



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:53 am BST

PDB ID : 1FAG
Title : STRUCTURE OF CYTOCHROME P450
Authors : Li, H.Y.; Poulos, T.L.
Deposited on : 1996-08-01
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

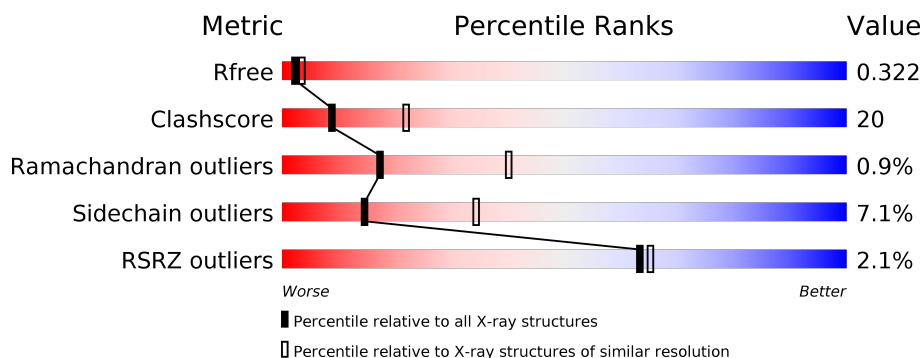
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	471	<div> <div>0%</div> <div> <div></div> <div>58%</div> <div>36%</div> <div>• •</div> </div> </div>
1	B	471	<div> <div>2%</div> <div> <div></div> <div>53%</div> <div>39%</div> <div>5%</div> <div>•</div> </div> </div>
1	C	471	<div> <div>3%</div> <div> <div></div> <div>52%</div> <div>42%</div> <div>• •</div> </div> </div>
1	D	471	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>40%</div> <div>• •</div> </div> </div>

2 Entry composition [i](#)

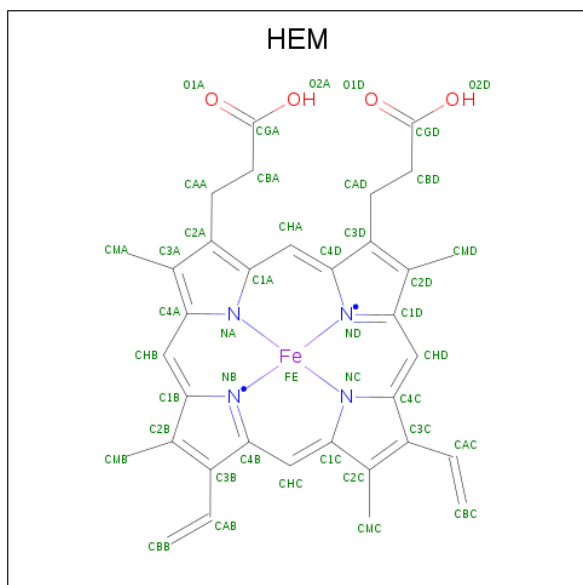
There are 3 unique types of molecules in this entry. The entry contains 14924 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CYTOCHROME P450 BM-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	0	0
			3670	2345	623	685	17			
1	B	455	Total	C	N	O	S	0	0	0
			3670	2345	623	685	17			
1	C	455	Total	C	N	O	S	0	0	0
			3670	2345	623	685	17			
1	D	455	Total	C	N	O	S	0	0	0
			3670	2345	623	685	17			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



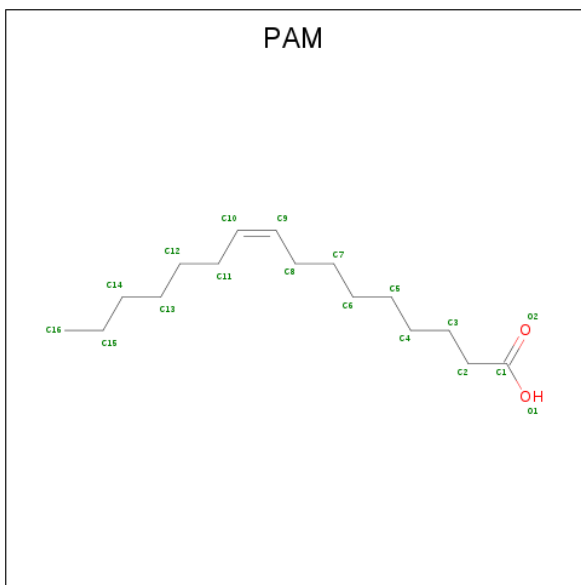
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N O	0	0
			43	34	1	4 4		
2	B	1	Total	C	Fe	N O	0	0
			43	34	1	4 4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 3 is PALMITOLEIC ACID (three-letter code: PAM) (formula: C₁₆H₃₀O₂).

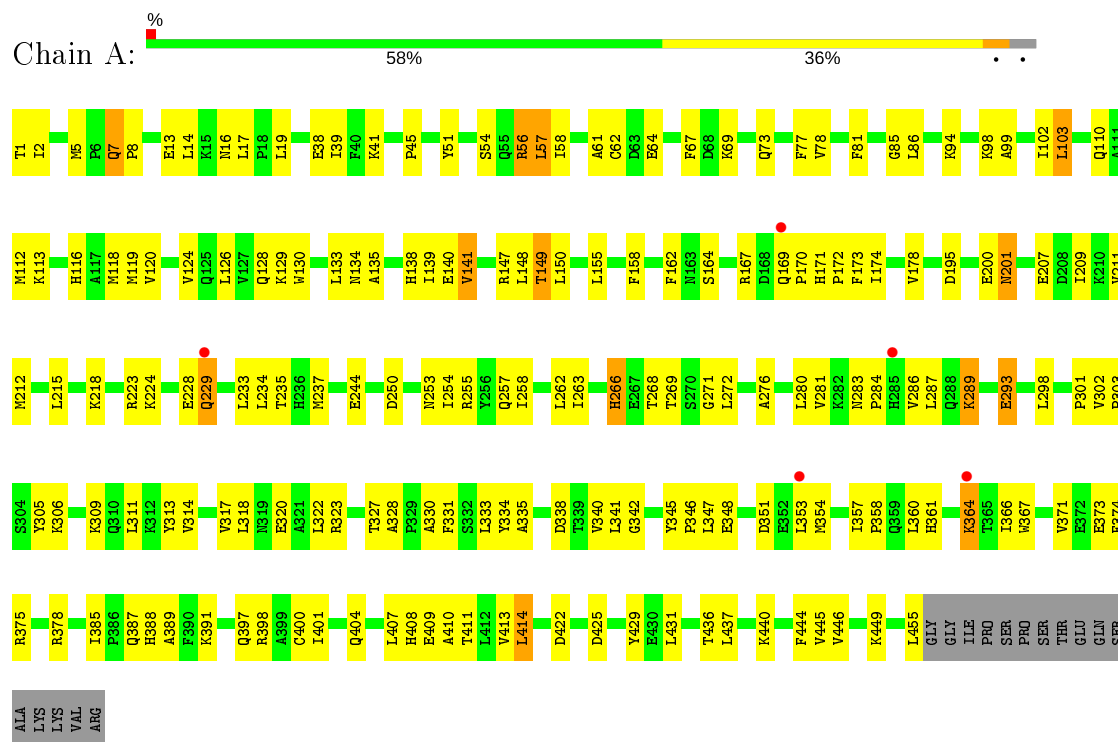


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O		
			18	16	2	0	0
3	B	1	Total	C	O		
			18	16	2	0	0
3	C	1	Total	C	O		
			18	16	2	0	0
3	D	1	Total	C	O		
			18	16	2	0	0

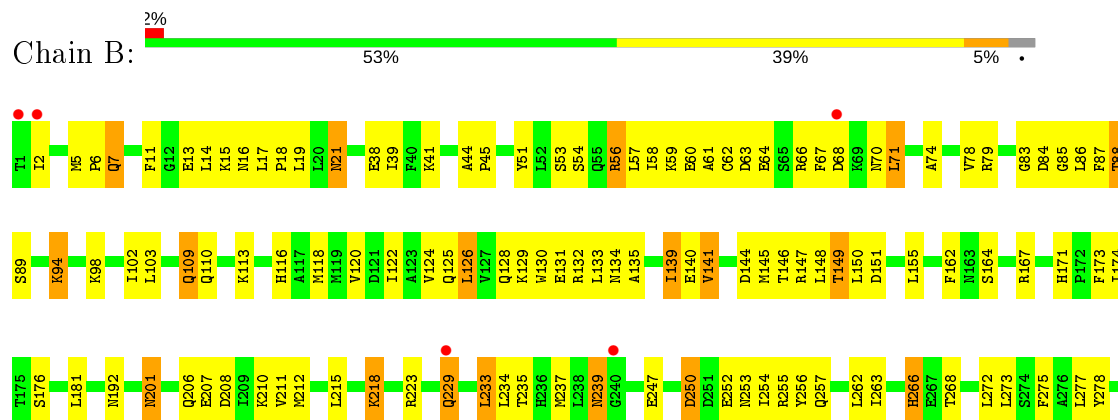
3 Residue-property plots

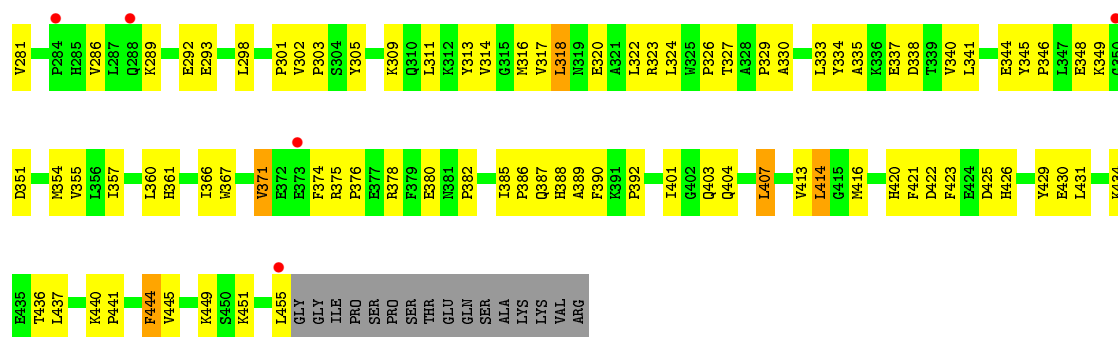
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: CYTOCHROME P450 BM-3

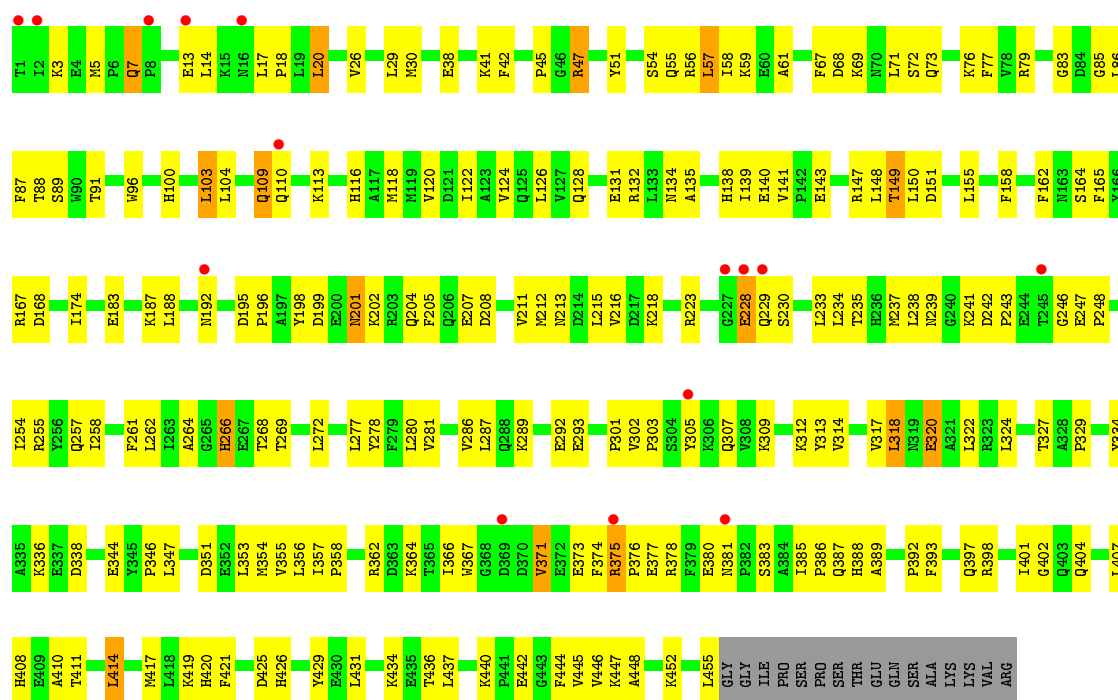


• Molecule 1: CYTOCHROME P450 BM-3

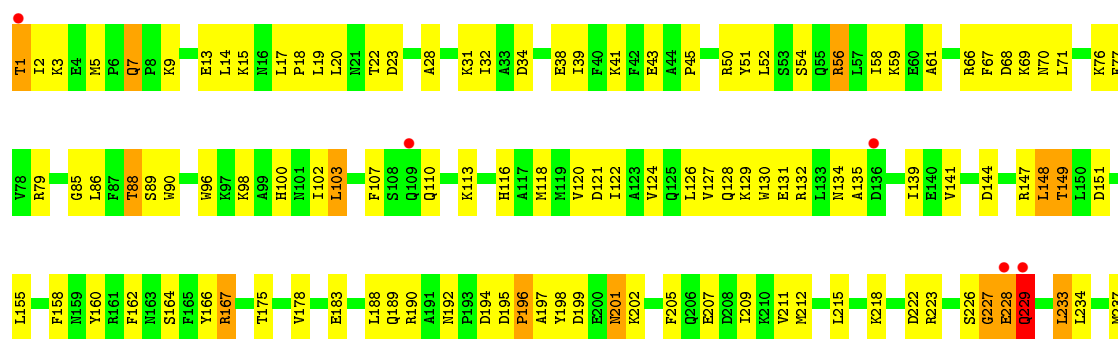


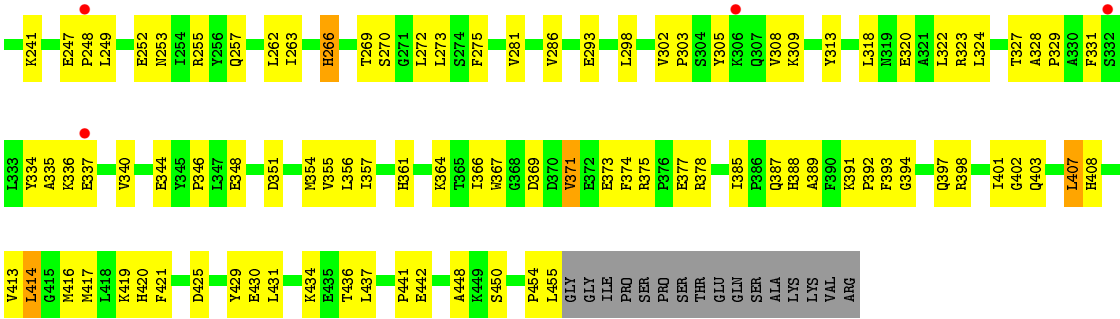


● Molecule 1: CYTOCHROME P450 BM-3



● Molecule 1: CYTOCHROME P450 BM-3





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	106.20 Å 165.20 Å 223.90 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70 19.90 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.4 (10.00-2.70) 99.8 (19.90-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.59 Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.246 , 0.353 0.234 , 0.322	Depositor DCC
R_{free} test set	6122 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å ²)	64.0	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 85.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14924	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.48	0/3755	0.69	3/5077 (0.1%)
1	B	0.46	0/3755	0.70	1/5077 (0.0%)
1	C	0.46	0/3755	0.67	0/5077
1	D	0.47	0/3755	0.71	1/5077 (0.0%)
All	All	0.47	0/15020	0.69	5/20308 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	333	LEU	CA-CB-CG	5.64	128.28	115.30
1	A	400	CYS	CA-CB-SG	-5.38	104.31	114.00
1	B	333	LEU	CA-CB-CG	5.22	127.30	115.30
1	D	328	ALA	N-CA-C	-5.10	97.22	111.00
1	A	328	ALA	N-CA-C	-5.09	97.27	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3670	0	3645	127	0
1	B	3670	0	3645	146	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3670	0	3645	164	0
1	D	3670	0	3645	164	0
2	A	43	0	30	2	0
2	B	43	0	30	3	0
2	C	43	0	30	5	0
2	D	43	0	30	7	0
3	A	18	0	29	1	0
3	B	18	0	29	2	0
3	C	18	0	29	3	0
3	D	18	0	29	0	0
All	All	14924	0	14816	606	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 20.

All (606) 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:C:241:LYS:HG2	1:C:248:PRO:HG3	1.29	1.14
1:D:241:LYS:HG2	1:D:248:PRO:HG3	1.38	1.03
1:D:5:MET:HG2	1:D:41:LYS:HB2	1.41	1.00
1:A:272:LEU:HD13	1:A:322:LEU:HD13	1.51	0.90
1:C:238:LEU:HD23	1:C:254:ILE:HD13	1.55	0.86
1:C:13:GLU:HG3	1:C:14:LEU:HD22	1.59	0.85
1:B:13:GLU:HG3	1:B:14:LEU:HD22	1.60	0.84
1:A:118:MET:HB3	1:A:155:LEU:HD23	1.59	0.84
1:C:47:ARG:HD3	1:C:73:GLN:HG3	1.60	0.82
1:A:120:VAL:HG11	1:A:302:VAL:HG13	1.62	0.82
1:B:301:PRO:HB3	1:B:455:LEU:HA	1.59	0.81
1:A:171:HIS:HD2	1:A:173:PHE:H	1.30	0.79
1:D:149:THR:HG21	1:D:269:THR:HB	1.64	0.79
1:D:223:ARG:HH21	1:D:234:LEU:HB3	1.47	0.78
1:D:320:GLU:HB3	1:D:374:PHE:CE1	2.19	0.78
1:B:61:ALA:HA	1:B:67:PHE:CD2	2.19	0.77
1:D:205:PHE:CE2	1:D:209:ILE:HD11	2.20	0.77
1:A:364:LYS:H	1:A:364:LYS:HD2	1.49	0.77
1:B:380:GLU:O	1:B:382:PRO:HD3	1.84	0.76
1:D:147:ARG:HG3	1:D:164:SER:HB3	1.67	0.76
1:B:57:LEU:HD12	1:B:341:LEU:HG	1.68	0.76
1:B:422:ASP:HB2	1:B:449:LYS:HB3	1.67	0.75
1:B:85:GLY:HA2	1:B:257:GLN:NE2	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:LEU:HD13	1:D:322:LEU:HD13	1.69	0.73
1:A:201:ASN:HD22	1:A:201:ASN:H	1.37	0.73
1:D:164:SER:HA	1:D:167:ARG:HD3	1.69	0.72
1:C:7:GLN:HB2	1:C:41:LYS:O	1.88	0.72
1:D:120:VAL:HG11	1:D:302:VAL:HG13	1.71	0.72
1:C:51:TYR:CE1	1:C:354:MET:HG2	2.25	0.71
1:C:86:LEU:HD23	1:C:401:ILE:HG13	1.70	0.71
1:D:128:GLN:O	1:D:132:ARG:HG3	1.90	0.71
1:B:103:LEU:HD11	1:B:237:MET:HG2	1.70	0.71
1:D:281:VAL:CG1	1:D:425:ASP:HB2	2.19	0.71
1:C:223:ARG:HH21	1:C:234:LEU:HB3	1.53	0.71
1:A:147:ARG:HG3	1:A:164:SER:HB3	1.72	0.71
1:D:1:THR:O	1:D:344:GLU:HA	1.91	0.70
1:D:201:ASN:HD22	1:D:201:ASN:H	1.39	0.70
1:D:131:GLU:HG2	1:D:421:PHE:HZ	1.54	0.70
1:A:13:GLU:HG3	1:A:14:LEU:HD22	1.73	0.69
1:A:51:TYR:CE2	1:A:354:MET:HG2	2.28	0.69
1:C:198:TYR:HA	1:C:201:ASN:ND2	2.06	0.69
1:C:312:LYS:HG3	1:C:313:TYR:H	1.58	0.69
1:C:367:TRP:HB2	1:C:371:VAL:HG12	1.74	0.69
1:D:252:GLU:HG3	1:D:255:ARG:NH2	2.07	0.69
1:B:281:VAL:CG1	1:B:425:ASP:HB2	2.24	0.68
1:A:281:VAL:CG1	1:A:425:ASP:HB2	2.24	0.68
1:B:367:TRP:HB2	1:B:371:VAL:HG12	1.74	0.68
1:A:56:ARG:HG3	1:A:57:LEU:HD22	1.76	0.67
2:B:472:HEM:HMC2	2:B:472:HEM:HBC2	1.77	0.67
1:C:286:VAL:HG13	1:C:313:TYR:OH	1.94	0.67
1:B:401:ILE:HG12	2:B:472:HEM:HBD2	1.77	0.67
1:C:147:ARG:HG3	1:C:164:SER:HB3	1.76	0.67
1:B:56:ARG:HA	1:B:59:LYS:HE3	1.76	0.67
1:C:281:VAL:CG1	1:C:425:ASP:HB2	2.25	0.67
1:D:58:ILE:HD12	1:D:355:VAL:HG22	1.77	0.67
1:C:100:HIS:HE1	1:C:104:LEU:HD22	1.60	0.66
1:C:198:TYR:O	1:C:202:LYS:HG3	1.95	0.66
1:C:138:HIS:HA	1:C:447:LYS:HD3	1.77	0.66
1:D:7:GLN:HB2	1:D:41:LYS:O	1.94	0.66
1:D:98:LYS:O	1:D:102:ILE:HG13	1.95	0.66
1:B:120:VAL:O	1:B:124:VAL:HG23	1.96	0.66
1:A:103:LEU:HD11	1:A:237:MET:HG2	1.77	0.66
1:B:122:ILE:HG22	1:B:148:LEU:HD12	1.78	0.66
1:C:150:LEU:HD22	1:C:174:ILE:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:PHE:HE2	1:D:237:MET:HE1	1.61	0.66
1:D:5:MET:HB3	1:D:41:LYS:NZ	2.11	0.66
1:D:131:GLU:HG2	1:D:421:PHE:CZ	2.31	0.66
1:C:87:PHE:CZ	3:C:473:PAM:H10	2.30	0.66
1:D:86:LEU:HD23	1:D:401:ILE:HG13	1.77	0.65
1:B:320:GLU:HB3	1:B:374:PHE:CE1	2.32	0.65
1:D:367:TRP:HB2	1:D:371:VAL:HG12	1.79	0.65
1:B:176:SER:HB3	1:B:208:ASP:HB3	1.79	0.65
1:C:122:ILE:HG22	1:C:148:LEU:HD12	1.79	0.65
1:B:54:SER:O	1:B:58:ILE:HG12	1.97	0.65
1:B:366:ILE:HG21	1:B:389:ALA:HB1	1.78	0.65
1:C:149:THR:HG21	1:C:269:THR:HB	1.78	0.64
1:C:85:GLY:HA2	1:C:257:GLN:NE2	2.12	0.64
1:A:7:GLN:HB2	1:A:41:LYS:O	1.97	0.64
1:C:289:LYS:O	1:C:292:GLU:HG3	1.98	0.63
1:C:56:ARG:HG3	1:C:57:LEU:HD22	1.80	0.63
1:C:397:GLN:HG2	1:C:398:ARG:HG2	1.80	0.63
1:C:419:LYS:HE3	1:C:420:HIS:CD2	2.33	0.63
1:B:329:PRO:HG2	3:B:473:PAM:H52	1.81	0.63
1:A:61:ALA:HA	1:A:67:PHE:CD2	2.33	0.63
1:D:13:GLU:HG3	1:D:14:LEU:HD22	1.81	0.63
1:B:229:GLN:OE1	1:B:229:GLN:HA	1.98	0.63
1:A:224:LYS:HA	1:A:224:LYS:HE2	1.81	0.62
1:D:17:LEU:HB3	1:D:18:PRO:HD3	1.81	0.62
1:A:401:ILE:HG12	2:A:472:HEM:HBD2	1.80	0.62
2:D:472:HEM:HMC2	2:D:472:HEM:HBC2	1.80	0.62
1:C:56:ARG:HA	1:C:59:LYS:HE3	1.80	0.62
1:C:401:ILE:HG12	2:C:472:HEM:HBD2	1.82	0.62
1:B:171:HIS:HD2	1:B:173:PHE:H	1.47	0.62
1:B:275:PHE:CE2	1:B:441:PRO:HD3	2.35	0.62
1:D:364:LYS:HD3	1:D:369:ASP:HA	1.80	0.62
2:A:472:HEM:HMC2	2:A:472:HEM:HBC2	1.82	0.62
1:C:201:ASN:H	1:C:201:ASN:HD22	1.47	0.62
1:C:96:TRP:CD1	1:C:398:ARG:NH2	2.67	0.62
1:D:56:ARG:HA	1:D:59:LYS:HE3	1.82	0.62
1:D:116:HIS:HD2	1:D:408:HIS:NE2	1.98	0.61
1:C:68:ASP:HB2	1:C:336:LYS:HE2	1.82	0.61
1:B:201:ASN:H	1:B:201:ASN:HD22	1.47	0.61
1:B:85:GLY:HA2	1:B:257:GLN:HE22	1.63	0.61
1:B:17:LEU:HB3	1:B:18:PRO:HD3	1.81	0.61
1:D:201:ASN:H	1:D:201:ASN:ND2	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:GLU:OE1	1:C:56:ARG:HD2	2.00	0.61
1:C:103:LEU:HD11	1:C:237:MET:HG2	1.82	0.61
1:D:103:LEU:HD11	1:D:237:MET:HG2	1.83	0.61
1:B:206:GLN:HB3	1:B:210:LYS:NZ	2.16	0.61
1:B:252:GLU:HG3	1:B:255:ARG:NH2	2.16	0.61
1:A:366:ILE:HG21	1:A:389:ALA:HB1	1.81	0.60
1:C:269:THR:O	1:C:272:LEU:HB3	2.01	0.60
1:C:68:ASP:HB3	1:C:334:TYR:CE1	2.36	0.60
1:D:397:GLN:HG3	1:D:398:ARG:HG2	1.81	0.60
1:B:218:LYS:HE3	1:B:218:LYS:HA	1.83	0.60
1:B:7:GLN:HB2	1:B:41:LYS:O	2.01	0.60
1:C:434:LYS:HD3	1:C:440:LYS:HE3	1.82	0.60
1:C:317:VAL:HG13	1:C:374:PHE:HZ	1.66	0.60
1:D:401:ILE:HG12	2:D:472:HEM:HBD2	1.83	0.60
1:C:120:VAL:HG11	1:C:302:VAL:HG13	1.84	0.60
1:D:281:VAL:HG11	1:D:425:ASP:HB2	1.82	0.60
1:C:213:ASN:OD1	1:C:255:ARG:HD2	2.01	0.60
1:D:118:MET:HB3	1:D:155:LEU:HD23	1.82	0.60
1:B:201:ASN:H	1:B:201:ASN:ND2	2.00	0.60
1:D:9:LYS:HE2	1:D:19:LEU:HD21	1.82	0.60
1:A:120:VAL:HG11	1:A:302:VAL:CG1	2.30	0.60
1:B:275:PHE:CE1	1:B:441:PRO:HG3	2.36	0.60
1:C:268:THR:O	1:C:327:THR:HG21	2.02	0.60
1:C:272:LEU:HD22	2:C:472:HEM:HBB1	1.84	0.60
1:A:78:VAL:HG11	3:A:473:PAM:H152	1.82	0.60
1:A:250:ASP:O	1:A:254:ILE:HG13	2.02	0.59
1:A:149:THR:HG21	1:A:269:THR:HB	1.82	0.59
1:A:320:GLU:HB3	1:A:374:PHE:CE1	2.36	0.59
1:B:103:LEU:HD11	1:B:237:MET:CG	2.31	0.59
1:C:216:VAL:HG11	1:C:255:ARG:HG3	1.84	0.59
1:A:301:PRO:HB3	1:A:455:LEU:HA	1.84	0.59
1:B:162:PHE:HE1	1:B:215:LEU:HD21	1.67	0.59
1:B:5:MET:SD	1:B:39:ILE:HG12	2.42	0.59
1:C:201:ASN:ND2	1:C:201:ASN:H	2.01	0.59
1:B:109:GLN:O	1:B:113:LYS:HG3	2.02	0.59
1:B:403:GLN:O	1:B:407:LEU:HD22	2.03	0.59
1:D:5:MET:SD	1:D:50:ARG:HG2	2.43	0.59
1:B:118:MET:HB3	1:B:155:LEU:HD23	1.85	0.58
1:B:286:VAL:HG13	1:B:313:TYR:OH	2.03	0.58
1:C:199:ASP:HA	1:C:202:LYS:HD2	1.84	0.58
1:B:51:TYR:CE2	1:B:354:MET:HG2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:ARG:HG2	1:B:361:HIS:HB3	1.84	0.58
1:C:207:GLU:O	1:C:211:VAL:HG23	2.03	0.58
1:A:158:PHE:HE1	1:A:237:MET:HE1	1.68	0.58
1:C:327:THR:OG1	2:C:472:HEM:HMB2	2.04	0.58
1:A:54:SER:O	1:A:58:ILE:HG12	2.04	0.58
1:C:54:SER:O	1:C:58:ILE:HG12	2.03	0.58
1:D:366:ILE:HG21	1:D:389:ALA:HB1	1.85	0.58
1:D:110:GLN:HA	1:D:113:LYS:HD2	1.85	0.58
1:C:305:TYR:O	1:C:309:LYS:HG2	2.04	0.57
1:C:162:PHE:CE1	1:C:215:LEU:HD21	2.40	0.57
1:C:5:MET:HG2	1:C:41:LYS:HB2	1.85	0.57
1:A:422:ASP:HB2	1:A:449:LYS:HB2	1.86	0.57
1:D:403:GLN:O	1:D:407:LEU:HD22	2.04	0.57
1:A:98:LYS:O	1:A:102:ILE:HG13	2.05	0.57
1:B:120:VAL:HG11	1:B:302:VAL:HG13	1.86	0.57
1:C:183:GLU:HG2	1:C:205:PHE:CD1	2.40	0.57
1:C:366:ILE:HG21	1:C:389:ALA:HB1	1.84	0.57
1:A:212:MET:HE2	1:A:263:ILE:HD11	1.87	0.57
1:B:272:LEU:HD13	1:B:322:LEU:HD13	1.87	0.57
1:C:312:LYS:HG3	1:C:313:TYR:N	2.19	0.57
1:C:262:LEU:O	1:C:266:HIS:HD2	1.88	0.57
1:C:208:ASP:O	1:C:212:MET:HG3	2.05	0.56
1:D:192:ASN:ND2	1:D:195:ASP:HB2	2.19	0.56
1:B:74:ALA:O	1:B:78:VAL:HG23	2.05	0.56
1:C:162:PHE:HE1	1:C:215:LEU:HD21	1.70	0.56
1:D:122:ILE:HG22	1:D:148:LEU:HD12	1.87	0.56
1:B:54:SER:OG	1:B:57:LEU:HD23	2.05	0.56
1:C:264:ALA:HB2	3:C:473:PAM:H141	1.88	0.56
1:A:5:MET:HG2	1:A:41:LYS:HB2	1.88	0.56
1:B:326:PRO:HG3	1:B:357:ILE:HG22	1.87	0.56
1:A:429:TYR:CE2	1:A:431:LEU:HA	2.41	0.56
1:B:130:TRP:CZ2	1:B:139:ILE:HD12	2.41	0.56
1:C:392:PRO:HG2	1:C:393:PHE:CD2	2.41	0.56
1:D:107:PHE:CD2	1:D:401:ILE:HG22	2.41	0.56
1:A:375:ARG:O	1:A:378:ARG:HG3	2.06	0.55
1:B:223:ARG:HH21	1:B:234:LEU:HB3	1.70	0.55
1:C:286:VAL:HG11	1:C:374:PHE:HE2	1.71	0.55
1:D:51:TYR:CE2	1:D:354:MET:HG2	2.41	0.55
1:A:17:LEU:HD22	1:A:45:PRO:HD2	1.88	0.55
1:B:375:ARG:O	1:B:378:ARG:HG3	2.06	0.55
1:B:181:LEU:HD22	1:B:437:LEU:HD12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:GLU:HG2	1:C:421:PHE:HZ	1.70	0.55
1:B:235:THR:O	1:B:239:ASN:HB2	2.07	0.55
1:C:116:HIS:HD2	1:C:408:HIS:NE2	2.05	0.55
1:B:21:ASN:HD22	1:B:21:ASN:N	2.05	0.55
1:D:158:PHE:CE2	1:D:237:MET:HE1	2.42	0.55
1:B:16:ASN:HB3	1:B:19:LEU:HD12	1.88	0.55
1:B:420:HIS:O	1:B:451:LYS:HB3	2.07	0.54
1:D:130:TRP:CZ2	1:D:139:ILE:HD12	2.43	0.54
1:D:331:PHE:CD2	1:D:357:ILE:HD11	2.42	0.54
1:B:212:MET:HE2	1:B:263:ILE:HD11	1.88	0.54
1:C:91:THR:OG1	1:C:398:ARG:HD2	2.07	0.54
1:B:140:GLU:HA	1:B:445:VAL:HG12	1.90	0.54
1:B:15:LYS:HB2	1:B:44:ALA:HA	1.90	0.54
1:D:228:GLU:HG3	1:D:229:GLN:H	1.72	0.54
1:B:318:LEU:CD1	1:B:414:LEU:HD12	2.37	0.54
2:C:472:HEM:HBC2	2:C:472:HEM:HMC2	1.90	0.54
1:D:262:LEU:O	1:D:266:HIS:HD2	1.90	0.54
1:D:68:ASP:HB2	1:D:336:LYS:HE3	1.89	0.54
1:B:273:LEU:HD11	1:B:413:VAL:HG11	1.90	0.53
1:A:8:PRO:HB2	1:A:19:LEU:HD11	1.90	0.53
1:C:100:HIS:CE1	1:C:104:LEU:HD22	2.40	0.53
1:C:89:SER:O	1:C:398:ARG:NH1	2.39	0.53
1:D:436:THR:O	1:D:437:LEU:HB2	2.06	0.53
1:A:207:GLU:O	1:A:211:VAL:HG23	2.07	0.53
1:A:323:ARG:HG2	1:A:361:HIS:HB3	1.90	0.53
1:C:158:PHE:HE2	1:C:258:ILE:HG12	1.72	0.53
1:C:277:LEU:HD22	1:C:417:MET:HE1	1.90	0.53
1:C:116:HIS:HE1	1:C:303:PRO:O	1.91	0.53
1:C:426:HIS:CD2	1:C:446:VAL:HA	2.44	0.53
1:D:28:ALA:O	1:D:32:ILE:HG13	2.09	0.53
1:D:66:ARG:O	1:D:336:LYS:HB2	2.08	0.53
1:A:280:LEU:HD21	1:A:317:VAL:CG1	2.39	0.53
1:A:38:GLU:HB2	1:A:54:SER:OG	2.09	0.53
1:A:140:GLU:HA	1:A:445:VAL:HG12	1.90	0.53
1:A:237:MET:HE1	1:A:258:ILE:HG12	1.88	0.53
1:B:162:PHE:CE1	1:B:215:LEU:HD21	2.43	0.53
1:D:237:MET:SD	1:D:257:GLN:HB2	2.49	0.53
1:C:131:GLU:HG2	1:C:421:PHE:CZ	2.43	0.53
1:A:357:ILE:N	1:A:358:PRO:HD2	2.24	0.53
1:C:305:TYR:CE2	1:C:309:LYS:HE3	2.44	0.53
1:A:223:ARG:HH21	1:A:234:LEU:HB3	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:LYS:HG3	1:B:60:GLU:N	2.23	0.53
1:D:1:THR:HG21	1:D:3:LYS:HE2	1.90	0.53
1:C:377:GLU:O	1:C:380:GLU:HB2	2.08	0.52
1:C:387:GLN:O	1:C:388:HIS:HB2	2.09	0.52
1:B:334:TYR:HA	1:B:351:ASP:O	2.09	0.52
1:D:5:MET:HB3	1:D:41:LYS:HZ1	1.74	0.52
1:B:164:SER:O	1:B:167:ARG:HG2	2.09	0.52
1:B:120:VAL:HG11	1:B:302:VAL:CG1	2.39	0.52
1:C:96:TRP:NE1	1:C:398:ARG:NH2	2.57	0.52
1:C:280:LEU:HD22	1:C:287:LEU:HA	1.92	0.52
1:D:305:TYR:O	1:D:309:LYS:HG2	2.09	0.52
1:D:9:LYS:CE	1:D:19:LEU:HD21	2.39	0.52
1:A:112:MET:HB3	1:A:305:TYR:HE2	1.73	0.52
1:A:364:LYS:HD2	1:A:364:LYS:N	2.23	0.52
1:D:198:TYR:O	1:D:202:LYS:HG3	2.09	0.52
1:D:31:LYS:O	1:D:34:ASP:HB2	2.10	0.52
1:D:375:ARG:O	1:D:378:ARG:HG3	2.10	0.52
1:D:14:LEU:N	1:D:14:LEU:HD22	2.25	0.52
1:D:212:MET:CE	1:D:263:ILE:HD11	2.39	0.52
1:A:280:LEU:HD21	1:A:317:VAL:HG11	1.91	0.51
1:C:85:GLY:HA2	1:C:257:GLN:HE22	1.74	0.51
1:D:110:GLN:O	1:D:113:LYS:HB2	2.10	0.51
1:A:305:TYR:O	1:A:309:LYS:HG2	2.10	0.51
1:D:320:GLU:OE2	1:D:378:ARG:HD2	2.10	0.51
1:A:150:LEU:HD22	1:A:174:ILE:HD11	1.91	0.51
1:C:61:ALA:HA	1:C:67:PHE:CD2	2.45	0.51
1:A:162:PHE:CE1	1:A:215:LEU:HD21	2.45	0.51
1:C:128:GLN:O	1:C:132:ARG:HG3	2.11	0.51
1:C:183:GLU:HG3	1:C:187:LYS:HE3	1.91	0.51
1:C:320:GLU:OE1	1:C:374:PHE:HA	2.10	0.51
1:D:68:ASP:HB3	1:D:334:TYR:CZ	2.45	0.51
1:A:201:ASN:H	1:A:201:ASN:ND2	2.04	0.51
1:B:421:PHE:HB2	1:B:423:PHE:CZ	2.45	0.51
1:C:281:VAL:HG11	1:C:425:ASP:HB2	1.92	0.51
1:B:62:CYS:HB3	1:B:388:HIS:NE2	2.26	0.51
1:C:72:SER:O	1:C:76:LYS:HG2	2.11	0.51
1:D:385:ILE:HD12	1:D:385:ILE:H	1.75	0.51
1:B:278:TYR:HA	1:B:444:PHE:CZ	2.46	0.51
1:C:362:ARG:HH11	1:C:362:ARG:HG3	1.76	0.51
1:C:42:PHE:HB3	1:C:51:TYR:HE2	1.76	0.51
1:C:71:LEU:O	1:C:76:LYS:HE3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ILE:O	1:A:178:VAL:HG22	2.10	0.51
1:A:228:GLU:O	1:A:229:GLN:HB2	2.12	0.50
1:B:68:ASP:HB3	1:B:334:TYR:CZ	2.46	0.50
1:B:98:LYS:O	1:B:102:ILE:HG13	2.10	0.50
1:A:16:ASN:HB3	1:A:19:LEU:HD12	1.93	0.50
1:B:262:LEU:O	1:B:266:HIS:HD2	1.94	0.50
1:D:151:ASP:OD1	1:D:162:PHE:HB2	2.11	0.50
1:A:341:LEU:N	1:A:345:TYR:O	2.43	0.50
1:C:305:TYR:CZ	1:C:309:LYS:HE3	2.47	0.50
1:A:57:LEU:HD12	1:A:341:LEU:HG	1.94	0.50
1:A:367:TRP:HB2	1:A:371:VAL:HG12	1.94	0.50
1:A:62:CYS:HB3	1:A:388:HIS:NE2	2.27	0.50
1:C:139:ILE:HD11	1:C:446:VAL:CG2	2.41	0.50
1:A:323:ARG:CG	1:A:361:HIS:HB3	2.42	0.50
1:A:436:THR:O	1:A:437:LEU:HB2	2.12	0.50
1:B:171:HIS:CD2	1:B:173:PHE:H	2.26	0.50
1:B:206:GLN:O	1:B:210:LYS:HG2	2.11	0.50
1:A:147:ARG:CG	1:A:164:SER:HB3	2.41	0.49
1:D:334:TYR:HA	1:D:351:ASP:O	2.12	0.49
1:C:110:GLN:O	1:C:113:LYS:HB2	2.12	0.49
1:C:421:PHE:HB3	1:C:448:ALA:HB1	1.94	0.49
1:C:71:LEU:HB3	1:C:76:LYS:HD3	1.94	0.49
1:D:194:ASP:O	1:D:195:ASP:C	2.49	0.49
1:C:79:ARG:HG3	1:C:83:GLY:O	2.13	0.49
1:B:58:ILE:HG21	1:B:360:LEU:HD22	1.93	0.49
1:C:195:ASP:CG	1:C:196:PRO:HD2	2.33	0.49
1:D:103:LEU:HD11	1:D:237:MET:CG	2.43	0.49
1:D:120:VAL:O	1:D:124:VAL:HG23	2.12	0.49
1:D:39:ILE:HG13	1:D:52:LEU:HD12	1.93	0.49
1:A:305:TYR:CE1	1:A:309:LYS:HE3	2.47	0.49
1:A:347:LEU:HD13	1:A:353:LEU:HD11	1.95	0.49
1:B:83:GLY:HA3	1:B:256:TYR:CD2	2.48	0.49
1:C:235:THR:O	1:C:239:ASN:HB2	2.13	0.49
1:D:120:VAL:HG11	1:D:302:VAL:CG1	2.42	0.49
1:D:7:GLN:HE22	1:D:43:GLU:HB2	1.78	0.49
1:A:305:TYR:CZ	1:A:309:LYS:HE3	2.48	0.49
1:B:212:MET:CE	1:B:263:ILE:HD11	2.43	0.49
1:B:132:ARG:HD2	1:D:166:TYR:CE2	2.48	0.49
1:D:149:THR:OG1	1:D:270:SER:HB3	2.13	0.49
1:D:323:ARG:HA	1:D:361:HIS:HD1	1.78	0.49
1:C:334:TYR:HA	1:C:351:ASP:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:VAL:CG2	1:A:411:THR:HG23	2.42	0.49
1:A:56:ARG:NH2	1:A:342:GLY:HA3	2.27	0.48
1:D:373:GLU:O	1:D:378:ARG:NH2	2.46	0.48
1:A:73:GLN:HG3	1:A:77:PHE:CE2	2.48	0.48
1:C:272:LEU:HD13	1:C:322:LEU:HD13	1.94	0.48
1:D:194:ASP:O	1:D:196:PRO:N	2.46	0.48
1:D:212:MET:HE1	1:D:263:ILE:HD11	1.94	0.48
1:D:286:VAL:HG13	1:D:313:TYR:OH	2.13	0.48
1:D:79:ARG:HG3	1:D:88:THR:HB	1.94	0.48
1:A:334:TYR:HA	1:A:351:ASP:O	2.14	0.48
1:B:116:HIS:HE1	1:B:303:PRO:O	1.97	0.48
1:B:305:TYR:O	1:B:309:LYS:HG2	2.13	0.48
1:B:340:VAL:HG22	1:B:346:PRO:HA	1.95	0.48
1:B:416:MET:O	1:B:420:HIS:HD2	1.96	0.48
1:B:131:GLU:HG2	1:B:421:PHE:CZ	2.48	0.48
1:D:305:TYR:CE2	1:D:309:LYS:HE3	2.48	0.48
1:B:44:ALA:HB1	1:B:45:PRO:HD2	1.95	0.48
1:A:1:THR:HG22	1:A:2:ILE:N	2.29	0.48
1:C:109:GLN:O	1:C:113:LYS:HG3	2.13	0.48
1:C:426:HIS:HD2	1:C:446:VAL:HA	1.78	0.48
1:A:388:HIS:HD2	1:A:391:LYS:HD2	1.77	0.48
1:B:206:GLN:HB3	1:B:210:LYS:HZ2	1.79	0.48
1:B:94:LYS:HD2	1:B:94:LYS:N	2.29	0.48
1:A:330:ALA:HA	1:A:357:ILE:HG13	1.96	0.48
1:D:61:ALA:HA	1:D:67:PHE:CD2	2.49	0.48
1:B:58:ILE:HD12	1:B:355:VAL:HG13	1.96	0.48
1:B:366:ILE:HG23	1:B:386:PRO:HG2	1.96	0.48
1:C:204:GLN:O	1:C:207:GLU:HB3	2.14	0.48
1:A:130:TRP:CZ2	1:A:139:ILE:HD12	2.49	0.47
1:B:132:ARG:HD2	1:D:166:TYR:HE2	1.78	0.47
1:D:218:LYS:N	1:D:218:LYS:HD2	2.29	0.47
1:A:272:LEU:HD13	1:A:322:LEU:CD1	2.34	0.47
1:C:357:ILE:N	1:C:358:PRO:HD2	2.28	0.47
1:B:86:LEU:HD23	1:B:401:ILE:HG13	1.95	0.47
1:B:413:VAL:HG13	1:B:414:LEU:N	2.29	0.47
1:C:381:ASN:N	1:C:381:ASN:OD1	2.48	0.47
1:C:54:SER:OG	1:C:57:LEU:HD23	2.14	0.47
1:A:124:VAL:O	1:A:128:GLN:HG2	2.15	0.47
1:B:128:GLN:O	1:B:132:ARG:HG3	2.14	0.47
1:B:318:LEU:O	1:B:322:LEU:HB2	2.14	0.47
1:B:131:GLU:HG2	1:B:421:PHE:HZ	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:GLU:O	1:D:45:PRO:HG3	2.15	0.47
1:D:196:PRO:HA	1:D:199:ASP:OD1	2.14	0.47
1:D:323:ARG:HG2	1:D:361:HIS:HB3	1.95	0.47
1:B:70:ASN:HB2	1:B:334:TYR:HD1	1.80	0.47
1:B:387:GLN:O	1:B:388:HIS:HB2	2.14	0.47
1:C:17:LEU:HB3	1:C:18:PRO:HD3	1.97	0.47
1:C:436:THR:O	1:C:437:LEU:HB2	2.15	0.47
1:C:118:MET:HB3	1:C:155:LEU:HD23	1.96	0.47
1:C:5:MET:CG	1:C:41:LYS:HB2	2.45	0.47
1:D:20:LEU:O	1:D:189:GLN:HG2	2.15	0.47
1:B:429:TYR:CE2	1:B:431:LEU:HA	2.51	0.47
1:C:257:GLN:O	1:C:261:PHE:HD1	1.98	0.47
1:C:373:GLU:O	1:C:378:ARG:NH2	2.48	0.47
1:D:38:GLU:HG3	1:D:39:ILE:HG22	1.96	0.47
1:D:327:THR:OG1	2:D:472:HEM:HMB2	2.14	0.47
1:A:331:PHE:CD2	1:A:357:ILE:HD11	2.50	0.46
1:A:58:ILE:HG21	1:A:360:LEU:HD22	1.96	0.46
1:D:385:ILE:N	1:D:385:ILE:HD12	2.30	0.46
1:D:192:ASN:O	1:D:198:TYR:HE2	1.98	0.46
1:D:218:LYS:O	1:D:222:ASP:HB2	2.16	0.46
1:B:61:ALA:HA	1:B:67:PHE:CE2	2.50	0.46
1:C:68:ASP:HB3	1:C:334:TYR:CZ	2.50	0.46
1:C:356:LEU:HD23	1:C:356:LEU:HA	1.83	0.46
1:D:127:VAL:HG11	1:D:455:LEU:HD22	1.97	0.46
1:D:305:TYR:CZ	1:D:309:LYS:HE3	2.50	0.46
1:D:331:PHE:CD2	1:D:394:GLY:HA2	2.50	0.46
2:B:472:HEM:CMC	2:B:472:HEM:HBC2	2.46	0.46
1:C:42:PHE:CB	1:C:51:TYR:HE2	2.29	0.46
1:D:195:ASP:O	1:D:197:ALA:N	2.49	0.46
1:D:69:LYS:O	1:D:334:TYR:HE1	1.99	0.46
1:A:38:GLU:HG3	1:A:39:ILE:HG22	1.96	0.46
1:B:147:ARG:HG3	1:B:164:SER:HB3	1.98	0.46
1:B:79:ARG:HH21	1:B:89:SER:HA	1.80	0.46
1:D:308:VAL:HG11	1:D:408:HIS:CE1	2.51	0.46
1:D:89:SER:O	1:D:398:ARG:NH1	2.46	0.46
1:B:268:THR:O	1:B:327:THR:HG21	2.15	0.46
1:D:318:LEU:CD1	1:D:414:LEU:HD12	2.46	0.46
1:D:413:VAL:HG13	1:D:414:LEU:N	2.29	0.46
1:B:149:THR:HG21	1:B:266:HIS:O	2.16	0.46
1:B:2:ILE:HG23	1:B:344:GLU:O	2.15	0.46
3:C:473:PAM:H111	3:C:473:PAM:H82	1.76	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:GLU:HB3	1:C:143:GLU:OE1	2.16	0.46
1:A:116:HIS:CD2	1:A:305:TYR:HA	2.50	0.46
1:A:306:LYS:HD3	1:A:306:LYS:N	2.30	0.46
1:A:86:LEU:HD11	1:A:99:ALA:CB	2.46	0.46
1:B:206:GLN:HB3	1:B:210:LYS:HZ1	1.80	0.46
1:B:305:TYR:CE1	1:B:309:LYS:HE3	2.51	0.46
1:A:162:PHE:HE1	1:A:215:LEU:HD21	1.81	0.45
1:B:141:VAL:CG1	1:B:277:LEU:HD23	2.47	0.45
1:B:250:ASP:O	1:B:254:ILE:HG13	2.16	0.45
1:C:301:PRO:HB2	1:C:455:LEU:HA	1.97	0.45
1:D:96:TRP:CZ2	1:D:100:HIS:HD2	2.35	0.45
1:A:298:LEU:HD21	1:A:311:LEU:HD11	1.98	0.45
1:A:340:VAL:HG22	1:A:346:PRO:HA	1.97	0.45
1:C:3:LYS:HB3	1:C:3:LYS:NZ	2.31	0.45
1:C:314:VAL:CG2	1:C:411:THR:HG23	2.46	0.45
1:D:327:THR:O	1:D:329:PRO:HD3	2.16	0.45
1:D:5:MET:HB3	1:D:41:LYS:HZ2	1.77	0.45
1:A:335:ALA:HB3	1:A:348:GLU:O	2.17	0.45
1:A:385:ILE:N	1:A:385:ILE:HD12	2.32	0.45
1:A:410:ALA:O	1:A:414:LEU:HB2	2.17	0.45
1:C:238:LEU:HD23	1:C:254:ILE:CD1	2.37	0.45
1:C:447:LYS:HD2	1:C:448:ALA:H	1.81	0.45
1:C:434:LYS:HB2	1:C:442:GLU:HB2	1.97	0.45
1:B:289:LYS:O	1:B:292:GLU:HG2	2.16	0.45
1:B:314:VAL:O	1:B:317:VAL:HB	2.16	0.45
1:B:38:GLU:HB2	1:B:54:SER:OG	2.16	0.45
1:C:324:LEU:HD12	1:C:362:ARG:NH2	2.31	0.45
1:C:419:LYS:HE3	1:C:420:HIS:NE2	2.31	0.45
1:A:309:LYS:NZ	1:A:404:GLN:NE2	2.64	0.45
1:A:5:MET:CG	1:A:41:LYS:HB2	2.47	0.45
1:D:318:LEU:O	1:D:322:LEU:HB2	2.17	0.45
1:D:429:TYR:CE2	1:D:431:LEU:HA	2.51	0.45
1:D:71:LEU:HD22	1:D:90:TRP:NE1	2.32	0.45
1:A:116:HIS:HE1	1:A:303:PRO:O	1.99	0.45
1:D:249:LEU:HD13	1:D:253:ASN:OD1	2.17	0.45
1:B:281:VAL:HG11	1:B:425:ASP:HB2	1.97	0.45
1:A:69:LYS:HD3	1:A:398:ARG:CZ	2.47	0.45
1:B:11:PHE:CD1	1:B:11:PHE:N	2.85	0.45
1:B:207:GLU:O	1:B:211:VAL:HG23	2.17	0.45
1:B:233:LEU:O	1:B:237:MET:HG3	2.16	0.45
1:B:421:PHE:HB2	1:B:423:PHE:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:58:ILE:HD12	1:C:355:VAL:HG13	1.97	0.45
1:D:116:HIS:HD2	1:D:408:HIS:CE1	2.35	0.45
1:D:275:PHE:CE2	1:D:441:PRO:HD3	2.52	0.45
1:B:390:PHE:CE2	1:B:392:PRO:HG3	2.52	0.44
1:B:84:ASP:HB2	1:B:89:SER:HB3	1.99	0.44
1:C:318:LEU:CD1	1:C:414:LEU:HD12	2.48	0.44
1:C:375:ARG:O	1:C:378:ARG:HG3	2.16	0.44
1:D:421:PHE:CE1	1:D:450:SER:HB3	2.52	0.44
1:B:253:ASN:O	1:B:257:GLN:HG2	2.18	0.44
1:C:55:GLN:O	1:C:59:LYS:HG2	2.16	0.44
1:D:207:GLU:O	1:D:211:VAL:HG23	2.18	0.44
1:D:392:PRO:HG2	1:D:393:PHE:CD2	2.52	0.44
1:C:17:LEU:HD22	1:C:45:PRO:HD2	1.98	0.44
1:D:196:PRO:HA	1:D:199:ASP:CG	2.38	0.44
1:D:85:GLY:HA2	1:D:257:GLN:NE2	2.31	0.44
1:B:305:TYR:CZ	1:B:309:LYS:HE3	2.52	0.44
1:D:237:MET:SD	1:D:257:GLN:CB	3.06	0.44
1:A:8:PRO:HB2	1:A:19:LEU:CD1	2.48	0.44
1:D:198:TYR:HA	1:D:201:ASN:ND2	2.32	0.44
1:D:227:GLY:O	1:D:228:GLU:HB2	2.17	0.44
1:B:298:LEU:HD22	1:B:303:PRO:HG3	1.99	0.44
1:C:54:SER:OG	1:C:57:LEU:CD2	2.65	0.44
1:C:5:MET:HG2	1:C:41:LYS:HE3	1.99	0.44
1:A:54:SER:OG	1:A:57:LEU:HD23	2.18	0.44
1:B:63:ASP:OD1	1:B:66:ARG:HB2	2.18	0.44
1:C:247:GLU:HA	1:C:248:PRO:HD3	1.70	0.44
1:C:385:ILE:HA	1:C:386:PRO:HD3	1.85	0.44
1:C:69:LYS:HD3	1:C:398:ARG:HD3	2.00	0.44
1:C:429:TYR:CD2	1:C:444:PHE:CD1	3.06	0.44
1:D:388:HIS:HD2	1:D:391:LYS:HD2	1.82	0.44
1:A:293:GLU:OE2	1:A:311:LEU:HA	2.18	0.43
1:A:397:GLN:HG3	1:A:398:ARG:HG2	1.99	0.43
1:C:303:PRO:HA	1:C:307:GLN:OE1	2.18	0.43
1:C:402:GLY:HA3	2:C:472:HEM:C3C	2.53	0.43
1:D:320:GLU:OE1	1:D:374:PHE:HA	2.18	0.43
1:D:434:LYS:HB2	1:D:442:GLU:HB2	2.00	0.43
1:B:129:LYS:O	1:B:133:LEU:HD13	2.17	0.43
1:B:83:GLY:HA3	1:B:256:TYR:CE2	2.53	0.43
1:C:286:VAL:HG11	1:C:374:PHE:CE2	2.53	0.43
1:C:344:GLU:O	1:C:346:PRO:HD3	2.17	0.43
1:C:116:HIS:HD2	1:C:408:HIS:CE1	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ASN:HA	1:A:284:PRO:HD2	1.79	0.43
1:B:5:MET:SD	1:B:6:PRO:HD2	2.59	0.43
1:D:130:TRP:CZ3	1:D:417:MET:HG2	2.53	0.43
1:A:218:LYS:HA	1:A:218:LYS:HE2	2.00	0.43
1:A:212:MET:CE	1:A:263:ILE:HD11	2.47	0.43
1:C:198:TYR:HA	1:C:201:ASN:HD22	1.80	0.43
1:D:308:VAL:HG11	1:D:408:HIS:ND1	2.33	0.43
1:A:124:VAL:O	1:A:128:GLN:CG	2.67	0.43
1:A:253:ASN:O	1:A:257:GLN:HG2	2.19	0.43
1:B:171:HIS:HD2	1:B:173:PHE:N	2.15	0.43
1:B:275:PHE:O	1:B:278:TYR:HB3	2.19	0.43
1:D:387:GLN:O	1:D:388:HIS:HB2	2.18	0.43
1:A:373:GLU:O	1:A:378:ARG:NH2	2.52	0.43
1:B:122:ILE:O	1:B:125:GLN:HB2	2.18	0.43
1:D:416:MET:O	1:D:420:HIS:HD2	2.02	0.43
1:A:286:VAL:HG13	1:A:313:TYR:OH	2.18	0.43
1:A:67:PHE:CD1	1:A:335:ALA:HA	2.54	0.43
1:C:96:TRP:CZ2	1:C:100:HIS:HD2	2.37	0.43
1:D:402:GLY:HA3	2:D:472:HEM:C3C	2.53	0.43
1:C:322:LEU:HA	1:C:322:LEU:HD12	1.80	0.43
1:D:298:LEU:HB2	1:D:419:LYS:HD2	2.01	0.43
1:D:54:SER:O	1:D:58:ILE:HG12	2.18	0.43
1:D:5:MET:HE2	1:D:5:MET:HB2	1.96	0.43
1:D:86:LEU:HB3	2:D:472:HEM:HAD1	2.01	0.43
1:A:129:LYS:O	1:A:133:LEU:HD13	2.19	0.43
1:C:278:TYR:HA	1:C:444:PHE:CZ	2.54	0.43
1:D:116:HIS:CD2	1:D:408:HIS:NE2	2.82	0.43
1:C:228:GLU:CG	1:C:229:GLN:H	2.32	0.42
1:C:238:LEU:CD2	1:C:254:ILE:HG21	2.49	0.42
1:D:201:ASN:ND2	1:D:201:ASN:N	2.65	0.42
1:D:116:HIS:HE1	1:D:303:PRO:O	2.02	0.42
1:A:171:HIS:CD2	1:A:173:PHE:H	2.21	0.42
1:A:320:GLU:OE1	1:A:374:PHE:HA	2.19	0.42
1:B:341:LEU:N	1:B:345:TYR:O	2.52	0.42
1:C:140:GLU:HA	1:C:445:VAL:HG12	2.00	0.42
1:D:393:PHE:CZ	1:D:407:LEU:HD21	2.54	0.42
1:A:409:GLU:O	1:A:413:VAL:HG12	2.19	0.42
1:C:147:ARG:NH1	1:C:167:ARG:O	2.53	0.42
1:D:77:PHE:HE2	1:D:188:LEU:HD23	1.84	0.42
1:D:356:LEU:HD23	1:D:356:LEU:HA	1.90	0.42
1:D:160:TYR:CE2	1:D:215:LEU:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:HIS:HB2	1:A:446:VAL:O	2.19	0.42
1:B:313:TYR:O	1:B:316:MET:HB2	2.19	0.42
1:C:147:ARG:HD2	1:C:165:PHE:CD1	2.54	0.42
1:D:272:LEU:HD22	2:D:472:HEM:HBB1	2.00	0.42
1:B:330:ALA:HB3	3:B:473:PAM:H51	2.02	0.42
1:D:377:GLU:CD	1:D:377:GLU:H	2.22	0.42
1:A:164:SER:O	1:A:167:ARG:HG2	2.20	0.42
1:A:56:ARG:NH2	1:A:342:GLY:CA	2.83	0.42
1:C:242:ASP:HA	1:C:243:PRO:HD3	1.93	0.42
1:C:77:PHE:CE2	1:C:188:LEU:HD23	2.55	0.42
1:D:129:LYS:HE2	1:D:144:ASP:OD1	2.20	0.42
1:D:96:TRP:CD1	1:D:398:ARG:NH2	2.87	0.42
1:D:70:ASN:HB2	1:D:334:TYR:HD1	1.85	0.42
1:B:275:PHE:CZ	1:B:441:PRO:HD3	2.55	0.42
1:A:271:GLY:HA2	1:A:440:LYS:HG3	2.01	0.42
1:C:29:LEU:HB3	1:C:356:LEU:HD11	2.01	0.42
1:D:15:LYS:HB3	1:D:43:GLU:O	2.20	0.42
1:D:183:GLU:OE1	1:D:190:ARG:NH2	2.53	0.42
1:A:149:THR:HG22	1:A:266:HIS:HA	2.02	0.42
1:A:449:LYS:HD3	1:A:449:LYS:HA	1.76	0.42
1:A:57:LEU:HD13	1:A:57:LEU:HA	1.86	0.42
1:B:141:VAL:HG11	1:B:277:LEU:HD23	2.02	0.42
1:C:120:VAL:O	1:C:124:VAL:HG23	2.20	0.42
1:C:410:ALA:O	1:C:414:LEU:HB2	2.20	0.42
1:C:278:TYR:CZ	1:C:431:LEU:HB2	2.55	0.42
1:C:69:LYS:HD3	1:C:398:ARG:NH1	2.35	0.41
1:A:103:LEU:HD11	1:A:237:MET:CG	2.45	0.41
1:A:169:GLN:HA	1:A:170:PRO:HD3	1.86	0.41
1:B:311:LEU:HB3	1:B:314:VAL:HG22	2.01	0.41
1:B:434:LYS:HD3	1:B:440:LYS:HZ2	1.85	0.41
1:B:71:LEU:HD21	1:B:88:THR:O	2.20	0.41
1:C:149:THR:HG21	1:C:266:HIS:O	2.20	0.41
1:B:126:LEU:HD11	1:B:145:MET:CE	2.50	0.41
1:C:309:LYS:HA	1:C:309:LYS:HD3	1.89	0.41
1:D:130:TRP:HZ3	1:D:417:MET:HG2	1.85	0.41
1:D:335:ALA:HB3	1:D:348:GLU:O	2.19	0.41
1:D:71:LEU:O	1:D:76:LYS:HE3	2.20	0.41
1:A:67:PHE:CE1	1:A:335:ALA:HA	2.55	0.41
1:B:13:GLU:HG3	1:B:14:LEU:CD2	2.42	0.41
1:B:150:LEU:HD22	1:B:174:ILE:HD11	2.02	0.41
1:C:318:LEU:HD13	1:C:414:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:LEU:O	1:D:237:MET:HG3	2.21	0.41
1:B:58:ILE:HG21	1:B:360:LEU:CD2	2.50	0.41
1:B:71:LEU:HD12	1:B:71:LEU:HA	1.91	0.41
1:D:273:LEU:HD11	1:D:413:VAL:HG11	2.03	0.41
1:A:262:LEU:HA	1:A:262:LEU:HD23	1.91	0.41
1:A:280:LEU:HB3	1:A:287:LEU:HG	2.03	0.41
1:C:347:LEU:HD13	1:C:353:LEU:HD11	2.03	0.41
1:C:77:PHE:HE2	1:C:188:LEU:HD23	1.84	0.41
1:D:77:PHE:CE2	1:D:188:LEU:HD23	2.56	0.41
1:B:110:GLN:O	1:B:113:LYS:HB2	2.21	0.41
1:C:218:LYS:HB2	1:C:218:LYS:HE3	1.93	0.41
1:A:110:GLN:O	1:A:113:LYS:HB2	2.19	0.41
1:A:85:GLY:HA2	1:A:257:GLN:NE2	2.36	0.41
1:B:436:THR:O	1:B:437:LEU:HB2	2.21	0.41
1:C:242:ASP:O	1:C:246:GLY:N	2.49	0.41
1:C:26:VAL:O	1:C:30:MET:HG3	2.21	0.41
1:D:175:THR:O	1:D:178:VAL:HG22	2.21	0.41
2:D:472:HEM:HBC2	2:D:472:HEM:CMC	2.51	0.41
1:A:158:PHE:HE1	1:A:237:MET:CE	2.33	0.41
1:A:81:PHE:HB3	1:A:209:ILE:HG12	2.02	0.41
1:D:96:TRP:CZ2	1:D:100:HIS:CD2	3.08	0.41
1:B:129:LYS:HE2	1:B:144:ASP:OD2	2.21	0.41
1:B:146:THR:HG23	1:B:266:HIS:CE1	2.56	0.41
1:D:247:GLU:HA	1:D:248:PRO:HD3	1.76	0.41
1:A:141:VAL:HG11	1:A:444:PHE:CE2	2.55	0.41
1:A:289:LYS:HB3	1:A:313:TYR:CE2	2.55	0.41
1:A:119:MET:SD	1:A:408:HIS:HD2	2.44	0.41
1:B:345:TYR:HA	1:B:346:PRO:HD3	1.88	0.41
1:B:318:LEU:HD11	1:B:414:LEU:HD12	2.02	0.41
1:D:421:PHE:HB3	1:D:448:ALA:HB1	2.02	0.41
1:A:268:THR:O	1:A:327:THR:HG21	2.22	0.40
1:A:281:VAL:HG13	1:A:425:ASP:HB2	2.02	0.40
1:C:149:THR:HG22	1:C:266:HIS:HA	2.02	0.40
1:D:22:THR:OG1	1:D:23:ASP:N	2.54	0.40
1:D:344:GLU:O	1:D:346:PRO:HD3	2.21	0.40
1:A:276:ALA:O	1:A:280:LEU:HG	2.21	0.40
1:C:183:GLU:O	1:C:187:LYS:HG3	2.21	0.40
1:B:286:VAL:CG1	1:B:376:PRO:HG2	2.52	0.40
1:C:20:LEU:HA	1:C:20:LEU:HD12	1.79	0.40
1:C:320:GLU:HG3	1:C:376:PRO:N	2.36	0.40
1:C:327:THR:O	1:C:329:PRO:HD3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:340:VAL:HG22	1:D:346:PRO:HA	2.04	0.40
1:A:149:THR:HG21	1:A:266:HIS:O	2.22	0.40
1:A:244:GLU:O	1:A:244:GLU:HG2	2.21	0.40
1:B:149:THR:HG22	1:B:266:HIS:HA	2.03	0.40
1:B:335:ALA:HB3	1:B:348:GLU:O	2.21	0.40
1:D:147:ARG:NH1	1:D:167:ARG:O	2.54	0.40
1:C:317:VAL:HG13	1:C:374:PHE:CZ	2.53	0.40
1:D:118:MET:O	1:D:121:ASP:HB3	2.20	0.40
1:D:9:LYS:HE2	1:D:19:LEU:CD2	2.49	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	453/471 (96%)	411 (91%)	39 (9%)	3 (1%)	22	46
1	B	453/471 (96%)	397 (88%)	52 (12%)	4 (1%)	17	40
1	C	453/471 (96%)	412 (91%)	38 (8%)	3 (1%)	22	46
1	D	453/471 (96%)	404 (89%)	42 (9%)	7 (2%)	10	26
All	All	1812/1884 (96%)	1624 (90%)	171 (9%)	17 (1%)	17	40

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	135	ALA
1	D	135	ALA
1	D	196	PRO
1	B	135	ALA
1	A	135	ALA
1	A	229	GLN

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Mol	Chain	Res	Type
1	D	141	VAL
1	D	229	GLN
1	A	141	VAL
1	B	426	HIS
1	D	454	PRO
1	D	227	GLY
1	B	141	VAL
1	D	371	VAL
1	B	371	VAL
1	C	141	VAL
1	C	371	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	399/412 (97%)	373 (94%)	26 (6%)	17	38
1	B	399/412 (97%)	363 (91%)	36 (9%)	9	22
1	C	399/412 (97%)	370 (93%)	29 (7%)	14	33
1	D	399/412 (97%)	376 (94%)	23 (6%)	20	43
All	All	1596/1648 (97%)	1482 (93%)	114 (7%)	14	34

All (114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	56	ARG
1	A	57	LEU
1	A	64	GLU
1	A	94	LYS
1	A	103	LEU
1	A	126	LEU
1	A	134	ASN
1	A	148	LEU
1	A	149	THR

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Mol	Chain	Res	Type
1	A	172	PRO
1	A	195	ASP
1	A	200	GLU
1	A	201	ASN
1	A	233	LEU
1	A	235	THR
1	A	255	ARG
1	A	266	HIS
1	A	289	LYS
1	A	293	GLU
1	A	318	LEU
1	A	338	ASP
1	A	364	LYS
1	A	387	GLN
1	A	407	LEU
1	A	414	LEU
1	B	7	GLN
1	B	21	ASN
1	B	53	SER
1	B	56	ARG
1	B	64	GLU
1	B	71	LEU
1	B	87	PHE
1	B	88	THR
1	B	94	LYS
1	B	109	GLN
1	B	126	LEU
1	B	134	ASN
1	B	139	ILE
1	B	149	THR
1	B	151	ASP
1	B	192	ASN
1	B	201	ASN
1	B	218	LYS
1	B	229	GLN
1	B	233	LEU
1	B	239	ASN
1	B	247	GLU
1	B	250	ASP
1	B	266	HIS
1	B	293	GLU
1	B	318	LEU

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Mol	Chain	Res	Type
1	B	324	LEU
1	B	337	GLU
1	B	338	ASP
1	B	349	LYS
1	B	385	ILE
1	B	404	GLN
1	B	407	LEU
1	B	414	LEU
1	B	430	GLU
1	B	444	PHE
1	C	7	GLN
1	C	20	LEU
1	C	47	ARG
1	C	57	LEU
1	C	88	THR
1	C	103	LEU
1	C	109	GLN
1	C	126	LEU
1	C	134	ASN
1	C	149	THR
1	C	151	ASP
1	C	168	ASP
1	C	192	ASN
1	C	201	ASN
1	C	228	GLU
1	C	230	SER
1	C	233	LEU
1	C	266	HIS
1	C	293	GLU
1	C	318	LEU
1	C	320	GLU
1	C	338	ASP
1	C	364	LYS
1	C	375	ARG
1	C	383	SER
1	C	404	GLN
1	C	407	LEU
1	C	414	LEU
1	C	452	LYS
1	D	1	THR
1	D	2	ILE
1	D	7	GLN

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Mol	Chain	Res	Type
1	D	56	ARG
1	D	88	THR
1	D	103	LEU
1	D	126	LEU
1	D	134	ASN
1	D	148	LEU
1	D	149	THR
1	D	167	ARG
1	D	201	ASN
1	D	226	SER
1	D	228	GLU
1	D	229	GLN
1	D	233	LEU
1	D	266	HIS
1	D	293	GLU
1	D	324	LEU
1	D	337	GLU
1	D	407	LEU
1	D	414	LEU
1	D	430	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	100	HIS
1	A	109	GLN
1	A	116	HIS
1	A	134	ASN
1	A	171	HIS
1	A	192	ASN
1	A	201	ASN
1	A	204	GLN
1	A	239	ASN
1	A	403	GLN
1	A	404	GLN
1	A	408	HIS
1	A	426	HIS
1	B	7	GLN
1	B	21	ASN
1	B	27	GLN
1	B	100	HIS

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Mol	Chain	Res	Type
1	B	116	HIS
1	B	171	HIS
1	B	201	ASN
1	B	239	ASN
1	B	266	HIS
1	B	307	GLN
1	B	310	GLN
1	B	403	GLN
1	C	7	GLN
1	C	21	ASN
1	C	27	GLN
1	C	100	HIS
1	C	116	HIS
1	C	171	HIS
1	C	192	ASN
1	C	201	ASN
1	C	204	GLN
1	C	239	ASN
1	C	310	GLN
1	C	403	GLN
1	C	426	HIS
1	D	7	GLN
1	D	92	HIS
1	D	100	HIS
1	D	116	HIS
1	D	134	ASN
1	D	201	ASN
1	D	388	HIS
1	D	403	GLN
1	D	420	HIS
1	D	426	HIS

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	HEM	D	472	1	27,50,50	1.65	6 (22%)	17,82,82	1.35	4 (23%)
2	HEM	A	472	1	27,50,50	1.54	3 (11%)	17,82,82	1.32	3 (17%)
3	PAM	C	473	-	14,17,17	0.45	0	13,17,17	0.36	0
2	HEM	C	472	1	27,50,50	1.54	3 (11%)	17,82,82	1.45	5 (29%)
2	HEM	B	472	1	27,50,50	1.80	6 (22%)	17,82,82	1.35	4 (23%)
3	PAM	B	473	-	14,17,17	0.45	0	13,17,17	0.47	0
3	PAM	A	473	-	14,17,17	0.40	0	13,17,17	0.64	0
3	PAM	D	473	-	14,17,17	0.41	0	13,17,17	0.55	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	D	472	1	-	0/6/54/54	-
2	HEM	A	472	1	-	0/6/54/54	-
3	PAM	C	473	-	-	4/13/15/15	-
2	HEM	C	472	1	-	0/6/54/54	-
2	HEM	B	472	1	-	0/6/54/54	-
3	PAM	B	473	-	-	3/13/15/15	-
3	PAM	A	473	-	-	6/13/15/15	-
3	PAM	D	473	-	-	4/13/15/15	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	472	HEM	C3B-CAB	-4.67	1.38	1.47
2	B	472	HEM	C3C-CAC	-4.55	1.38	1.47
2	D	472	HEM	C3C-CAC	-4.22	1.39	1.47
2	D	472	HEM	C3B-CAB	-3.98	1.39	1.47
2	A	472	HEM	C3C-CAC	-3.95	1.39	1.47
2	B	472	HEM	C3B-CAB	-3.79	1.40	1.47
2	A	472	HEM	C3B-CAB	-3.61	1.40	1.47
2	C	472	HEM	C3C-CAC	-3.00	1.41	1.47
2	B	472	HEM	C3C-C2C	-2.61	1.36	1.40
2	B	472	HEM	C3B-C2B	-2.43	1.37	1.40
2	B	472	HEM	C1C-C2C	2.33	1.47	1.42
2	D	472	HEM	C3C-C2C	-2.31	1.37	1.40
2	B	472	HEM	C1B-C2B	2.30	1.47	1.42
2	D	472	HEM	C1A-CHA	-2.29	1.34	1.41
2	C	472	HEM	C1D-ND	2.27	1.40	1.36
2	D	472	HEM	C3B-C2B	-2.26	1.37	1.40
2	A	472	HEM	C1C-C2C	2.06	1.47	1.42
2	D	472	HEM	C1B-C2B	2.02	1.47	1.42

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	472	HEM	CBD-CAD-C3D	-2.98	106.99	112.48
2	B	472	HEM	C4C-C3C-C2C	-2.82	104.93	106.90
2	C	472	HEM	CMB-C2B-C3B	2.80	129.92	124.68
2	D	472	HEM	CMB-C2B-C3B	2.69	129.70	124.68
2	B	472	HEM	CMB-C2B-C3B	2.54	129.43	124.68
2	A	472	HEM	C4C-C3C-C2C	-2.52	105.14	106.90
2	D	472	HEM	C4C-C3C-C2C	-2.48	105.17	106.90
2	B	472	HEM	C3B-C4B-NB	2.32	112.21	109.21
2	A	472	HEM	CMB-C2B-C3B	2.28	128.95	124.68
2	D	472	HEM	CBD-CAD-C3D	-2.26	108.31	112.48
2	C	472	HEM	CBD-CAD-C3D	-2.24	108.36	112.48
2	C	472	HEM	C4C-C3C-C2C	-2.22	105.35	106.90
2	D	472	HEM	C1D-C2D-C3D	-2.20	105.46	107.00
2	B	472	HEM	CBD-CAD-C3D	-2.16	108.50	112.48
2	C	472	HEM	CMC-C2C-C3C	2.05	128.51	124.68
2	C	472	HEM	C1D-C2D-C3D	-2.04	105.58	107.00

There are no chirality outliers.

All (17) torsion outliers are listed below:

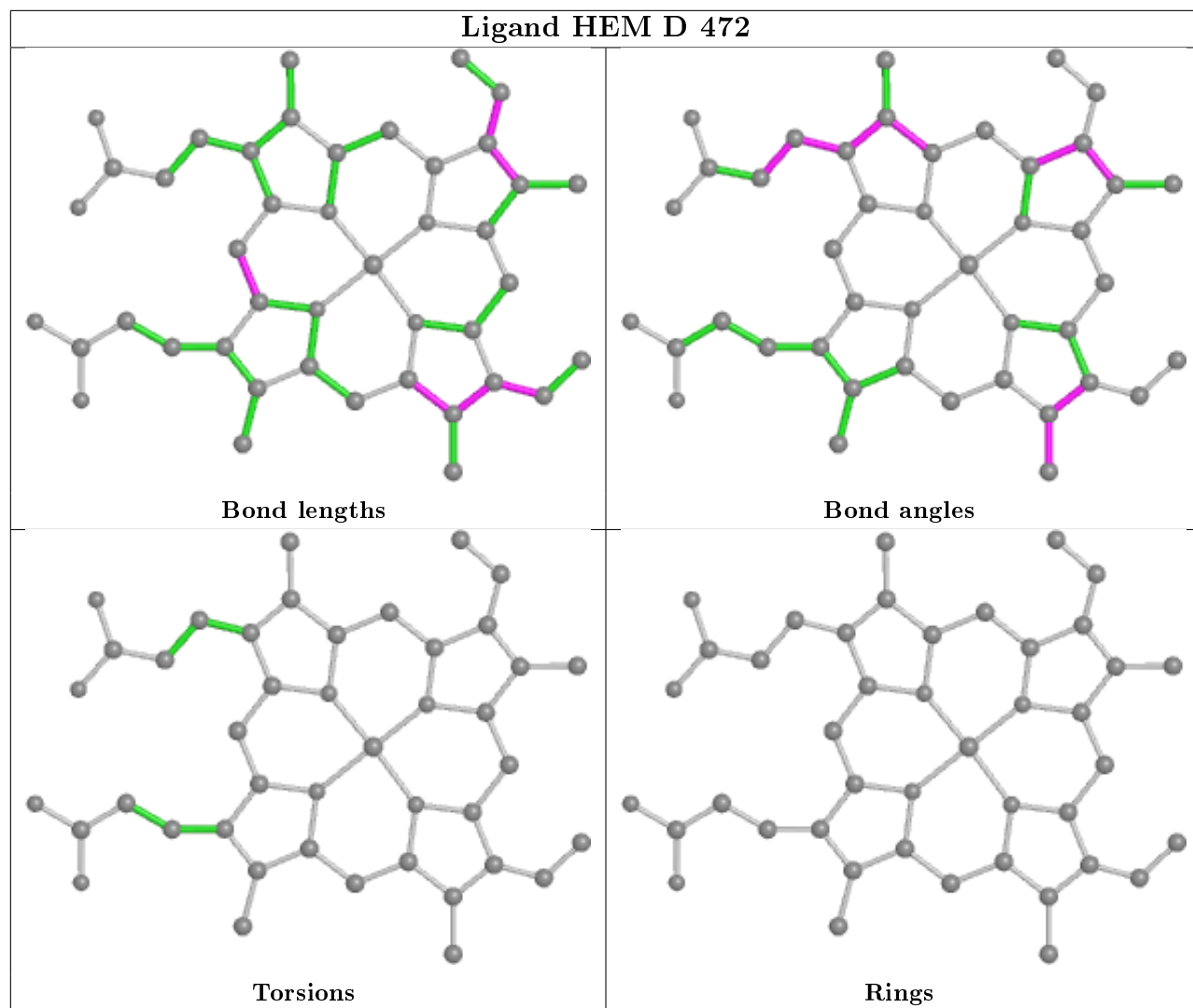
Mol	Chain	Res	Type	Atoms
3	C	473	PAM	C11-C12-C13-C14
3	C	473	PAM	C6-C7-C8-C9
3	D	473	PAM	C6-C7-C8-C9
3	A	473	PAM	C13-C14-C15-C16
3	D	473	PAM	C2-C3-C4-C5
3	A	473	PAM	C12-C13-C14-C15
3	A	473	PAM	C3-C4-C5-C6
3	A	473	PAM	C1-C2-C3-C4
3	A	473	PAM	C9-C10-C11-C12
3	D	473	PAM	C12-C13-C14-C15
3	A	473	PAM	C2-C3-C4-C5
3	B	473	PAM	C4-C5-C6-C7
3	B	473	PAM	C7-C8-C9-C10
3	C	473	PAM	C2-C3-C4-C5
3	B	473	PAM	C9-C10-C11-C12
3	D	473	PAM	C9-C10-C11-C12
3	C	473	PAM	C5-C6-C7-C8

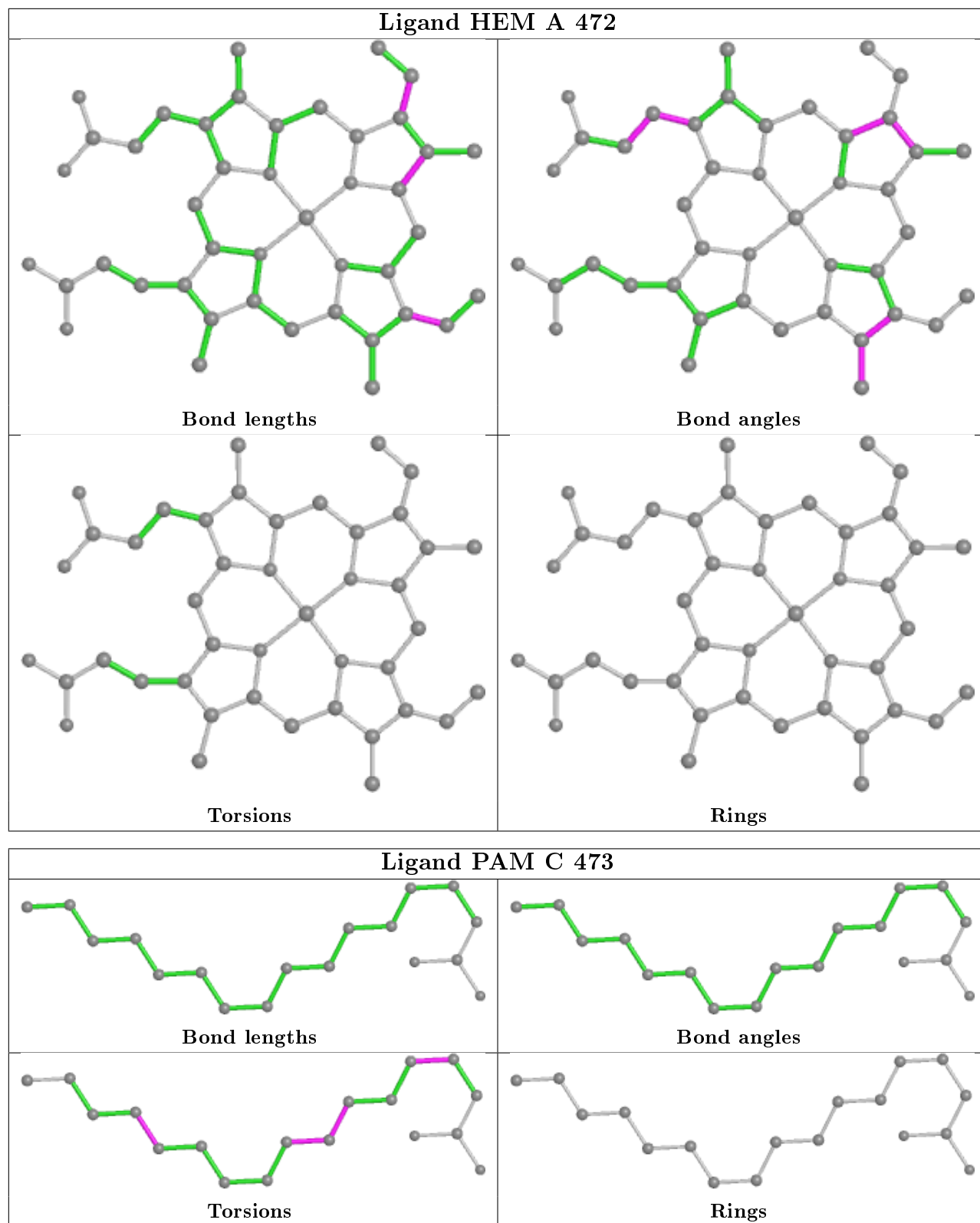
There are no ring outliers.

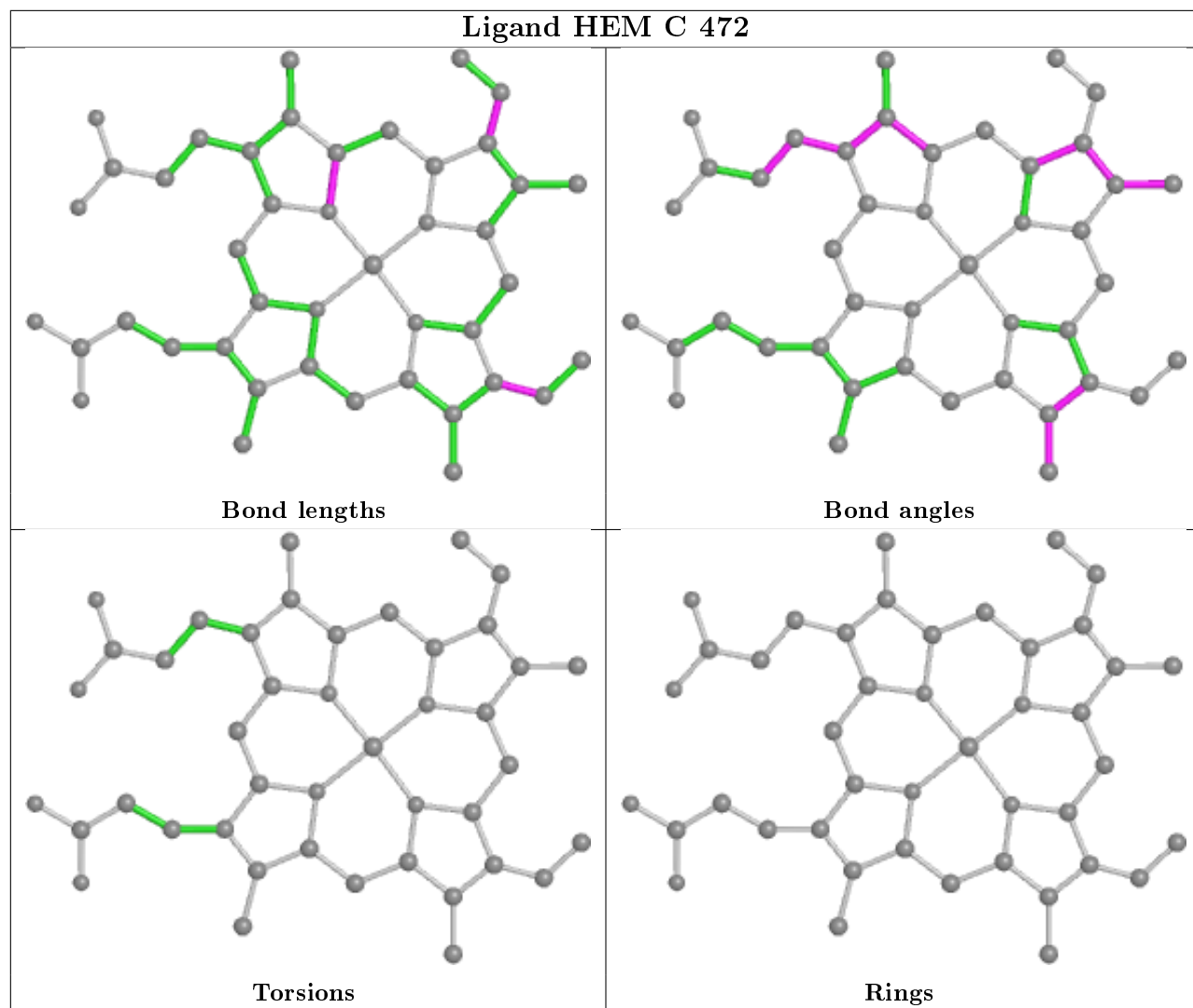
7 monomers are involved in 23 short contacts:

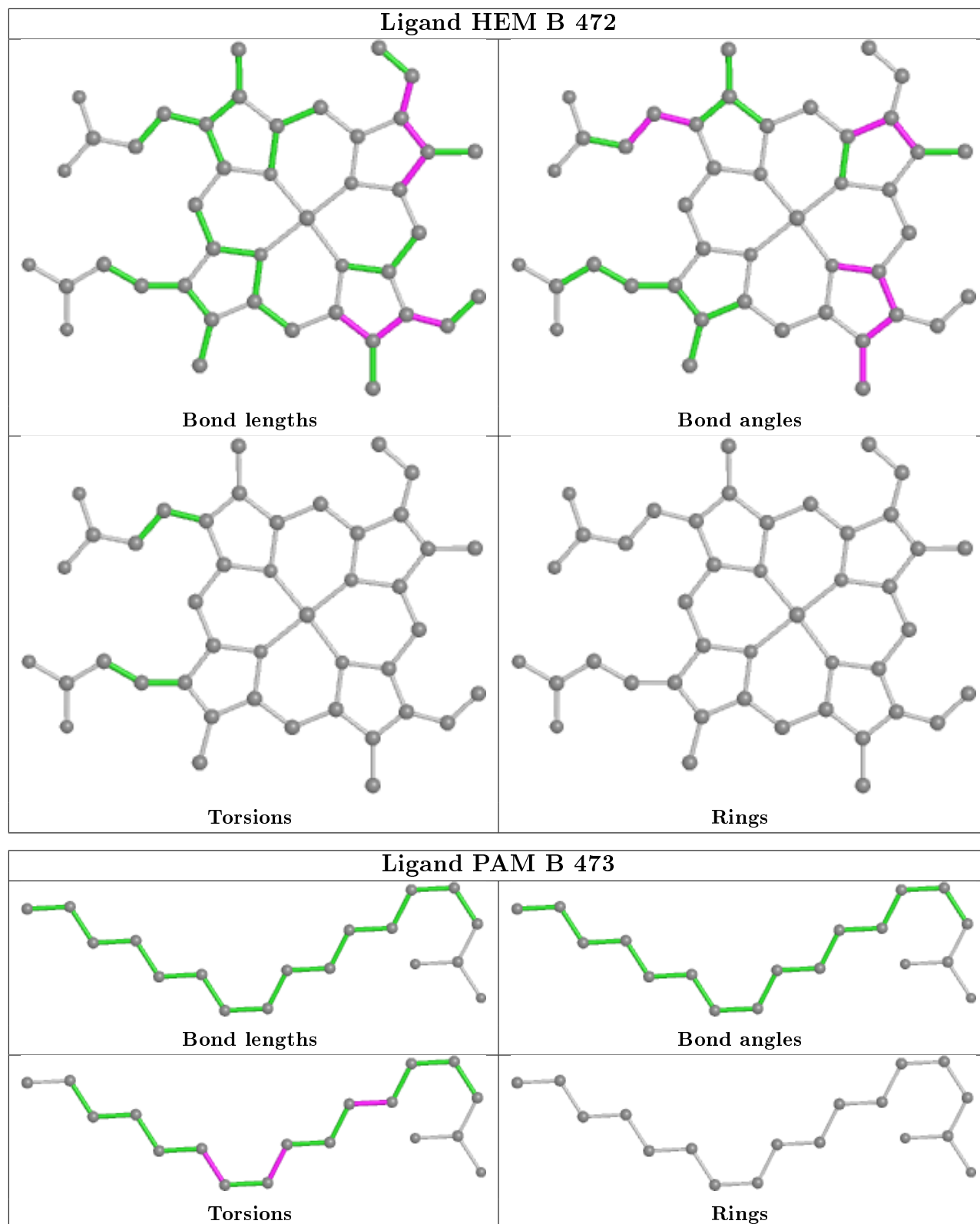
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	472	HEM	7	0
2	A	472	HEM	2	0
3	C	473	PAM	3	0
2	C	472	HEM	5	0
2	B	472	HEM	3	0
3	B	473	PAM	2	0
3	A	473	PAM	1	0

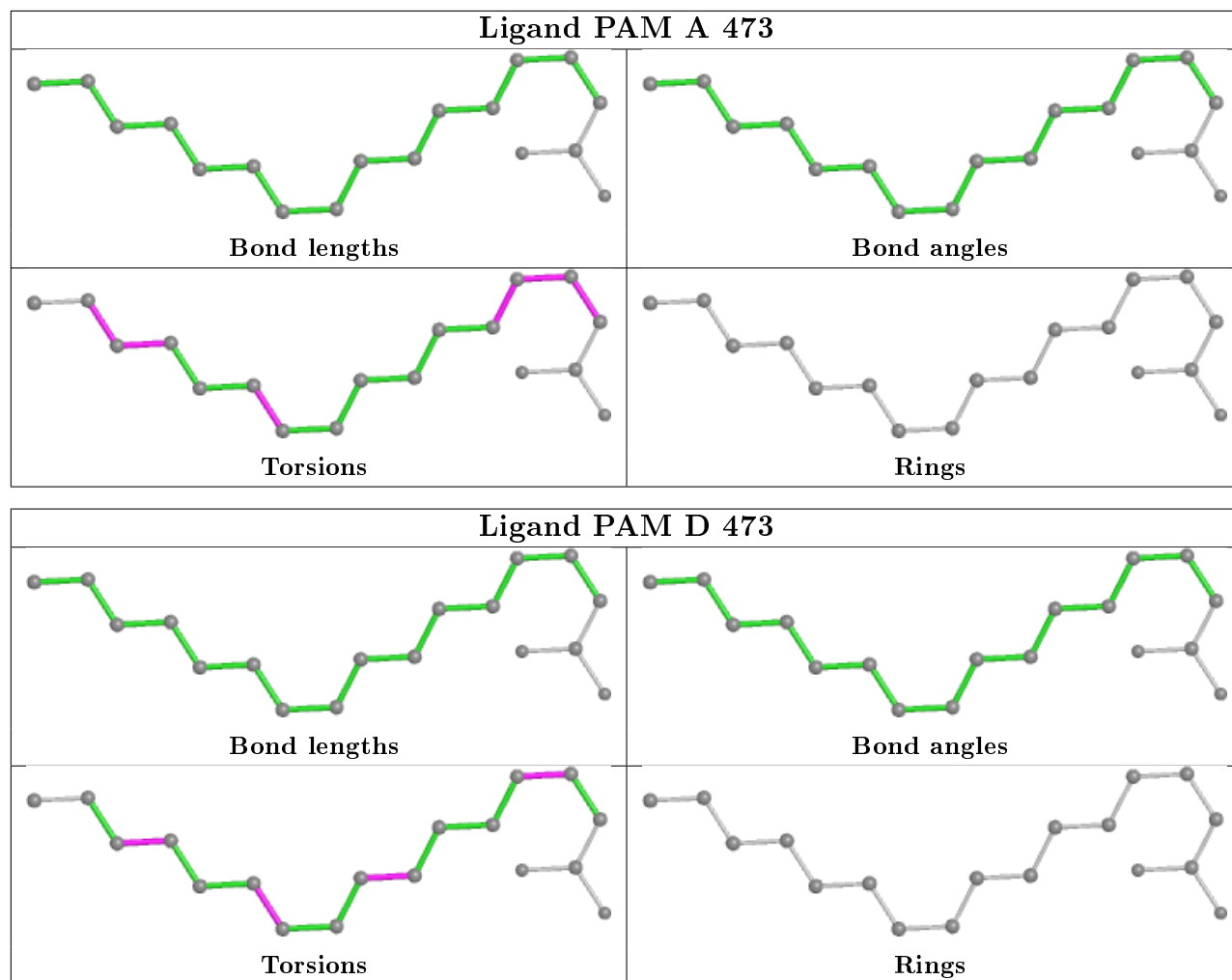
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	455/471 (96%)	-0.24	5 (1%) 80 82	18, 45, 84, 100	0
1	B	455/471 (96%)	0.04	10 (2%) 62 63	26, 54, 89, 100	0
1	C	455/471 (96%)	0.00	15 (3%) 46 46	25, 56, 89, 100	0
1	D	455/471 (96%)	-0.11	9 (1%) 65 67	22, 50, 90, 100	0
All	All	1820/1884 (96%)	-0.08	39 (2%) 63 65	18, 52, 89, 100	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	229	GLN	5.9
1	C	229	GLN	5.0
1	C	228	GLU	4.7
1	B	229	GLN	4.6
1	B	240	GLY	4.5
1	B	455	LEU	4.1
1	B	288	GLN	3.5
1	B	350	GLY	3.5
1	D	1	THR	3.3
1	A	364	LYS	2.9
1	C	2	ILE	2.9
1	D	228	GLU	2.9
1	C	305	TYR	2.7
1	C	227	GLY	2.7
1	A	169	GLN	2.7
1	B	373	GLU	2.7
1	D	332	SER	2.7
1	C	16	ASN	2.5
1	C	245	THR	2.4
1	D	306	LYS	2.4
1	C	375	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	229	GLN	2.4
1	C	13	GLU	2.3
1	D	337	GLU	2.3
1	C	192	ASN	2.3
1	C	110	GLN	2.3
1	C	381	ASN	2.3
1	A	285	HIS	2.2
1	B	284	PRO	2.2
1	C	369	ASP	2.1
1	B	2	ILE	2.1
1	B	68	ASP	2.1
1	D	136	ASP	2.1
1	B	1	THR	2.1
1	C	8	PRO	2.0
1	C	1	THR	2.0
1	D	109	GLN	2.0
1	A	353	LEU	2.0
1	D	248	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

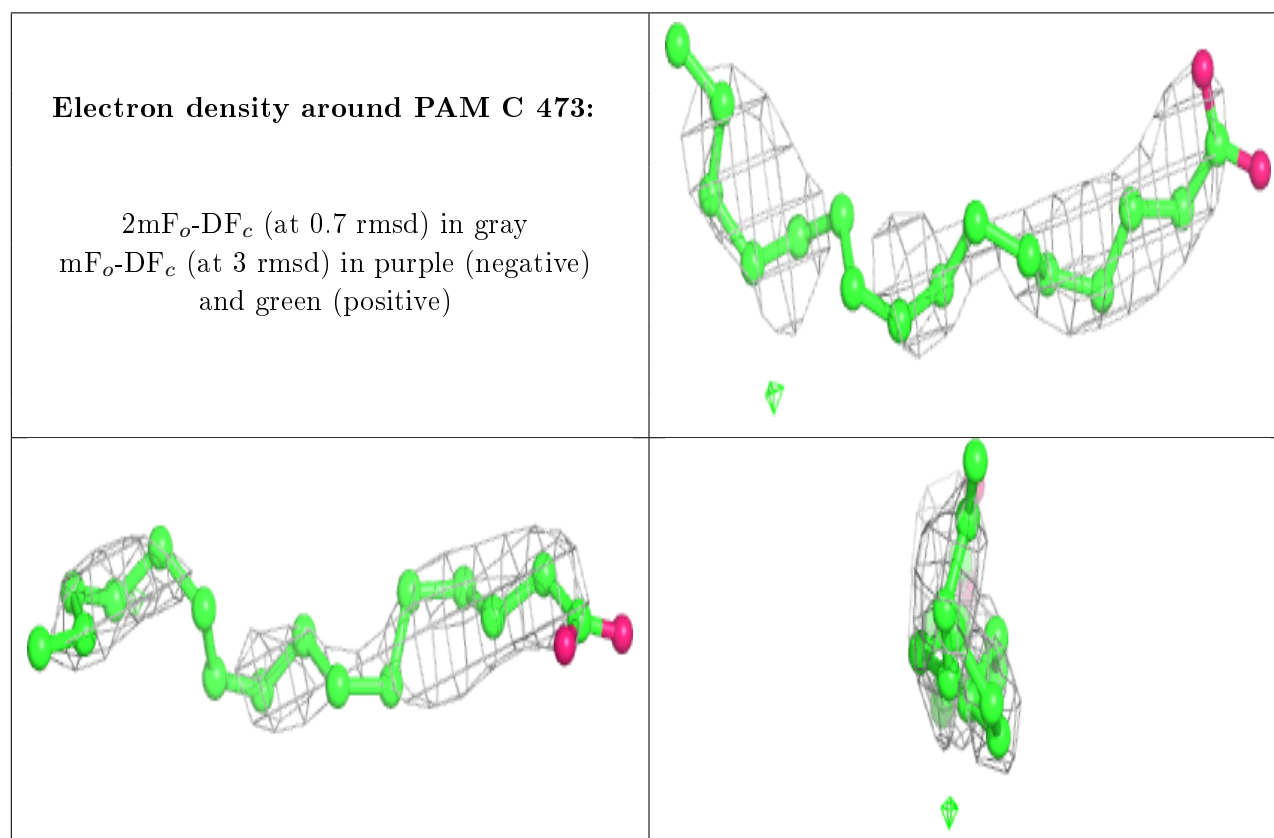
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PAM	C	473	18/18	0.83	0.30	58,69,96,99	0
3	PAM	B	473	18/18	0.89	0.27	45,52,77,80	0
3	PAM	A	473	18/18	0.89	0.23	28,48,80,83	0
3	PAM	D	473	18/18	0.89	0.22	31,49,64,66	0
2	HEM	C	472	43/43	0.94	0.15	19,38,52,56	0

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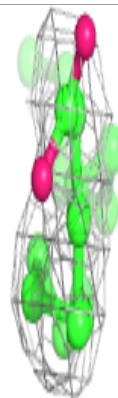
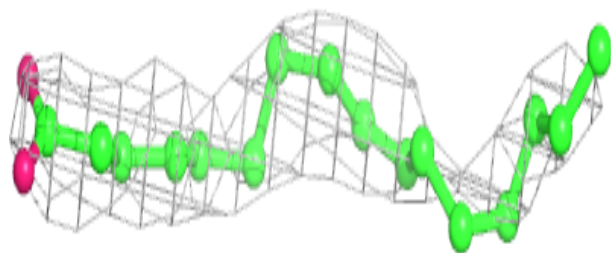
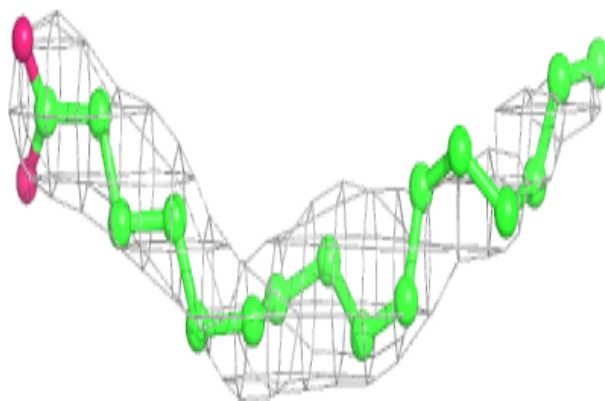
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	HEM	A	472	43/43	0.95	0.15	15,30,46,51	0
2	HEM	B	472	43/43	0.96	0.14	19,29,54,68	0
2	HEM	D	472	43/43	0.97	0.10	15,30,44,68	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

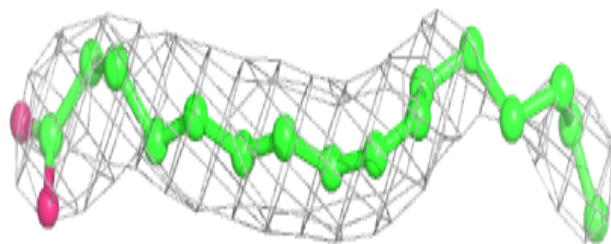
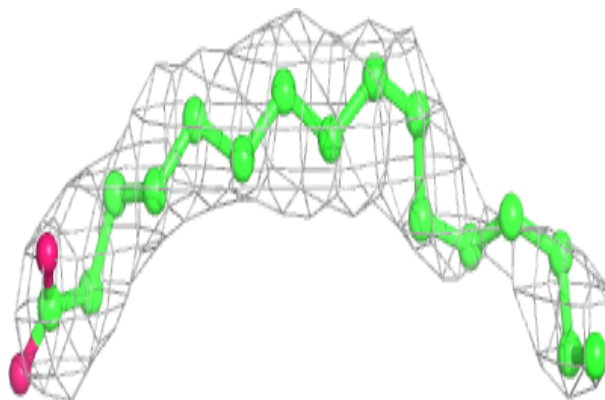


Electron density around PAM B 473:

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

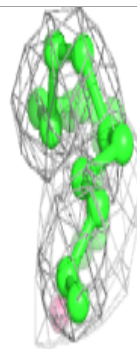
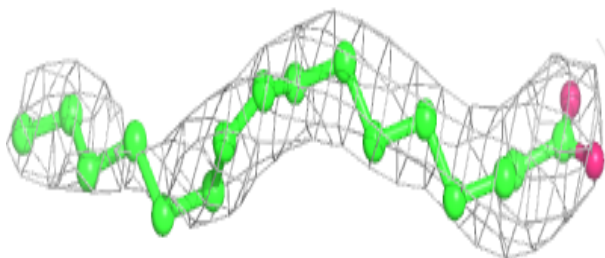
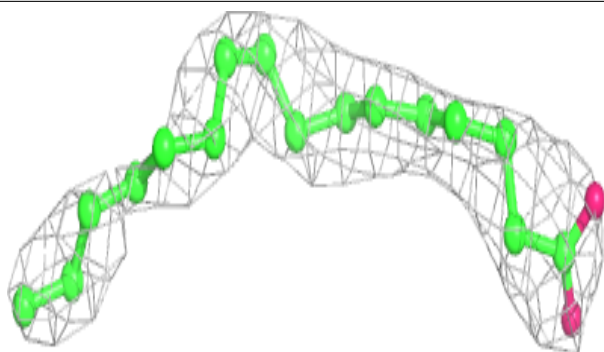
**Electron density around PAM A 473:**

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



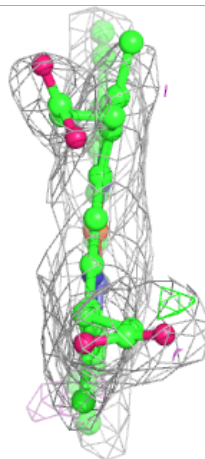
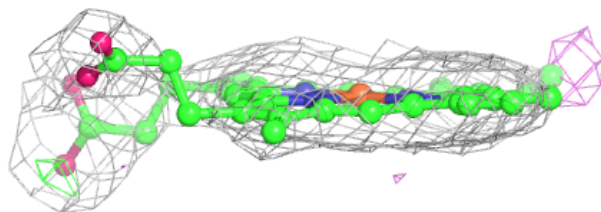
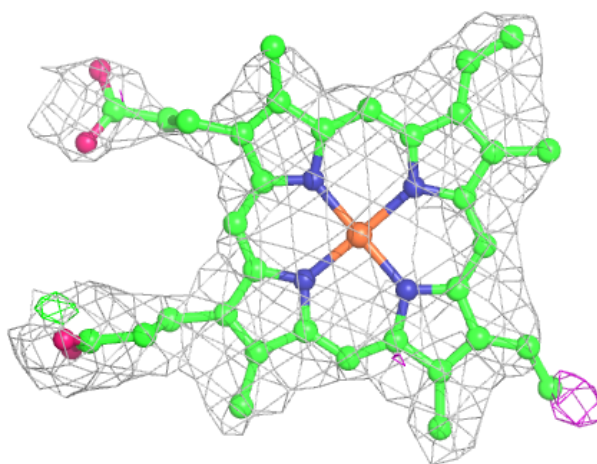
Electron density around PAM D 473:

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



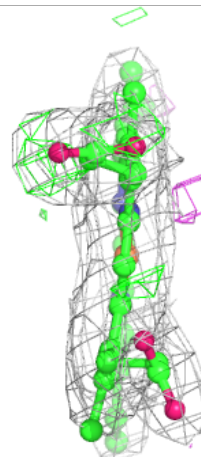
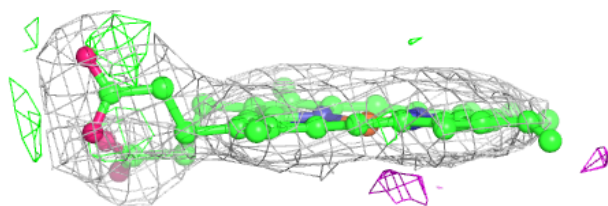
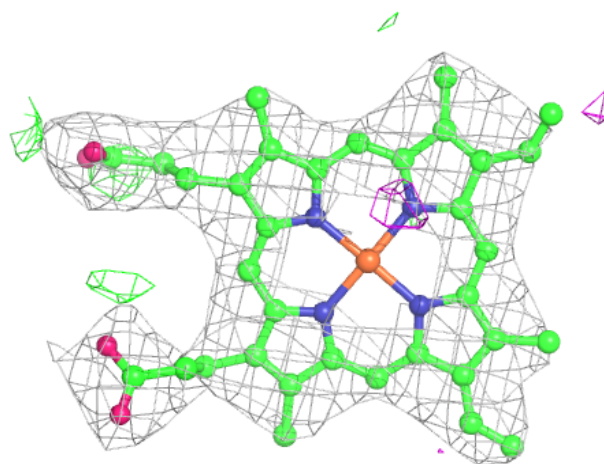
Electron density around HEM C 472:

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



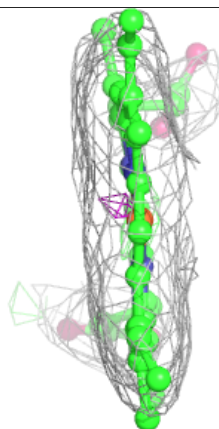
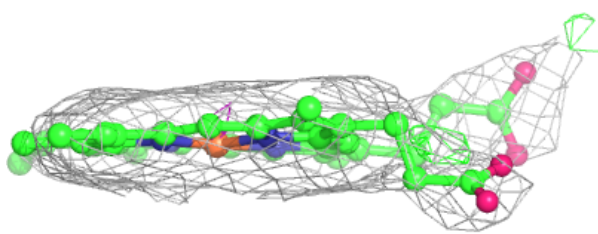
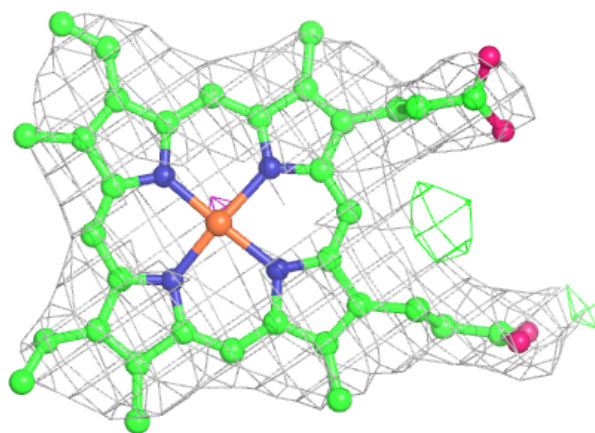
Electron density around HEM A 472:

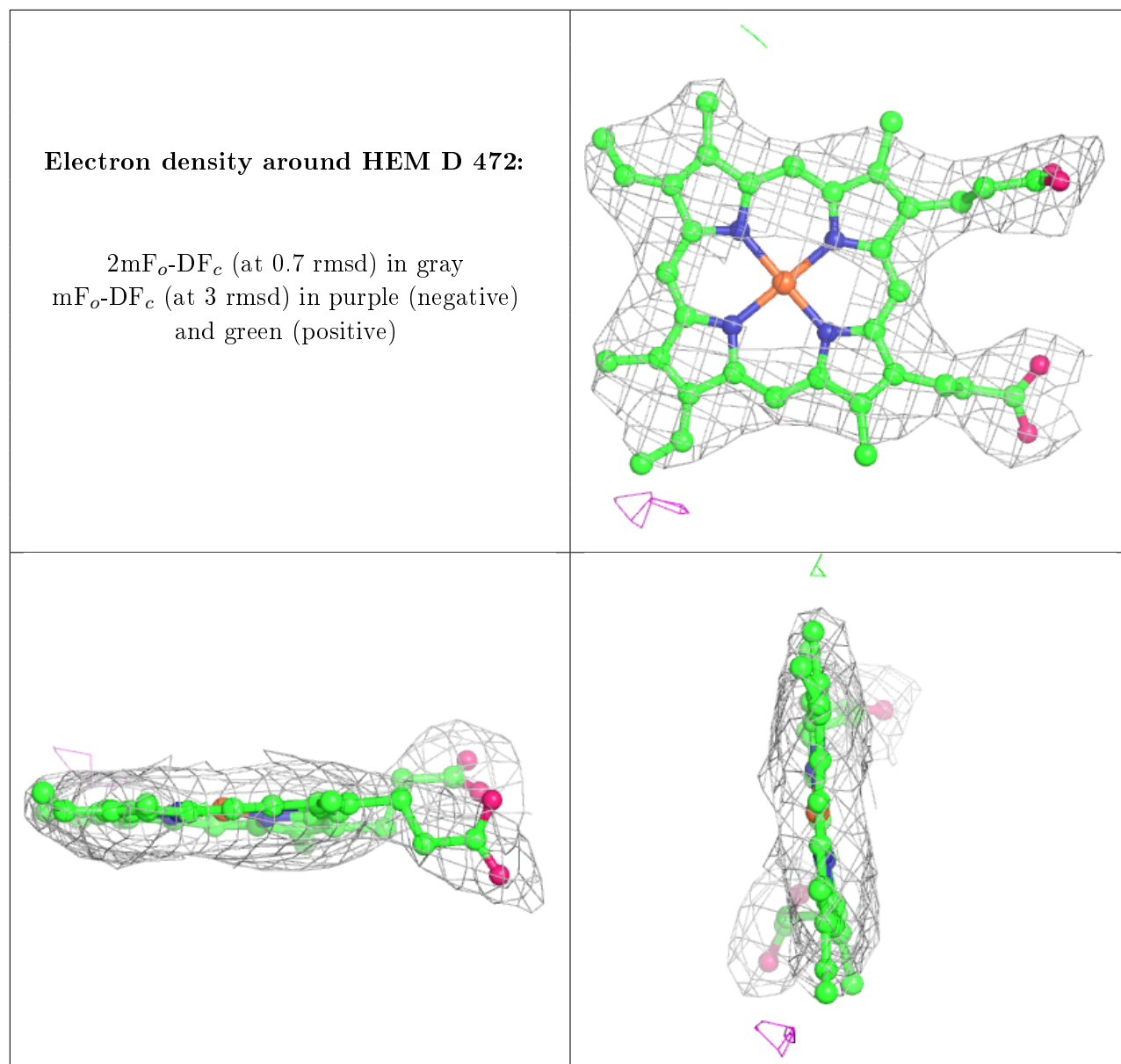
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 472:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.