARG:O	1:B:3638:ARG:NH1	2.42	0.47
1:B:3100:ALA:HA	1:B:3137:LEU:HD21	1.96	0.47
1:B:3170:LEU:HD23	1:B:3170:LEU:C	2.39	0.47
1:C:868:LEU:CD1	1:C:934:LEU:HD11	2.43	0.47
1:C:1273:LEU:HD22	1:C:1290:LEU:HD11	1.96	0.47
1:C:2528:LEU:HD23	1:C:2531:MET:HE3	1.96	0.47
1:D:2257:TYR:CZ	1:D:2261:ASN:OD1	2.67	0.47
1:D:3369:ARG:O	1:D:3373:VAL:HG23	2.14	0.47
1:A:2863:LEU:HD22	1:A:2929:LYS:CB	2.45	0.47
1:A:3100:ALA:HA	1:A:3137:LEU:HD21	1.96	0.47
1:B:2751:LYS:O	1:B:2936:TYR:OH	2.26	0.47
1:C:592:ASP:HA	1:C:632:LEU:HD21	1.95	0.47
1:D:592:ASP:HA	1:D:632:LEU:HD21	1.95	0.47
1:D:2863:LEU:HD22	1:D:2929:LYS:CB	2.45	0.47
1:B:859:THR:HG21	1:B:932:THR:HG22	1.96	0.47
1:B:2817:MET:CE	1:B:2879:LEU:HD11	2.43	0.47
1:B:4835:LEU:HD21	1:B:4934:ILE:HD11	1.96	0.47
1:B:4902:PRO:HB3	1:B:4911:ARG:HG2	1.96	0.47
1:C:2234:CYS:O	1:C:2238:CYS:CB	2.62	0.47
1:D:139:GLN:NE2	1:D:141:ASP:O	2.47	0.47
1:A:139:GLN:NE2	1:A:141:ASP:O	2.47	0.47
1:A:729:ARG:NH2	1:A:1490:CYS:SG	2.87	0.47
1:A:3671:GLU:OE1	1:A:3671:GLU:N	2.46	0.47
1:B:2234:CYS:C	1:B:2238:CYS:HB2	2.39	0.47
1:B:2480:LEU:HD11	1:B:2484:GLY:HA2	1.96	0.47
1:C:2265:GLY:O	1:C:2267:GLY:N	2.42	0.47
1:C:4835:LEU:HD21	1:C:4934:ILE:HD11	1.96	0.47
1:A:2234:CYS:O	1:A:2238:CYS:CB	2.62	0.47
1:A:2234:CYS:C	1:A:2238:CYS:HB2	2.39	0.47
1:A:2875:MET:HE3	1:A:2938:VAL:HG12	1.96	0.47
1:B:1273:LEU:HD22	1:B:1290:LEU:HD11	1.95	0.47
1:B:2875:MET:HE2	1:B:2938:VAL:HG12	1.95	0.47
1:B:2909:TYR:HA	1:B:2912:LEU:HD12	1.97	0.47
1:B:3582:GLY:N	1:B:3584:GLU:OE1	2.48	0.47
1:C:2234:CYS:C	1:C:2238:CYS:HB2	2.39	0.47
1:C:5033:GLN:OE1	1:C:5033:GLN:N	2.48	0.47
1:D:2480:LEU:HD11	1:D:2484:GLY:HA2	1.96	0.47
1:D:2875:MET:HE2	1:D:2938:VAL:HG12	1.95	0.47
1:A:592:ASP:HA	1:A:632:LEU:HD21	1.95	0.47
1:A:1685:ALA:HA	2:E:91:ILE:HD11	1.97	0.47
1:A:2438:ALA:HB2	1:A:2510:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2997:LYS:O	1:A:2998:PHE:C	2.56	0.47
1:A:3369:ARG:O	1:A:3373:VAL:HG23	2.14	0.47
1:A:5033:GLN:OE1	1:A:5033:GLN:N	2.48	0.47
1:B:868:LEU:HD22	1:B:930:LEU:HD12	1.96	0.47
1:B:1642:ILE:HD11	1:B:1649:MET:HE3	1.95	0.47
1:B:2234:CYS:O	1:B:2238:CYS:HB2	2.15	0.47
1:B:2997:LYS:O	1:B:2998:PHE:C	2.56	0.47
1:B:4694:ASP:OD2	1:B:4697:GLY:N	2.44	0.47
1:C:2457:ILE:O	1:C:2461:LEU:HD13	2.14	0.47
1:C:3384:ALA:O	1:C:3388:ALA:N	2.40	0.47
1:C:3847:LEU:HD13	1:D:77:ARG:NH1	2.29	0.47
1:D:868:LEU:HD22	1:D:930:LEU:HD12	1.96	0.47
1:D:2457:ILE:O	1:D:2461:LEU:HD13	2.14	0.47
1:D:2997:LYS:O	1:D:2998:PHE:C	2.56	0.47
1:D:3170:LEU:HD23	1:D:3170:LEU:C	2.39	0.47
1:A:2480:LEU:HD11	1:A:2484:GLY:HA2	1.96	0.47
1:A:2876:ALA:HB3	1:A:2921:ARG:NH1	2.29	0.47
1:A:4066:ASP:OD1	1:A:4172:SER:OG	2.26	0.47
1:B:3328:LEU:HD23	1:B:3365:ARG:HH12	1.80	0.47
1:B:3384:ALA:O	1:B:3388:ALA:N	2.40	0.47
1:C:3582:GLY:N	1:C:3584:GLU:OE1	2.48	0.47
1:D:2817:MET:CE	1:D:2879:LEU:HD11	2.44	0.47
1:D:3582:GLY:N	1:D:3584:GLU:OE1	2.48	0.47
1:A:4902:PRO:HB3	1:A:4911:ARG:HG2	1.96	0.47
1:B:973:LEU:O	1:B:973:LEU:HD12	2.15	0.47
1:C:2234:CYS:O	1:C:2238:CYS:HB2	2.15	0.47
1:C:2480:LEU:HD11	1:C:2484:GLY:HA2	1.96	0.47
1:C:2863:LEU:HD22	1:C:2929:LYS:CB	2.44	0.47
1:D:2234:CYS:O	1:D:2238:CYS:HB2	2.15	0.47
1:A:2909:TYR:HA	1:A:2912:LEU:HD12	1.97	0.47
1:B:673:ALA:O	1:B:681:THR:OG1	2.29	0.47
1:B:2528:LEU:HD23	1:B:2531:MET:HE3	1.96	0.47
1:C:2817:MET:CE	1:C:2879:LEU:HD11	2.43	0.47
1:C:2875:MET:HE3	1:C:2938:VAL:HG12	1.96	0.47
1:D:4546:ARG:O	1:D:4550:LEU:HD23	2.15	0.47
1:C:973:LEU:HD12	1:C:973:LEU:O	2.15	0.46
1:D:3328:LEU:HD23	1:D:3365:ARG:HH12	1.80	0.46
1:A:3582:GLY:N	1:A:3584:GLU:OE1	2.48	0.46
1:B:5033:GLN:OE1	1:B:5033:GLN:N	2.48	0.46
1:C:3100:ALA:HA	1:C:3137:LEU:HD21	1.96	0.46
1:C:4546:ARG:O	1:C:4550:LEU:HD23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:973:LEU:HD12	1:D:973:LEU:O	2.15	0.46
1:D:2528:LEU:HD23	1:D:2531:MET:HE3	1.96	0.46
1:D:2564:THR:HG22	1:D:2607:CYS:CA	2.44	0.46
1:D:3529:THR:HG23	1:D:3574:MET:HE3	1.98	0.46
1:D:4902:PRO:HB3	1:D:4911:ARG:HG2	1.96	0.46
1:D:5033:GLN:OE1	1:D:5033:GLN:N	2.48	0.46
1:A:973:LEU:HD12	1:A:973:LEU:O	2.15	0.46
1:A:2166:LEU:CB	1:A:2179:MET:HE1	2.46	0.46
1:A:3018:PHE:O	1:A:3037:LYS:NZ	2.48	0.46
1:C:2564:THR:HG22	1:C:2607:CYS:CA	2.44	0.46
1:C:3687:GLU:OE1	1:C:3695:LYS:NZ	2.45	0.46
1:A:3529:THR:HG23	1:A:3574:MET:HE3	1.98	0.46
1:B:1973:ASN:HD21	1:B:2025:PRO:CD	2.29	0.46
1:B:2166:LEU:CB	1:B:2179:MET:HE1	2.46	0.46
1:C:3353:GLU:OE1	1:C:3353:GLU:N	2.44	0.46
1:D:3100:ALA:HA	1:D:3137:LEU:HD21	1.96	0.46
1:A:868:LEU:HD22	1:A:930:LEU:HD12	1.96	0.46
1:A:1973:ASN:HD21	1:A:2025:PRO:CD	2.29	0.46
1:A:3847:LEU:HD13	1:B:77:ARG:NH1	2.30	0.46
1:A:4835:LEU:HD21	1:A:4934:ILE:HD11	1.96	0.46
1:B:3018:PHE:O	1:B:3037:LYS:NZ	2.48	0.46
1:B:3529:THR:HG23	1:B:3574:MET:HE3	1.98	0.46
1:C:2909:TYR:HA	1:C:2912:LEU:HD12	1.97	0.46
1:C:3529:THR:HG23	1:C:3574:MET:HE3	1.98	0.46
1:C:3730:MET:O	1:C:3733:SER:OG	2.28	0.46
1:D:2875:MET:HE3	1:D:2938:VAL:HG12	1.96	0.46
1:D:4989:PHE:HE2	1:D:5008:VAL:HG11	1.80	0.46
1:A:2234:CYS:O	1:A:2238:CYS:HB2	2.15	0.46
1:A:2817:MET:CE	1:A:2879:LEU:HD11	2.43	0.46
1:A:4546:ARG:O	1:A:4550:LEU:HD23	2.15	0.46
1:B:2863:LEU:HD22	1:B:2929:LYS:CB	2.45	0.46
1:C:1300:GLN:OE1	1:C:1546:ASN:ND2	2.48	0.46
1:C:4989:PHE:HE2	1:C:5008:VAL:HG11	1.81	0.46
1:D:2166:LEU:CB	1:D:2179:MET:HE1	2.46	0.46
1:D:4835:LEU:HD21	1:D:4934:ILE:HD11	1.96	0.46
1:A:962:MET:HG2	1:A:966:TYR:O	2.16	0.46
1:A:2528:LEU:HD23	1:A:2531:MET:HE3	1.96	0.46
1:A:2000:ARG:O	1:A:3638:ARG:NH1	2.42	0.46
1:B:3357:SER:OG	1:B:3358:HIS:ND1	2.37	0.46
1:D:2909:TYR:HA	1:D:2912:LEU:HD12	1.97	0.46
1:A:2482:LYS:HD2	1:A:2483:ASP:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2875:MET:HE3	1:B:2938:VAL:HG12	1.96	0.46
1:B:4546:ARG:O	1:B:4550:LEU:HD23	2.15	0.46
1:C:962:MET:HG2	1:C:966:TYR:O	2.16	0.46
1:C:1659:ASP:OD1	1:C:1659:ASP:N	2.49	0.46
1:C:2166:LEU:CB	1:C:2179:MET:HE1	2.46	0.46
1:C:2482:LYS:HD2	1:C:2483:ASP:H	1.81	0.46
1:C:2815:LYS:HA	1:C:2818:ILE:HD12	1.97	0.46
1:D:2815:LYS:HA	1:D:2818:ILE:HD12	1.97	0.46
2:E:26:HIS:CE1	2:E:105:LEU:HD11	2.51	0.46
1:B:3380:LEU:HD21	1:B:3391:GLY:C	2.41	0.46
1:A:3380:LEU:HD21	1:A:3391:GLY:C	2.41	0.45
1:C:4653:PHE:N	1:C:4794:MET:HE1	2.31	0.45
1:D:3595:ARG:O	1:D:3599:GLU:OE1	2.35	0.45
1:A:2505:LEU:HD23	1:A:2505:LEU:C	2.42	0.45
1:B:1825:GLY:O	1:B:1827:HIS:ND1	2.49	0.45
1:C:218:GLY:N	1:C:263:LEU:O	2.47	0.45
1:C:225:HIS:N	1:C:230:GLU:O	2.48	0.45
1:C:1825:GLY:O	1:C:1827:HIS:ND1	2.49	0.45
1:D:881:GLU:OE2	1:D:966:TYR:OH	2.34	0.45
1:D:1973:ASN:HD21	1:D:2025:PRO:CD	2.29	0.45
1:D:2820:TRP:CH2	1:D:2882:ASN:HB2	2.51	0.45
1:A:1095:ALA:HB1	1:A:1101:MET:HE1	1.98	0.45
1:A:2564:THR:HG22	1:A:2607:CYS:CA	2.44	0.45
1:B:249:GLU:OE1	1:B:374:LYS:NZ	2.47	0.45
1:C:3380:LEU:HD21	1:C:3391:GLY:C	2.41	0.45
1:A:2482:LYS:HD2	1:A:2483:ASP:N	2.32	0.45
1:B:2789:HIS:CD2	1:B:2790:PRO:HD2	2.52	0.45
1:D:2505:LEU:HD23	1:D:2505:LEU:C	2.42	0.45
1:A:4989:PHE:HE2	1:A:5008:VAL:HG11	1.81	0.45
1:C:1734:GLU:HG2	1:C:2202:LEU:HD23	1.98	0.45
1:C:2577:ALA:HA	1:C:2619:MET:HE1	1.98	0.45
1:C:3328:LEU:HD23	1:C:3365:ARG:HH12	1.80	0.45
1:D:962:MET:HG2	1:D:966:TYR:O	2.15	0.45
1:A:881:GLU:OE2	1:A:966:TYR:OH	2.34	0.45
1:A:1734:GLU:HG2	1:A:2202:LEU:HD23	1.98	0.45
1:A:3328:LEU:HD23	1:A:3365:ARG:HH12	1.80	0.45
1:C:862:ILE:HG22	1:C:862:ILE:O	2.17	0.45
1:C:1973:ASN:HD21	1:C:2025:PRO:CD	2.29	0.45
1:C:3684:GLN:OE1	1:C:3684:GLN:N	2.45	0.45
1:C:4244:THR:CG2	1:C:4248:MET:HE3	2.47	0.45
1:D:4653:PHE:N	1:D:4794:MET:HE1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:862:ILE:O	1:B:862:ILE:HG22	2.17	0.45
1:B:1300:GLN:OE1	1:B:1546:ASN:ND2	2.47	0.45
1:B:3671:GLU:OE1	1:B:3671:GLU:N	2.46	0.45
1:B:4989:PHE:HE2	1:B:5008:VAL:HG11	1.81	0.45
1:C:2505:LEU:C	1:C:2505:LEU:HD23	2.42	0.45
1:D:3380:LEU:HD21	1:D:3391:GLY:C	2.41	0.45
1:D:4244:THR:CG2	1:D:4248:MET:HE3	2.47	0.45
1:A:1810:ARG:NE	1:A:1855:VAL:O	2.50	0.45
1:A:3974:GLY:N	1:A:3975:PRO:HA	2.32	0.45
1:B:1734:GLU:HG2	1:B:2202:LEU:HD23	1.98	0.45
1:B:2505:LEU:HD23	1:B:2505:LEU:C	2.42	0.45
1:B:2577:ALA:HA	1:B:2619:MET:HE1	1.98	0.45
1:B:2815:LYS:HA	1:B:2818:ILE:HD12	1.97	0.45
1:C:881:GLU:OE2	1:C:966:TYR:OH	2.35	0.45
1:C:2096:GLN:HA	1:C:2128:GLN:HE21	1.82	0.45
1:C:3398:GLU:O	1:C:3401:VAL:HG12	2.17	0.45
1:D:1734:GLU:HG2	1:D:2202:LEU:HD23	1.98	0.45
1:D:1810:ARG:NE	1:D:1855:VAL:O	2.50	0.45
1:D:2482:LYS:HD2	1:D:2483:ASP:H	1.81	0.45
1:D:3267:MET:HG3	1:D:3267:MET:O	2.17	0.45
1:A:1825:GLY:O	1:A:1827:HIS:ND1	2.49	0.45
1:A:2820:TRP:CH2	1:A:2882:ASN:HB2	2.52	0.45
1:B:2564:THR:HG22	1:B:2607:CYS:CA	2.44	0.45
1:B:4244:THR:CG2	1:B:4248:MET:HE3	2.47	0.45
1:C:2215:VAL:HG11	1:C:2229:MET:HG2	1.99	0.45
1:C:2482:LYS:HD2	1:C:2483:ASP:N	2.32	0.45
1:C:3037:LYS:O	1:C:3040:ILE:HG22	2.17	0.45
1:D:2096:GLN:HA	1:D:2128:GLN:HE21	1.82	0.45
1:D:3018:PHE:O	1:D:3037:LYS:NZ	2.48	0.45
1:D:3398:GLU:O	1:D:3401:VAL:HG12	2.17	0.45
1:A:2789:HIS:CD2	1:A:2790:PRO:HD2	2.52	0.45
1:A:3037:LYS:O	1:A:3040:ILE:HG22	2.17	0.45
1:A:4044:ALA:O	1:A:4048:VAL:HG23	2.17	0.45
1:B:2820:TRP:CH2	1:B:2882:ASN:HB2	2.52	0.45
1:C:2820:TRP:CH2	1:C:2882:ASN:HB2	2.52	0.45
1:C:3018:PHE:O	1:C:3037:LYS:NZ	2.48	0.45
1:C:3357:SER:OG	1:C:3358:HIS:ND1	2.37	0.45
1:D:3037:LYS:O	1:D:3040:ILE:HG22	2.17	0.45
1:D:3353:GLU:OE1	1:D:3353:GLU:N	2.44	0.45
1:D:4694:ASP:OD2	1:D:4697:GLY:N	2.44	0.45
1:A:2215:VAL:HG11	1:A:2229:MET:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2815:LYS:HA	1:A:2818:ILE:HD12	1.97	0.44
1:A:3384:ALA:O	1:A:3388:ALA:N	2.40	0.44
1:A:4244:THR:CG2	1:A:4248:MET:HE3	2.47	0.44
1:A:4653:PHE:N	1:A:4794:MET:HE1	2.31	0.44
1:B:962:MET:HG2	1:B:966:TYR:O	2.16	0.44
1:B:4066:ASP:OD1	1:B:4172:SER:OG	2.26	0.44
1:A:3267:MET:HG3	1:A:3267:MET:O	2.17	0.44
2:G:88:HIS:NE2	1:C:1788:LEU:HD21	2.32	0.44
1:B:1810:ARG:NE	1:B:1855:VAL:O	2.50	0.44
1:C:2789:HIS:CD2	1:C:2790:PRO:HD2	2.52	0.44
1:C:4044:ALA:O	1:C:4048:VAL:HG23	2.17	0.44
1:D:929:THR:HG23	1:D:930:LEU:CD2	2.46	0.44
1:D:1825:GLY:O	1:D:1827:HIS:ND1	2.49	0.44
1:D:2000:ARG:O	1:D:3638:ARG:NH1	2.42	0.44
1:D:2215:VAL:HG11	1:D:2229:MET:HG2	1.99	0.44
1:D:2234:CYS:C	1:D:2238:CYS:CB	2.91	0.44
1:D:2482:LYS:HD2	1:D:2483:ASP:N	2.32	0.44
1:D:4044:ALA:O	1:D:4048:VAL:HG23	2.17	0.44
1:A:3398:GLU:O	1:A:3401:VAL:HG12	2.17	0.44
1:B:2482:LYS:HD2	1:B:2483:ASP:N	2.32	0.44
1:B:3974:GLY:N	1:B:3975:PRO:HA	2.32	0.44
1:C:3869:ILE:O	1:C:3869:ILE:HG22	2.17	0.44
1:C:3974:GLY:N	1:C:3975:PRO:HA	2.32	0.44
1:D:2789:HIS:CD2	1:D:2790:PRO:HD2	2.52	0.44
1:B:881:GLU:OE2	1:B:966:TYR:OH	2.34	0.44
1:C:2234:CYS:C	1:C:2238:CYS:CB	2.91	0.44
1:C:3267:MET:HG3	1:C:3267:MET:O	2.17	0.44
1:C:3528:PRO:HG2	1:C:3574:MET:HE2	2.00	0.44
1:C:4720:ARG:HE	1:C:4720:ARG:HB3	1.61	0.44
1:D:554:ARG:NH2	1:D:556:GLU:OE2	2.48	0.44
1:D:1095:ALA:HB1	1:D:1101:MET:HE1	1.98	0.44
1:D:2577:ALA:HA	1:D:2619:MET:HE1	1.98	0.44
1:D:2922:GLU:O	1:D:2926:GLU:HG2	2.18	0.44
1:D:3016:LEU:HD22	1:D:3026:LEU:CD1	2.47	0.44
1:A:77:ARG:NH1	1:D:3847:LEU:HD13	2.32	0.44
1:A:1659:ASP:N	1:A:1659:ASP:OD1	2.49	0.44
1:A:2577:ALA:HA	1:A:2619:MET:HE1	1.98	0.44
1:A:3016:LEU:HD22	1:A:3026:LEU:CD1	2.47	0.44
1:A:3202:MET:HE3	1:A:3204:VAL:HG12	2.00	0.44
1:B:2096:GLN:HA	1:B:2128:GLN:HE21	1.82	0.44
1:B:2971:SER:O	1:B:2975:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3595:ARG:O	1:B:3599:GLU:OE1	2.35	0.44
1:C:3595:ARG:O	1:C:3599:GLU:OE1	2.35	0.44
1:D:3515:LEU:HD21	1:D:3603:VAL:HG13	2.00	0.44
1:A:1871:GLU:O	1:A:1874:ARG:HD2	2.18	0.44
1:A:2766:LYS:HZ1	1:A:2860:PRO:HB2	1.83	0.44
1:A:2940:ARG:HB3	1:A:2942:LEU:HD12	2.00	0.44
1:A:2971:SER:O	1:A:2975:ILE:HG12	2.18	0.44
1:B:267:ARG:NH2	1:B:332:VAL:O	2.49	0.44
1:B:1095:ALA:HB1	1:B:1101:MET:HE1	1.98	0.44
1:B:2234:CYS:C	1:B:2238:CYS:CB	2.91	0.44
1:B:2922:GLU:O	1:B:2926:GLU:HG2	2.18	0.44
1:C:2922:GLU:O	1:C:2926:GLU:HG2	2.18	0.44
1:C:2971:SER:O	1:C:2975:ILE:HG12	2.18	0.44
1:D:3671:GLU:OE1	1:D:3671:GLU:N	2.46	0.44
1:D:3869:ILE:HG22	1:D:3869:ILE:O	2.17	0.44
1:A:3595:ARG:O	1:A:3599:GLU:OE1	2.35	0.44
1:B:929:THR:HG23	1:B:930:LEU:CD2	2.46	0.44
1:B:3016:LEU:HD22	1:B:3026:LEU:CD1	2.47	0.44
1:B:3037:LYS:O	1:B:3040:ILE:HG22	2.17	0.44
1:B:3267:MET:O	1:B:3267:MET:HG3	2.17	0.44
1:B:3528:PRO:HG2	1:B:3574:MET:HE2	2.00	0.44
1:B:4653:PHE:N	1:B:4794:MET:HE1	2.31	0.44
1:C:3016:LEU:HD22	1:C:3026:LEU:CD1	2.47	0.44
1:D:218:GLY:N	1:D:263:LEU:O	2.47	0.44
1:D:3410:TYR:N	1:D:3411:PRO:HD2	2.33	0.44
1:D:3528:PRO:HG2	1:D:3574:MET:HE2	2.00	0.44
1:D:3974:GLY:N	1:D:3975:PRO:HA	2.32	0.44
1:A:2096:GLN:HA	1:A:2128:GLN:HE21	1.82	0.44
1:A:3347:VAL:HG11	1:A:3415:ARG:HB2	2.00	0.44
1:A:3515:LEU:HD21	1:A:3603:VAL:HG13	2.00	0.44
1:B:2215:VAL:HG11	1:B:2229:MET:HG2	1.99	0.44
1:D:711:ASP:OD1	1:D:711:ASP:N	2.51	0.44
1:A:2234:CYS:C	1:A:2238:CYS:CB	2.91	0.44
2:H:91:ILE:HD11	1:D:1685:ALA:HA	2.00	0.44
1:B:2482:LYS:HD2	1:B:2483:ASP:H	1.81	0.44
1:B:2875:MET:SD	1:B:2940:ARG:HB2	2.58	0.44
1:C:1810:ARG:NE	1:C:1855:VAL:O	2.50	0.44
1:D:2940:ARG:HB3	1:D:2942:LEU:HD12	2.00	0.44
1:D:2971:SER:O	1:D:2975:ILE:HG12	2.18	0.44
1:D:3202:MET:HE3	1:D:3204:VAL:HG12	2.00	0.44
1:A:673:ALA:O	1:A:681:THR:OG1	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:731:VAL:HG21	1:B:765:VAL:HG12	2.00	0.43
1:B:1659:ASP:OD1	1:B:1659:ASP:N	2.49	0.43
1:B:2265:GLY:HA2	1:B:2268:MET:HE3	2.00	0.43
1:B:3202:MET:HE3	1:B:3204:VAL:HG12	2.00	0.43
1:B:3347:VAL:HG11	1:B:3415:ARG:HB2	2.00	0.43
1:B:4044:ALA:O	1:B:4048:VAL:HG23	2.17	0.43
1:C:1871:GLU:O	1:C:1874:ARG:HD2	2.18	0.43
1:A:225:HIS:NE2	1:A:386:ASP:O	2.52	0.43
1:A:862:ILE:O	1:A:862:ILE:HG22	2.17	0.43
1:A:929:THR:HG23	1:A:930:LEU:CD2	2.46	0.43
1:A:2690:LYS:O	1:A:2994:GLN:NE2	2.51	0.43
1:B:1871:GLU:O	1:B:1874:ARG:HD2	2.18	0.43
1:B:3515:LEU:O	1:B:3516:LYS:C	2.61	0.43
1:C:731:VAL:HG21	1:C:765:VAL:HG12	2.00	0.43
1:C:929:THR:HG23	1:C:930:LEU:CD2	2.46	0.43
1:D:225:HIS:NE2	1:D:386:ASP:O	2.52	0.43
1:D:888:ILE:CD1	1:D:893:THR:HG22	2.48	0.43
1:A:1300:GLN:OE1	1:A:1546:ASN:ND2	2.48	0.43
1:A:3004:LEU:HB2	1:A:3005:PRO:HD3	2.01	0.43
1:B:263:LEU:HD12	1:B:275:LEU:HD11	2.00	0.43
1:B:1067:GLN:OE1	1:B:1069:ARG:NH2	2.51	0.43
1:B:3004:LEU:HB2	1:B:3005:PRO:HD3	2.01	0.43
1:C:1095:ALA:HB1	1:C:1101:MET:HE1	1.98	0.43
1:C:2265:GLY:HA2	1:C:2268:MET:HE3	2.00	0.43
1:C:3202:MET:HE3	1:C:3204:VAL:HG12	2.00	0.43
1:C:3347:VAL:HG11	1:C:3415:ARG:HB2	2.00	0.43
1:C:3553:PHE:O	1:C:3556:ASN:OD1	2.37	0.43
1:D:263:LEU:HD12	1:D:275:LEU:HD11	2.00	0.43
1:D:1067:GLN:OE1	1:D:1069:ARG:NH2	2.51	0.43
1:D:1973:ASN:HD21	1:D:2025:PRO:HD3	1.84	0.43
1:D:3553:PHE:O	1:D:3556:ASN:OD1	2.37	0.43
1:B:711:ASP:N	1:B:711:ASP:OD1	2.51	0.43
1:B:3398:GLU:O	1:B:3401:VAL:HG12	2.17	0.43
1:B:3591:GLU:HA	1:B:3594:VAL:HG22	2.00	0.43
1:C:711:ASP:OD1	1:C:711:ASP:N	2.51	0.43
1:C:1067:GLN:OE1	1:C:1069:ARG:NH2	2.51	0.43
1:C:1793:ALA:C	1:C:1794:THR:HG1	2.17	0.43
1:C:3110:ASN:O	1:C:3113:LEU:HD12	2.18	0.43
1:C:3874:GLY:O	1:C:3875:GLU:C	2.62	0.43
1:D:3347:VAL:HG11	1:D:3415:ARG:HB2	2.00	0.43
1:D:3591:GLU:HA	1:D:3594:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4632:GLU:OE1	1:D:4632:GLU:HA	2.19	0.43
1:A:2124:LEU:O	1:A:2128:GLN:HG2	2.18	0.43
1:A:3410:TYR:N	1:A:3411:PRO:HD2	2.33	0.43
1:A:3528:PRO:HG2	1:A:3574:MET:HE2	2.00	0.43
1:A:3591:GLU:HA	1:A:3594:VAL:HG22	2.00	0.43
1:A:3869:ILE:O	1:A:3869:ILE:HG22	2.18	0.43
1:B:704:GLY:N	1:B:1648:CYS:SG	2.91	0.43
1:B:3410:TYR:N	1:B:3411:PRO:HD2	2.33	0.43
1:C:2124:LEU:O	1:C:2128:GLN:HG2	2.19	0.43
1:C:2940:ARG:HE	1:C:2942:LEU:HG	1.84	0.43
1:C:3458:ASN:O	1:C:3459:PHE:C	2.62	0.43
1:C:4679:LEU:HD11	1:C:4704:LEU:HD22	2.01	0.43
1:D:1871:GLU:O	1:D:1874:ARG:HD2	2.18	0.43
1:D:2940:ARG:HE	1:D:2942:LEU:HG	1.84	0.43
1:D:3110:ASN:O	1:D:3113:LEU:HD12	2.18	0.43
1:D:4679:LEU:HD11	1:D:4704:LEU:HD22	2.01	0.43
1:A:294:LEU:HD13	1:A:379:LEU:HD12	2.01	0.43
1:A:1067:GLN:OE1	1:A:1069:ARG:NH2	2.51	0.43
1:A:3874:GLY:O	1:A:3875:GLU:C	2.62	0.43
1:B:490:ASN:O	1:B:494:ARG:HG2	2.19	0.43
1:B:2940:ARG:HB3	1:B:2942:LEU:HD12	2.00	0.43
1:B:2940:ARG:HE	1:B:2942:LEU:HG	1.84	0.43
1:B:4632:GLU:OE1	1:B:4632:GLU:HA	2.18	0.43
1:C:490:ASN:O	1:C:494:ARG:HG2	2.19	0.43
1:C:2875:MET:SD	1:C:2940:ARG:HB2	2.58	0.43
1:C:3004:LEU:HB2	1:C:3005:PRO:HD3	2.01	0.43
1:C:3671:GLU:OE1	1:C:3671:GLU:N	2.46	0.43
1:C:4835:LEU:CD2	1:C:4934:ILE:HD11	2.49	0.43
1:D:704:GLY:N	1:D:1648:CYS:SG	2.91	0.43
1:D:1659:ASP:OD1	1:D:1659:ASP:N	2.49	0.43
1:D:2875:MET:SD	1:D:2940:ARG:HB2	2.58	0.43
1:D:3377:GLU:OE2	1:D:3451:ASN:ND2	2.52	0.43
1:A:2875:MET:SD	1:A:2940:ARG:HB2	2.58	0.43
1:A:3377:GLU:OE2	1:A:3451:ASN:ND2	2.52	0.43
1:A:3772:ARG:O	1:A:3776:ARG:HD2	2.19	0.43
1:A:4706:THR:HG21	1:A:4773:TYR:HD1	1.83	0.43
1:B:888:ILE:CD1	1:B:893:THR:HG22	2.48	0.43
1:B:3377:GLU:OE2	1:B:3451:ASN:ND2	2.52	0.43
1:B:3752:VAL:HG22	1:B:3753:GLU:N	2.34	0.43
1:C:673:ALA:O	1:C:681:THR:OG1	2.29	0.43
1:C:3515:LEU:O	1:C:3516:LYS:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4765:TRP:O	1:C:4769:ILE:HG13	2.19	0.43
1:D:294:LEU:HD13	1:D:379:LEU:HD12	2.01	0.43
1:A:225:HIS:N	1:A:230:GLU:O	2.48	0.43
1:A:704:GLY:N	1:A:1648:CYS:SG	2.92	0.43
1:A:888:ILE:CD1	1:A:893:THR:HG22	2.48	0.43
1:A:909:VAL:HG12	1:A:910:ASN:N	2.34	0.43
1:A:2891:LYS:O	1:A:2895:LEU:HG	2.19	0.43
1:A:3553:PHE:O	1:A:3556:ASN:OD1	2.37	0.43
1:B:874:LYS:HZ1	1:B:951:LEU:HD11	1.84	0.43
1:B:1973:ASN:HD21	1:B:2025:PRO:HD3	1.84	0.43
1:B:2124:LEU:O	1:B:2128:GLN:HG2	2.18	0.43
1:B:3869:ILE:O	1:B:3869:ILE:HG22	2.18	0.43
1:C:704:GLY:N	1:C:1648:CYS:SG	2.92	0.43
1:C:903:ARG:HH11	1:C:903:ARG:C	2.27	0.43
1:D:3546:THR:HG23	1:D:3549:GLU:H	1.84	0.43
1:D:3589:ASP:OD2	1:D:3591:GLU:HG3	2.19	0.43
1:D:3962:LYS:HG3	1:D:4025:ASP:OD1	2.19	0.43
1:D:4835:LEU:CD2	1:D:4934:ILE:HD11	2.49	0.43
1:A:903:ARG:HH11	1:A:903:ARG:C	2.27	0.43
1:A:2922:GLU:O	1:A:2926:GLU:HG2	2.18	0.43
1:A:4226:ASN:ND2	1:A:4227:GLU:OE1	2.46	0.43
1:A:4632:GLU:OE1	1:A:4632:GLU:HA	2.19	0.43
2:F:91:ILE:HD11	1:B:1685:ALA:HA	2.00	0.43
1:B:903:ARG:C	1:B:903:ARG:HH11	2.27	0.43
1:B:909:VAL:HG12	1:B:910:ASN:N	2.34	0.43
1:B:2891:LYS:O	1:B:2895:LEU:HG	2.19	0.43
1:B:2981:VAL:O	1:B:2986:ARG:NH2	2.51	0.43
1:B:3772:ARG:O	1:B:3776:ARG:HD2	2.19	0.43
1:B:3962:LYS:HG3	1:B:4025:ASP:OD1	2.19	0.43
1:C:284:ARG:NH1	1:C:291:TYR:OH	2.52	0.43
1:C:2887:TRP:CD1	1:C:2891:LYS:HZ1	2.37	0.43
1:C:2891:LYS:O	1:C:2895:LEU:HG	2.19	0.43
1:C:3377:GLU:OE2	1:C:3451:ASN:ND2	2.52	0.43
1:C:3410:TYR:N	1:C:3411:PRO:HD2	2.33	0.43
1:D:490:ASN:O	1:D:494:ARG:HG2	2.19	0.43
1:D:2124:LEU:O	1:D:2128:GLN:HG2	2.18	0.43
1:D:2751:LYS:O	1:D:2936:TYR:OH	2.26	0.43
1:D:3874:GLY:O	1:D:3875:GLU:C	2.62	0.43
1:A:263:LEU:HD12	1:A:275:LEU:HD11	2.00	0.43
1:A:2265:GLY:HA2	1:A:2268:MET:HE3	2.00	0.43
1:A:3546:THR:HG23	1:A:3549:GLU:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3589:ASP:OD2	1:A:3591:GLU:HG3	2.19	0.43
1:B:979:THR:O	1:B:983:THR:HG23	2.19	0.43
1:B:3684:GLN:OE1	1:B:3684:GLN:N	2.45	0.43
1:B:4835:LEU:CD2	1:B:4934:ILE:HD11	2.49	0.43
1:C:1499:GLY:HA2	1:C:1502:VAL:HG12	2.01	0.43
1:C:3515:LEU:HD21	1:C:3603:VAL:HG13	2.00	0.43
1:C:4632:GLU:OE1	1:C:4632:GLU:HA	2.18	0.43
1:C:4816:MET:O	1:C:4822:ARG:NH1	2.51	0.43
1:D:862:ILE:O	1:D:862:ILE:HG22	2.17	0.43
1:D:2265:GLY:HA2	1:D:2268:MET:HE3	2.01	0.43
1:D:2891:LYS:O	1:D:2895:LEU:HG	2.19	0.43
1:D:3004:LEU:HB2	1:D:3005:PRO:HD3	2.01	0.43
1:D:3772:ARG:O	1:D:3776:ARG:HD2	2.19	0.43
1:A:4024:LYS:N	1:A:4142:ILE:HD13	2.34	0.42
1:A:4765:TRP:O	1:A:4769:ILE:HG13	2.19	0.42
1:B:2978:LEU:HD22	1:B:3057:LEU:CD2	2.49	0.42
1:B:3515:LEU:O	1:B:3518:MET:N	2.52	0.42
1:B:4679:LEU:HD11	1:B:4704:LEU:HD22	2.01	0.42
1:C:2748:ILE:HD12	1:C:2818:ILE:HD11	2.01	0.42
1:C:2940:ARG:HB3	1:C:2942:LEU:HD12	2.00	0.42
1:C:4024:LYS:N	1:C:4142:ILE:HD13	2.34	0.42
1:C:4706:THR:HG21	1:C:4773:TYR:HD1	1.83	0.42
1:C:4975:THR:HA	1:C:4978:LEU:HD12	2.01	0.42
1:D:903:ARG:HH11	1:D:903:ARG:C	2.27	0.42
1:D:1964:GLU:HA	1:D:3651:CYS:SG	2.59	0.42
1:D:3167:TYR:OH	1:D:3204:VAL:HG11	2.19	0.42
1:D:3458:ASN:O	1:D:3459:PHE:C	2.62	0.42
1:A:979:THR:O	1:A:983:THR:HG23	2.19	0.42
1:A:1695:LEU:HB3	1:A:1716:LEU:HD12	2.01	0.42
1:A:1964:GLU:HA	1:A:3651:CYS:SG	2.60	0.42
1:A:4679:LEU:HD11	1:A:4704:LEU:HD22	2.01	0.42
2:H:91:ILE:N	2:H:91:ILE:HD12	2.34	0.42
1:B:2887:TRP:CD1	1:B:2891:LYS:HZ1	2.37	0.42
1:B:3458:ASN:O	1:B:3459:PHE:C	2.62	0.42
1:B:3515:LEU:HD21	1:B:3603:VAL:HG13	2.00	0.42
1:B:3589:ASP:OD2	1:B:3591:GLU:HG3	2.19	0.42
1:B:4024:LYS:N	1:B:4142:ILE:HD13	2.34	0.42
1:B:4700:ASP:C	1:B:4702:LEU:H	2.27	0.42
1:B:4706:THR:HG21	1:B:4773:TYR:HD1	1.83	0.42
1:D:1499:GLY:HA2	1:D:1502:VAL:HG12	2.01	0.42
1:D:1793:ALA:C	1:D:1794:THR:HG1	2.15	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2483:ASP:O	1:D:2483:ASP:OD2	2.37	0.42
1:D:3515:LEU:O	1:D:3516:LYS:C	2.61	0.42
1:A:3515:LEU:O	1:A:3516:LYS:C	2.61	0.42
1:A:4700:ASP:C	1:A:4702:LEU:H	2.27	0.42
1:B:3553:PHE:O	1:B:3556:ASN:OD1	2.37	0.42
1:B:4226:ASN:ND2	1:B:4227:GLU:OE1	2.47	0.42
1:C:888:ILE:HG12	1:C:960:TYR:HA	2.01	0.42
1:C:2978:LEU:HD22	1:C:3057:LEU:CD2	2.50	0.42
1:C:4706:THR:HG23	1:C:4708:SER:H	1.84	0.42
1:C:4902:PRO:O	1:C:4903:ALA:C	2.63	0.42
1:D:225:HIS:N	1:D:230:GLU:O	2.48	0.42
1:D:4765:TRP:O	1:D:4769:ILE:HG13	2.19	0.42
1:A:249:GLU:OE1	1:A:374:LYS:NZ	2.47	0.42
1:A:782:VAL:HG13	1:A:782:VAL:O	2.20	0.42
1:A:888:ILE:HG12	1:A:960:TYR:HA	2.01	0.42
1:A:2887:TRP:CD1	1:A:2891:LYS:HZ1	2.37	0.42
1:A:4835:LEU:CD2	1:A:4934:ILE:HD11	2.49	0.42
1:B:2523:LEU:HD11	1:B:2563:ILE:HD13	2.02	0.42
1:B:4706:THR:HG23	1:B:4708:SER:H	1.84	0.42
1:C:927:GLY:O	1:C:931:LYS:HG3	2.20	0.42
1:C:979:THR:O	1:C:983:THR:HG23	2.19	0.42
1:C:3167:TYR:OH	1:C:3204:VAL:HG11	2.19	0.42
1:C:3591:GLU:HA	1:C:3594:VAL:HG22	2.00	0.42
1:D:4900:GLU:O	1:D:4911:ARG:NH2	2.44	0.42
1:A:490:ASN:O	1:A:494:ARG:HG2	2.19	0.42
1:A:731:VAL:HG21	1:A:765:VAL:HG12	2.00	0.42
1:A:1788:LEU:HD21	2:E:88:HIS:CD2	2.54	0.42
1:B:2136:LEU:HD21	1:B:3664:LEU:HD13	2.02	0.42
1:B:3316:LEU:HD23	1:B:3346:ILE:HD13	2.01	0.42
1:C:263:LEU:HD12	1:C:275:LEU:HD11	2.00	0.42
1:C:909:VAL:HG12	1:C:910:ASN:N	2.34	0.42
1:C:2002:PRO:HG2	1:C:3865:ASP:HB2	2.02	0.42
1:C:2523:LEU:HD11	1:C:2563:ILE:HD13	2.02	0.42
1:C:3546:THR:HG23	1:C:3549:GLU:H	1.84	0.42
1:C:4079:ALA:O	1:C:4082:ASP:HB2	2.19	0.42
1:D:3316:LEU:HD23	1:D:3346:ILE:HD13	2.01	0.42
1:A:215:VAL:HG12	1:A:275:LEU:HD12	2.02	0.42
1:A:2483:ASP:O	1:A:2483:ASP:OD2	2.37	0.42
1:A:3962:LYS:HG3	1:A:4025:ASP:OD1	2.19	0.42
1:A:4575:LEU:O	1:A:4578:TYR:HB2	2.20	0.42
1:B:225:HIS:N	1:B:230:GLU:O	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2756:ILE:HG13	1:B:2814:LEU:CD1	2.49	0.42
1:B:2982:VAL:O	1:B:2986:ARG:NH2	2.53	0.42
1:B:4765:TRP:O	1:B:4769:ILE:HG13	2.19	0.42
1:C:554:ARG:NH2	1:C:556:GLU:OE2	2.49	0.42
1:C:888:ILE:CD1	1:C:893:THR:HG22	2.48	0.42
1:C:1964:GLU:HA	1:C:3651:CYS:SG	2.59	0.42
1:C:2600:GLN:O	1:C:2604:ILE:HG13	2.20	0.42
1:C:2690:LYS:O	1:C:2994:GLN:NE2	2.51	0.42
1:D:215:VAL:HG12	1:D:275:LEU:HD12	2.02	0.42
1:D:4700:ASP:C	1:D:4702:LEU:H	2.27	0.42
1:A:1973:ASN:HD21	1:A:2025:PRO:HD3	1.84	0.42
1:A:1978:TYR:HB2	1:A:1999:PHE:CE1	2.55	0.42
1:A:3458:ASN:O	1:A:3459:PHE:C	2.62	0.42
1:A:3752:VAL:HG22	1:A:3753:GLU:N	2.34	0.42
1:B:294:LEU:HD13	1:B:379:LEU:HD12	2.01	0.42
1:B:2748:ILE:HD12	1:B:2818:ILE:HD11	2.01	0.42
1:B:3110:ASN:O	1:B:3113:LEU:HD12	2.18	0.42
1:C:4900:GLU:O	1:C:4911:ARG:NH2	2.44	0.42
1:D:731:VAL:HG21	1:D:765:VAL:HG12	2.00	0.42
1:D:2002:PRO:HG2	1:D:3865:ASP:HB2	2.02	0.42
1:D:2887:TRP:CD1	1:D:2891:LYS:HZ1	2.37	0.42
1:D:3515:LEU:O	1:D:3518:MET:N	2.52	0.42
1:D:4024:LYS:N	1:D:4142:ILE:HD13	2.34	0.42
1:A:576:LEU:CD2	1:A:607:LEU:HD23	2.50	0.42
1:A:3257:LEU:HB3	1:A:3267:MET:HE1	2.02	0.42
1:A:3353:GLU:OE1	1:A:3353:GLU:N	2.44	0.42
1:A:4741:MET:HE2	1:A:4746:LEU:HD11	2.02	0.42
1:B:284:ARG:NH1	1:B:291:TYR:OH	2.52	0.42
1:C:294:LEU:HD13	1:C:379:LEU:HD12	2.01	0.42
1:C:1102:ARG:HG2	1:C:1126:ASN:HB2	2.01	0.42
1:C:1973:ASN:HD21	1:C:2025:PRO:HD3	1.84	0.42
1:C:2981:VAL:O	1:C:2986:ARG:NH2	2.51	0.42
1:C:3515:LEU:O	1:C:3518:MET:N	2.52	0.42
1:C:3772:ARG:O	1:C:3776:ARG:HD2	2.19	0.42
1:D:576:LEU:CD2	1:D:607:LEU:HD23	2.50	0.42
1:D:888:ILE:HG12	1:D:960:TYR:HA	2.02	0.42
1:D:1064:VAL:HG23	1:D:1065:ASP:N	2.35	0.42
1:D:4720:ARG:HE	1:D:4720:ARG:HB3	1.61	0.42
1:A:2136:LEU:HD21	1:A:3664:LEU:HD13	2.02	0.42
1:A:2940:ARG:HE	1:A:2942:LEU:HG	1.84	0.42
1:A:3316:LEU:HD23	1:A:3346:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3515:LEU:O	1:A:3518:MET:N	2.52	0.42
2:H:88:HIS:CD2	1:D:1788:LEU:HD21	2.55	0.42
1:B:576:LEU:CD2	1:B:607:LEU:HD23	2.50	0.42
1:B:3057:LEU:O	1:B:3057:LEU:HD23	2.20	0.42
1:B:4987:MET:O	1:B:4991:MET:HG3	2.19	0.42
1:C:3076:LEU:HD23	1:C:3077:ASP:N	2.35	0.42
1:C:3257:LEU:HB3	1:C:3267:MET:HE1	2.02	0.42
1:D:782:VAL:HG13	1:D:782:VAL:O	2.20	0.42
1:D:2600:GLN:O	1:D:2604:ILE:HG13	2.20	0.42
1:D:2982:VAL:O	1:D:2986:ARG:NH2	2.53	0.42
1:D:4707:PRO:HD2	1:D:4770:ASP:CG	2.45	0.42
1:D:4902:PRO:O	1:D:4903:ALA:C	2.62	0.42
1:A:1064:VAL:HG23	1:A:1065:ASP:N	2.35	0.42
1:A:1499:GLY:HA2	1:A:1502:VAL:HG12	2.01	0.42
1:A:1576:LEU:HD23	1:A:1576:LEU:HA	1.93	0.42
1:A:2748:ILE:HD12	1:A:2818:ILE:HD11	2.01	0.42
1:A:3076:LEU:HD23	1:A:3077:ASP:N	2.35	0.42
1:A:3987:ARG:NH2	1:B:161:GLY:O	2.53	0.42
1:A:4706:THR:HG23	1:A:4708:SER:H	1.85	0.42
1:B:575:VAL:O	1:B:579:ILE:HG12	2.20	0.42
1:B:1964:GLU:HA	1:B:3651:CYS:SG	2.59	0.42
1:B:4079:ALA:O	1:B:4082:ASP:HB2	2.19	0.42
1:B:4741:MET:HE2	1:B:4746:LEU:HD11	2.02	0.42
1:B:4902:PRO:O	1:B:4903:ALA:C	2.62	0.42
1:C:575:VAL:O	1:C:579:ILE:HG12	2.20	0.42
1:C:2136:LEU:HD21	1:C:3664:LEU:HD13	2.02	0.42
1:C:3589:ASP:OD2	1:C:3591:GLU:HG3	2.19	0.42
1:C:3752:VAL:HG22	1:C:3753:GLU:N	2.34	0.42
1:C:4575:LEU:O	1:C:4578:TYR:HB2	2.20	0.42
1:D:284:ARG:NH1	1:D:291:TYR:OH	2.52	0.42
1:D:760:ILE:O	1:D:760:ILE:HG23	2.20	0.42
1:D:927:GLY:O	1:D:931:LYS:HG3	2.20	0.42
1:D:1978:TYR:HB2	1:D:1999:PHE:CE1	2.55	0.42
1:D:2136:LEU:HD21	1:D:3664:LEU:HD13	2.02	0.42
1:D:2981:VAL:O	1:D:2986:ARG:NH2	2.51	0.42
1:D:4706:THR:HG21	1:D:4773:TYR:HD1	1.83	0.42
1:D:4975:THR:HA	1:D:4978:LEU:HD12	2.01	0.42
1:D:4987:MET:O	1:D:4991:MET:HG3	2.19	0.42
1:A:760:ILE:HG23	1:A:760:ILE:O	2.20	0.41
1:A:927:GLY:O	1:A:931:LYS:HG3	2.20	0.41
1:A:2756:ILE:HG13	1:A:2814:LEU:CD1	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3110:ASN:O	1:A:3113:LEU:HD12	2.19	0.41
1:A:3167:TYR:OH	1:A:3204:VAL:HG11	2.19	0.41
1:A:4707:PRO:HD2	1:A:4770:ASP:CG	2.45	0.41
1:B:1499:GLY:HA2	1:B:1502:VAL:HG12	2.02	0.41
1:B:4707:PRO:HD2	1:B:4770:ASP:CG	2.45	0.41
1:C:753:VAL:HB	1:C:754:PRO:C	2.45	0.41
1:C:1064:VAL:HG23	1:C:1065:ASP:N	2.35	0.41
1:C:2756:ILE:HG13	1:C:2814:LEU:CD1	2.49	0.41
1:C:3962:LYS:HG3	1:C:4025:ASP:OD1	2.19	0.41
1:D:2413:GLU:HG3	1:D:2413:GLU:O	2.20	0.41
1:D:3638:ARG:HH11	1:D:3640:THR:HG22	1.85	0.41
1:A:79:LEU:O	1:A:80:GLN:C	2.62	0.41
1:A:711:ASP:N	1:A:711:ASP:OD1	2.51	0.41
1:A:3638:ARG:HH11	1:A:3640:THR:HG22	1.85	0.41
1:A:3684:GLN:OE1	1:A:3684:GLN:N	2.45	0.41
1:B:753:VAL:HB	1:B:754:PRO:C	2.45	0.41
1:B:782:VAL:O	1:B:782:VAL:HG13	2.20	0.41
1:B:3546:THR:HG23	1:B:3549:GLU:H	1.84	0.41
1:B:3987:ARG:NH2	1:C:161:GLY:O	2.53	0.41
1:B:4975:THR:HA	1:B:4978:LEU:HD12	2.01	0.41
1:C:576:LEU:CD2	1:C:607:LEU:HD23	2.50	0.41
1:C:3987:ARG:NH2	1:D:161:GLY:O	2.53	0.41
1:C:4987:MET:O	1:C:4991:MET:HG3	2.19	0.41
1:D:914:LEU:O	1:D:915:PRO:C	2.63	0.41
1:D:979:THR:O	1:D:983:THR:HG23	2.19	0.41
1:D:1102:ARG:HG2	1:D:1126:ASN:HB2	2.01	0.41
1:D:2748:ILE:HD12	1:D:2818:ILE:HD11	2.01	0.41
1:D:3076:LEU:HD23	1:D:3077:ASP:N	2.35	0.41
1:A:2600:GLN:O	1:A:2604:ILE:HG13	2.20	0.41
1:A:2982:VAL:O	1:A:2986:ARG:NH2	2.53	0.41
1:A:4079:ALA:O	1:A:4082:ASP:HB2	2.19	0.41
1:A:4902:PRO:O	1:A:4903:ALA:C	2.62	0.41
1:B:79:LEU:O	1:B:80:GLN:C	2.62	0.41
1:B:221:LEU:C	1:B:221:LEU:HD12	2.45	0.41
1:B:903:ARG:HH22	1:B:908:LEU:HD12	1.86	0.41
1:B:1695:LEU:HB3	1:B:1716:LEU:HD12	2.01	0.41
1:B:1978:TYR:HB2	1:B:1999:PHE:CE1	2.55	0.41
1:B:4575:LEU:O	1:B:4578:TYR:HB2	2.20	0.41
1:B:4886:TYR:OH	1:C:4915:ASP:OD2	2.34	0.41
1:C:79:LEU:O	1:C:80:GLN:C	2.62	0.41
1:C:215:VAL:HG12	1:C:275:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3181:ASN:OD1	1:C:3182:PRO:HD2	2.21	0.41
1:D:627:LEU:N	1:D:628:PRO:HD2	2.36	0.41
1:D:2771:LYS:HE3	1:D:2789:HIS:CG	2.55	0.41
1:A:2002:PRO:HG2	1:A:3865:ASP:HB2	2.02	0.41
1:A:2748:ILE:HG23	1:A:2748:ILE:O	2.20	0.41
1:A:2964:LEU:O	1:A:2968:MET:HG2	2.20	0.41
1:A:3181:ASN:OD1	1:A:3182:PRO:HD2	2.21	0.41
1:A:4975:THR:HA	1:A:4978:LEU:HD12	2.01	0.41
1:A:4987:MET:O	1:A:4991:MET:HG3	2.19	0.41
2:F:88:HIS:CD2	1:B:1788:LEU:HD21	2.55	0.41
2:F:91:ILE:HD12	2:F:91:ILE:N	2.34	0.41
1:B:218:GLY:N	1:B:263:LEU:O	2.47	0.41
1:B:927:GLY:O	1:B:931:LYS:HG3	2.20	0.41
1:B:1064:VAL:HG23	1:B:1065:ASP:N	2.35	0.41
1:B:2002:PRO:HG2	1:B:3865:ASP:HB2	2.02	0.41
1:B:2964:LEU:O	1:B:2968:MET:HG2	2.20	0.41
1:B:3167:TYR:OH	1:B:3204:VAL:HG11	2.19	0.41
1:C:1978:TYR:HB2	1:C:1999:PHE:CE1	2.55	0.41
1:C:3057:LEU:O	1:C:3057:LEU:HD23	2.20	0.41
1:C:3316:LEU:HD23	1:C:3346:ILE:HD13	2.01	0.41
1:C:4707:PRO:HD2	1:C:4770:ASP:CG	2.45	0.41
1:D:267:ARG:NH2	1:D:332:VAL:O	2.49	0.41
1:D:909:VAL:HG12	1:D:910:ASN:N	2.34	0.41
1:A:221:LEU:C	1:A:221:LEU:HD12	2.45	0.41
1:A:267:ARG:NH2	1:A:332:VAL:O	2.49	0.41
1:A:753:VAL:HB	1:A:754:PRO:C	2.45	0.41
2:G:91:ILE:HD12	2:G:91:ILE:N	2.35	0.41
1:B:1229:ILE:HG23	1:B:1230:ASN:H	1.85	0.41
1:B:2600:GLN:O	1:B:2604:ILE:HG13	2.20	0.41
1:B:2748:ILE:HD12	1:B:2818:ILE:CD1	2.51	0.41
1:B:3257:LEU:HB3	1:B:3267:MET:HE1	2.02	0.41
1:C:2139:LEU:N	1:C:2140:PRO:HD2	2.35	0.41
1:C:2748:ILE:O	1:C:2748:ILE:HG23	2.20	0.41
1:C:2752:LEU:HD21	1:C:2824:VAL:HG11	2.03	0.41
1:D:221:LEU:C	1:D:221:LEU:HD12	2.45	0.41
1:D:892:TRP:HB3	1:D:903:ARG:HE	1.86	0.41
1:D:2748:ILE:O	1:D:2748:ILE:HG23	2.20	0.41
1:D:2752:LEU:HD21	1:D:2824:VAL:HG11	2.03	0.41
1:D:3257:LEU:HB3	1:D:3267:MET:HE1	2.02	0.41
1:D:3526:CYS:SG	1:D:3600:VAL:HG21	2.61	0.41
1:D:4079:ALA:O	1:D:4082:ASP:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4706:THR:HG23	1:D:4708:SER:H	1.84	0.41
1:A:1102:ARG:HG2	1:A:1126:ASN:HB2	2.01	0.41
1:A:4835:LEU:HD11	1:A:4934:ILE:HD11	2.02	0.41
2:G:91:ILE:HD11	1:C:1685:ALA:HA	2.01	0.41
1:B:215:VAL:HG12	1:B:275:LEU:HD12	2.02	0.41
1:B:500:THR:HG23	1:B:503:HIS:H	1.86	0.41
1:B:787:GLY:N	1:B:1631:CYS:O	2.45	0.41
1:B:888:ILE:HG12	1:B:960:TYR:HA	2.01	0.41
1:B:2771:LYS:HB3	1:B:2776:TRP:HB2	2.02	0.41
1:B:2771:LYS:HE3	1:B:2789:HIS:CG	2.56	0.41
1:B:4720:ARG:HE	1:B:4720:ARG:HB3	1.61	0.41
1:C:221:LEU:C	1:C:221:LEU:HD12	2.45	0.41
1:C:627:LEU:N	1:C:628:PRO:HD2	2.35	0.41
1:C:782:VAL:O	1:C:782:VAL:HG13	2.20	0.41
1:C:892:TRP:HB3	1:C:903:ARG:HE	1.85	0.41
1:C:2873:GLN:O	1:C:2877:GLU:HG2	2.21	0.41
1:C:2982:VAL:O	1:C:2986:ARG:NH2	2.53	0.41
1:D:1229:ILE:HG23	1:D:1230:ASN:H	1.85	0.41
1:D:1300:GLN:OE1	1:D:1546:ASN:ND2	2.48	0.41
1:D:2756:ILE:HG13	1:D:2814:LEU:CD1	2.49	0.41
1:A:2523:LEU:HD11	1:A:2563:ILE:HD13	2.02	0.41
1:A:2771:LYS:HE3	1:A:2789:HIS:CG	2.55	0.41
2:E:91:ILE:N	2:E:91:ILE:HD12	2.36	0.41
1:B:141:ASP:OD1	1:B:141:ASP:N	2.53	0.41
1:B:2634:LEU:HD12	1:B:2686:SER:CB	2.51	0.41
1:B:2817:MET:HB2	1:B:2822:TRP:HB2	2.03	0.41
1:B:4835:LEU:HD11	1:B:4934:ILE:HD11	2.02	0.41
1:C:1695:LEU:HB3	1:C:1716:LEU:HD12	2.01	0.41
1:C:3526:CYS:SG	1:C:3600:VAL:HG21	2.61	0.41
1:D:249:GLU:OE1	1:D:374:LYS:NZ	2.47	0.41
1:D:753:VAL:HB	1:D:754:PRO:C	2.45	0.41
1:D:2964:LEU:O	1:D:2968:MET:HG2	2.20	0.41
1:D:3181:ASN:OD1	1:D:3182:PRO:HD2	2.21	0.41
1:D:4763:LEU:HD12	1:D:4764:THR:N	2.36	0.41
1:A:500:THR:HG23	1:A:503:HIS:H	1.85	0.41
1:A:892:TRP:HB3	1:A:903:ARG:HE	1.86	0.41
1:A:914:LEU:O	1:A:915:PRO:C	2.63	0.41
1:B:554:ARG:NH2	1:B:556:GLU:OE2	2.48	0.41
1:B:627:LEU:N	1:B:628:PRO:HD2	2.35	0.41
1:B:1793:ALA:C	1:B:1794:THR:HG1	2.18	0.41
1:B:2139:LEU:N	1:B:2140:PRO:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2413:GLU:O	1:B:2413:GLU:HG3	2.20	0.41
1:B:2483:ASP:O	1:B:2483:ASP:OD2	2.37	0.41
1:B:3076:LEU:HD23	1:B:3077:ASP:N	2.35	0.41
1:C:2483:ASP:O	1:C:2483:ASP:OD2	2.37	0.41
1:C:2748:ILE:HD12	1:C:2818:ILE:CD1	2.51	0.41
1:C:2964:LEU:O	1:C:2968:MET:HG2	2.20	0.41
1:C:3638:ARG:HH11	1:C:3640:THR:HG22	1.85	0.41
1:C:4835:LEU:HD11	1:C:4934:ILE:HD11	2.02	0.41
1:D:500:THR:HG23	1:D:503:HIS:H	1.85	0.41
1:D:2523:LEU:HD11	1:D:2563:ILE:HD13	2.02	0.41
1:D:2690:LYS:O	1:D:2994:GLN:NE2	2.51	0.41
1:D:2771:LYS:HB3	1:D:2776:TRP:HB2	2.02	0.41
1:D:3413:LEU:HD11	1:D:3435:LEU:HD21	2.03	0.41
1:D:3752:VAL:HG22	1:D:3753:GLU:N	2.34	0.41
1:D:4221:ILE:HD13	1:D:4952:MET:HE2	2.03	0.41
1:D:4741:MET:HE2	1:D:4746:LEU:HD11	2.02	0.41
1:A:909:VAL:O	1:A:910:ASN:C	2.64	0.41
1:A:2413:GLU:HG3	1:A:2413:GLU:O	2.20	0.41
1:A:2634:LEU:HD12	1:A:2686:SER:CB	2.51	0.41
1:A:2752:LEU:HD21	1:A:2824:VAL:HG11	2.03	0.41
1:A:3057:LEU:HD23	1:A:3057:LEU:O	2.20	0.41
1:A:3078:ALA:HB3	1:A:3157:VAL:HG21	2.03	0.41
1:A:3294:PRO:HB2	1:A:3298:PRO:HD3	2.03	0.41
1:A:3526:CYS:SG	1:A:3600:VAL:HG21	2.61	0.41
1:A:3771:SER:HA	1:A:3774:HIS:CD2	2.56	0.41
2:F:101:ASP:OD1	2:F:101:ASP:C	2.64	0.41
1:B:225:HIS:NE2	1:B:386:ASP:O	2.51	0.41
1:B:843:PRO:O	1:B:1197:PRO:HA	2.21	0.41
1:B:910:ASN:O	1:B:914:LEU:N	2.54	0.41
1:B:1102:ARG:HG2	1:B:1126:ASN:HB2	2.01	0.41
1:B:2000:ARG:HH11	1:B:2000:ARG:HG3	1.86	0.41
1:B:2748:ILE:HG23	1:B:2748:ILE:O	2.20	0.41
1:B:2752:LEU:HD21	1:B:2824:VAL:HG11	2.03	0.41
1:B:3638:ARG:HH11	1:B:3640:THR:HG22	1.85	0.41
1:B:3874:GLY:O	1:B:3875:GLU:C	2.61	0.41
1:C:860:ILE:HG13	1:C:861:GLN:N	2.36	0.41
1:C:1460:GLN:OE1	1:C:1471:ARG:HG2	2.21	0.41
1:C:2000:ARG:HH11	1:C:2000:ARG:HG3	1.86	0.41
1:C:2391:PRO:C	1:C:2393:ARG:H	2.29	0.41
1:C:2391:PRO:O	1:C:2392:ALA:HB3	2.20	0.41
1:C:2634:LEU:HD12	1:C:2686:SER:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4700:ASP:C	1:C:4702:LEU:H	2.27	0.41
1:C:4741:MET:HE2	1:C:4746:LEU:HD11	2.02	0.41
7:C:8006:PCW:H482	7:C:8006:PCW:C44	2.51	0.41
1:D:141:ASP:OD1	1:D:141:ASP:N	2.53	0.41
1:D:575:VAL:O	1:D:579:ILE:HG12	2.20	0.41
1:D:903:ARG:HH22	1:D:908:LEU:HD12	1.85	0.41
1:D:2000:ARG:HG3	1:D:2000:ARG:HH11	1.86	0.41
1:D:2139:LEU:N	1:D:2140:PRO:HD2	2.35	0.41
1:D:2873:GLN:O	1:D:2877:GLU:HG2	2.21	0.41
1:D:2978:LEU:HD22	1:D:3057:LEU:CD2	2.49	0.41
1:D:3057:LEU:HD23	1:D:3057:LEU:O	2.20	0.41
1:D:3771:SER:HA	1:D:3774:HIS:CD2	2.56	0.41
1:D:4575:LEU:O	1:D:4578:TYR:HB2	2.20	0.41
1:D:4835:LEU:HD11	1:D:4934:ILE:HD11	2.02	0.41
7:D:8006:PCW:H482	7:D:8006:PCW:C44	2.51	0.41
1:A:1793:ALA:C	1:A:1794:THR:HG1	2.16	0.41
1:A:2000:ARG:HG3	1:A:2000:ARG:HH11	1.86	0.41
1:A:2224:ILE:HD11	1:A:2268:MET:HE2	2.03	0.41
1:A:4763:LEU:HD12	1:A:4764:THR:N	2.36	0.41
1:B:1576:LEU:HD23	1:B:1576:LEU:HA	1.93	0.41
1:B:2766:LYS:HZ1	1:B:2860:PRO:HB2	1.85	0.41
1:B:2793:ARG:NH1	1:B:2797:THR:O	2.54	0.41
1:B:2873:GLN:O	1:B:2877:GLU:HG2	2.21	0.41
1:B:3861:MET:HE1	1:B:3870:ASN:HA	2.04	0.41
1:B:4730:PHE:HD2	1:B:4735:ILE:HG12	1.85	0.41
1:C:225:HIS:NE2	1:C:386:ASP:O	2.52	0.41
1:C:2413:GLU:HG3	1:C:2413:GLU:O	2.20	0.41
1:C:3815:VAL:O	1:C:3819:MET:HG3	2.21	0.41
1:D:2634:LEU:HD12	1:D:2686:SER:CB	2.51	0.41
1:D:3534:ILE:HD12	1:D:3534:ILE:H	1.86	0.41
1:D:3820:LEU:CD2	1:D:3901:ASP:HB3	2.51	0.41
1:D:4217:LYS:NZ	5:D:8003:ATP:O1A	2.53	0.41
1:A:1481:GLN:OE1	1:A:1481:GLN:N	2.52	0.40
1:A:2771:LYS:HB3	1:A:2776:TRP:HB2	2.02	0.40
1:A:2981:VAL:O	1:A:2986:ARG:NH2	2.51	0.40
1:A:3413:LEU:HD11	1:A:3435:LEU:HD21	2.03	0.40
1:A:3820:LEU:CD2	1:A:3901:ASP:HB3	2.51	0.40
1:B:914:LEU:O	1:B:915:PRO:C	2.63	0.40
1:B:3294:PRO:HB2	1:B:3298:PRO:HD3	2.03	0.40
1:B:3526:CYS:SG	1:B:3600:VAL:HG21	2.61	0.40
1:C:843:PRO:O	1:C:1197:PRO:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:893:THR:O	1:C:903:ARG:CZ	2.69	0.40
1:C:903:ARG:HH22	1:C:908:LEU:HD12	1.86	0.40
1:C:2432:ASP:OD2	1:C:2436:ARG:NE	2.44	0.40
1:C:4221:ILE:HD13	1:C:4952:MET:HE2	2.03	0.40
1:C:4730:PHE:HD2	1:C:4735:ILE:HG12	1.85	0.40
1:D:1460:GLN:OE1	1:D:1471:ARG:HG2	2.21	0.40
1:A:332:VAL:HG22	1:A:333:GLU:N	2.36	0.40
1:A:627:LEU:N	1:A:628:PRO:HD2	2.35	0.40
1:A:1028:LEU:HD21	1:A:1032:THR:CG2	2.52	0.40
1:A:1229:ILE:HG23	1:A:1230:ASN:H	1.85	0.40
1:A:1460:GLN:OE1	1:A:1471:ARG:HG2	2.21	0.40
1:A:2139:LEU:N	1:A:2140:PRO:HD2	2.35	0.40
1:A:2391:PRO:C	1:A:2393:ARG:H	2.29	0.40
1:A:4221:ILE:HD13	1:A:4952:MET:HE2	2.03	0.40
1:A:4720:ARG:HE	1:A:4720:ARG:HB3	1.61	0.40
1:A:4730:PHE:HD2	1:A:4735:ILE:HG12	1.85	0.40
1:B:332:VAL:HG22	1:B:333:GLU:N	2.36	0.40
1:B:909:VAL:O	1:B:910:ASN:C	2.64	0.40
1:B:2391:PRO:O	1:B:2392:ALA:HB3	2.20	0.40
1:B:3355:LEU:HD22	1:B:3424:TRP:CZ2	2.56	0.40
1:B:3771:SER:HA	1:B:3774:HIS:CD2	2.56	0.40
1:C:2771:LYS:HE3	1:C:2789:HIS:CG	2.56	0.40
1:C:4226:ASN:ND2	1:C:4227:GLU:OE1	2.46	0.40
1:C:4763:LEU:HD12	1:C:4764:THR:N	2.36	0.40
1:D:843:PRO:O	1:D:1197:PRO:HA	2.21	0.40
1:D:1028:LEU:HD21	1:D:1032:THR:CG2	2.52	0.40
1:D:1695:LEU:HB3	1:D:1716:LEU:HD12	2.01	0.40
1:D:2391:PRO:O	1:D:2392:ALA:HB3	2.20	0.40
1:D:3355:LEU:HD22	1:D:3424:TRP:CZ2	2.56	0.40
1:D:3861:MET:HE1	1:D:3870:ASN:HA	2.04	0.40
1:A:665:PHE:CE1	1:A:747:CYS:HB2	2.57	0.40
1:A:843:PRO:O	1:A:1197:PRO:HA	2.21	0.40
1:A:2748:ILE:HD12	1:A:2818:ILE:CD1	2.51	0.40
1:A:2817:MET:HB2	1:A:2822:TRP:HB2	2.03	0.40
1:B:1028:LEU:HD21	1:B:1032:THR:CG2	2.51	0.40
1:B:4086:ASP:OD1	1:B:4088:ARG:NH2	2.49	0.40
1:C:557:ALA:O	1:C:561:ILE:HD12	2.22	0.40
1:C:760:ILE:HG23	1:C:760:ILE:O	2.20	0.40
1:C:1028:LEU:HD21	1:C:1032:THR:CG2	2.52	0.40
1:C:2768:ALA:HA	1:C:2771:LYS:HE2	2.04	0.40
1:C:2771:LYS:HB3	1:C:2776:TRP:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3820:LEU:CD2	1:C:3901:ASP:HB3	2.51	0.40
1:D:79:LEU:O	1:D:80:GLN:C	2.62	0.40
1:D:3406:LEU:HD13	1:D:3511:ILE:HD12	2.04	0.40
1:A:557:ALA:O	1:A:561:ILE:HD12	2.22	0.40
1:A:2414:GLU:HB2	1:A:2490:LYS:HZ3	1.87	0.40
1:A:2748:ILE:HD11	1:A:2752:LEU:HB3	2.04	0.40
1:A:2978:LEU:HD22	1:A:3057:LEU:CD2	2.49	0.40
1:A:3355:LEU:HD22	1:A:3424:TRP:CZ2	2.56	0.40
1:B:860:ILE:HG13	1:B:861:GLN:N	2.36	0.40
1:B:1460:GLN:OE1	1:B:1471:ARG:HG2	2.21	0.40
1:B:1466:ASP:OD1	1:B:1466:ASP:C	2.65	0.40
1:B:2414:GLU:HB2	1:B:2490:LYS:HZ3	1.87	0.40
1:B:2918:ALA:HA	1:B:2921:ARG:HB3	2.03	0.40
1:C:665:PHE:CE1	1:C:747:CYS:HB2	2.57	0.40
1:D:70:LEU:HD23	1:D:110:LEU:HD23	2.04	0.40
1:D:332:VAL:HG22	1:D:333:GLU:N	2.36	0.40
1:D:910:ASN:O	1:D:914:LEU:N	2.54	0.40
1:D:2748:ILE:HD12	1:D:2818:ILE:CD1	2.51	0.40
1:D:2817:MET:HB2	1:D:2822:TRP:HB2	2.03	0.40
1:D:2918:ALA:HA	1:D:2921:ARG:HB3	2.03	0.40
1:D:4730:PHE:HD2	1:D:4735:ILE:HG12	1.85	0.40
1:A:619:GLN:OE1	1:A:1679:ASN:ND2	2.50	0.40
1:A:860:ILE:HG13	1:A:861:GLN:N	2.36	0.40
1:A:903:ARG:HH22	1:A:908:LEU:HD12	1.86	0.40
1:A:2391:PRO:O	1:A:2392:ALA:HB3	2.20	0.40
1:A:3815:VAL:O	1:A:3819:MET:HG3	2.21	0.40
1:B:665:PHE:CE1	1:B:747:CYS:HB2	2.57	0.40
1:B:881:GLU:OE1	1:B:969:ALA:N	2.40	0.40
1:B:1781:PRO:HA	1:B:1782:PRO:HD3	1.99	0.40
1:B:2690:LYS:O	1:B:2994:GLN:NE2	2.51	0.40
1:B:3820:LEU:CD2	1:B:3901:ASP:HB3	2.51	0.40
1:C:332:VAL:HG22	1:C:333:GLU:N	2.36	0.40
1:C:500:THR:HG23	1:C:503:HIS:H	1.85	0.40
1:C:914:LEU:O	1:C:915:PRO:C	2.63	0.40
1:C:3294:PRO:HB2	1:C:3298:PRO:HD3	2.03	0.40
1:C:3771:SER:HA	1:C:3774:HIS:CD2	2.56	0.40
1:D:538:CYS:SG	1:D:571:GLU:HB2	2.62	0.40
1:D:2281:VAL:O	1:D:2281:VAL:HG22	2.22	0.40
1:D:2482:LYS:HD2	1:D:2483:ASP:CG	2.47	0.40
1:D:3684:GLN:OE1	1:D:3684:GLN:N	2.45	0.40
1:D:4034:LEU:HG	1:D:4047:MET:HE1	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	4345/5035 (86%)	4201 (97%)	144 (3%)	0	100	100
1	B	4345/5035 (86%)	4200 (97%)	145 (3%)	0	100	100
1	C	4345/5035 (86%)	4203 (97%)	142 (3%)	0	100	100
1	D	4345/5035 (86%)	4201 (97%)	144 (3%)	0	100	100
2	E	105/108 (97%)	100 (95%)	5 (5%)	0	100	100
2	F	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	G	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	H	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
All	All	17800/20572 (86%)	17210 (97%)	590 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	3806/4296 (89%)	3799 (100%)	7 (0%)	92	96
1	B	3806/4296 (89%)	3799 (100%)	7 (0%)	92	96
1	C	3806/4296 (89%)	3799 (100%)	7 (0%)	92	96
1	D	3806/4296 (89%)	3799 (100%)	7 (0%)	92	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	89/90 (99%)	89 (100%)	0	100	100
2	F	89/90 (99%)	89 (100%)	0	100	100
2	G	89/90 (99%)	89 (100%)	0	100	100
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	15580/17544 (89%)	15552 (100%)	28 (0%)	91	96

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	HIS
1	A	4102	SER
1	A	4706	THR
1	A	4718	VAL
1	A	4720	ARG
1	A	4735	ILE
1	A	4771	VAL
1	B	219	HIS
1	B	4102	SER
1	B	4706	THR
1	B	4718	VAL
1	B	4720	ARG
1	B	4735	ILE
1	B	4771	VAL
1	C	219	HIS
1	C	4102	SER
1	C	4706	THR
1	C	4718	VAL
1	C	4720	ARG
1	C	4735	ILE
1	C	4771	VAL
1	D	219	HIS
1	D	4102	SER
1	D	4706	THR
1	D	4718	VAL
1	D	4720	ARG
1	D	4735	ILE
1	D	4771	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (129) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	204	ASN
1	A	350	GLN
1	A	534	ASN
1	A	640	ASN
1	A	766	GLN
1	A	922	ASN
1	A	1207	GLN
1	A	1460	GLN
1	A	1591	GLN
1	A	1632	GLN
1	A	1973	ASN
1	A	2126	HIS
1	A	2261	ASN
1	A	2418	HIS
1	A	2963	GLN
1	A	3212	ASN
1	A	3327	ASN
1	A	3450	HIS
1	A	3557	ASN
1	A	3612	HIS
1	A	3930	GLN
1	A	3963	GLN
1	A	3973	GLN
1	A	3981	GLN
1	A	4156	HIS
1	A	4165	ASN
1	A	4545	GLN
1	A	4834	GLN
2	E	95	HIS
2	F	26	HIS
2	F	44	ASN
2	F	95	HIS
2	G	95	HIS
2	H	44	ASN
2	H	95	HIS
1	B	24	GLN
1	B	204	ASN
1	B	350	GLN
1	B	413	ASN
1	B	534	ASN
1	B	577	ASN
1	B	640	ASN

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Mol	Chain	Res	Type
1	B	922	ASN
1	B	1207	GLN
1	B	1301	HIS
1	B	1460	GLN
1	B	1591	GLN
1	B	1632	GLN
1	B	1692	GLN
1	B	1973	ASN
1	B	2126	HIS
1	B	2261	ASN
1	B	2418	HIS
1	B	2963	GLN
1	B	3212	ASN
1	B	3327	ASN
1	B	3419	ASN
1	B	3450	HIS
1	B	3557	ASN
1	B	3612	HIS
1	B	3873	ASN
1	B	3963	GLN
1	B	3981	GLN
1	B	4156	HIS
1	B	4165	ASN
1	B	4545	GLN
1	B	4774	GLN
1	B	4834	GLN
1	C	24	GLN
1	C	204	ASN
1	C	350	GLN
1	C	534	ASN
1	C	640	ASN
1	C	922	ASN
1	C	1207	GLN
1	C	1460	GLN
1	C	1512	HIS
1	C	1591	GLN
1	C	1632	GLN
1	C	1778	HIS
1	C	1973	ASN
1	C	2126	HIS
1	C	2261	ASN
1	C	2418	HIS

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Mol	Chain	Res	Type
1	C	2963	GLN
1	C	3212	ASN
1	C	3327	ASN
1	C	3450	HIS
1	C	3557	ASN
1	C	3612	HIS
1	C	3963	GLN
1	C	3981	GLN
1	C	4156	HIS
1	C	4165	ASN
1	C	4545	GLN
1	C	4774	GLN
1	C	4834	GLN
1	D	24	GLN
1	D	204	ASN
1	D	350	GLN
1	D	413	ASN
1	D	534	ASN
1	D	640	ASN
1	D	922	ASN
1	D	1460	GLN
1	D	1512	HIS
1	D	1591	GLN
1	D	1632	GLN
1	D	1778	HIS
1	D	1973	ASN
1	D	2126	HIS
1	D	2261	ASN
1	D	2418	HIS
1	D	2775	ASN
1	D	2963	GLN
1	D	3212	ASN
1	D	3327	ASN
1	D	3450	HIS
1	D	3557	ASN
1	D	3612	HIS
1	D	3892	GLN
1	D	3963	GLN
1	D	3981	GLN
1	D	4156	HIS
1	D	4165	ASN
1	D	4545	GLN

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Mol	Chain	Res	Type
1	D	4774	GLN
1	D	4834	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 28 ligands modelled in this entry, 8 are monoatomic - leaving 20 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CFF	B	8002	-	8,15,15	2.08	3 (37%)	8,23,23	1.40	1 (12%)
7	PCW	B	8006	-	53,53,53	1.24	7 (13%)	59,61,61	1.07	3 (5%)
7	PCW	D	8006	-	53,53,53	1.24	7 (13%)	59,61,61	1.07	3 (5%)
7	PCW	C	8006	-	53,53,53	1.24	7 (13%)	59,61,61	1.07	3 (5%)
7	PCW	A	8005	-	53,53,53	1.26	7 (13%)	59,61,61	1.15	4 (6%)
7	PCW	A	8006	-	53,53,53	1.24	7 (13%)	59,61,61	1.07	3 (5%)
4	CFF	D	8002	-	8,15,15	2.08	3 (37%)	8,23,23	1.40	1 (12%)
4	CFF	C	8002	-	8,15,15	2.08	3 (37%)	8,23,23	1.39	1 (12%)
5	ATP	B	8007	-	28,33,33	0.65	0	34,52,52	0.92	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CFF	A	8002	-	8,15,15	2.08	3 (37%)	8,23,23	1.39	1 (12%)
5	ATP	C	8007	-	28,33,33	0.65	0	34,52,52	0.92	1 (2%)
5	ATP	A	8007	-	28,33,33	0.65	0	34,52,52	0.92	1 (2%)
5	ATP	B	8003	-	28,33,33	0.64	0	34,52,52	0.88	1 (2%)
5	ATP	C	8003	-	28,33,33	0.63	0	34,52,52	0.89	1 (2%)
7	PCW	B	8005	-	53,53,53	1.26	7 (13%)	59,61,61	1.15	4 (6%)
5	ATP	A	8003	-	28,33,33	0.64	0	34,52,52	0.89	1 (2%)
5	ATP	D	8007	-	28,33,33	0.65	0	34,52,52	0.92	1 (2%)
7	PCW	C	8005	-	53,53,53	1.26	7 (13%)	59,61,61	1.15	4 (6%)
7	PCW	D	8005	-	53,53,53	1.26	7 (13%)	59,61,61	1.15	4 (6%)
5	ATP	D	8003	-	28,33,33	0.63	0	34,52,52	0.89	1 (2%)

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	CFF	B	8002	-	-	-	0/2/2/2
7	PCW	B	8006	-	-	22/57/57/57	-
7	PCW	D	8006	-	-	22/57/57/57	-
7	PCW	C	8006	-	-	22/57/57/57	-
7	PCW	A	8005	-	-	26/57/57/57	-
7	PCW	A	8006	-	-	22/57/57/57	-
4	CFF	C	8002	-	-	-	0/2/2/2
4	CFF	D	8002	-	-	-	0/2/2/2
5	ATP	B	8007	-	-	6/18/38/38	0/3/3/3
4	CFF	A	8002	-	-	-	0/2/2/2
5	ATP	C	8007	-	-	6/18/38/38	0/3/3/3
5	ATP	A	8007	-	-	6/18/38/38	0/3/3/3
5	ATP	B	8003	-	-	4/18/38/38	0/3/3/3
5	ATP	C	8003	-	-	4/18/38/38	0/3/3/3
7	PCW	B	8005	-	-	26/57/57/57	-
5	ATP	A	8003	-	-	4/18/38/38	0/3/3/3
5	ATP	D	8007	-	-	6/18/38/38	0/3/3/3
7	PCW	C	8005	-	-	26/57/57/57	-
7	PCW	D	8005	-	-	26/57/57/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ATP	D	8003	-	-	4/18/38/38	0/3/3/3

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8002	CFF	C5-C4	-3.44	1.33	1.39
4	D	8002	CFF	C5-C4	-3.44	1.33	1.39
4	A	8002	CFF	C5-C4	-3.42	1.33	1.39
4	C	8002	CFF	C5-C4	-3.42	1.33	1.39
4	A	8002	CFF	C6-N1	-3.26	1.32	1.38
4	C	8002	CFF	C6-N1	-3.26	1.32	1.38
4	B	8002	CFF	C6-N1	-3.22	1.32	1.38
4	D	8002	CFF	C6-N1	-3.22	1.32	1.38
7	B	8005	PCW	O3-C11	3.08	1.42	1.33
7	A	8005	PCW	O3-C11	3.07	1.42	1.33
7	D	8005	PCW	O3-C11	3.07	1.42	1.33
7	B	8006	PCW	O3-C11	3.06	1.42	1.33
7	C	8005	PCW	O3-C11	3.05	1.42	1.33
7	A	8006	PCW	O3-C11	3.03	1.42	1.33
7	C	8006	PCW	O3-C11	3.03	1.42	1.33
7	D	8006	PCW	O3-C11	3.03	1.42	1.33
7	B	8005	PCW	O2-C31	2.88	1.42	1.34
7	A	8005	PCW	O2-C31	2.87	1.42	1.34
7	D	8005	PCW	O2-C31	2.87	1.42	1.34
7	A	8006	PCW	O2-C31	2.86	1.42	1.34
7	B	8006	PCW	O2-C31	2.86	1.42	1.34
7	D	8006	PCW	O2-C31	2.86	1.42	1.34
7	C	8005	PCW	O2-C31	2.86	1.42	1.34
7	C	8006	PCW	O2-C31	2.84	1.42	1.34
7	C	8005	PCW	P-O4P	2.57	1.69	1.59
7	D	8005	PCW	P-O4P	2.57	1.69	1.59
7	A	8005	PCW	P-O4P	2.56	1.69	1.59
7	B	8005	PCW	P-O4P	2.55	1.69	1.59
7	B	8006	PCW	P-O4P	2.54	1.69	1.59
7	D	8006	PCW	P-O4P	2.54	1.69	1.59
7	A	8006	PCW	P-O4P	2.53	1.69	1.59
7	C	8006	PCW	P-O4P	2.53	1.69	1.59
4	A	8002	CFF	O13-C6	-2.49	1.18	1.24
4	B	8002	CFF	O13-C6	-2.49	1.18	1.24
4	D	8002	CFF	O13-C6	-2.49	1.18	1.24
4	C	8002	CFF	O13-C6	-2.49	1.18	1.24
7	B	8005	PCW	O2-C2	-2.42	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	8005	PCW	O2-C2	-2.41	1.40	1.46
7	C	8005	PCW	O2-C2	-2.41	1.40	1.46
7	D	8005	PCW	O2-C2	-2.40	1.41	1.46
7	A	8005	PCW	C5-C4	2.38	1.58	1.51
7	B	8005	PCW	C5-C4	2.38	1.58	1.51
7	D	8005	PCW	C5-C4	2.38	1.58	1.51
7	C	8005	PCW	C5-C4	2.36	1.58	1.51
7	A	8006	PCW	O2-C2	-2.30	1.41	1.46
7	B	8006	PCW	O2-C2	-2.30	1.41	1.46
7	D	8006	PCW	O2-C2	-2.30	1.41	1.46
7	C	8006	PCW	O2-C2	-2.29	1.41	1.46
7	B	8005	PCW	C32-C31	2.28	1.57	1.50
7	D	8005	PCW	C32-C31	2.28	1.57	1.50
7	A	8005	PCW	C32-C31	2.27	1.57	1.50
7	C	8005	PCW	C32-C31	2.27	1.57	1.50
7	A	8005	PCW	P-O3P	2.22	1.68	1.59
7	C	8005	PCW	P-O3P	2.22	1.68	1.59
7	D	8005	PCW	P-O3P	2.22	1.68	1.59
7	B	8005	PCW	P-O3P	2.21	1.68	1.59
7	C	8006	PCW	C32-C31	2.17	1.57	1.50
7	B	8006	PCW	C5-C4	2.16	1.57	1.51
7	C	8006	PCW	C5-C4	2.14	1.57	1.51
7	D	8006	PCW	C5-C4	2.14	1.57	1.51
7	A	8006	PCW	C32-C31	2.14	1.56	1.50
7	B	8006	PCW	C32-C31	2.14	1.56	1.50
7	D	8006	PCW	C32-C31	2.14	1.56	1.50
7	A	8006	PCW	C5-C4	2.14	1.57	1.51
7	D	8006	PCW	P-O3P	2.09	1.67	1.59
7	B	8006	PCW	P-O3P	2.07	1.67	1.59
7	A	8006	PCW	P-O3P	2.07	1.67	1.59
7	C	8006	PCW	P-O3P	2.06	1.67	1.59

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	8005	PCW	O2-C31-C32	4.11	120.38	111.48
7	A	8005	PCW	O2-C31-C32	4.10	120.36	111.48
7	D	8005	PCW	O2-C31-C32	4.09	120.34	111.48
7	B	8005	PCW	O2-C31-C32	4.08	120.32	111.48
7	B	8005	PCW	C21-C20-C19	4.08	155.39	124.83
7	A	8005	PCW	C21-C20-C19	4.07	155.36	124.83
7	C	8005	PCW	C21-C20-C19	4.07	155.36	124.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	8005	PCW	C21-C20-C19	4.07	155.31	124.83
7	A	8006	PCW	O2-C31-C32	3.95	120.02	111.48
7	B	8006	PCW	O2-C31-C32	3.95	120.02	111.48
7	C	8006	PCW	O2-C31-C32	3.95	120.02	111.48
7	D	8006	PCW	O2-C31-C32	3.95	120.02	111.48
7	C	8006	PCW	C21-C20-C19	3.88	153.87	124.83
7	D	8006	PCW	C21-C20-C19	3.88	153.87	124.83
7	A	8006	PCW	C21-C20-C19	3.87	153.84	124.83
7	B	8006	PCW	C21-C20-C19	3.87	153.81	124.83
4	B	8002	CFF	C14-N7-C8	-3.05	110.76	125.43
4	D	8002	CFF	C14-N7-C8	-3.05	110.76	125.43
4	A	8002	CFF	C14-N7-C8	-3.04	110.80	125.43
4	C	8002	CFF	C14-N7-C8	-3.04	110.82	125.43
7	D	8005	PCW	C18-C19-C20	2.77	145.58	124.83
7	C	8005	PCW	C18-C19-C20	2.76	145.55	124.83
7	B	8005	PCW	C18-C19-C20	2.76	145.54	124.83
7	A	8005	PCW	C18-C19-C20	2.76	145.54	124.83
7	D	8006	PCW	O3-C11-C12	2.59	119.72	111.83
7	A	8006	PCW	O3-C11-C12	2.59	119.72	111.83
7	B	8006	PCW	O3-C11-C12	2.59	119.72	111.83
7	C	8006	PCW	O3-C11-C12	2.58	119.69	111.83
7	D	8005	PCW	O3-C11-C12	2.48	119.40	111.83
7	A	8005	PCW	O3-C11-C12	2.47	119.36	111.83
7	C	8005	PCW	O3-C11-C12	2.46	119.33	111.83
7	B	8005	PCW	O3-C11-C12	2.45	119.31	111.83
5	A	8003	ATP	C5-C6-N6	2.33	123.87	120.31
5	D	8003	ATP	C5-C6-N6	2.32	123.85	120.31
5	C	8003	ATP	C5-C6-N6	2.32	123.85	120.31
5	A	8007	ATP	C5-C6-N6	2.31	123.83	120.31
5	B	8003	ATP	C5-C6-N6	2.31	123.83	120.31
5	C	8007	ATP	C5-C6-N6	2.30	123.82	120.31
5	D	8007	ATP	C5-C6-N6	2.29	123.80	120.31
5	B	8007	ATP	C5-C6-N6	2.29	123.80	120.31

There are no chirality outliers.

All (232) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	8003	ATP	C5'-O5'-PA-O2A
5	A	8003	ATP	C5'-O5'-PA-O3A
5	B	8003	ATP	C5'-O5'-PA-O2A
5	B	8003	ATP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
5	C	8003	ATP	C5'-O5'-PA-O2A
5	C	8003	ATP	C5'-O5'-PA-O3A
5	D	8003	ATP	C5'-O5'-PA-O2A
5	D	8003	ATP	C5'-O5'-PA-O3A
7	A	8005	PCW	C32-C31-O2-C2
7	A	8006	PCW	O4P-C4-C5-N
7	A	8006	PCW	C1-O3P-P-O2P
7	A	8006	PCW	C4-O4P-P-O2P
7	A	8006	PCW	C4-O4P-P-O3P
7	B	8005	PCW	C32-C31-O2-C2
7	B	8006	PCW	O4P-C4-C5-N
7	B	8006	PCW	C1-O3P-P-O2P
7	B	8006	PCW	C4-O4P-P-O2P
7	B	8006	PCW	C4-O4P-P-O3P
7	C	8005	PCW	C32-C31-O2-C2
7	C	8006	PCW	O4P-C4-C5-N
7	C	8006	PCW	C1-O3P-P-O2P
7	C	8006	PCW	C4-O4P-P-O2P
7	C	8006	PCW	C4-O4P-P-O3P
7	D	8005	PCW	C32-C31-O2-C2
7	D	8006	PCW	O4P-C4-C5-N
7	D	8006	PCW	C1-O3P-P-O2P
7	D	8006	PCW	C4-O4P-P-O2P
7	D	8006	PCW	C4-O4P-P-O3P
7	A	8005	PCW	O31-C31-O2-C2
7	B	8005	PCW	O31-C31-O2-C2
7	C	8005	PCW	O31-C31-O2-C2
7	D	8005	PCW	O31-C31-O2-C2
7	B	8005	PCW	C41-C42-C43-C44
7	A	8005	PCW	C41-C42-C43-C44
7	C	8005	PCW	C41-C42-C43-C44
7	D	8005	PCW	C41-C42-C43-C44
7	A	8006	PCW	C31-C32-C33-C34
7	B	8006	PCW	C31-C32-C33-C34
7	C	8006	PCW	C31-C32-C33-C34
7	D	8006	PCW	C31-C32-C33-C34
7	A	8006	PCW	C20-C21-C22-C23
7	B	8006	PCW	C20-C21-C22-C23
7	C	8006	PCW	C20-C21-C22-C23
7	D	8006	PCW	C20-C21-C22-C23
7	A	8006	PCW	C11-C12-C13-C14
7	B	8006	PCW	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
7	C	8006	PCW	C11-C12-C13-C14
7	D	8006	PCW	C11-C12-C13-C14
7	A	8005	PCW	C21-C22-C23-C24
7	B	8005	PCW	C21-C22-C23-C24
7	C	8005	PCW	C21-C22-C23-C24
7	D	8005	PCW	C21-C22-C23-C24
7	C	8006	PCW	C35-C36-C37-C38
7	A	8006	PCW	C35-C36-C37-C38
7	B	8006	PCW	C35-C36-C37-C38
7	D	8006	PCW	C35-C36-C37-C38
7	A	8006	PCW	C40-C41-C42-C43
7	B	8006	PCW	C40-C41-C42-C43
7	D	8006	PCW	C40-C41-C42-C43
5	A	8003	ATP	C4'-C5'-O5'-PA
5	B	8003	ATP	C4'-C5'-O5'-PA
5	C	8003	ATP	C4'-C5'-O5'-PA
5	D	8003	ATP	C4'-C5'-O5'-PA
7	A	8006	PCW	C32-C31-O2-C2
7	B	8006	PCW	C32-C31-O2-C2
7	C	8006	PCW	C32-C31-O2-C2
7	D	8006	PCW	C32-C31-O2-C2
7	B	8005	PCW	C32-C33-C34-C35
7	A	8005	PCW	C32-C33-C34-C35
7	C	8005	PCW	C32-C33-C34-C35
7	D	8005	PCW	C32-C33-C34-C35
7	C	8006	PCW	C40-C41-C42-C43
7	A	8005	PCW	C36-C37-C38-C39
7	B	8005	PCW	C36-C37-C38-C39
7	C	8005	PCW	C36-C37-C38-C39
7	D	8005	PCW	C36-C37-C38-C39
7	D	8006	PCW	C15-C16-C17-C18
7	A	8006	PCW	C15-C16-C17-C18
7	B	8006	PCW	C15-C16-C17-C18
7	C	8006	PCW	C15-C16-C17-C18
7	A	8006	PCW	O31-C31-O2-C2
7	C	8006	PCW	O31-C31-O2-C2
7	D	8006	PCW	O31-C31-O2-C2
7	B	8006	PCW	O31-C31-O2-C2
7	A	8005	PCW	C20-C21-C22-C23
7	B	8005	PCW	C20-C21-C22-C23
7	C	8005	PCW	C20-C21-C22-C23
7	D	8005	PCW	C20-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
7	A	8005	PCW	C15-C16-C17-C18
7	B	8005	PCW	C15-C16-C17-C18
7	C	8005	PCW	C15-C16-C17-C18
7	D	8005	PCW	C15-C16-C17-C18
7	A	8005	PCW	C16-C17-C18-C19
7	B	8005	PCW	C16-C17-C18-C19
7	C	8005	PCW	C16-C17-C18-C19
7	D	8005	PCW	C16-C17-C18-C19
7	A	8006	PCW	C43-C44-C45-C46
7	B	8006	PCW	C43-C44-C45-C46
7	C	8006	PCW	C43-C44-C45-C46
7	D	8006	PCW	C43-C44-C45-C46
7	A	8006	PCW	C41-C42-C43-C44
7	C	8006	PCW	C41-C42-C43-C44
7	D	8006	PCW	C41-C42-C43-C44
7	B	8006	PCW	C41-C42-C43-C44
5	A	8003	ATP	PA-O3A-PB-O3B
5	B	8003	ATP	PA-O3A-PB-O3B
5	C	8003	ATP	PA-O3A-PB-O3B
5	D	8003	ATP	PA-O3A-PB-O3B
7	A	8006	PCW	O3P-C1-C2-O2
7	B	8006	PCW	O3P-C1-C2-O2
7	C	8006	PCW	O3P-C1-C2-O2
7	D	8006	PCW	O3P-C1-C2-O2
7	A	8005	PCW	C23-C24-C25-C26
7	B	8005	PCW	C23-C24-C25-C26
7	C	8005	PCW	C23-C24-C25-C26
7	D	8005	PCW	C23-C24-C25-C26
7	A	8006	PCW	O3P-C1-C2-C3
7	B	8006	PCW	O3P-C1-C2-C3
7	C	8006	PCW	O3P-C1-C2-C3
7	D	8006	PCW	O3P-C1-C2-C3
5	A	8007	ATP	PG-O3B-PB-O2B
5	B	8007	ATP	PG-O3B-PB-O2B
5	C	8007	ATP	PG-O3B-PB-O2B
5	D	8007	ATP	PG-O3B-PB-O2B
7	A	8005	PCW	C19-C20-C21-C22
7	B	8005	PCW	C19-C20-C21-C22
7	C	8005	PCW	C19-C20-C21-C22
7	D	8005	PCW	C19-C20-C21-C22
7	A	8005	PCW	C2-C1-O3P-P
7	B	8005	PCW	C2-C1-O3P-P

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Mol	Chain	Res	Type	Atoms
7	C	8005	PCW	C2-C1-O3P-P
7	D	8005	PCW	C2-C1-O3P-P
7	A	8005	PCW	C25-C26-C27-C28
7	B	8005	PCW	C25-C26-C27-C28
7	C	8005	PCW	C25-C26-C27-C28
7	D	8005	PCW	C25-C26-C27-C28
7	A	8005	PCW	C33-C34-C35-C36
7	D	8005	PCW	C33-C34-C35-C36
7	C	8005	PCW	C33-C34-C35-C36
7	B	8005	PCW	C33-C34-C35-C36
7	D	8006	PCW	C45-C46-C47-C48
7	B	8006	PCW	C45-C46-C47-C48
7	A	8006	PCW	C45-C46-C47-C48
7	C	8006	PCW	C45-C46-C47-C48
7	C	8005	PCW	C45-C46-C47-C48
7	A	8005	PCW	C45-C46-C47-C48
7	B	8005	PCW	C45-C46-C47-C48
7	D	8005	PCW	C45-C46-C47-C48
7	C	8006	PCW	C25-C26-C27-C28
7	A	8006	PCW	C25-C26-C27-C28
7	B	8006	PCW	C25-C26-C27-C28
7	D	8006	PCW	C25-C26-C27-C28
5	A	8007	ATP	C4'-C5'-O5'-PA
5	B	8007	ATP	C4'-C5'-O5'-PA
5	C	8007	ATP	C4'-C5'-O5'-PA
5	D	8007	ATP	C4'-C5'-O5'-PA
7	A	8006	PCW	C16-C17-C18-C19
7	B	8006	PCW	C16-C17-C18-C19
7	C	8006	PCW	C16-C17-C18-C19
7	D	8006	PCW	C16-C17-C18-C19
5	A	8007	ATP	PB-O3A-PA-O1A
5	B	8007	ATP	PB-O3A-PA-O1A
5	C	8007	ATP	PB-O3A-PA-O1A
5	D	8007	ATP	PB-O3A-PA-O1A
7	C	8005	PCW	C31-C32-C33-C34
7	A	8005	PCW	C31-C32-C33-C34
7	B	8005	PCW	C31-C32-C33-C34
7	D	8005	PCW	C31-C32-C33-C34
7	D	8005	PCW	C43-C44-C45-C46
7	A	8005	PCW	C43-C44-C45-C46
7	B	8005	PCW	C43-C44-C45-C46
7	C	8005	PCW	C43-C44-C45-C46

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Mol	Chain	Res	Type	Atoms
7	A	8005	PCW	C4-C5-N-C6
7	B	8005	PCW	C4-C5-N-C6
7	C	8005	PCW	C4-C5-N-C6
7	D	8005	PCW	C4-C5-N-C6
7	A	8005	PCW	C5-C4-O4P-P
7	B	8005	PCW	C5-C4-O4P-P
7	C	8005	PCW	C5-C4-O4P-P
7	D	8005	PCW	C5-C4-O4P-P
7	A	8006	PCW	O2-C31-C32-C33
7	B	8006	PCW	O2-C31-C32-C33
7	D	8006	PCW	O2-C31-C32-C33
5	A	8007	ATP	PG-O3B-PB-O1B
5	B	8007	ATP	PG-O3B-PB-O1B
5	C	8007	ATP	PG-O3B-PB-O1B
5	D	8007	ATP	PG-O3B-PB-O1B
7	C	8006	PCW	O2-C31-C32-C33
5	A	8007	ATP	O4'-C4'-C5'-O5'
5	B	8007	ATP	O4'-C4'-C5'-O5'
5	C	8007	ATP	O4'-C4'-C5'-O5'
5	D	8007	ATP	O4'-C4'-C5'-O5'
7	A	8005	PCW	C4-C5-N-C7
7	B	8005	PCW	C4-C5-N-C7
7	C	8005	PCW	C4-C5-N-C7
7	D	8005	PCW	C4-C5-N-C7
7	A	8005	PCW	O2-C31-C32-C33
7	B	8005	PCW	O2-C31-C32-C33
7	C	8005	PCW	O2-C31-C32-C33
7	D	8005	PCW	O2-C31-C32-C33
7	A	8005	PCW	C37-C38-C39-C40
7	B	8005	PCW	C37-C38-C39-C40
7	D	8005	PCW	C34-C35-C36-C37
7	C	8005	PCW	C37-C38-C39-C40
7	D	8005	PCW	C37-C38-C39-C40
7	B	8005	PCW	C34-C35-C36-C37
7	A	8005	PCW	C34-C35-C36-C37
7	C	8005	PCW	C34-C35-C36-C37
7	A	8005	PCW	O31-C31-C32-C33
7	C	8005	PCW	O31-C31-C32-C33
7	B	8005	PCW	O31-C31-C32-C33
7	D	8005	PCW	O31-C31-C32-C33
7	A	8006	PCW	O31-C31-C32-C33
7	C	8006	PCW	O31-C31-C32-C33

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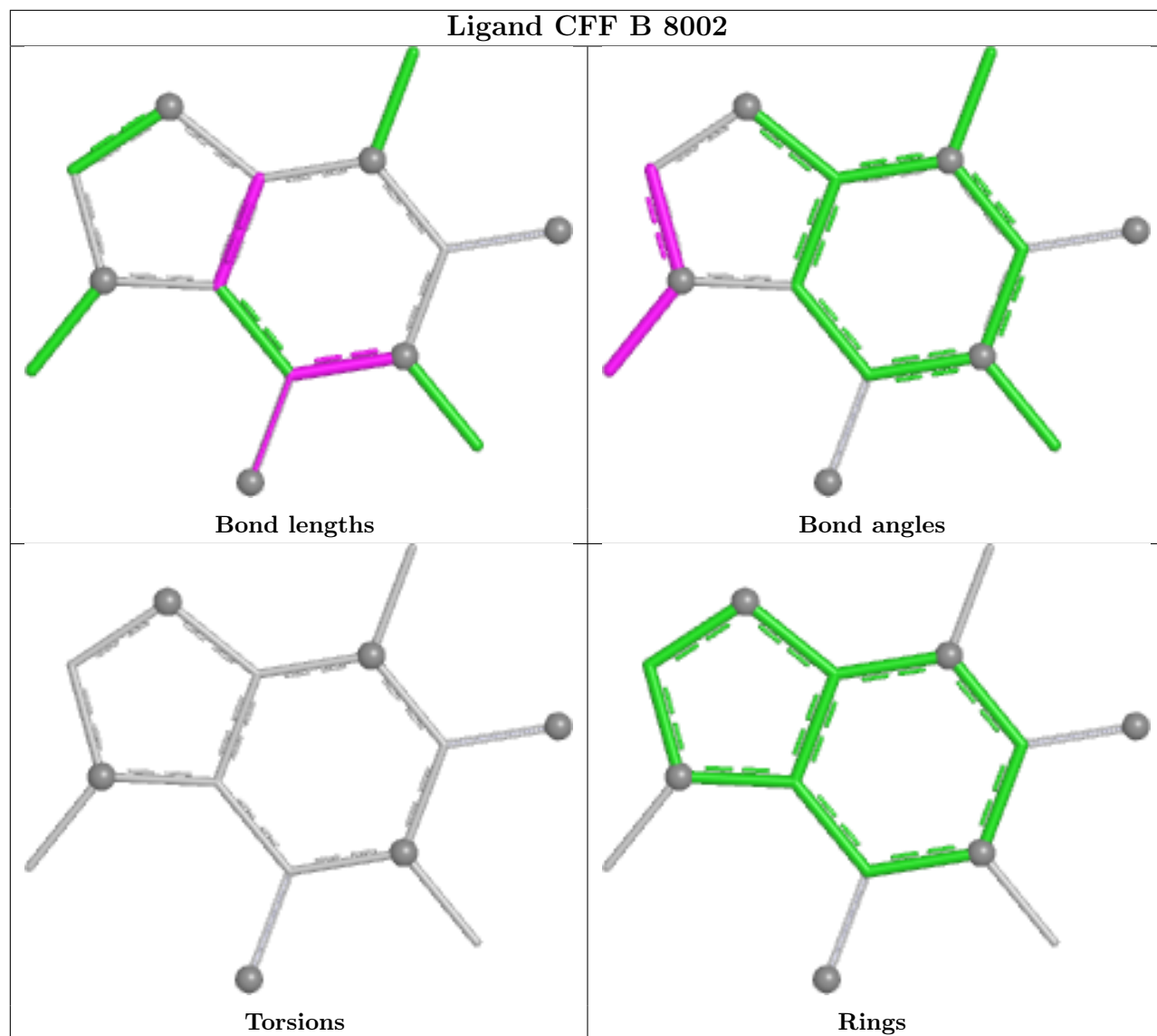
Mol	Chain	Res	Type	Atoms
7	D	8006	PCW	O31-C31-C32-C33
7	B	8006	PCW	O31-C31-C32-C33
7	A	8005	PCW	C1-C2-C3-O3
7	B	8005	PCW	C1-C2-C3-O3
7	C	8005	PCW	C1-C2-C3-O3
7	D	8005	PCW	C1-C2-C3-O3
7	A	8005	PCW	C4-C5-N-C8
7	B	8005	PCW	C4-C5-N-C8
7	C	8005	PCW	C4-C5-N-C8
7	D	8005	PCW	C4-C5-N-C8
7	D	8006	PCW	C33-C34-C35-C36
7	C	8006	PCW	C33-C34-C35-C36
7	A	8006	PCW	C33-C34-C35-C36
7	B	8006	PCW	C33-C34-C35-C36
5	A	8007	ATP	PB-O3A-PA-O2A
5	B	8007	ATP	PB-O3A-PA-O2A
5	C	8007	ATP	PB-O3A-PA-O2A
5	D	8007	ATP	PB-O3A-PA-O2A

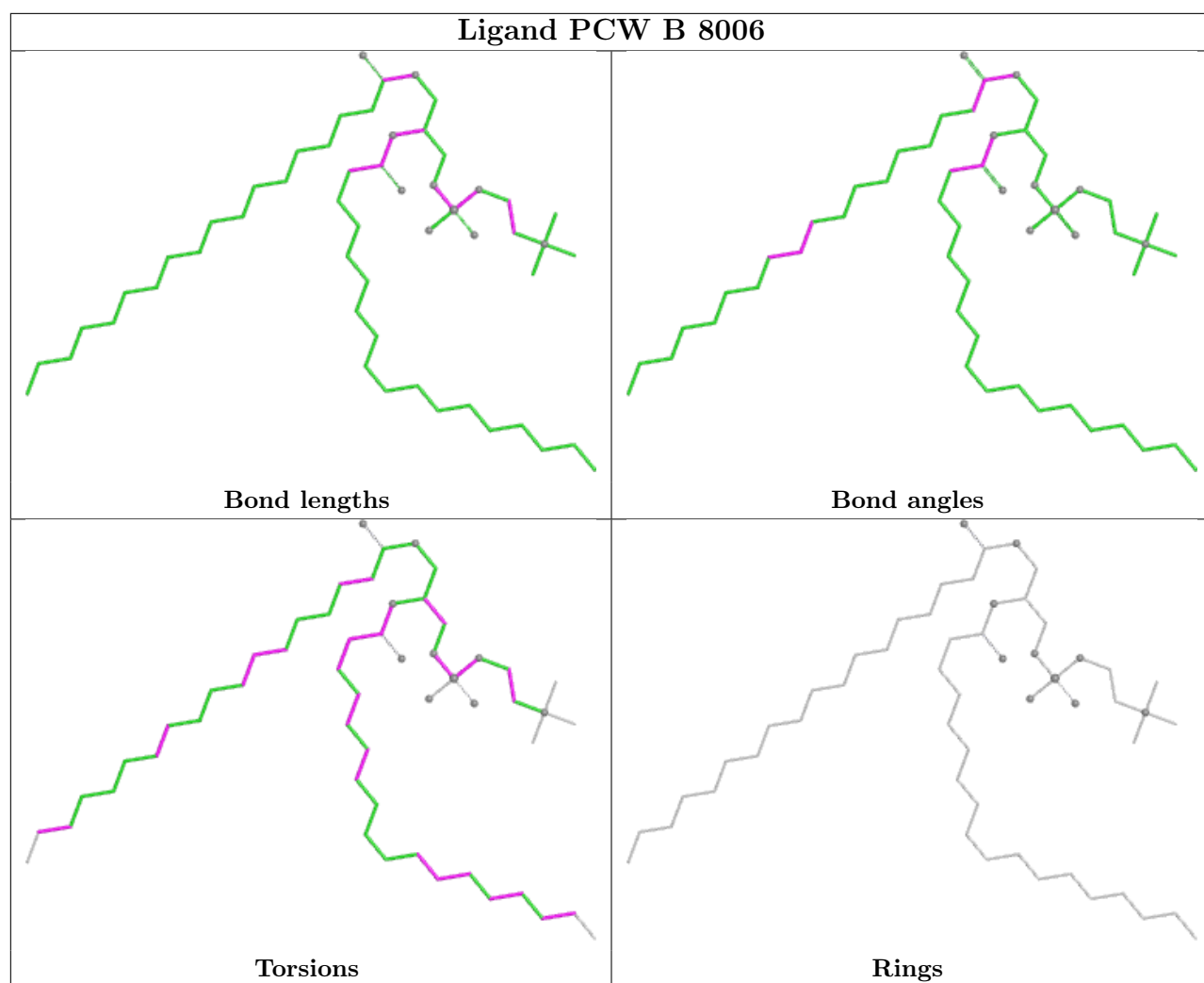
There are no ring outliers.

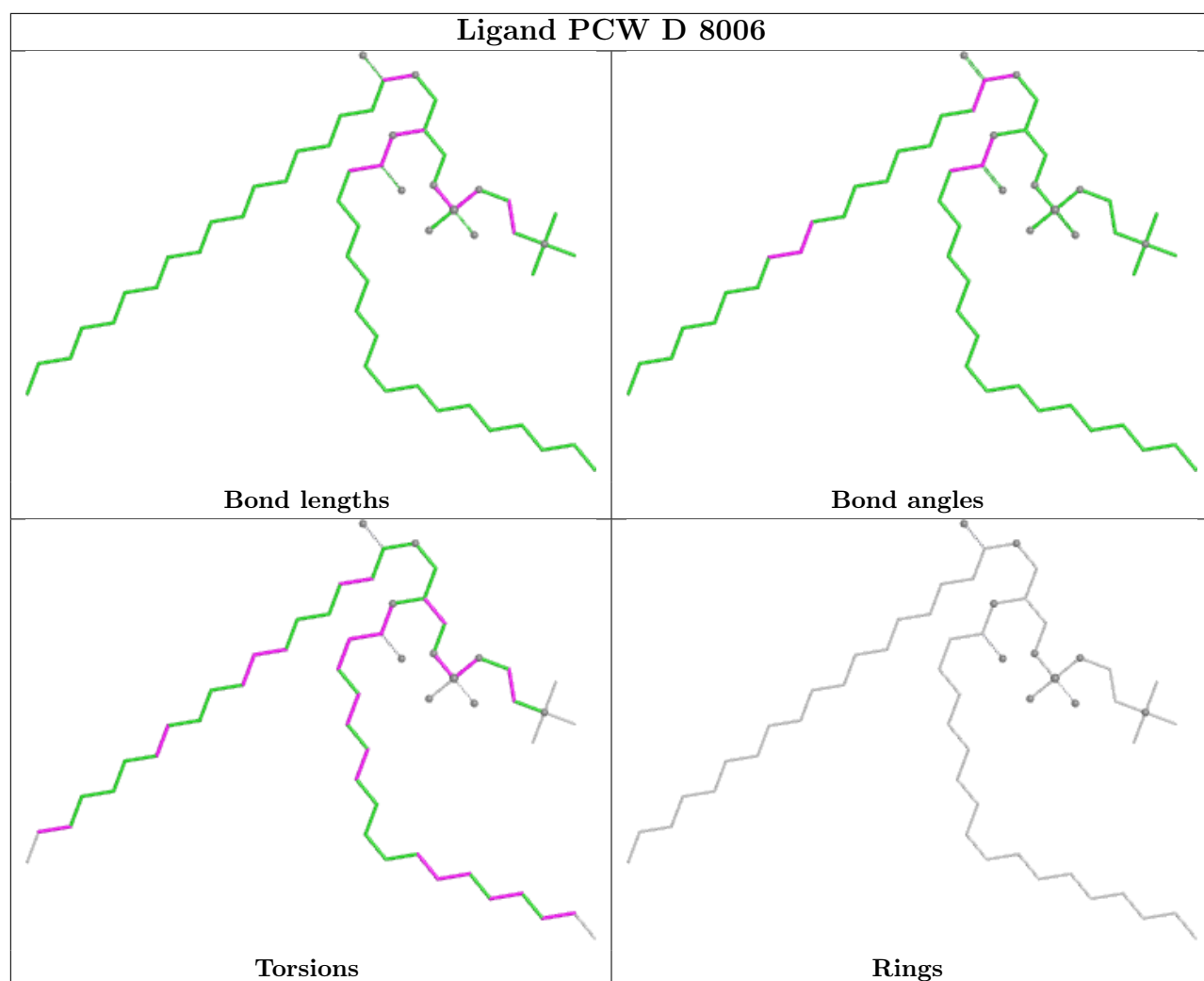
6 monomers are involved in 7 short contacts:

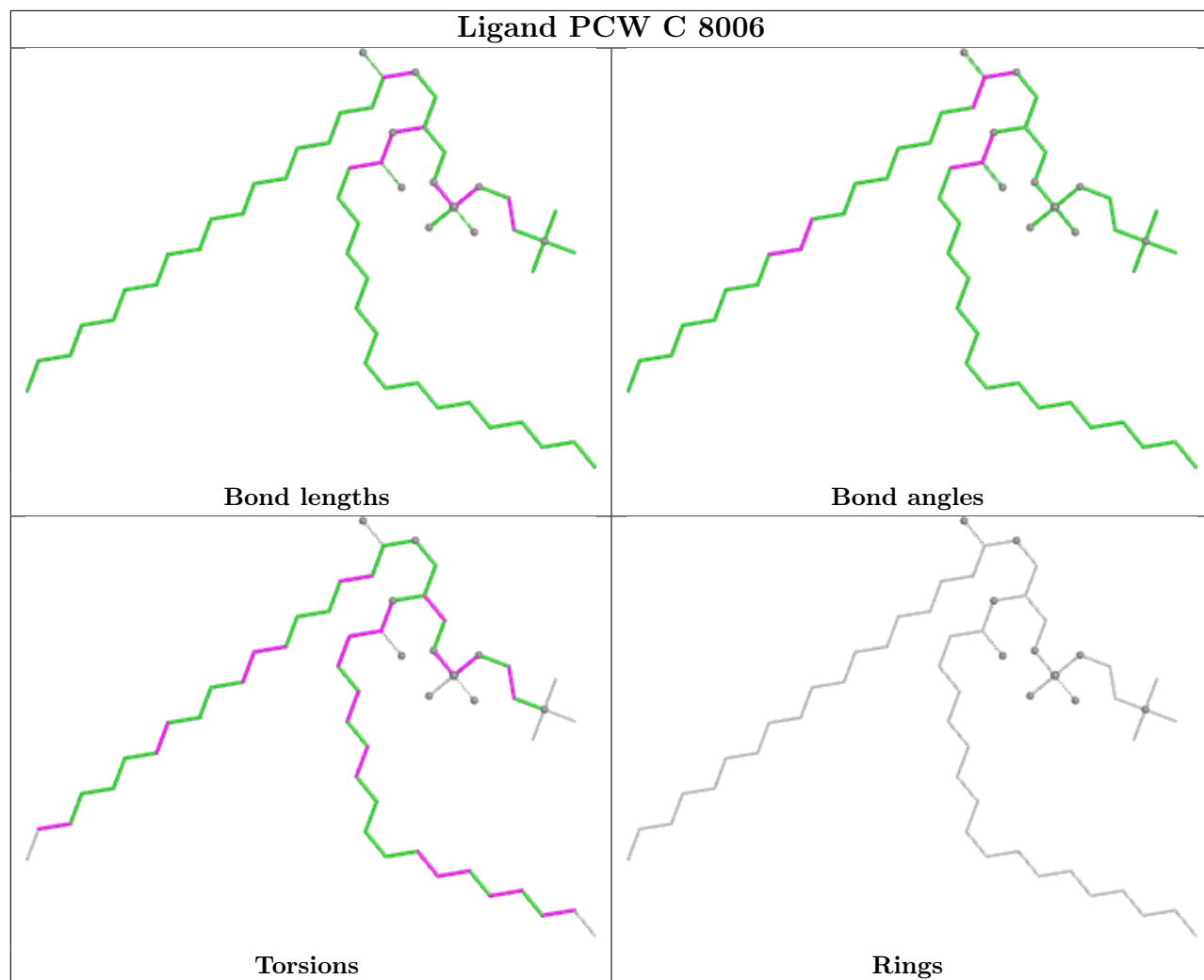
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	8006	PCW	1	0
7	C	8006	PCW	1	0
5	B	8003	ATP	1	0
5	C	8003	ATP	1	0
5	A	8003	ATP	1	0
5	D	8003	ATP	2	0

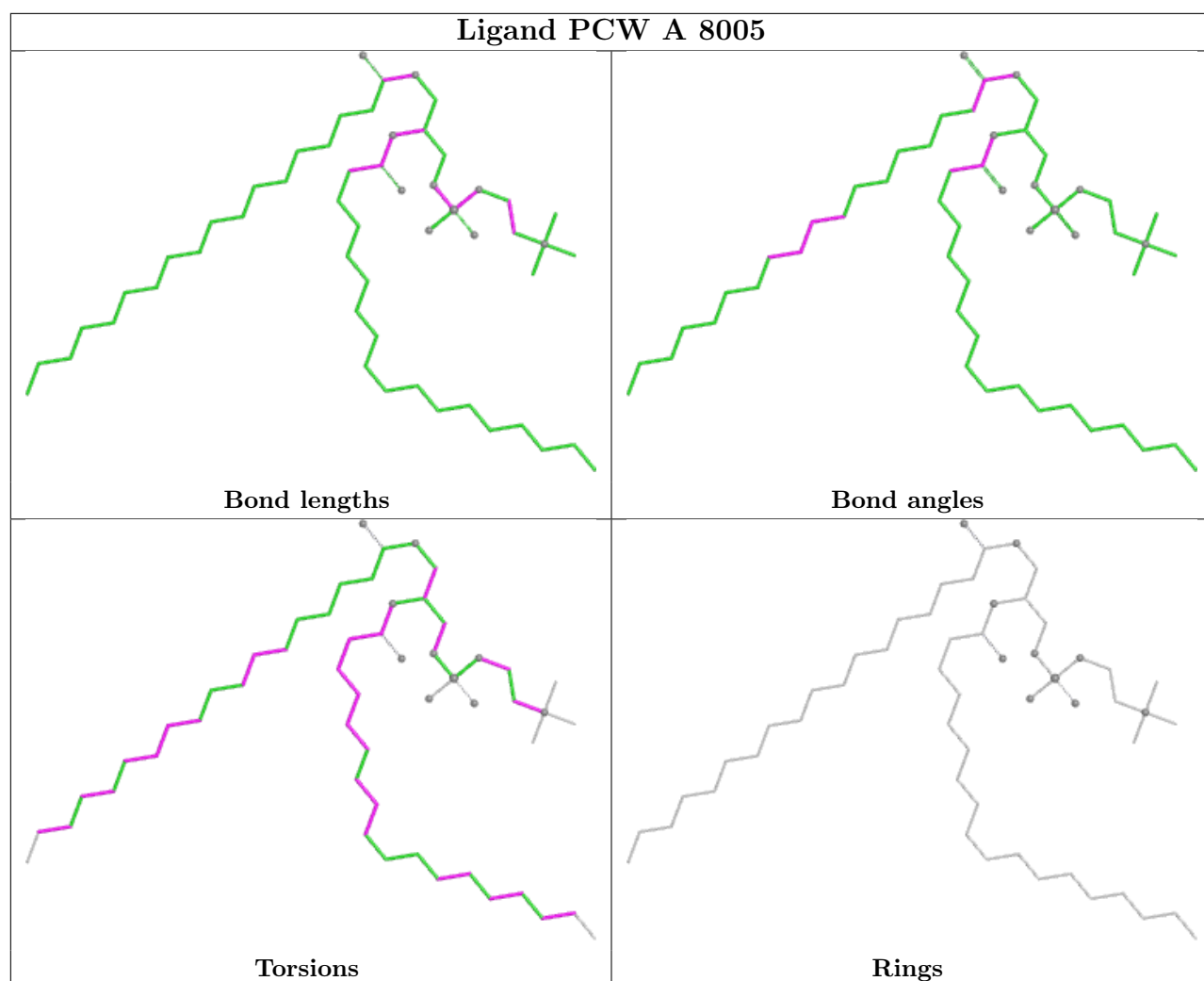
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

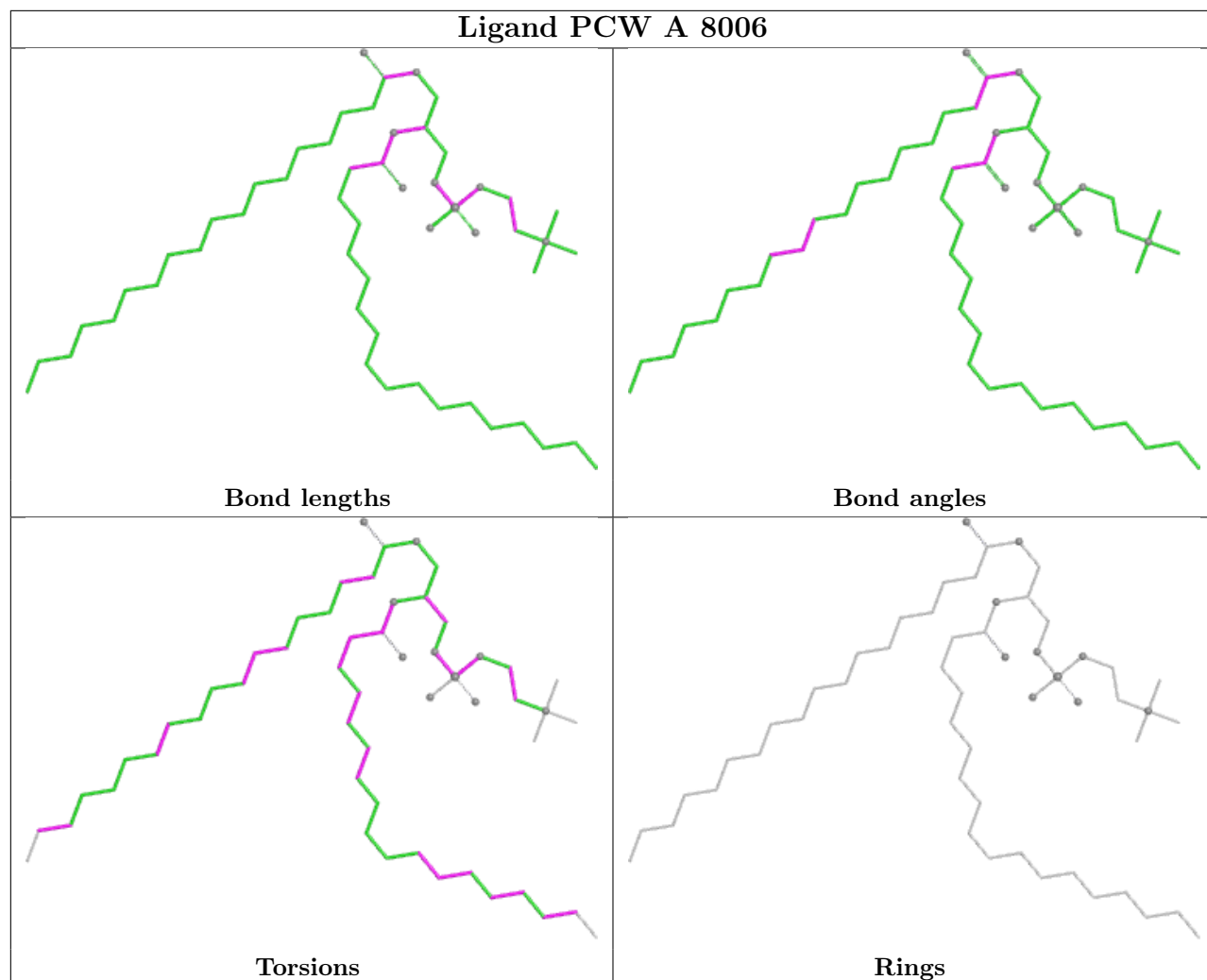


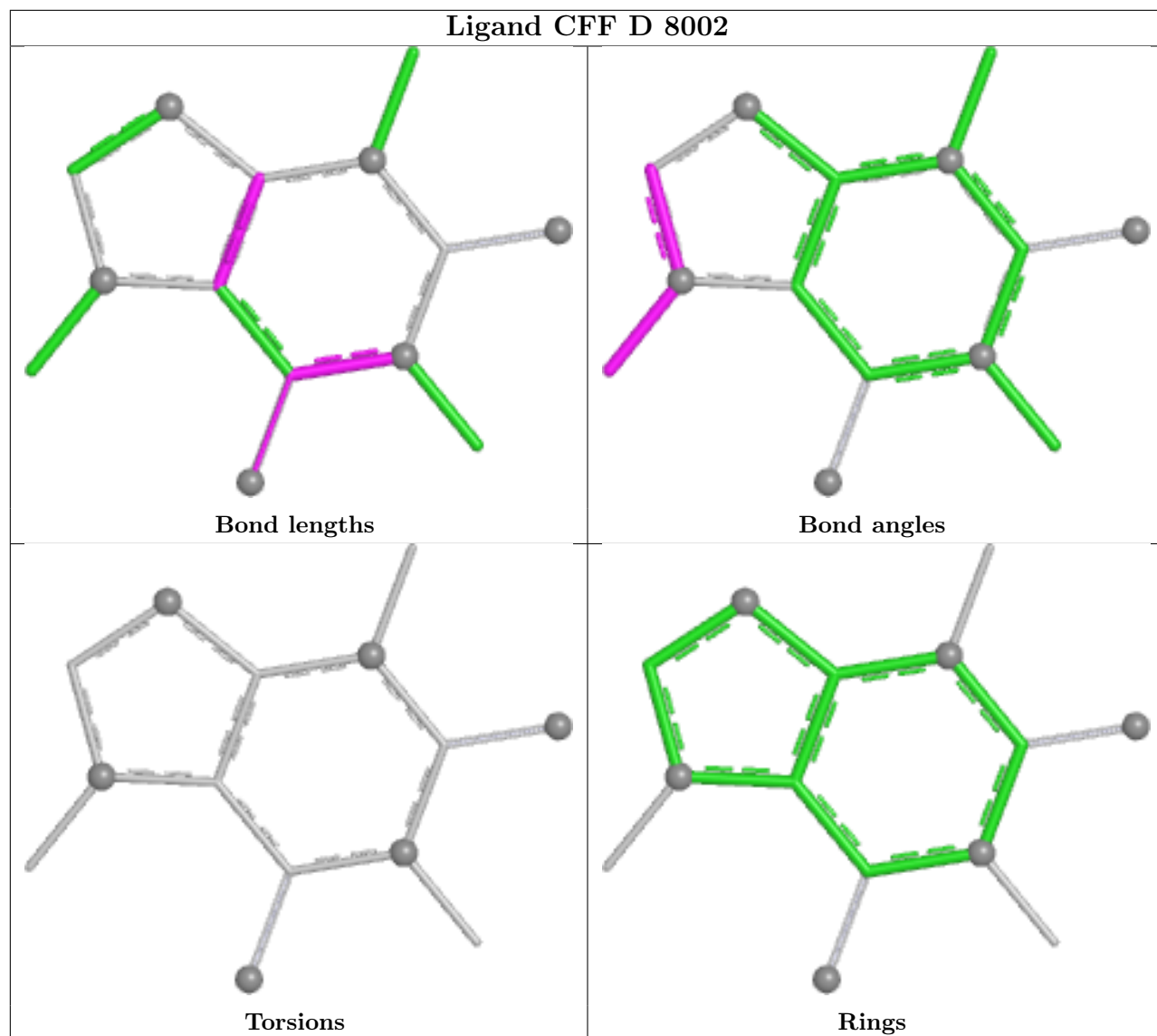


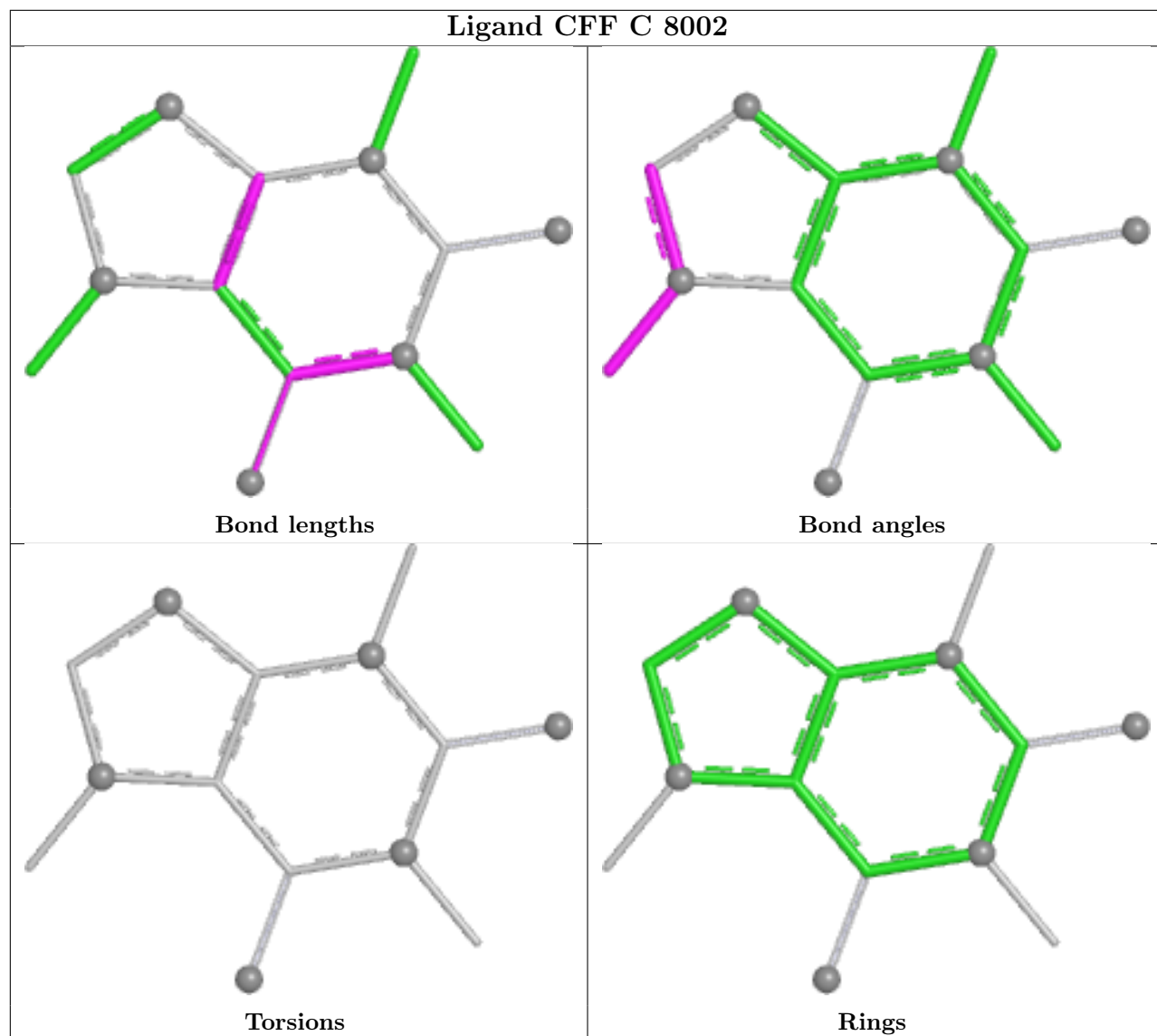


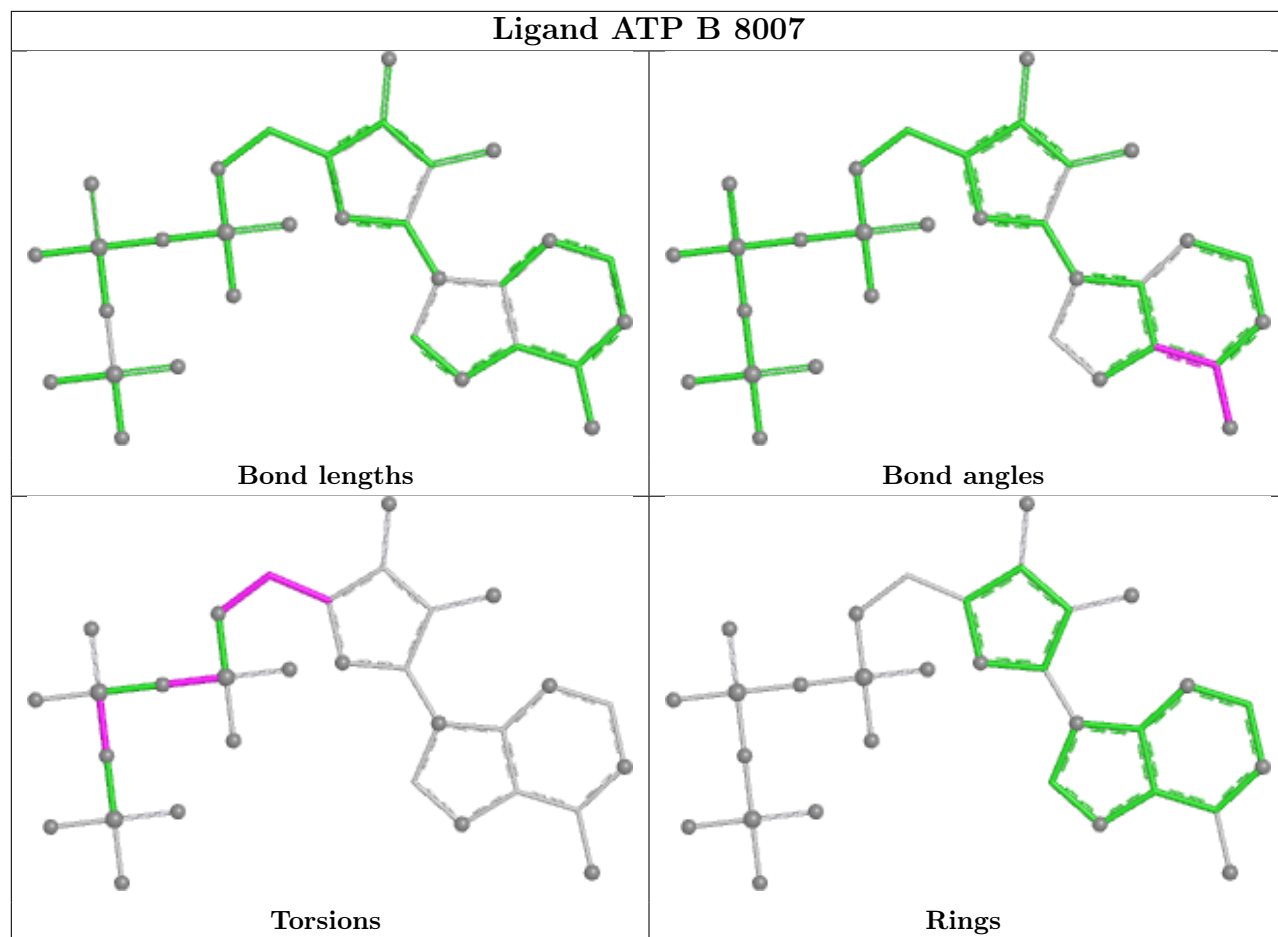


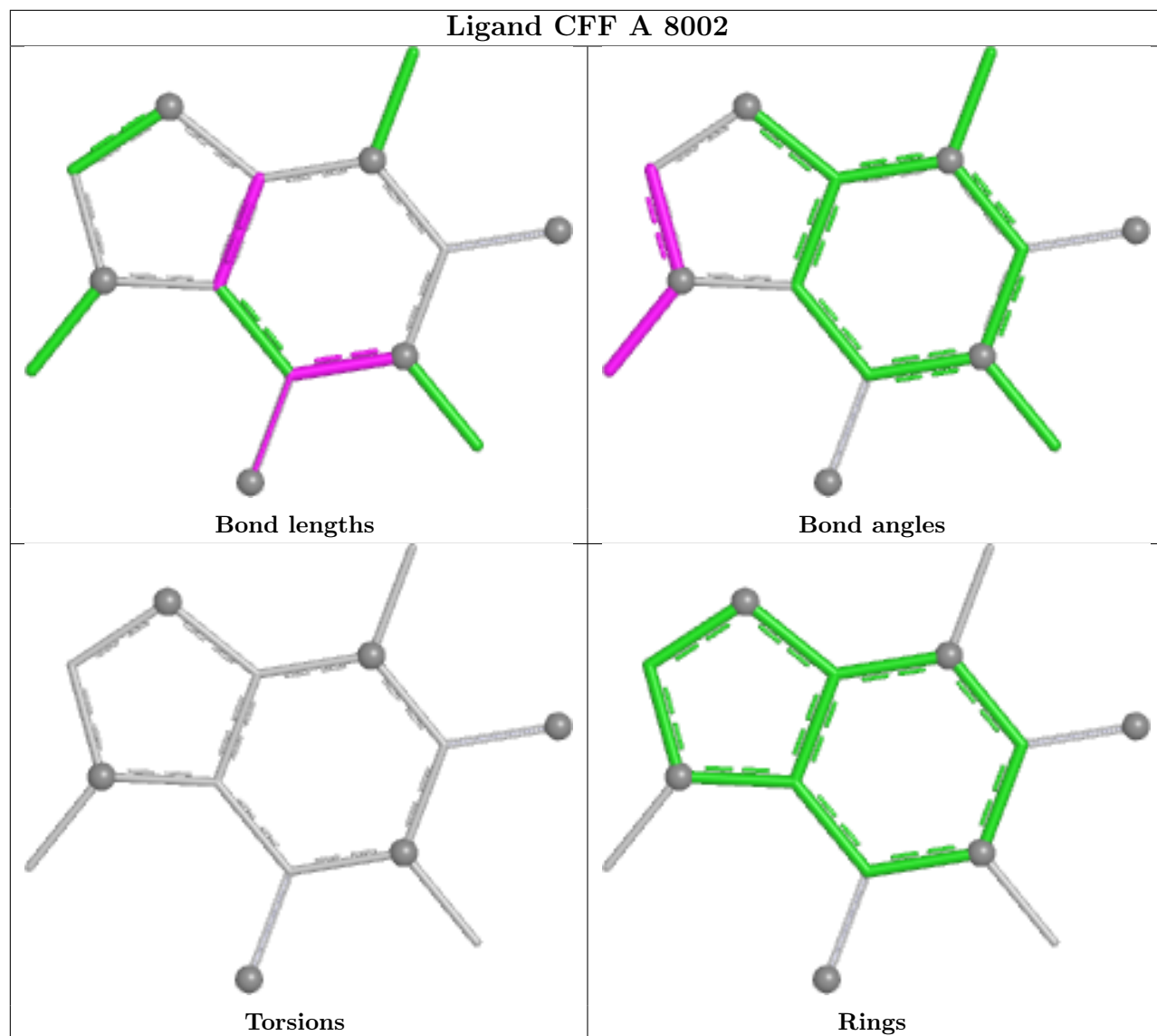


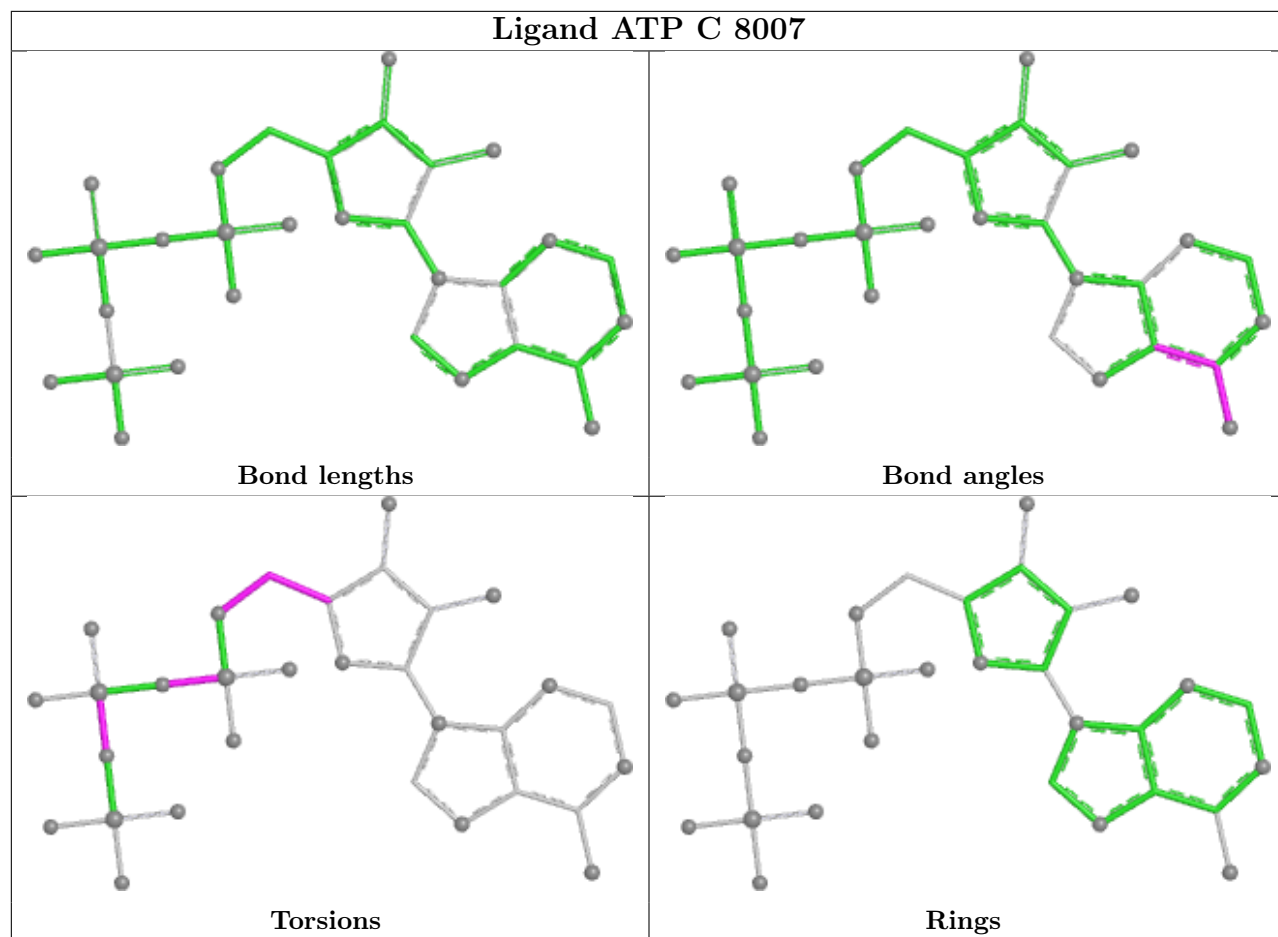


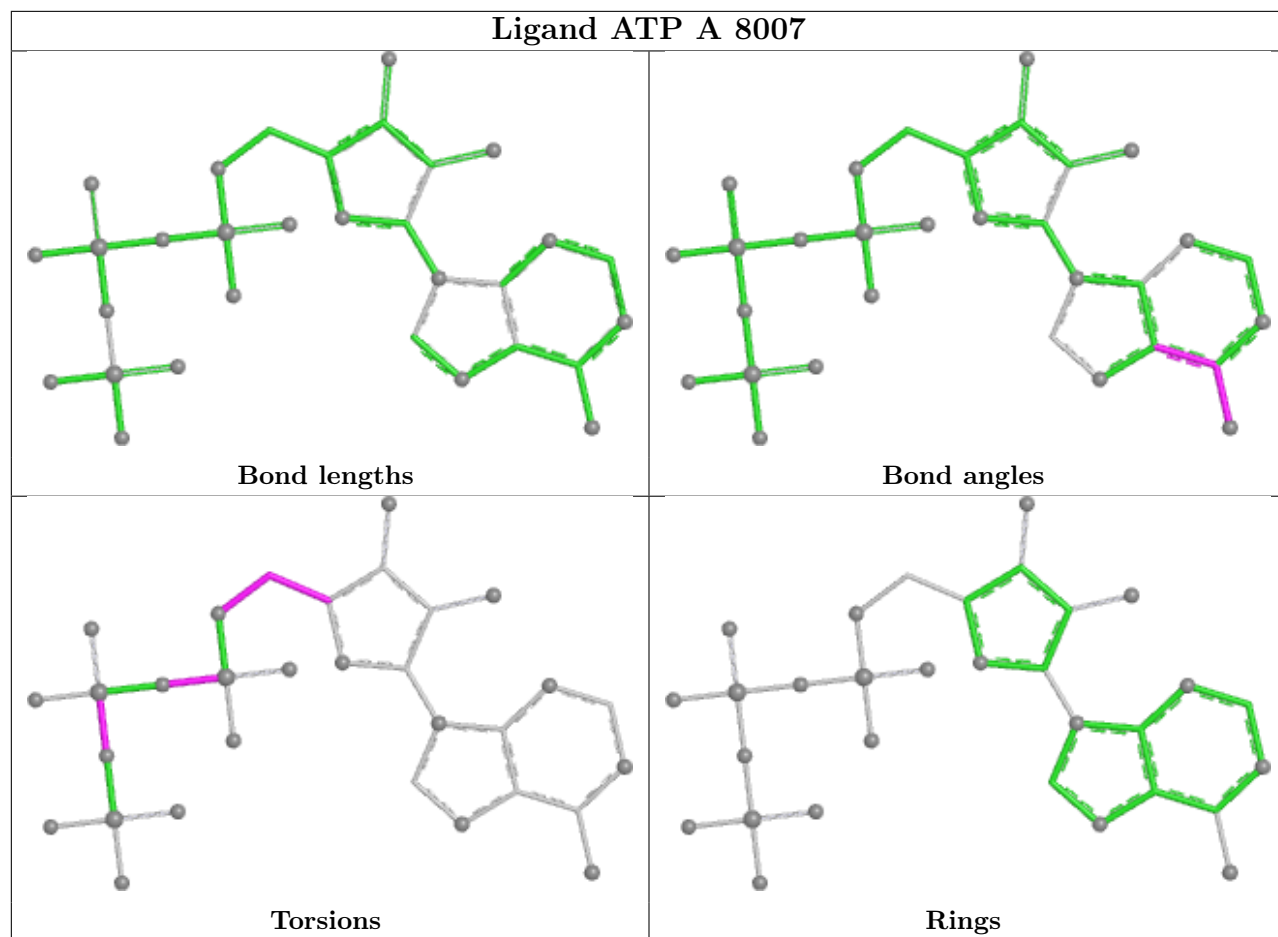


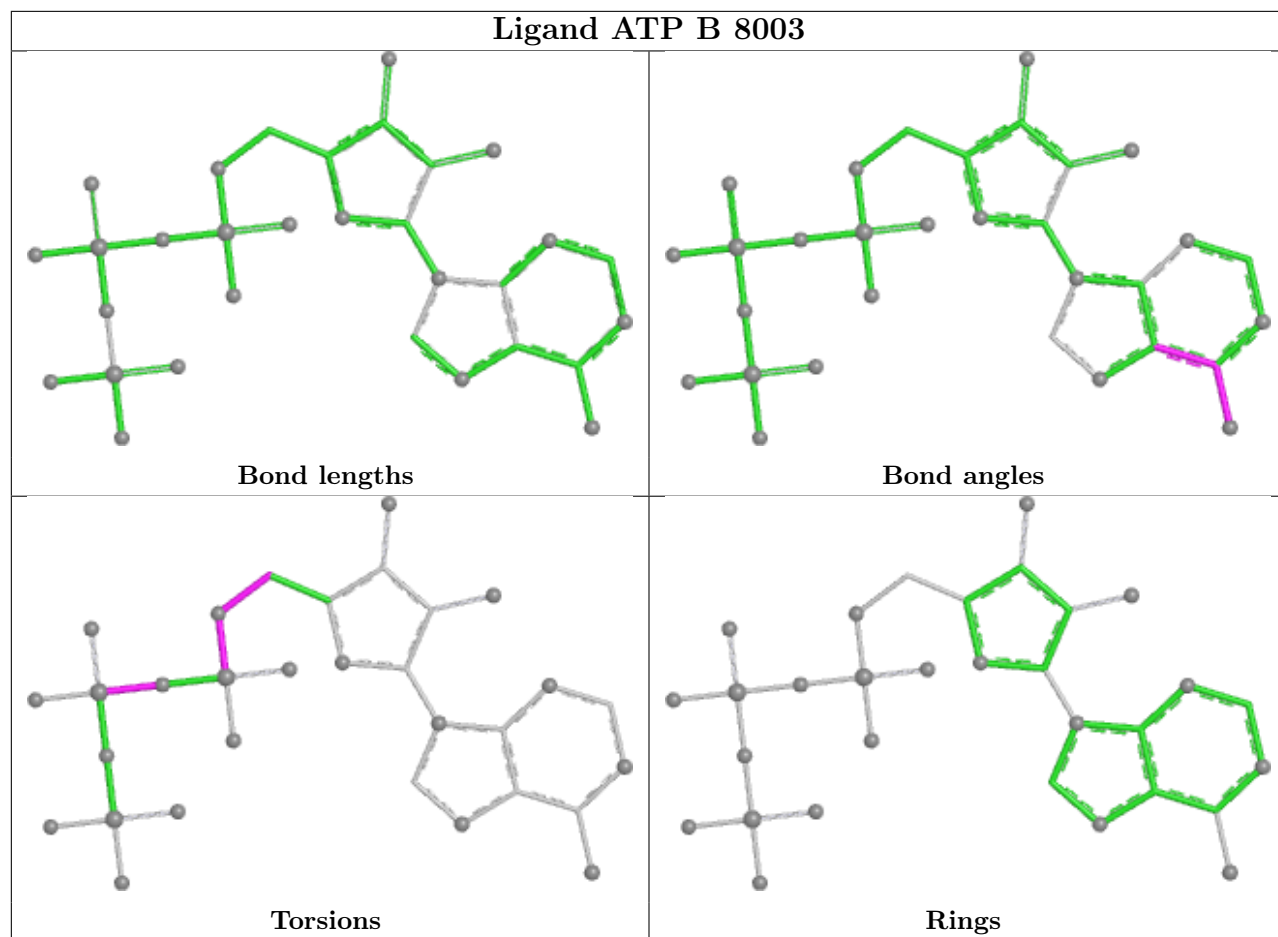


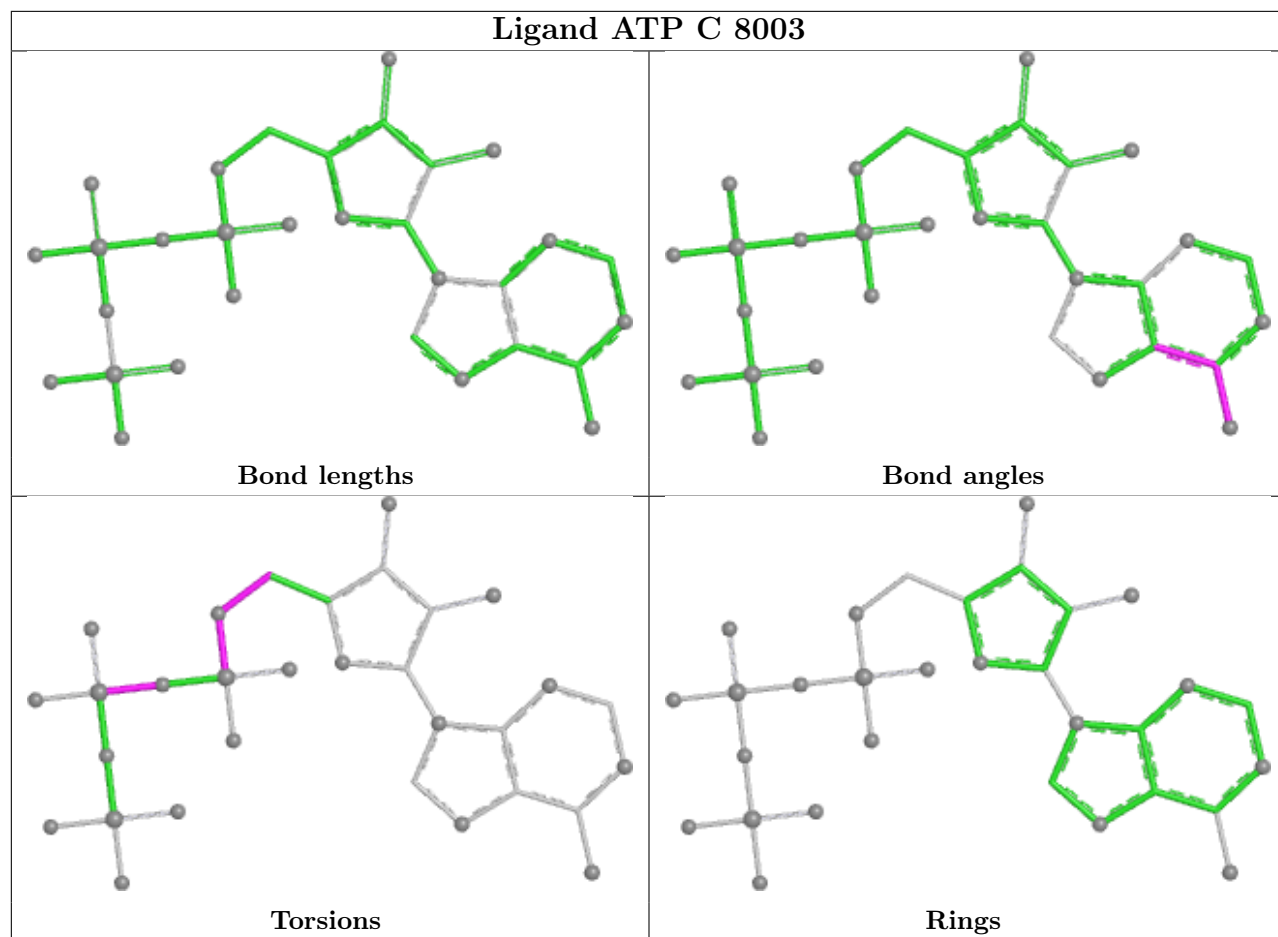


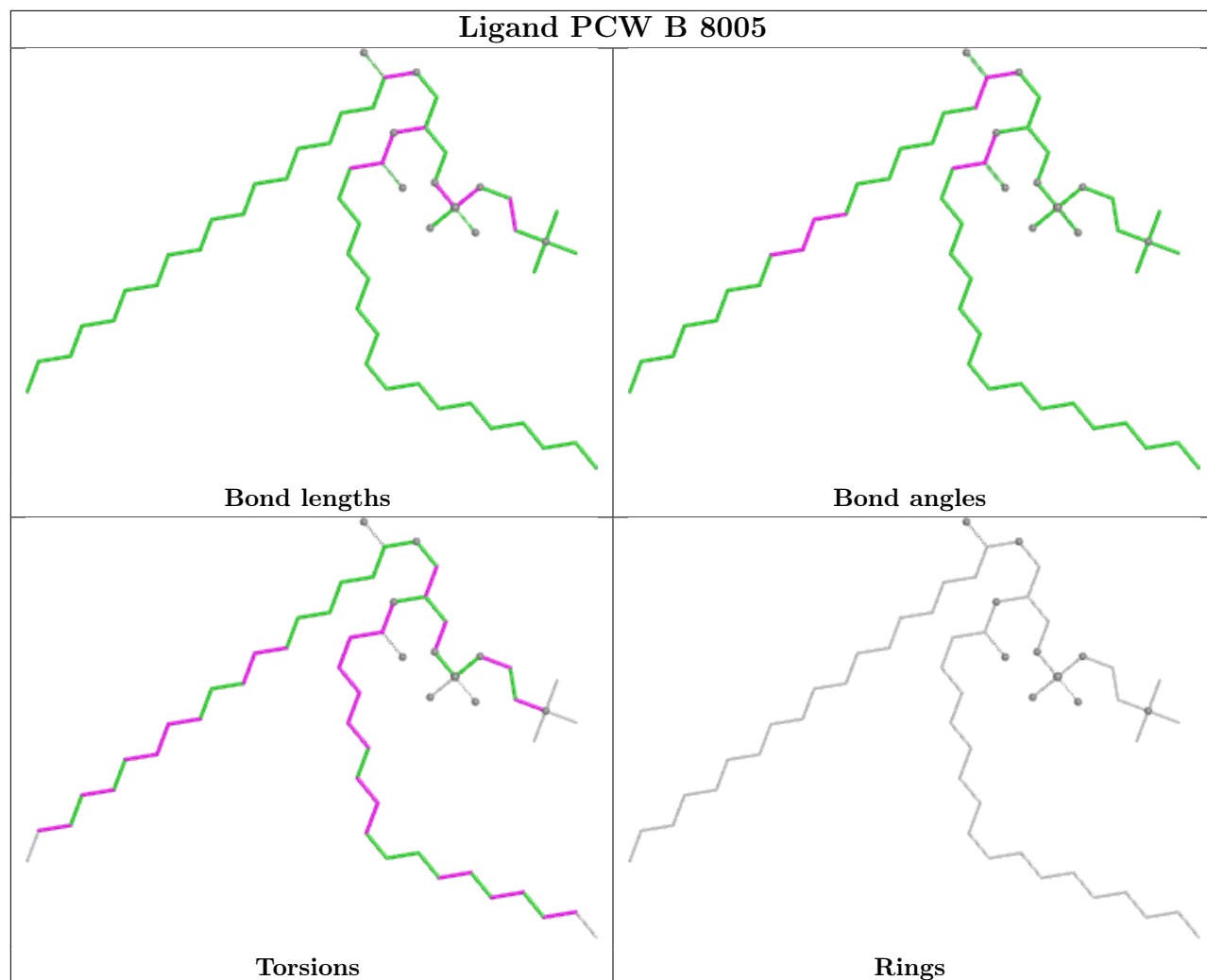


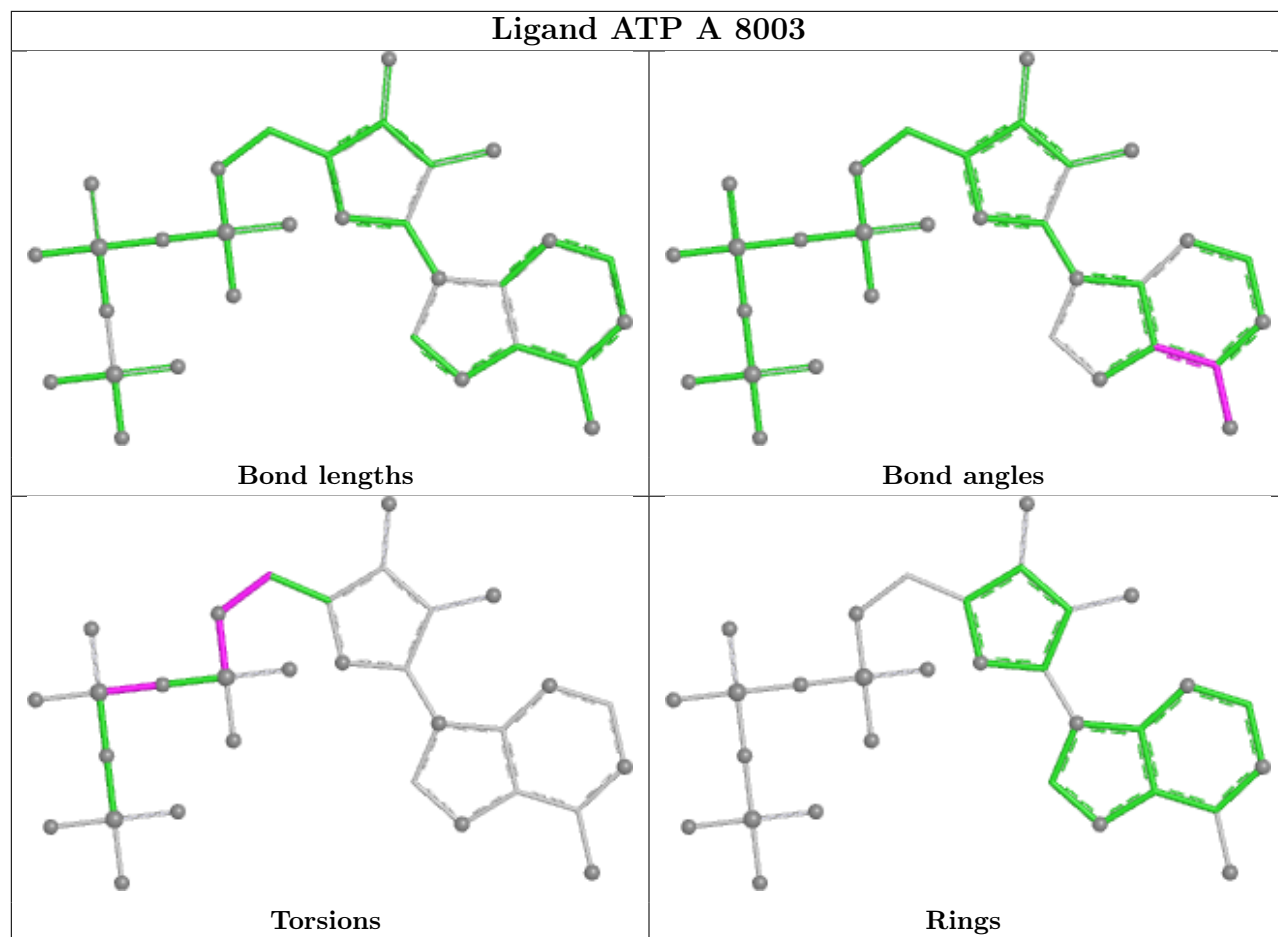


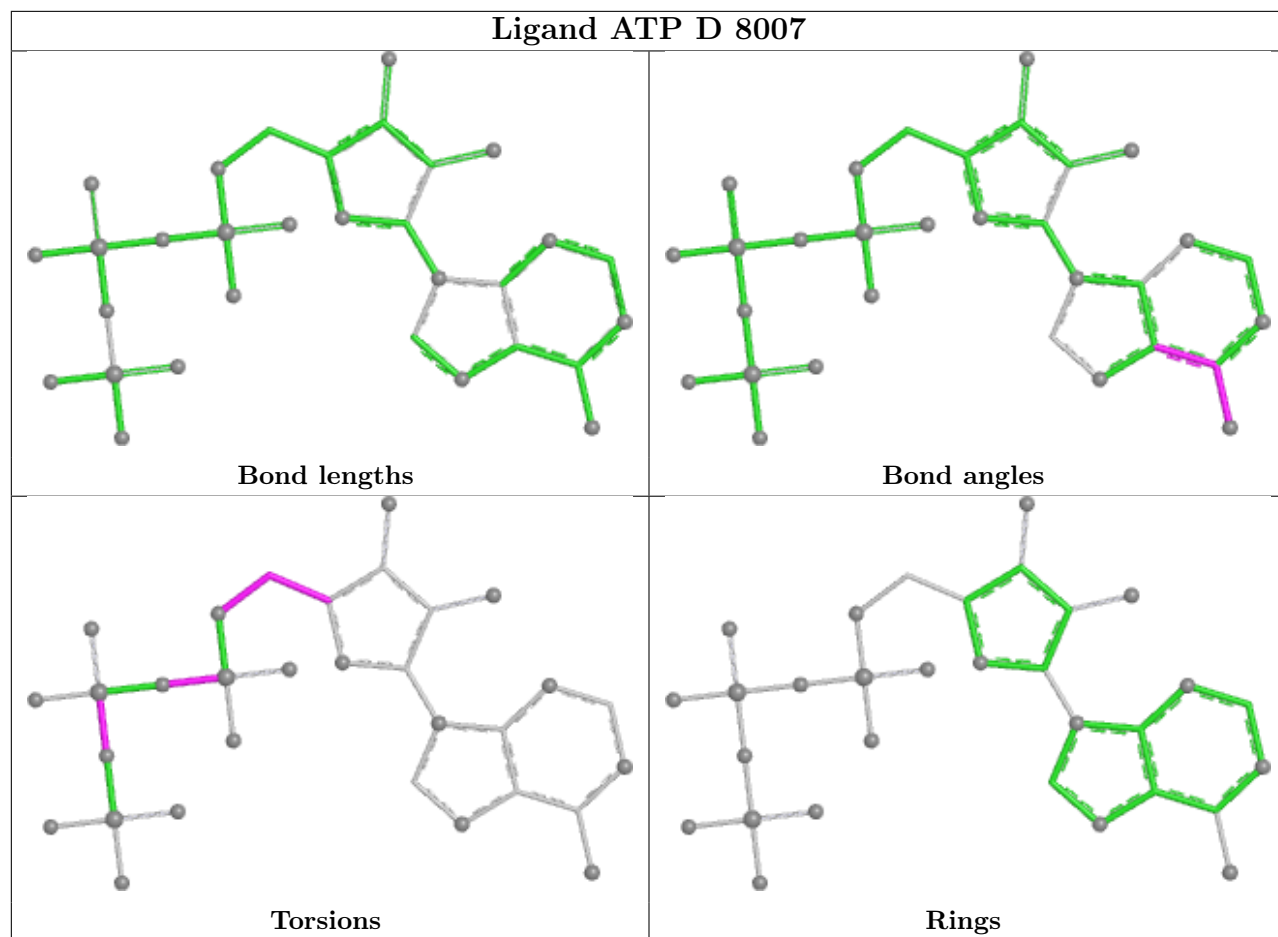


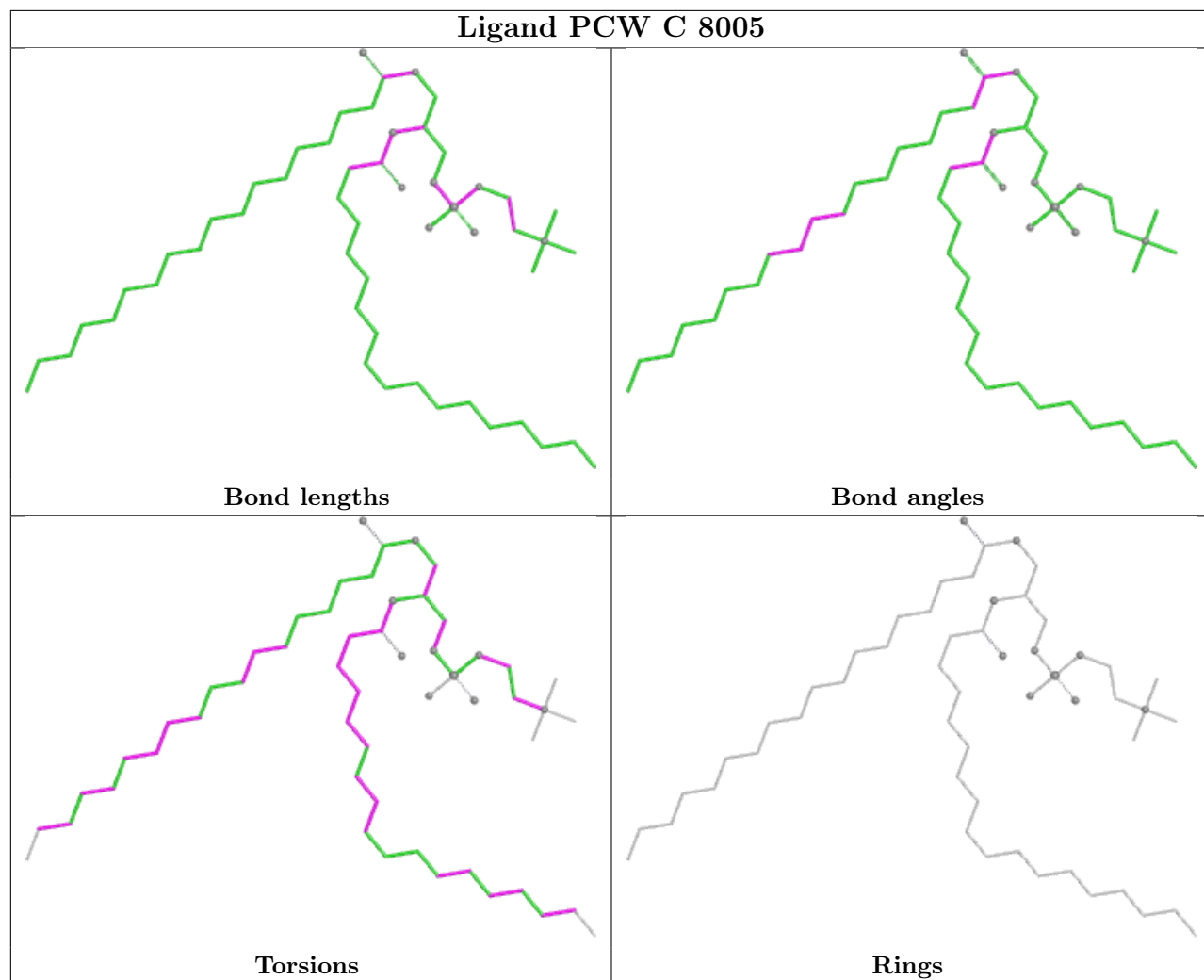


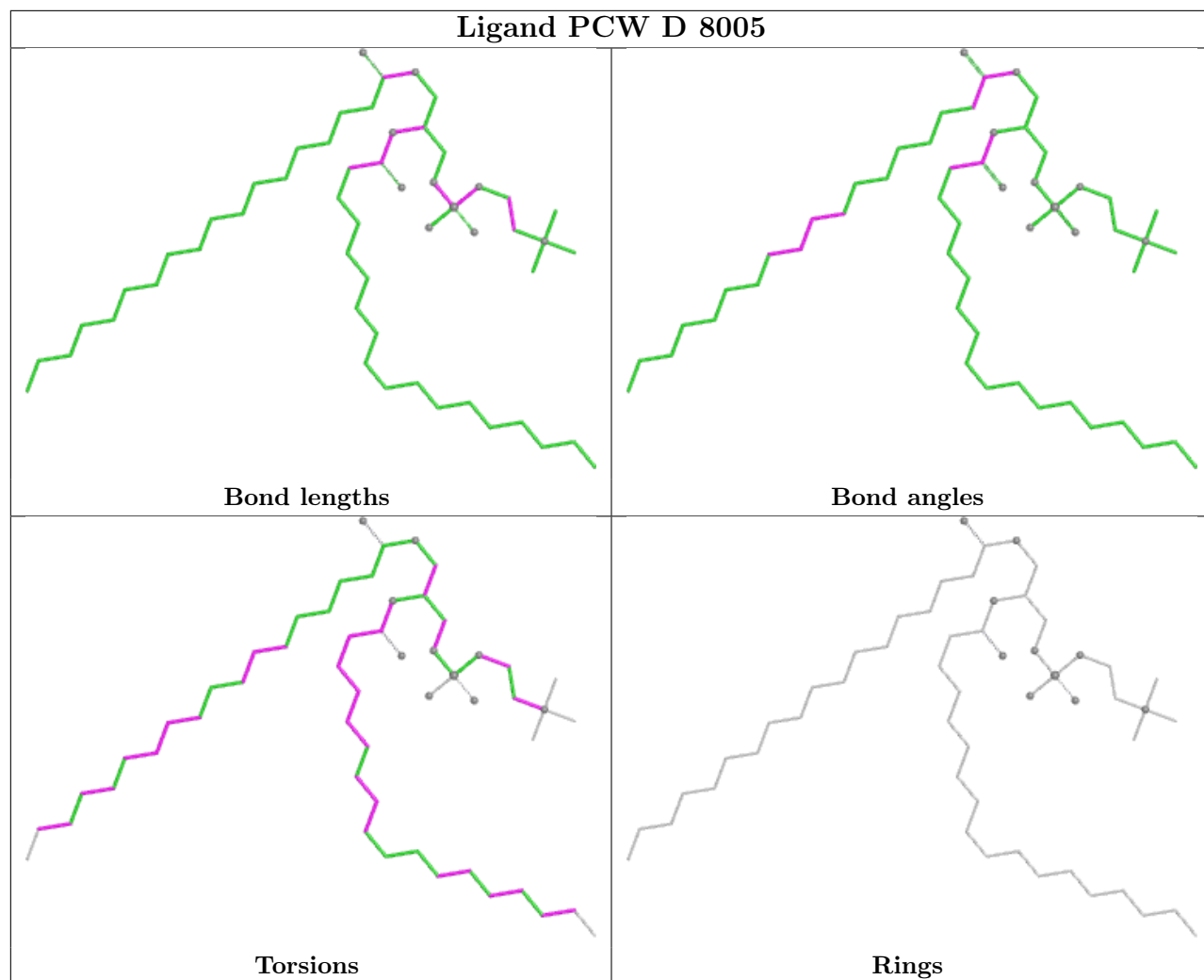


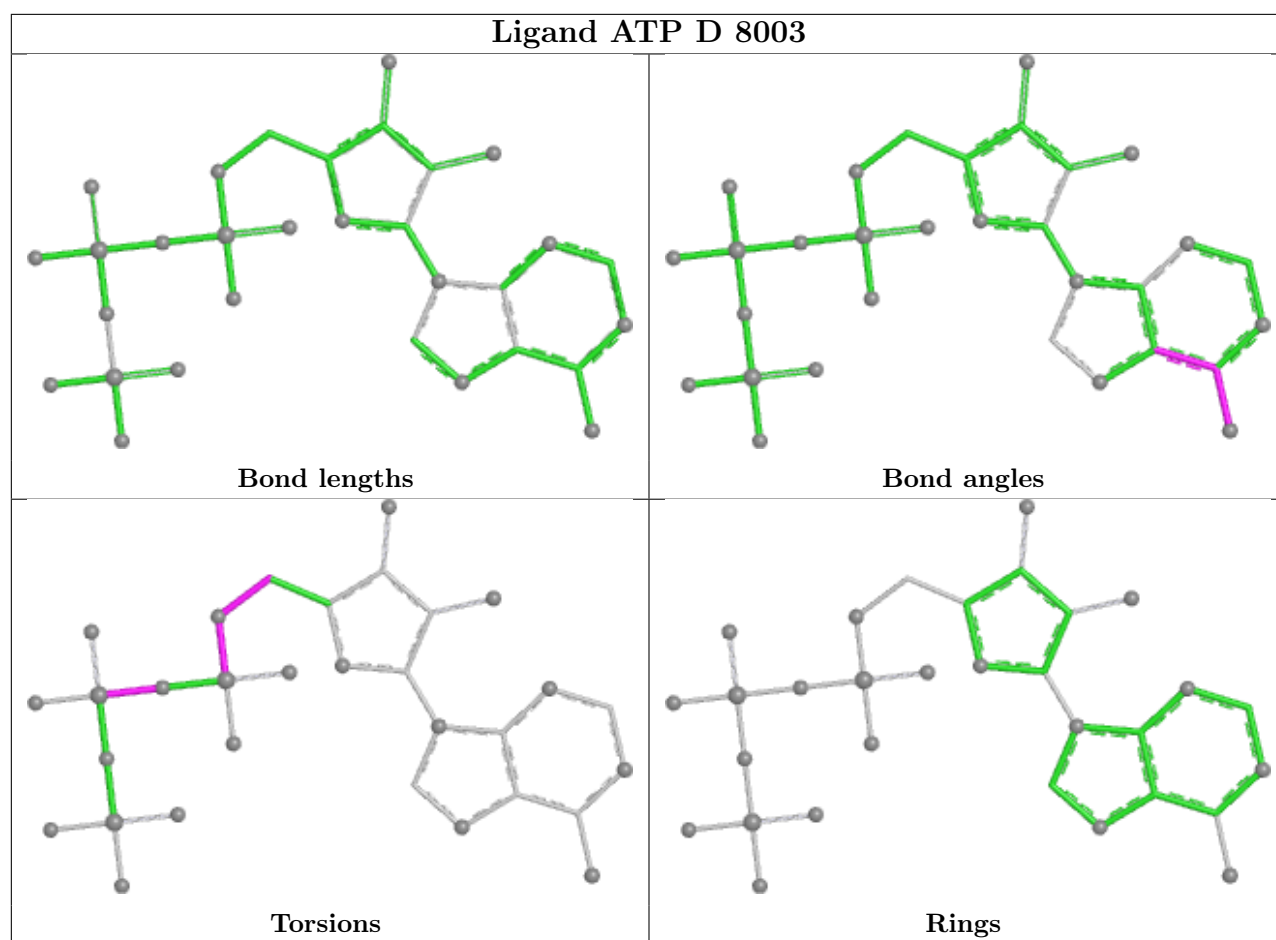












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

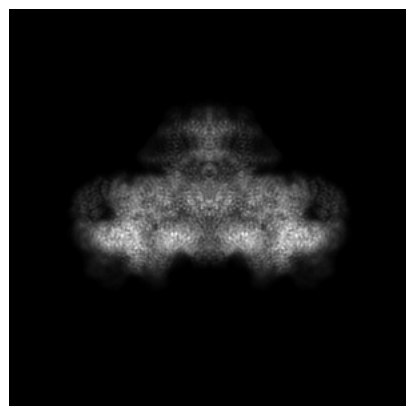
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49534. These allow visual inspection of the internal detail of the map and identification of artifacts.

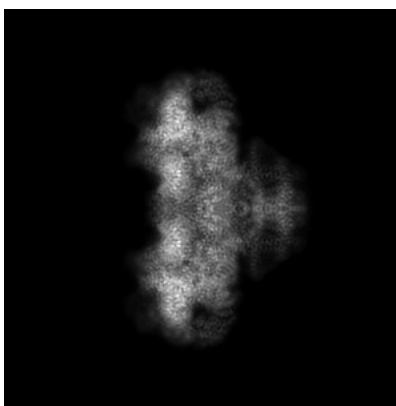
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

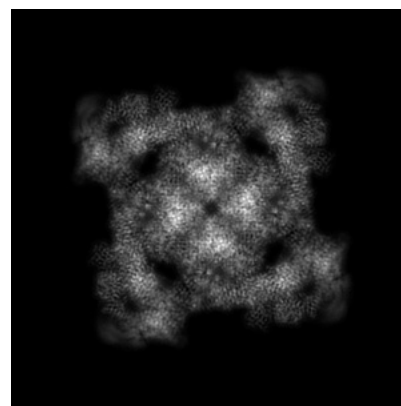
6.1.1 Primary map



X

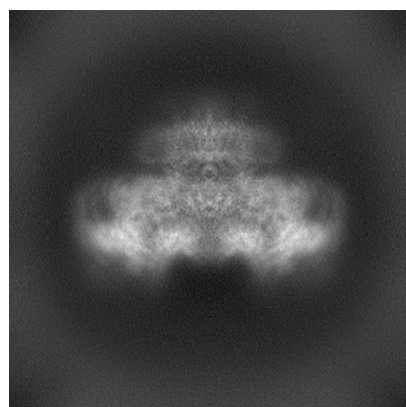


Y

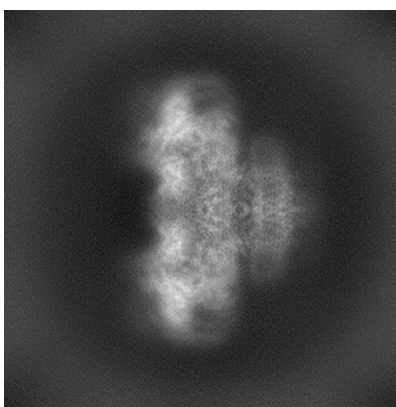


Z

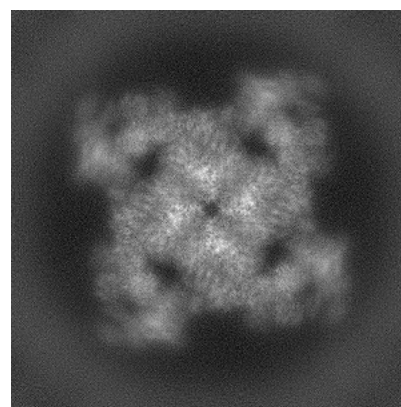
6.1.2 Raw map



X



Y

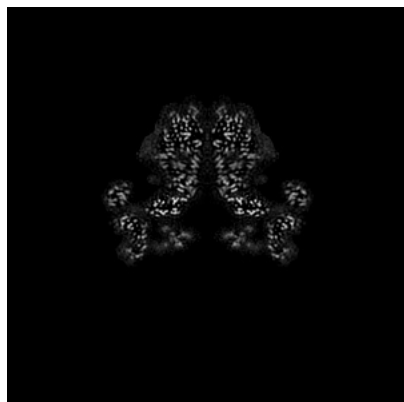


Z

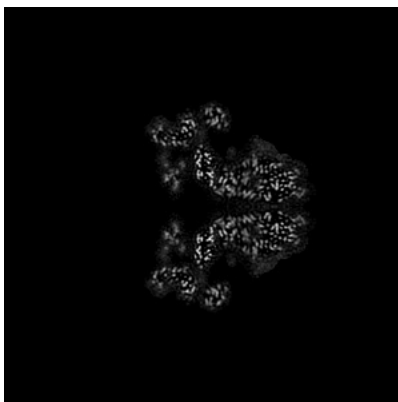
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

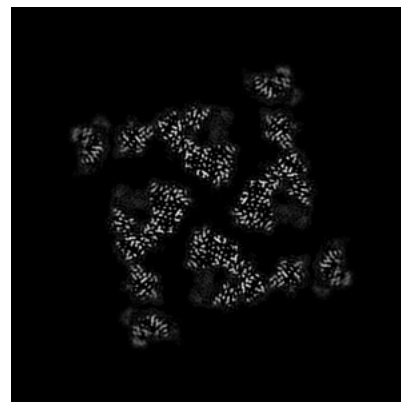
6.2.1 Primary map



X Index: 256

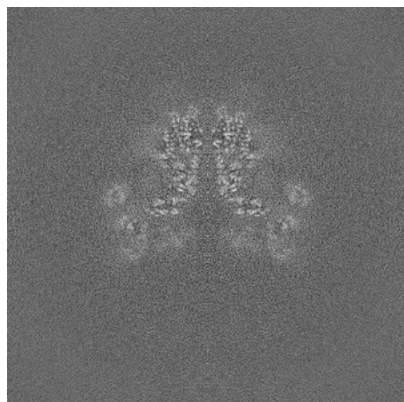


Y Index: 256

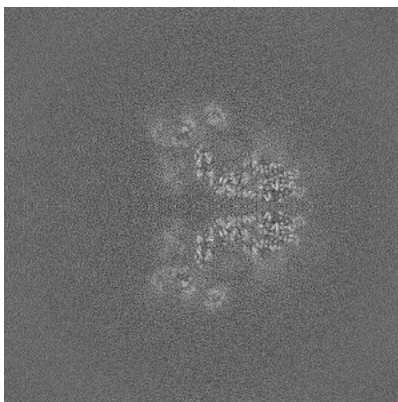


Z Index: 256

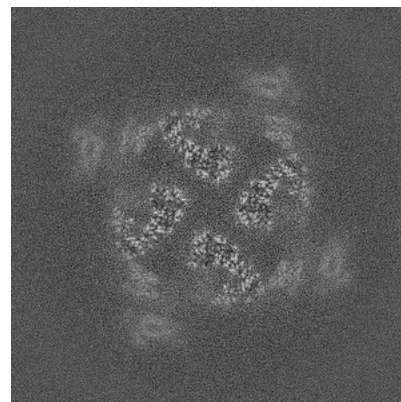
6.2.2 Raw map



X Index: 256



Y Index: 256

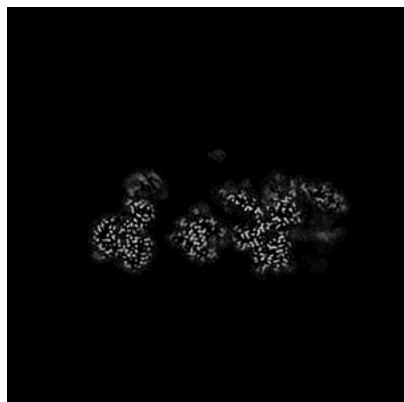


Z Index: 256

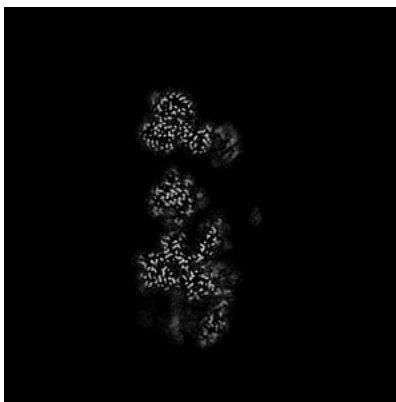
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

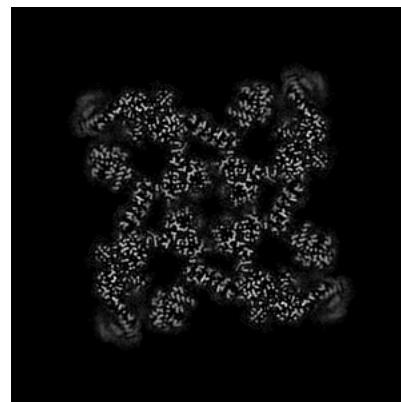
6.3.1 Primary map



X Index: 348

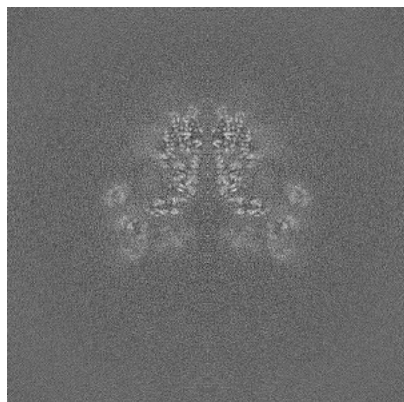


Y Index: 348

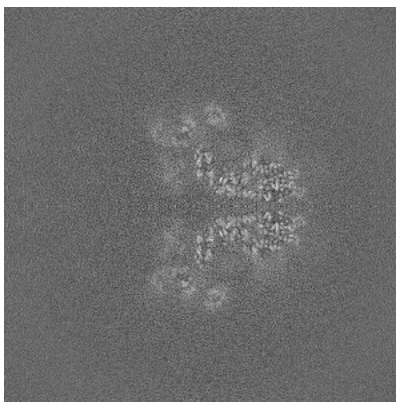


Z Index: 224

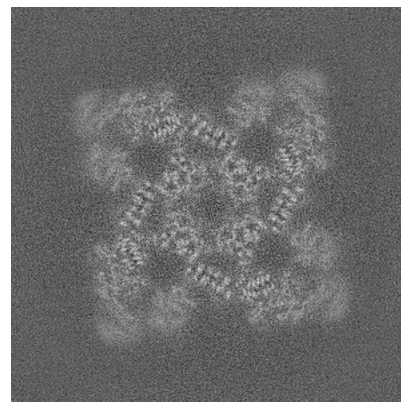
6.3.2 Raw map



X Index: 256



Y Index: 256

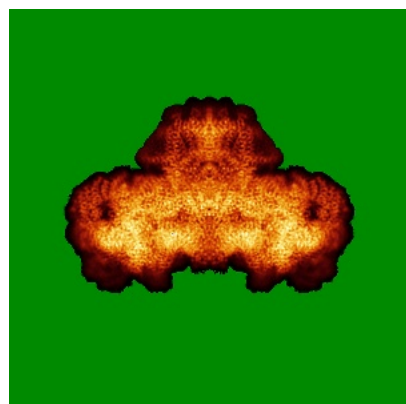


Z Index: 225

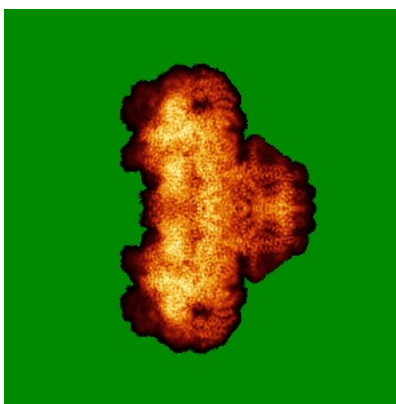
The images above show the largest variance slices of the map in three orthogonal directions.

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

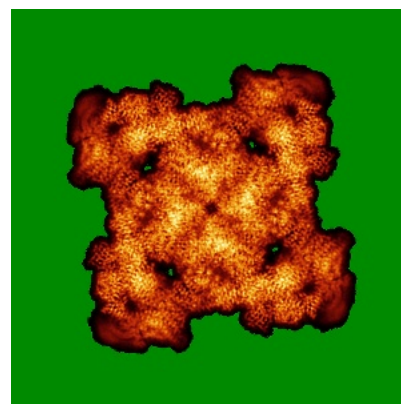
6.4.1 Primary map



X

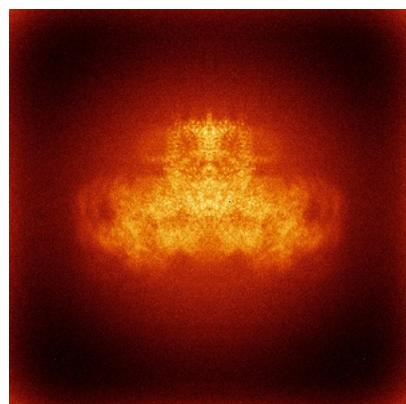


Y

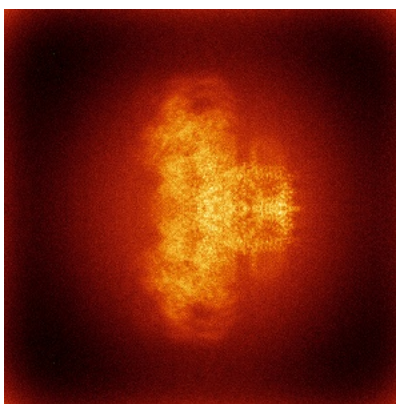


Z

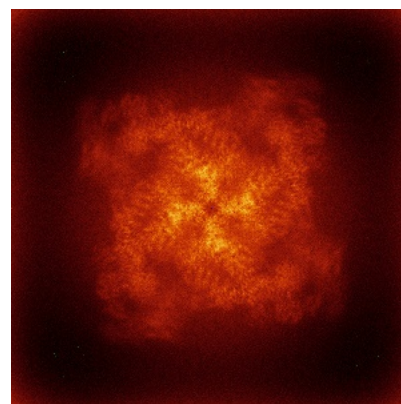
6.4.2 Raw map



X



Y

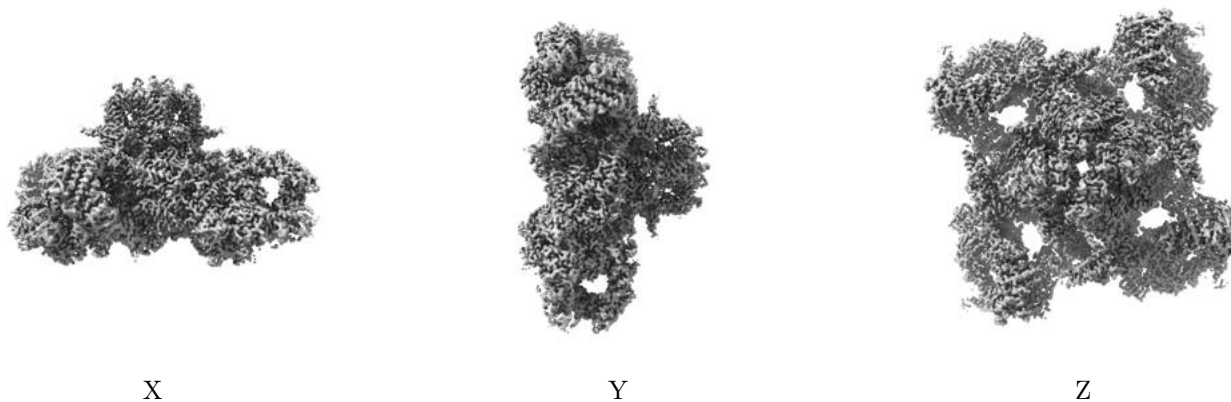


Z

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.

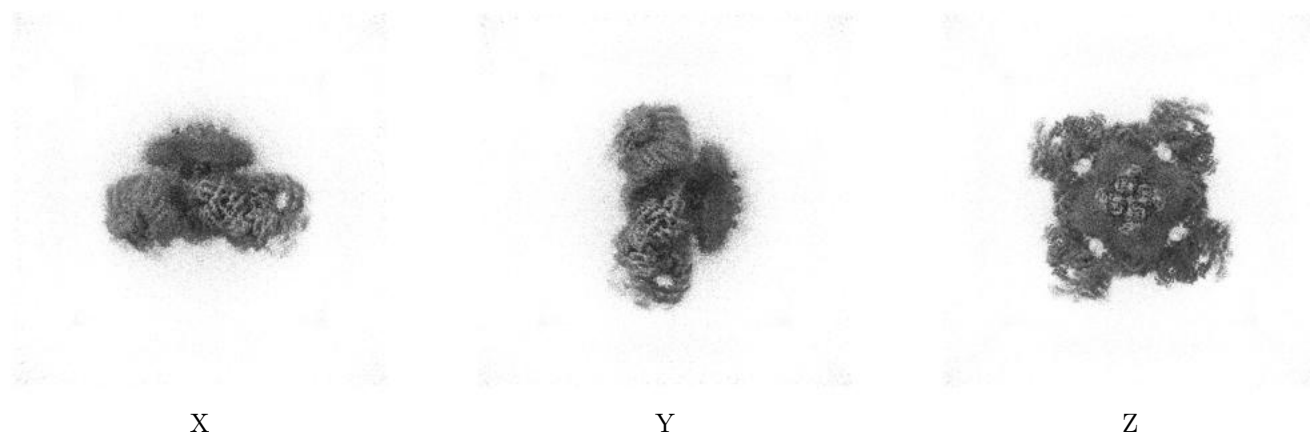
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

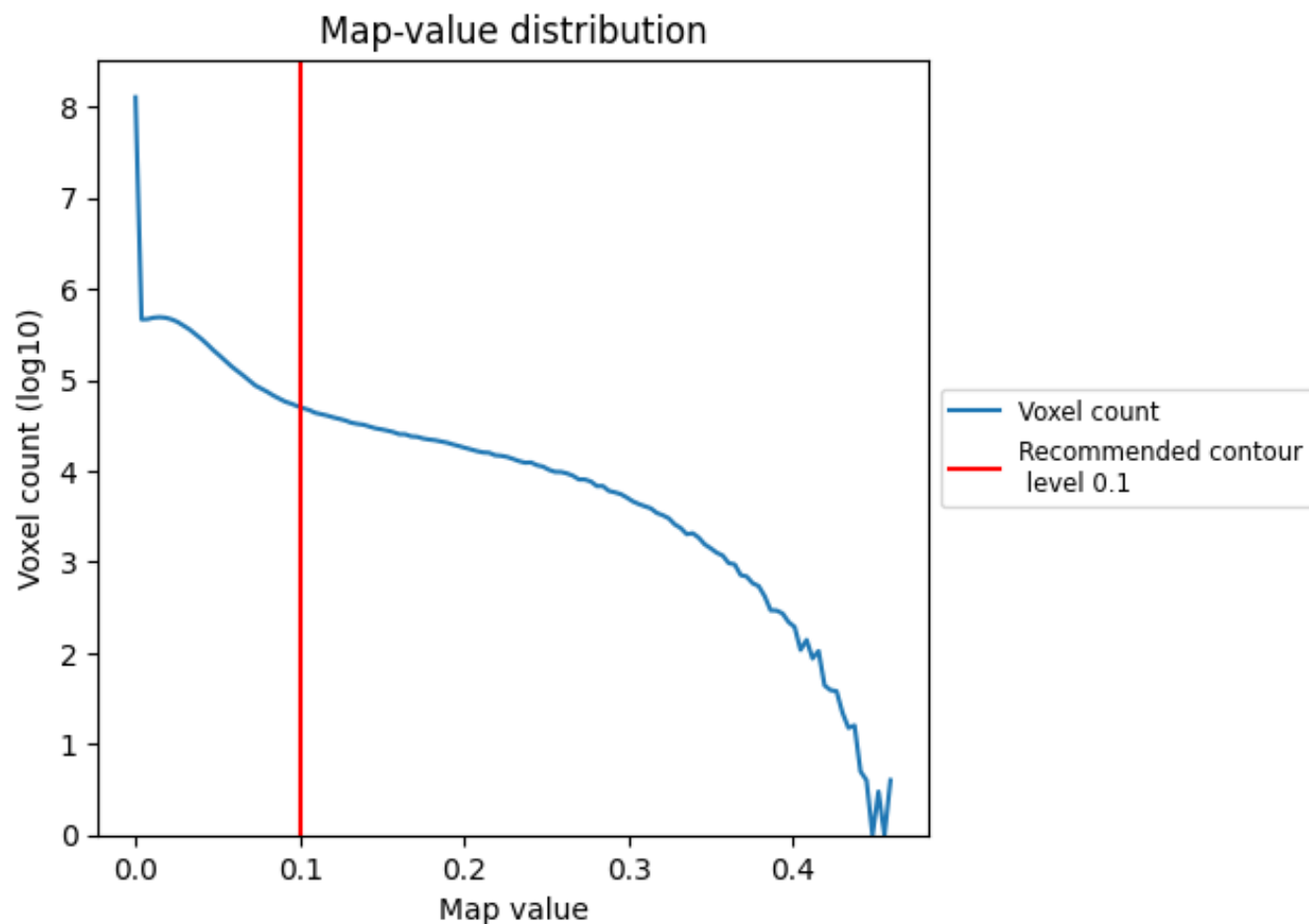
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

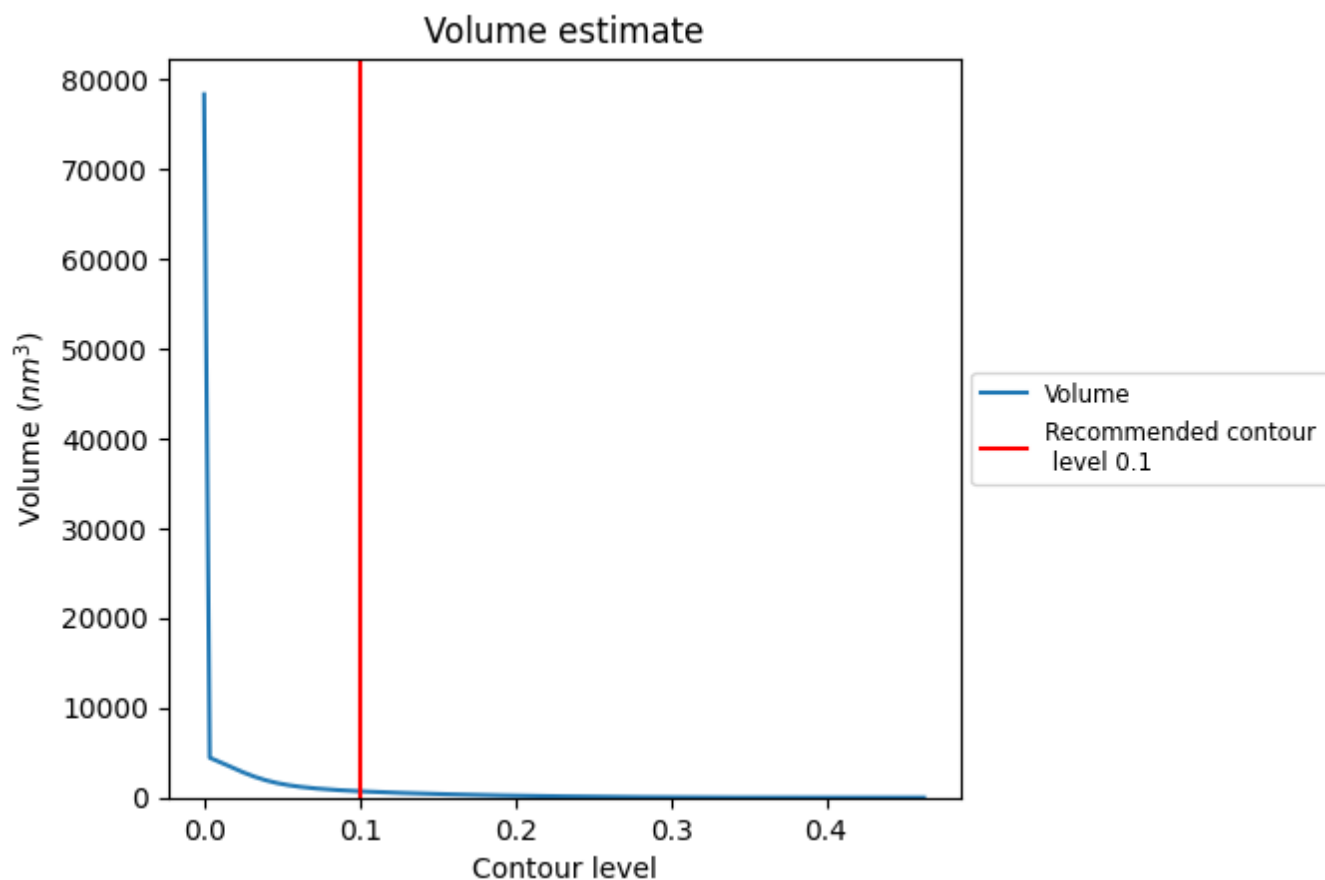
This section contains the results of statistical analysis of the map.

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.

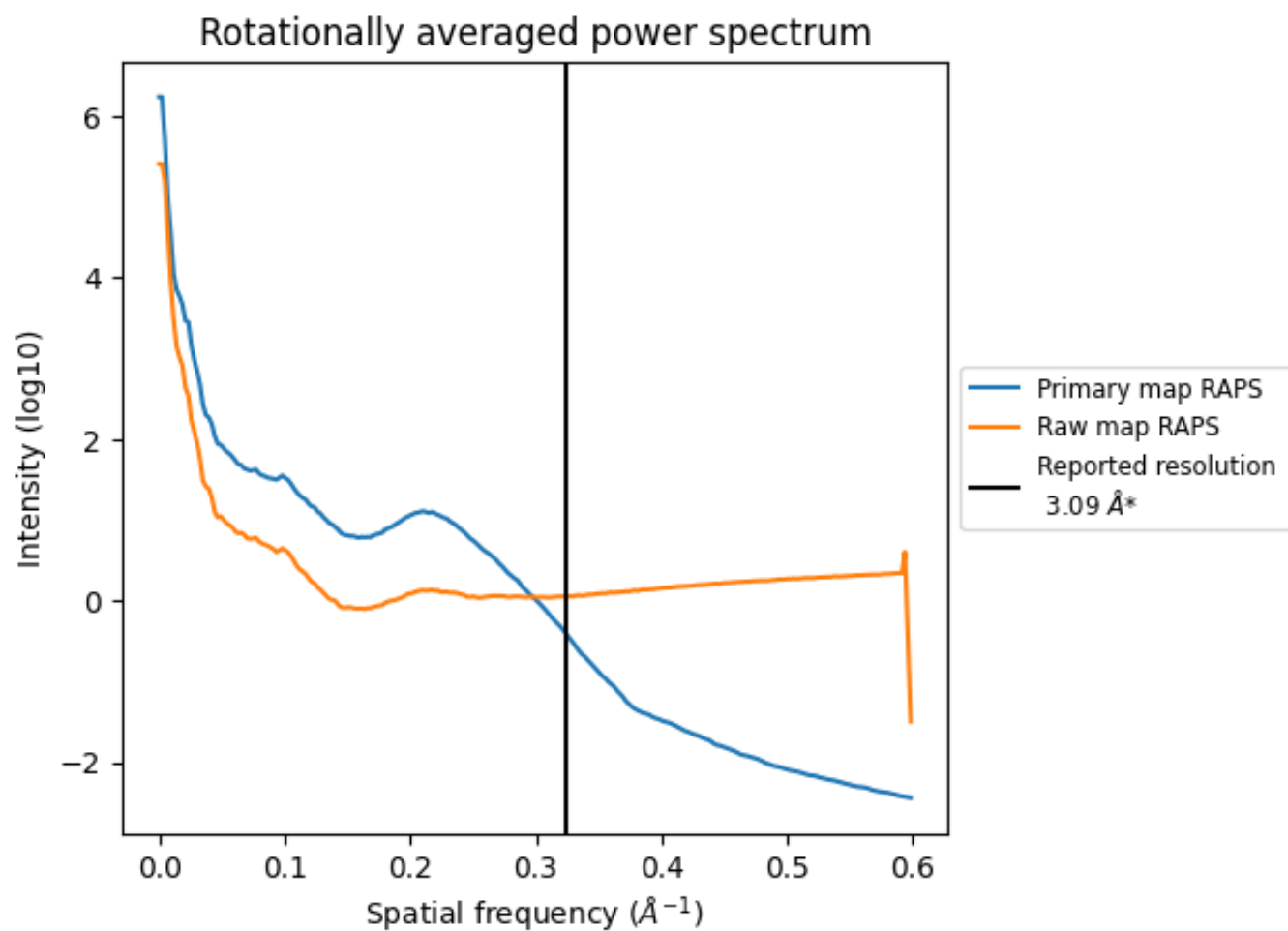
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 703 nm³; this corresponds to an approximate mass of 635 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 ⓘ

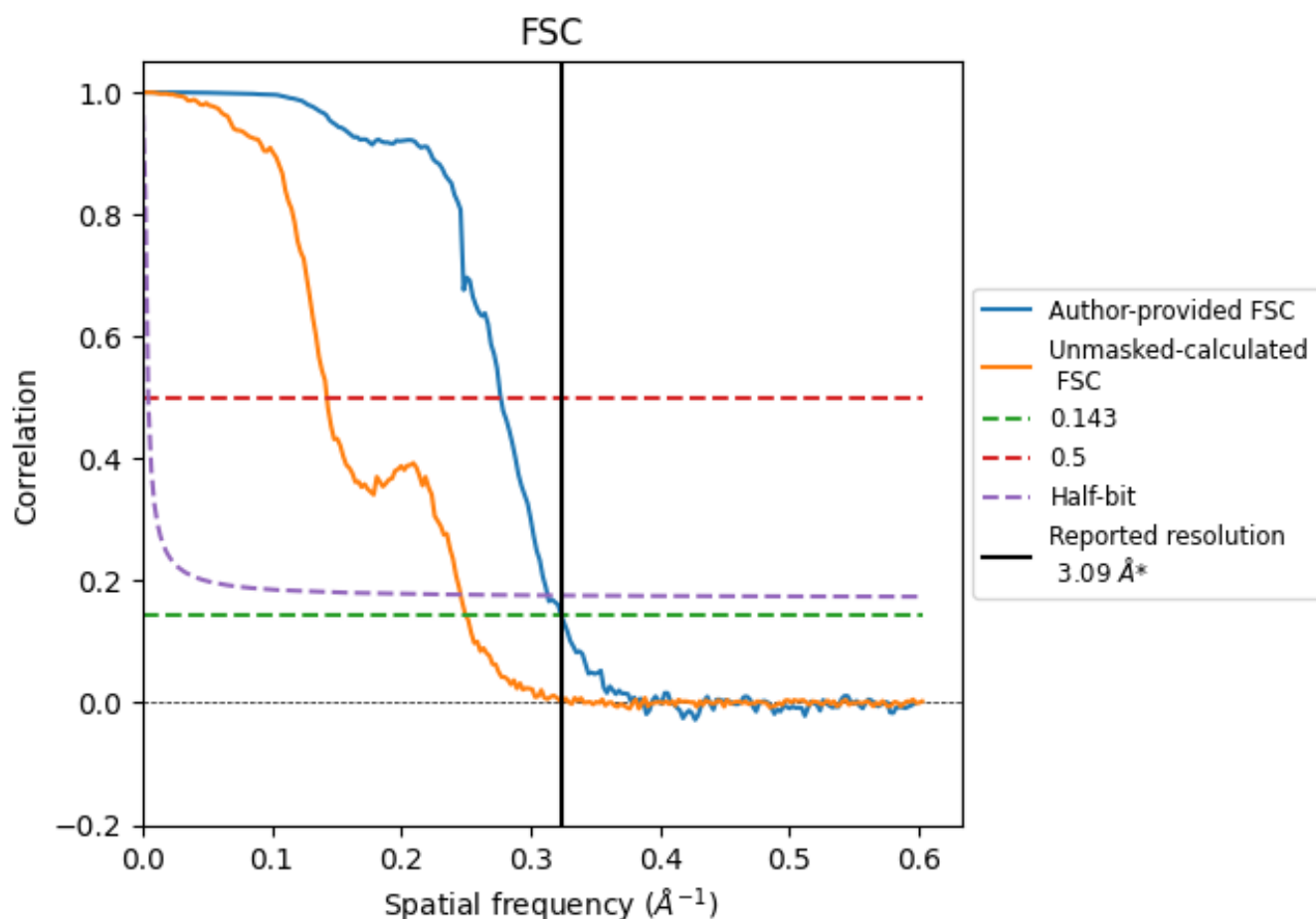


*Reported resolution corresponds to spatial frequency of 0.324 \AA^{-1}

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 0.324 \AA^{-1}

8.2 Resolution estimates [i](#)

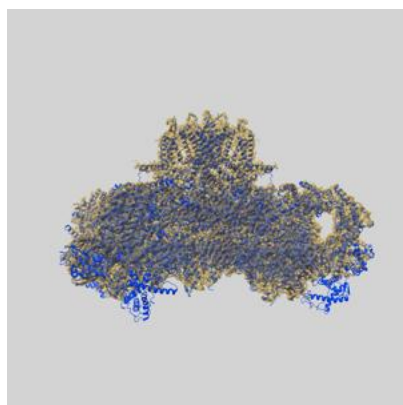
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	3.09	3.61	3.19
Unmasked-calculated*	4.00	7.01	4.07

*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 4.00 differs from the reported value 3.09 by more than 10 %

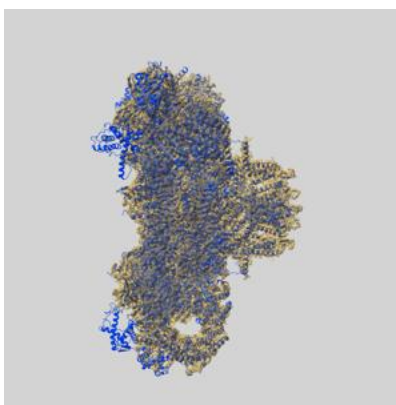
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49534 and PDB model 9NMN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

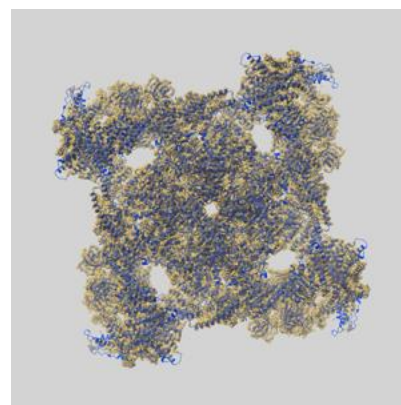
9.1 Map-model overlay [i](#)



X



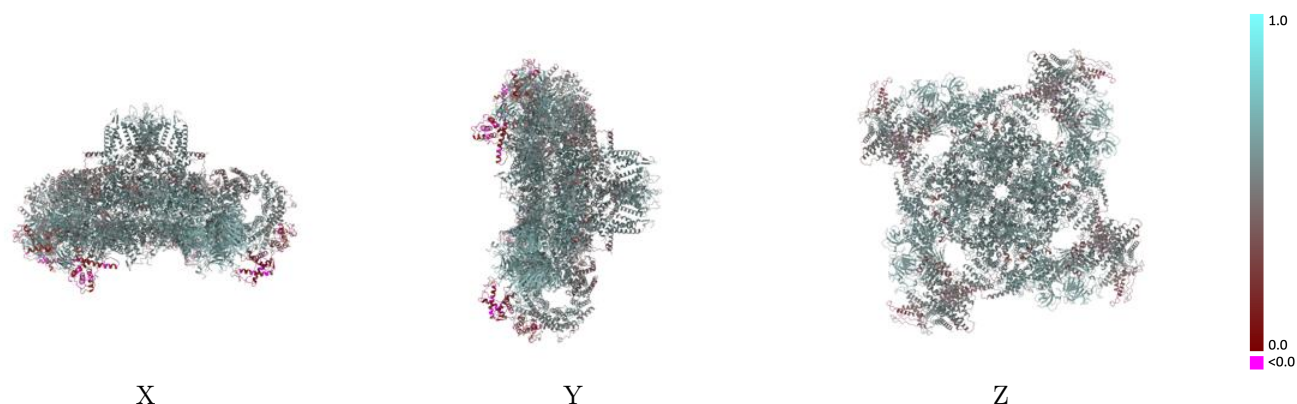
Y



Z

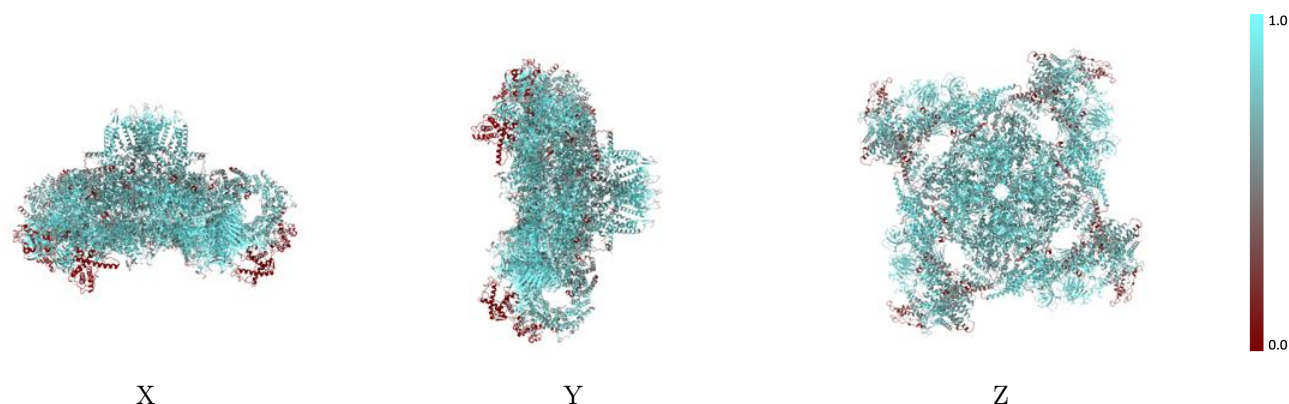
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



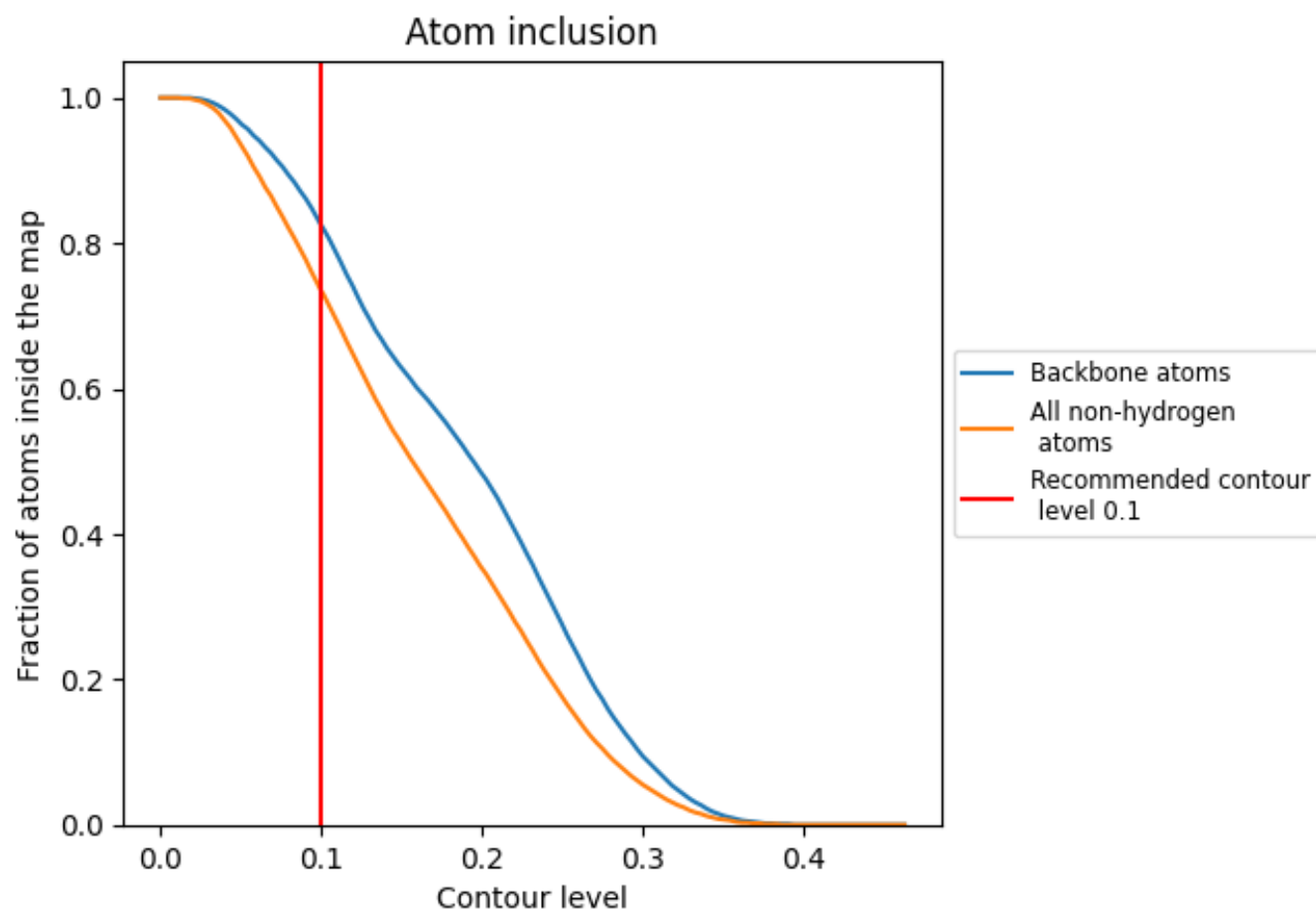
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 73% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7340	<div></div> 0.5250
A	<div></div> 0.7320	<div></div> 0.5230
B	<div></div> 0.7320	<div></div> 0.5230
C	<div></div> 0.7320	<div></div> 0.5230
D	<div></div> 0.7320	<div></div> 0.5230
E	<div></div> 0.8480	<div></div> 0.6050
F	<div></div> 0.8440	<div></div> 0.6060
G	<div></div> 0.8430	<div></div> 0.6070
H	<div></div> 0.8400	<div></div> 0.6050

