



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 10:00 am GMT

PDB ID : 4CK8
Title : STEROL 14-ALPHA DEMETHYLASE (CYP51)FROM TRYPANOSOMA CRUZI IN COMPLEX WITH (R)-1-(2,4-dichlorophenyl)-2-(1H-imidazol-1-yl)ethyl 4-(4-(3,4-dichlorophenyl)piperazin-1-yl)phenylcarbamate (LFD)
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Deposited on : 2013-12-30
Resolution : 2.62 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

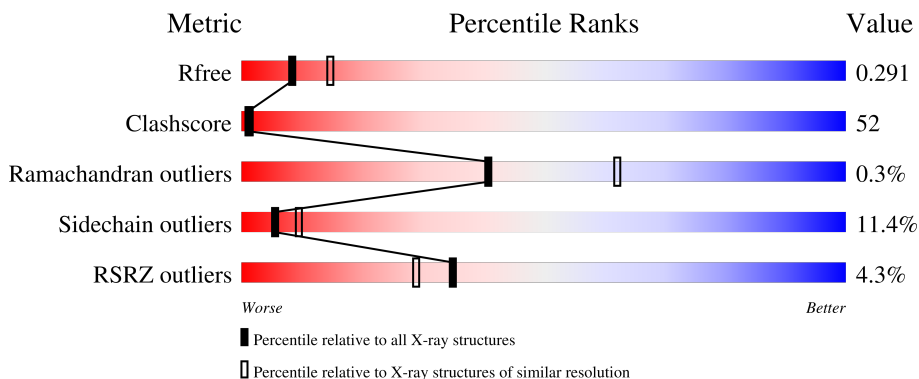
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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

Mol	Chain	Length	Quality of chain
1	A	460	 3% 40% 50% 7%
1	B	460	 5% 43% 47% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7377 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 STEROL 14-ALPHA DEMETHYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	449	3592	2294	630	640	28	0	0	0
1	B	450	3597	2297	631	641	28	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

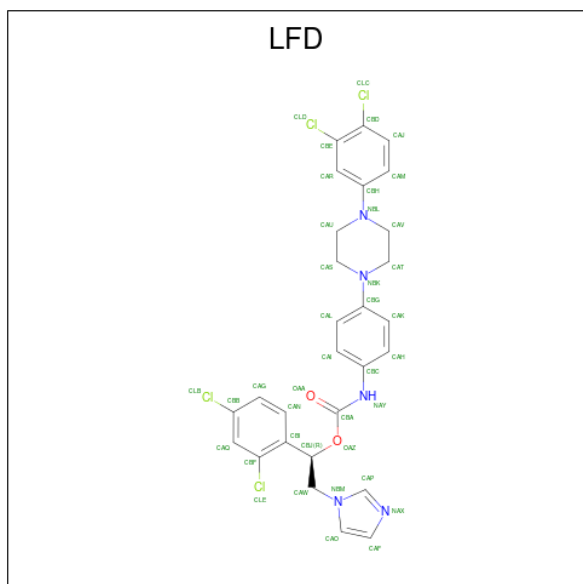
Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ALA	-	expression tag	UNP Q7Z1V1
A	29	LYS	-	expression tag	UNP Q7Z1V1
A	30	LYS	-	expression tag	UNP Q7Z1V1
A	31	THR	-	expression tag	UNP Q7Z1V1
A	482	HIS	-	expression tag	UNP Q7Z1V1
A	483	HIS	-	expression tag	UNP Q7Z1V1
A	484	HIS	-	expression tag	UNP Q7Z1V1
A	485	HIS	-	expression tag	UNP Q7Z1V1
A	486	HIS	-	expression tag	UNP Q7Z1V1
A	487	HIS	-	expression tag	UNP Q7Z1V1
B	28	ALA	-	expression tag	UNP Q7Z1V1
B	29	LYS	-	expression tag	UNP Q7Z1V1
B	30	LYS	-	expression tag	UNP Q7Z1V1
B	31	THR	-	expression tag	UNP Q7Z1V1
B	482	HIS	-	expression tag	UNP Q7Z1V1
B	483	HIS	-	expression tag	UNP Q7Z1V1
B	484	HIS	-	expression tag	UNP Q7Z1V1
B	485	HIS	-	expression tag	UNP Q7Z1V1
B	486	HIS	-	expression tag	UNP Q7Z1V1
B	487	HIS	-	expression tag	UNP Q7Z1V1

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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		

- Molecule 3 is (1R)-1-(2,4-dichlorophenyl)-2-(1H-imidazol-1-yl)ethyl {4-[4-(3,4-dichlorophenyl)piperazin-1-yl]phenyl}carbamate (three-letter code: LFD) (formula: C₂₈H₂₅Cl₄N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	Cl	N	O	0	0
			39	28	4	5	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
3	B	1	39	28	4	5	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	O	0	0
			13	13		
4	B	11	Total	O	0	0
			11	11		

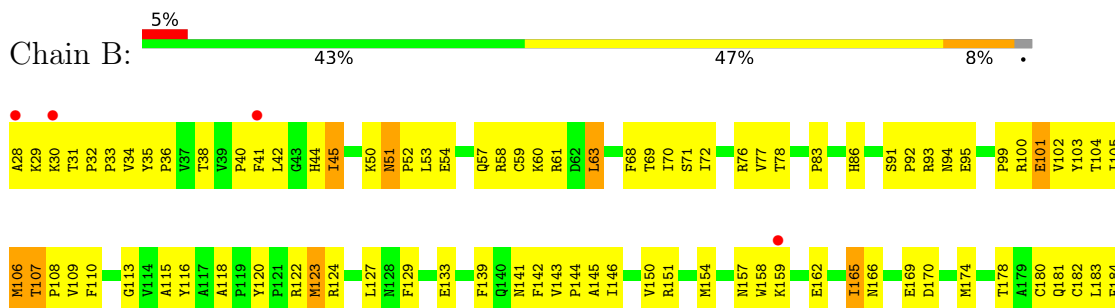
3 Residue-property plots [i](#)

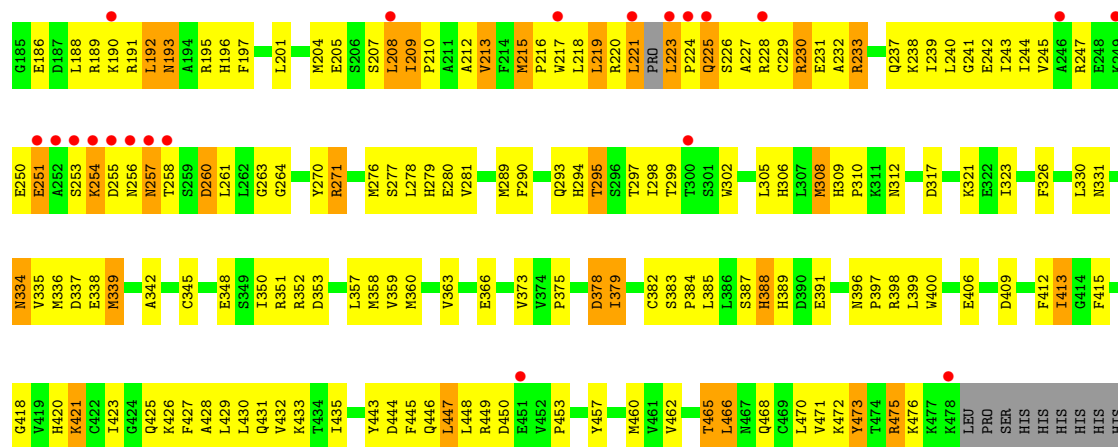
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: STEROL 14-ALPHA DEMETHYLASE



• Molecule 1: STEROL 14-ALPHA DEMETHYLASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.90Å 137.18Å 152.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.62 29.76 – 2.62	Depositor EDS
% Data completeness (in resolution range)	98.9 (30.00-2.62) 99.0 (29.76-2.62)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.14 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.235 , 0.286 0.242 , 0.291	Depositor DCC
R_{free} test set	1905 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	52.9	Xtrriage
Anisotropy	0.383	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7377	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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: LFD, HEM

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/3675	0.58	1/4964 (0.0%)
1	B	0.30	0/3680	0.58	0/4971
All	All	0.32	0/7355	0.58	1/9935 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	460	MET	CB-CG-SD	-5.64	95.47	112.40

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	3592	0	3624	352	0
1	B	3597	0	3629	399	0
2	A	43	0	30	8	0
2	B	43	0	30	19	0
3	A	39	0	25	10	0
3	B	39	0	25	11	0
4	A	13	0	0	5	0
4	B	11	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7377	0	7363	761	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 52.

All (761) 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:B:105:ILE:CG2	1:B:213:VAL:HG23	1.58	1.33
1:A:233:ARG:HH12	1:A:279:HIS:CD2	1.49	1.29
1:B:277:SER:O	1:B:281:VAL:HG23	1.26	1.28
1:B:33:PRO:HB2	1:B:63:LEU:CD1	1.65	1.25
1:B:219:LEU:CD1	1:B:220:ARG:H	1.52	1.21
1:A:103:TYR:HD2	1:A:116:TYR:CE2	1.60	1.18
1:A:212:ALA:HB1	1:A:219:LEU:HD21	1.19	1.18
1:A:257:ASN:HB2	4:A:2006:HOH:O	1.40	1.18
1:B:220:ARG:HB3	1:B:221:LEU:HB3	1.21	1.17
1:B:58:ARG:HG3	1:B:61:ARG:HH22	1.03	1.16
1:A:33:PRO:HB2	1:A:63:LEU:CD1	1.78	1.14
1:A:116:TYR:CD1	1:A:123:MET:CE	2.32	1.11
1:A:116:TYR:CD1	1:A:123:MET:HE3	1.86	1.10
1:B:207:SER:HB3	1:B:225:GLN:NE2	1.66	1.10
1:A:215:MET:O	1:A:218:LEU:HG	1.49	1.09
1:A:250:GLU:HG2	1:A:255:ASP:OD2	1.52	1.09
1:B:331:ASN:H	1:B:334:ASN:ND2	1.49	1.09
1:B:207:SER:CA	1:B:225:GLN:HG3	1.84	1.07
1:B:44:HIS:CD2	1:B:71:SER:H	1.74	1.06
1:B:254:LYS:HE2	1:B:254:LYS:HA	1.34	1.06
1:A:33:PRO:CB	1:A:63:LEU:HD12	1.85	1.06
1:B:105:ILE:HG23	1:B:213:VAL:HG23	1.09	1.06
1:B:209:ILE:HG12	1:B:212:ALA:HB2	1.07	1.04
1:B:207:SER:CB	1:B:225:GLN:HE21	1.69	1.04
1:B:255:ASP:O	1:B:256:ASN:HB2	1.56	1.04
1:B:192:LEU:HD11	1:B:197:PHE:HB2	1.40	1.03
1:A:44:HIS:CD2	1:A:71:SER:H	1.76	1.03
1:A:103:TYR:CD2	1:A:116:TYR:CE2	2.47	1.02
1:B:220:ARG:HB3	1:B:221:LEU:CB	1.90	1.02
1:B:209:ILE:CG1	1:B:212:ALA:HB2	1.89	1.01
1:A:116:TYR:HD1	1:A:123:MET:CE	1.67	1.01
1:B:460:MET:HE2	3:B:1490:LFD:HAH	1.39	1.01
1:B:219:LEU:HD12	1:B:220:ARG:H	1.20	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:PRO:CB	1:A:63:LEU:CD1	2.37	1.00
1:A:104:THR:O	1:A:107:THR:HG23	1.60	1.00
1:B:290:PHE:CD2	3:B:1490:LFD:CLE	2.51	1.00
1:A:33:PRO:HB2	1:A:63:LEU:HD12	1.02	1.00
1:B:33:PRO:HB2	1:B:63:LEU:HD12	1.38	1.00
1:B:103:TYR:CD2	1:B:116:TYR:CE2	2.49	1.00
1:B:103:TYR:CD2	1:B:116:TYR:HE2	1.78	1.00
1:A:233:ARG:NH1	1:A:279:HIS:CD2	2.30	1.00
1:B:207:SER:HA	1:B:225:GLN:HG3	1.00	0.99
1:B:233:ARG:HH22	1:B:279:HIS:CD2	1.79	0.99
1:B:429:LEU:O	1:B:433:LYS:HG3	1.62	0.99
1:B:219:LEU:CD1	1:B:220:ARG:N	2.26	0.98
1:B:460:MET:CE	3:B:1490:LFD:HAH	1.92	0.98
1:A:447:LEU:CD1	1:A:449:ARG:HB2	1.93	0.98
1:B:217:TRP:CZ2	1:B:218:LEU:HD23	1.99	0.97
1:A:98:SER:CB	1:A:364:LYS:HE2	1.95	0.96
1:B:207:SER:HB3	1:B:225:GLN:HE21	1.23	0.96
1:B:210:PRO:HB3	3:B:1490:LFD:HAV	1.47	0.96
1:B:44:HIS:HD2	1:B:71:SER:H	1.08	0.96
1:A:223:LEU:N	1:A:224:PRO:HD3	1.80	0.96
1:A:116:TYR:CD1	1:A:123:MET:HE1	2.00	0.96
1:B:33:PRO:HB2	1:B:63:LEU:HD13	1.47	0.96
1:B:223:LEU:HD22	1:B:224:PRO:HD3	1.45	0.95
1:B:277:SER:O	1:B:281:VAL:CG2	2.14	0.95
1:B:217:TRP:O	1:B:219:LEU:HD12	1.66	0.94
1:B:221:LEU:O	1:B:223:LEU:HB3	1.65	0.94
1:B:223:LEU:HD22	1:B:224:PRO:CD	1.96	0.94
1:A:227:ALA:O	1:A:230:ARG:HB2	1.68	0.94
1:B:219:LEU:HD13	1:B:220:ARG:H	1.29	0.94
1:B:58:ARG:HG3	1:B:61:ARG:NH2	1.81	0.94
1:B:247:ARG:NH2	1:B:258:THR:HG21	1.82	0.93
1:B:209:ILE:HG12	1:B:212:ALA:CB	1.98	0.93
1:A:98:SER:HB2	1:A:364:LYS:HE2	1.49	0.93
1:A:116:TYR:HD1	1:A:123:MET:HE3	1.22	0.93
1:A:187:ASP:HA	1:A:190:LYS:HG3	1.50	0.93
1:A:165:ILE:HD13	1:A:165:ILE:H	1.33	0.92
1:B:207:SER:HA	1:B:225:GLN:CG	1.96	0.92
1:A:447:LEU:HD11	1:A:449:ARG:HB2	1.52	0.91
1:B:217:TRP:CE2	1:B:218:LEU:HD23	2.05	0.91
2:A:1480:HEM:HMB2	2:A:1480:HEM:HBB2	1.52	0.91
1:B:180:CYS:O	1:B:184:PHE:HB2	1.71	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:LYS:HG3	1:A:66:GLY:HA2	1.52	0.90
1:B:331:ASN:H	1:B:334:ASN:HD21	1.19	0.90
1:A:293:GLN:O	1:A:297:THR:HG22	1.71	0.90
2:B:1480:HEM:HBB2	2:B:1480:HEM:HMB2	1.53	0.90
1:B:166:ASN:HD21	1:B:466:LEU:CD1	1.85	0.90
1:B:388:HIS:HE1	1:B:413:ILE:H	1.14	0.90
1:B:219:LEU:HD13	1:B:220:ARG:N	1.83	0.90
1:B:150:VAL:HG12	1:B:154:MET:HE2	1.53	0.90
1:B:105:ILE:HG23	1:B:213:VAL:CG2	2.00	0.89
1:B:151:ARG:HA	1:B:154:MET:HE3	1.51	0.89
1:B:251:GLU:OE1	1:B:254:LYS:HE3	1.73	0.89
1:B:221:LEU:H	1:B:223:LEU:HD12	1.37	0.89
1:A:105:ILE:HG21	1:A:213:VAL:HG22	1.53	0.89
1:A:478:LYS:HD3	1:A:478:LYS:C	1.93	0.89
1:B:217:TRP:O	1:B:219:LEU:CD1	2.20	0.88
1:A:385:LEU:O	1:A:389:HIS:HD2	1.57	0.88
1:B:254:LYS:HA	1:B:254:LYS:CE	2.00	0.88
2:B:1480:HEM:HMC2	2:B:1480:HEM:HBC2	1.56	0.87
1:B:192:LEU:C	1:B:192:LEU:HD12	1.93	0.87
1:B:290:PHE:HD2	3:B:1490:LFD:CLE	1.91	0.87
1:B:444:ASP:OD2	1:B:476:LYS:HE2	1.74	0.87
1:B:450:ASP:CB	4:B:2010:HOH:O	2.22	0.87
1:B:221:LEU:N	1:B:223:LEU:HD12	1.89	0.87
1:A:116:TYR:CE1	1:A:123:MET:HE1	2.10	0.87
1:B:105:ILE:CG2	1:B:213:VAL:CG2	2.50	0.87
1:B:217:TRP:CZ2	1:B:218:LEU:CD2	2.57	0.87
1:A:476:LYS:O	1:A:477:LYS:HG3	1.74	0.86
1:B:106:MET:C	1:B:108:PRO:HD2	1.96	0.85
1:B:207:SER:CB	1:B:225:GLN:NE2	2.34	0.85
1:B:334:ASN:O	1:B:338:GLU:HB2	1.78	0.84
1:B:105:ILE:HG21	1:B:213:VAL:HG23	1.57	0.84
1:A:233:ARG:HH12	1:A:279:HIS:HD2	1.17	0.83
1:A:250:GLU:HB3	1:A:255:ASP:CG	1.99	0.83
1:A:388:HIS:HE1	1:A:413:ILE:H	1.24	0.83
1:B:133:GLU:HB3	1:B:261:LEU:HD12	1.60	0.83
1:A:250:GLU:CG	1:A:255:ASP:OD2	2.27	0.82
1:A:191:ARG:HH12	1:A:242:GLU:CD	1.82	0.82
1:A:309:HIS:CD2	1:A:310:PRO:HD2	2.14	0.82
1:A:141:ASN:O	1:A:144:PRO:HD2	1.79	0.82
1:A:45:ILE:HD11	3:A:1490:LFD:CLD	2.16	0.82
1:B:107:THR:N	1:B:108:PRO:HD2	1.95	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:ASN:HD21	1:B:466:LEU:HD12	1.44	0.81
1:B:221:LEU:C	1:B:223:LEU:HB3	2.01	0.81
1:A:158:TRP:HB3	1:A:473:TYR:CE2	2.15	0.81
1:B:331:ASN:N	1:B:334:ASN:ND2	2.29	0.81
1:B:209:ILE:HD13	1:B:209:ILE:N	1.96	0.81
1:A:253:SER:O	1:A:254:LYS:HB2	1.80	0.81
1:B:116:TYR:HA	1:B:123:MET:HE2	1.63	0.81
1:A:233:ARG:NH1	1:A:279:HIS:NE2	2.29	0.80
1:B:221:LEU:N	1:B:221:LEU:HD13	1.97	0.80
1:A:238:LYS:CE	1:A:242:GLU:OE2	2.29	0.80
1:B:50:LYS:HB2	1:B:50:LYS:NZ	1.96	0.80
1:B:205:GLU:O	1:B:208:LEU:HG	1.82	0.79
1:B:220:ARG:HB3	1:B:221:LEU:CA	2.12	0.79
1:B:447:LEU:HD23	1:B:471:VAL:HG22	1.64	0.79
1:A:212:ALA:CB	1:A:219:LEU:HD21	2.08	0.79
1:B:93:ARG:CD	1:B:95:GLU:OE1	2.30	0.79
1:B:423:ILE:HD11	2:B:1480:HEM:CMD	2.13	0.79
2:B:1480:HEM:HBB2	2:B:1480:HEM:CMB	2.09	0.79
1:B:335:VAL:O	1:B:339:MET:HG3	1.82	0.79
1:B:221:LEU:C	1:B:223:LEU:HD12	2.03	0.78
1:A:225:GLN:O	1:A:228:ARG:HB2	1.82	0.78
1:B:33:PRO:CB	1:B:63:LEU:HD12	2.13	0.78
2:A:1480:HEM:HBB2	2:A:1480:HEM:CMB	2.11	0.78
1:A:250:GLU:HB3	1:A:255:ASP:OD1	1.83	0.78
1:B:45:ILE:HD12	1:B:72:ILE:HG23	1.67	0.77
1:A:136:ILE:HB	1:A:332:TYR:OH	1.83	0.77
1:A:227:ALA:O	1:A:230:ARG:CB	2.32	0.77
1:B:223:LEU:N	1:B:223:LEU:HD13	2.00	0.76
1:A:221:LEU:HA	1:A:223:LEU:HD21	1.65	0.76
1:B:207:SER:HB2	1:B:225:GLN:HE21	1.48	0.76
1:A:103:TYR:HD2	1:A:116:TYR:CD2	2.03	0.76
1:A:447:LEU:HD13	1:A:449:ARG:HB2	1.65	0.76
1:B:58:ARG:CG	1:B:61:ARG:HH22	1.92	0.76
1:A:33:PRO:HB3	1:A:63:LEU:CD1	2.15	0.76
1:B:290:PHE:CE2	3:B:1490:LFD:CLE	2.75	0.75
1:A:150:VAL:HG12	1:A:154:MET:HE2	1.69	0.74
1:B:133:GLU:HB3	1:B:261:LEU:CD1	2.16	0.74
1:A:223:LEU:N	1:A:224:PRO:CD	2.50	0.74
1:B:44:HIS:HD2	1:B:71:SER:N	1.85	0.74
1:B:227:ALA:HA	1:B:230:ARG:HG2	1.67	0.74
1:B:309:HIS:CD2	1:B:310:PRO:HD2	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:ASN:OD1	1:B:196:HIS:HB3	1.87	0.74
1:A:102:VAL:HG11	1:A:360:MET:HB2	1.69	0.74
1:A:358:MET:HE3	1:A:360:MET:HE2	1.69	0.74
1:B:460:MET:CE	3:B:1490:LFD:CAH	2.66	0.74
1:A:165:ILE:HD13	1:A:165:ILE:N	2.03	0.73
1:A:210:PRO:O	1:A:213:VAL:HG23	1.88	0.73
1:A:216:PRO:O	1:A:219:LEU:N	2.20	0.73
1:B:93:ARG:HD3	1:B:95:GLU:OE1	1.88	0.73
1:B:106:MET:O	1:B:109:VAL:N	2.21	0.73
1:B:174:MET:O	1:B:178:THR:HG23	1.88	0.73
1:A:98:SER:HB2	1:A:364:LYS:CE	2.17	0.73
1:B:143:VAL:HB	1:B:144:PRO:HD3	1.70	0.73
1:B:388:HIS:CE1	1:B:413:ILE:H	2.04	0.73
1:A:357:LEU:HD22	1:A:385:LEU:HD22	1.71	0.72
1:A:418:GLY:O	1:A:421:LYS:HG2	1.90	0.72
1:A:180:CYS:O	1:A:184:PHE:HB2	1.90	0.72
1:A:255:ASP:OD1	1:A:256:ASN:ND2	2.22	0.72
1:A:204:MET:O	1:A:229:CYS:SG	2.47	0.72
1:B:226:SER:O	1:B:230:ARG:HB3	1.90	0.72
2:B:1480:HEM:HBC2	2:B:1480:HEM:CMC	2.20	0.72
1:B:466:LEU:HD12	1:B:466:LEU:O	1.89	0.72
1:B:93:ARG:HG2	1:B:94:ASN:N	2.04	0.72
1:B:423:ILE:HD11	2:B:1480:HEM:HMD2	1.69	0.72
1:B:115:ALA:O	1:B:118:ALA:HB3	1.89	0.71
1:A:107:THR:N	1:A:108:PRO:HD2	2.06	0.71
1:A:33:PRO:HB3	1:A:63:LEU:HD13	1.71	0.71
1:A:271:ARG:HG3	1:A:271:ARG:HH11	1.55	0.71
1:A:44:HIS:HD2	1:A:71:SER:H	1.38	0.71
1:A:212:ALA:HB1	1:A:219:LEU:CD2	2.11	0.71
1:A:447:LEU:HD12	1:A:449:ARG:O	1.90	0.70
1:B:154:MET:HG2	1:B:158:TRP:CE3	2.26	0.70
1:B:220:ARG:CB	1:B:221:LEU:HA	2.20	0.70
1:B:141:ASN:O	1:B:144:PRO:HD2	1.92	0.70
1:B:215:MET:HB2	1:B:218:LEU:HG	1.72	0.70
1:B:385:LEU:O	1:B:389:HIS:HD2	1.75	0.70
1:A:30:LYS:HD2	1:A:31:THR:H	1.56	0.70
1:B:50:LYS:HB2	1:B:50:LYS:HZ3	1.54	0.70
1:B:357:LEU:HD22	1:B:385:LEU:HD22	1.73	0.70
1:B:460:MET:HE3	3:B:1490:LFD:CAH	2.20	0.70
1:B:449:ARG:NH1	1:B:468:GLN:OE1	2.24	0.70
1:B:158:TRP:NE1	1:B:165:ILE:HG21	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:LEU:HD12	1:B:220:ARG:N	1.97	0.69
1:A:447:LEU:CD1	1:A:449:ARG:CB	2.70	0.69
1:B:133:GLU:CB	1:B:261:LEU:HD12	2.21	0.69
1:A:225:GLN:O	1:A:228:ARG:N	2.23	0.69
1:B:237:GLN:OE1	1:B:279:HIS:HA	1.93	0.69
1:B:107:THR:N	1:B:108:PRO:CD	2.56	0.69
1:B:120:TYR:CD1	1:B:123:MET:HE3	2.28	0.68
1:A:238:LYS:HE3	1:A:242:GLU:OE2	1.93	0.68
1:B:348:GLU:OE1	1:B:348:GLU:HA	1.93	0.68
1:B:465:THR:HG22	1:B:468:GLN:HG3	1.74	0.68
1:A:209:ILE:CD1	1:A:212:ALA:HB2	2.24	0.68
1:A:277:SER:O	1:A:281:VAL:HG23	1.94	0.68
1:A:150:VAL:O	1:A:154:MET:HG3	1.94	0.68
1:B:233:ARG:NH2	1:B:279:HIS:CD2	2.60	0.68
1:A:95:GLU:OE1	1:A:95:GLU:N	2.26	0.68
1:A:388:HIS:CE1	1:A:413:ILE:H	2.10	0.68
1:A:228:ARG:O	1:A:231:GLU:N	2.28	0.67
1:A:176:ILE:HD11	1:A:197:PHE:HD2	1.59	0.67
1:A:326:PHE:HB3	1:A:330:LEU:HD21	1.75	0.67
1:A:331:ASN:H	1:A:334:ASN:ND2	1.92	0.67
1:B:221:LEU:HD22	1:B:223:LEU:CD1	2.24	0.67
1:B:326:PHE:HB3	1:B:330:LEU:CD2	2.24	0.67
1:B:151:ARG:HA	1:B:154:MET:CE	2.25	0.67
1:B:447:LEU:CD2	1:B:471:VAL:HG22	2.24	0.67
1:B:223:LEU:N	1:B:224:PRO:HD2	2.10	0.67
1:B:427:PHE:O	1:B:430:LEU:HB3	1.95	0.67
1:A:238:LYS:HE2	1:A:242:GLU:OE2	1.95	0.66
1:B:223:LEU:CD2	1:B:224:PRO:HD3	2.21	0.66
1:B:193:ASN:OD1	1:B:196:HIS:CB	2.42	0.66
1:A:300:THR:O	1:A:304:MET:HG3	1.96	0.66
1:B:389:HIS:CE1	1:B:398:ARG:HH11	2.14	0.66
1:A:106:MET:C	1:A:108:PRO:HD2	2.16	0.66
1:B:225:GLN:OE1	1:B:228:ARG:NE	2.27	0.66
1:B:105:ILE:HG21	1:B:213:VAL:CG2	2.22	0.65
1:B:221:LEU:H	1:B:223:LEU:CD1	2.07	0.65
1:A:209:ILE:HD12	1:A:212:ALA:HB2	1.77	0.65
1:B:220:ARG:CB	1:B:221:LEU:CA	2.73	0.65
1:B:366:GLU:HG2	1:B:373:VAL:CG1	2.27	0.65
1:A:34:VAL:HG12	1:A:35:TYR:N	2.11	0.65
1:B:116:TYR:HA	1:B:123:MET:CE	2.26	0.65
1:B:225:GLN:O	1:B:228:ARG:N	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:PRO:O	1:B:41:PHE:HB3	1.95	0.65
1:B:239:ILE:O	1:B:243:ILE:HG12	1.97	0.65
1:A:447:LEU:HD13	1:A:449:ARG:N	2.12	0.65
1:B:154:MET:HG2	1:B:158:TRP:CZ3	2.32	0.64
1:B:193:ASN:HD21	1:B:195:ARG:CZ	2.09	0.64
1:A:44:HIS:CD2	1:A:70:ILE:HB	2.31	0.64
1:A:89:PHE:HE1	1:A:380:ILE:HG23	1.60	0.64
1:A:101:GLU:HG3	1:A:362:MET:HG2	1.79	0.64
1:B:93:ARG:HG2	1:B:94:ASN:H	1.61	0.64
1:B:465:THR:HG21	1:B:468:GLN:HE21	1.61	0.64
1:A:328:ALA:HA	1:A:441:ARG:CZ	2.27	0.64
1:B:116:TYR:HD1	1:B:123:MET:SD	2.19	0.64
1:A:187:ASP:CA	1:A:190:LYS:HG3	2.25	0.64
1:A:228:ARG:HG2	1:A:228:ARG:HH11	1.62	0.64
1:A:44:HIS:CD2	1:A:71:SER:N	2.59	0.64
1:B:209:ILE:HD13	1:B:209:ILE:H	1.60	0.64
1:A:120:TYR:HA	1:A:123:MET:HG2	1.80	0.64
1:B:31:THR:HB	1:B:32:PRO:HD2	1.80	0.64
1:A:165:ILE:N	1:A:165:ILE:CD1	2.61	0.64
1:B:58:ARG:CG	1:B:61:ARG:NH2	2.57	0.64
1:A:147:GLN:NE2	1:A:328:ALA:O	2.27	0.63
1:B:215:MET:O	1:B:217:TRP:N	2.31	0.63
1:A:186:GLU:O	1:A:190:LYS:HG2	1.99	0.63
1:A:422:CYS:HB2	2:A:1480:HEM:C1A	2.34	0.63
1:B:418:GLY:O	1:B:421:LYS:HE2	1.98	0.63
1:A:352:ARG:NH1	1:A:353:ASP:OD2	2.31	0.63
1:A:399:LEU:HD12	1:A:400:TRP:N	2.13	0.63
1:B:106:MET:HG2	1:B:110:PHE:CZ	2.34	0.63
1:A:322:GLU:OE2	1:A:339:MET:HA	1.99	0.63
1:A:327:PRO:HG2	1:A:329:GLN:O	1.99	0.63
1:A:385:LEU:O	1:A:389:HIS:CD2	2.46	0.63
1:B:450:ASP:HB2	4:B:2010:HOH:O	1.94	0.63
1:A:271:ARG:HG3	1:A:271:ARG:NH1	2.13	0.62
1:A:192:LEU:HD11	1:A:197:PHE:HB2	1.80	0.62
1:B:166:ASN:HD21	1:B:466:LEU:HD11	1.64	0.62
1:B:326:PHE:HB3	1:B:330:LEU:HD21	1.82	0.62
1:A:165:ILE:H	1:A:165:ILE:CD1	2.09	0.62
1:B:102:VAL:HG11	1:B:360:MET:HB2	1.81	0.62
1:B:159:LYS:HB2	1:B:159:LYS:NZ	2.13	0.62
1:B:443:TYR:CD1	1:B:475:ARG:HA	2.34	0.62
1:B:142:PHE:O	1:B:146:ILE:HD12	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:SER:HB3	1:A:364:LYS:HE2	1.79	0.62
1:B:420:HIS:CA	2:B:1480:HEM:O2D	2.48	0.62
1:B:193:ASN:OD1	1:B:196:HIS:N	2.31	0.62
1:B:475:ARG:HG3	1:B:475:ARG:HH11	1.62	0.62
1:A:176:ILE:HB	1:A:293:GLN:HE22	1.65	0.61
1:A:217:TRP:CZ3	1:A:218:LEU:HD23	2.35	0.61
1:B:247:ARG:HH22	1:B:258:THR:HG21	1.65	0.61
1:B:221:LEU:CA	1:B:223:LEU:HD12	2.31	0.61
1:B:295:THR:HB	2:B:1480:HEM:CAB	2.31	0.61
1:B:28:ALA:O	1:B:29:LYS:HB2	2.00	0.61
1:A:250:GLU:HB3	1:A:255:ASP:OD2	2.01	0.61
1:B:166:ASN:ND2	1:B:466:LEU:CD1	2.62	0.61
1:A:210:PRO:CA	3:A:1490:LFD:HAUA	2.30	0.61
1:A:302:TRP:O	1:A:306:HIS:CD2	2.54	0.61
1:B:124:ARG:O	1:B:124:ARG:HD3	2.01	0.61
1:B:192:LEU:HD12	1:B:193:ASN:N	2.14	0.61
1:A:466:LEU:HD12	1:A:466:LEU:O	2.01	0.60
1:B:166:ASN:ND2	1:B:466:LEU:HD11	2.16	0.60
1:A:215:MET:O	1:A:218:LEU:CG	2.39	0.60
1:B:116:TYR:CD1	1:B:123:MET:SD	2.94	0.60
1:A:146:ILE:HD11	1:A:182:CYS:SG	2.42	0.60
1:A:348:GLU:HB2	1:A:402:PRO:HA	1.83	0.60
1:A:389:HIS:CE1	1:A:398:ARG:HH11	2.19	0.60
1:B:399:LEU:HD12	1:B:400:TRP:N	2.16	0.60
1:B:415:PHE:CD1	1:B:425:GLN:HG3	2.36	0.60
1:B:423:ILE:HD11	2:B:1480:HEM:HMD1	1.84	0.60
1:B:93:ARG:HD2	1:B:95:GLU:OE1	2.01	0.60
1:A:271:ARG:O	1:A:273:GLY:N	2.36	0.59
1:B:51:ASN:C	1:B:51:ASN:HD22	2.03	0.59
1:B:466:LEU:HD12	1:B:466:LEU:C	2.22	0.59
1:A:251:GLU:OE1	1:A:254:LYS:HE2	2.02	0.59
1:B:450:ASP:HB3	4:B:2010:HOH:O	1.94	0.59
1:A:389:HIS:HE1	1:A:398:ARG:NH1	1.99	0.59
1:B:213:VAL:O	1:B:213:VAL:HG13	2.00	0.59
1:B:223:LEU:N	1:B:224:PRO:CD	2.66	0.59
1:A:191:ARG:NH1	1:A:242:GLU:OE1	2.35	0.59
1:A:406:GLU:O	1:A:406:GLU:HG3	2.02	0.59
1:B:444:ASP:OD2	1:B:476:LYS:CE	2.49	0.59
1:B:93:ARG:HD2	1:B:95:GLU:HB2	1.84	0.59
1:A:220:ARG:HH11	1:A:220:ARG:CG	2.15	0.59
1:A:139:PHE:CD2	1:A:430:LEU:HD22	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:LEU:HA	1:A:226:SER:OG	2.03	0.59
1:B:77:VAL:HG13	1:B:379:ILE:HG22	1.84	0.59
1:B:120:TYR:HD1	1:B:123:MET:HE3	1.68	0.59
1:B:226:SER:O	1:B:230:ARG:CB	2.51	0.59
1:A:308:MET:HE2	1:A:445:PHE:HB3	1.85	0.58
1:B:219:LEU:HD12	1:B:219:LEU:N	2.18	0.58
1:B:192:LEU:C	1:B:192:LEU:CD1	2.66	0.58
1:A:106:MET:O	1:A:109:VAL:N	2.36	0.58
1:A:221:LEU:HA	1:A:223:LEU:CD2	2.34	0.58
1:A:331:ASN:OD1	1:A:334:ASN:ND2	2.35	0.58
1:A:251:GLU:CB	4:A:2005:HOH:O	2.49	0.58
1:B:186:GLU:OE1	1:B:190:LYS:NZ	2.31	0.58
1:B:91:SER:N	1:B:92:PRO:CD	2.67	0.58
1:B:227:ALA:CA	1:B:230:ARG:HG2	2.33	0.58
1:A:102:VAL:O	1:A:213:VAL:HG13	2.04	0.58
1:A:332:TYR:O	1:A:335:VAL:N	2.35	0.58
1:B:260:ASP:OD1	1:B:263:GLY:N	2.28	0.58
1:B:447:LEU:C	1:B:449:ARG:H	2.06	0.58
1:A:227:ALA:O	1:A:230:ARG:N	2.37	0.58
1:A:116:TYR:HA	1:A:123:MET:HE3	1.86	0.58
1:A:192:LEU:HD12	1:A:193:ASN:N	2.19	0.58
1:A:348:GLU:HG3	1:A:400:TRP:CD1	2.39	0.58
1:A:331:ASN:H	1:A:334:ASN:HD22	1.51	0.57
1:B:158:TRP:HE1	1:B:165:ILE:HG21	1.68	0.57
1:A:32:PRO:HA	1:A:372:TYR:CD1	2.39	0.57
1:B:384:PRO:O	1:B:388:HIS:CG	2.57	0.57
1:A:160:GLU:OE1	1:A:160:GLU:N	2.38	0.57
1:A:447:LEU:HD11	1:A:449:ARG:CB	2.29	0.57
1:B:352:ARG:NH1	1:B:353:ASP:OD2	2.34	0.57
1:B:103:TYR:CE2	1:B:116:TYR:HE2	2.21	0.57
1:B:216:PRO:O	1:B:219:LEU:HG	2.04	0.57
1:A:358:MET:CE	1:A:360:MET:HE2	2.32	0.57
1:B:189:ARG:C	1:B:191:ARG:H	2.08	0.57
1:B:326:PHE:CE1	1:B:334:ASN:HB3	2.39	0.57
1:A:228:ARG:HH11	1:A:228:ARG:CG	2.18	0.56
1:B:58:ARG:HA	1:B:61:ARG:NH2	2.19	0.56
1:B:225:GLN:HE22	1:B:228:ARG:HB3	1.70	0.56
1:B:308:MET:HE2	1:B:445:PHE:CB	2.35	0.56
1:B:357:LEU:HD11	1:B:462:VAL:HG21	1.87	0.56
1:B:389:HIS:HE1	1:B:398:ARG:HH11	1.51	0.56
1:A:389:HIS:HE1	1:A:398:ARG:HH11	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:GLU:CD	1:B:472:LYS:HE3	2.25	0.56
1:B:223:LEU:HD22	1:B:223:LEU:N	2.19	0.56
1:B:351:ARG:O	1:B:388:HIS:HD2	1.89	0.56
1:A:107:THR:N	1:A:108:PRO:CD	2.68	0.56
1:A:288:ALA:O	1:A:291:ALA:HB3	2.04	0.56
1:A:151:ARG:HA	1:A:154:MET:HE3	1.87	0.56
1:A:213:VAL:HG21	3:A:1490:LFD:HAS	1.87	0.56
1:A:447:LEU:HD13	1:A:449:ARG:CB	2.36	0.56
2:A:1480:HEM:HBD1	2:A:1480:HEM:HHA	1.88	0.56
1:B:35:TYR:CD1	1:B:36:PRO:HD2	2.40	0.56
1:A:251:GLU:HB3	4:A:2005:HOH:O	2.04	0.56
1:B:351:ARG:HA	1:B:388:HIS:CD2	2.40	0.56
1:A:292:GLY:O	1:A:296:SER:HB2	2.06	0.56
1:A:250:GLU:CB	1:A:255:ASP:OD2	2.54	0.55
1:A:446:GLN:O	1:A:471:VAL:HG13	2.06	0.55
1:B:420:HIS:O	2:B:1480:HEM:O2D	2.23	0.55
1:B:221:LEU:N	1:B:221:LEU:CD1	2.69	0.55
1:B:139:PHE:CD2	1:B:430:LEU:HD22	2.41	0.55
1:A:133:GLU:OE2	1:A:264:GLY:HA3	2.07	0.55
1:A:166:ASN:CG	1:A:169:GLU:HG3	2.26	0.55
1:B:217:TRP:CE2	1:B:218:LEU:CD2	2.81	0.55
1:B:221:LEU:C	1:B:221:LEU:HD22	2.27	0.55
1:A:205:GLU:O	1:A:207:SER:N	2.39	0.55
1:B:465:THR:CG2	1:B:468:GLN:HE21	2.19	0.55
1:A:89:PHE:CE1	1:A:380:ILE:HG23	2.40	0.55
1:A:220:ARG:NH1	1:A:220:ARG:HG3	2.21	0.55
1:B:293:GLN:O	1:B:297:THR:HG22	2.05	0.55
1:B:104:THR:O	1:B:107:THR:HG23	2.06	0.55
1:B:204:MET:HA	1:B:229:CYS:HA	1.89	0.55
1:B:215:MET:C	1:B:217:TRP:H	2.09	0.55
1:A:447:LEU:CD1	1:A:449:ARG:O	2.55	0.55
1:A:204:MET:HA	1:A:229:CYS:HA	1.88	0.54
1:B:113:GLY:O	1:B:118:ALA:HB2	2.08	0.54
1:B:473:TYR:CD1	1:B:473:TYR:C	2.80	0.54
1:A:154:MET:HE2	1:A:438:THR:HG22	1.88	0.54
1:A:331:ASN:O	1:A:334:ASN:HB2	2.08	0.54
1:B:446:GLN:O	1:B:471:VAL:HG13	2.07	0.54
1:B:133:GLU:CB	1:B:261:LEU:CD1	2.83	0.54
1:B:193:ASN:HD21	1:B:195:ARG:NH1	2.06	0.54
1:B:289:MET:O	1:B:293:GLN:HB2	2.08	0.54
1:A:330:LEU:HA	1:A:334:ASN:HD22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:TRP:CH2	1:B:218:LEU:HD23	2.42	0.54
1:B:375:PRO:O	1:B:378:ASP:HB2	2.08	0.54
1:A:120:TYR:HB3	4:A:2002:HOH:O	2.08	0.54
1:A:123:MET:HG3	1:A:124:ARG:N	2.22	0.54
1:A:389:HIS:CE1	1:A:398:ARG:NH1	2.75	0.54
1:A:48:PHE:O	1:A:52:PRO:HG3	2.08	0.53
1:B:86:HIS:NE2	1:B:387:SER:OG	2.40	0.53
1:A:154:MET:HE2	1:A:438:THR:CG2	2.37	0.53
1:B:221:LEU:C	1:B:223:LEU:CB	2.76	0.53
1:A:150:VAL:HG12	1:A:154:MET:CE	2.38	0.53
1:A:191:ARG:HH12	1:A:242:GLU:CB	2.22	0.53
1:A:478:LYS:C	1:A:478:LYS:CD	2.63	0.53
1:B:106:MET:C	1:B:108:PRO:CD	2.72	0.53
1:B:308:MET:HE2	1:B:445:PHE:HB3	1.90	0.53
1:A:186:GLU:O	1:A:190:LYS:CG	2.56	0.53
1:A:192:LEU:HD12	1:A:193:ASN:O	2.08	0.53
1:B:351:ARG:O	1:B:388:HIS:CD2	2.62	0.53
1:A:165:ILE:HD13	1:A:471:VAL:O	2.09	0.53
1:A:271:ARG:C	1:A:273:GLY:H	2.12	0.53
1:B:428:ALA:O	1:B:432:VAL:HG23	2.08	0.53
1:A:412:PHE:CD1	1:A:412:PHE:C	2.82	0.53
1:B:221:LEU:H	1:B:221:LEU:HD13	1.74	0.53
1:B:473:TYR:CD1	1:B:473:TYR:O	2.62	0.52
1:A:59:CYS:O	1:A:63:LEU:HB2	2.09	0.52
1:B:100:ARG:HA	1:B:116:TYR:HB3	1.91	0.52
1:B:193:ASN:OD1	1:B:193:ASN:C	2.48	0.52
1:B:396:ASN:HB3	1:B:399:LEU:HB3	1.90	0.52
1:A:302:TRP:O	1:A:306:HIS:HD2	1.92	0.52
1:A:45:ILE:CD1	3:A:1490:LFD:CLD	2.93	0.52
1:A:448:LEU:O	1:A:449:ARG:HG3	2.10	0.52
1:B:221:LEU:HD22	1:B:223:LEU:HD12	1.91	0.52
1:B:238:LYS:O	1:B:239:ILE:C	2.48	0.52
1:B:255:ASP:O	1:B:256:ASN:CB	2.39	0.52
1:A:166:ASN:HD21	1:A:466:LEU:HD12	1.75	0.52
1:B:76:ARG:NE	1:B:378:ASP:OD1	2.42	0.52
1:B:420:HIS:HA	2:B:1480:HEM:O2D	2.10	0.52
1:B:105:ILE:HG21	1:B:213:VAL:CB	2.40	0.52
1:B:127:LEU:HD13	2:B:1480:HEM:O1D	2.10	0.52
1:A:220:ARG:CG	1:A:220:ARG:NH1	2.73	0.52
1:B:102:VAL:HG12	1:B:102:VAL:O	2.09	0.52
2:B:1480:HEM:HMB2	2:B:1480:HEM:CBB	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ALA:O	1:A:118:ALA:HB3	2.10	0.51
1:A:352:ARG:NE	1:A:398:ARG:O	2.37	0.51
1:A:210:PRO:HA	3:A:1490:LFD:HAUA	1.93	0.51
1:A:294:HIS:O	1:A:298:ILE:HD12	2.10	0.51
1:A:223:LEU:C	1:A:226:SER:OG	2.49	0.51
1:A:373:VAL:HG12	1:A:374:VAL:N	2.25	0.51
1:B:183:LEU:HB3	1:B:261:LEU:HD22	1.92	0.51
1:A:44:HIS:HD2	1:A:71:SER:N	2.05	0.51
1:A:228:ARG:O	1:A:232:ALA:N	2.30	0.51
1:B:294:HIS:HA	1:B:297:THR:CG2	2.41	0.51
1:A:154:MET:CE	1:A:438:THR:HG22	2.40	0.51
1:A:158:TRP:O	1:A:475:ARG:NH2	2.44	0.51
1:B:277:SER:OG	1:B:280:GLU:HG3	2.09	0.51
1:B:308:MET:CE	1:B:445:PHE:HB3	2.41	0.51
1:A:30:LYS:CD	1:A:31:THR:H	2.22	0.51
1:A:101:GLU:HG3	1:A:362:MET:CG	2.40	0.51
1:A:330:LEU:HA	1:A:334:ASN:ND2	2.25	0.51
1:B:253:SER:HB2	1:B:255:ASP:HB3	1.92	0.51
1:B:123:MET:CG	1:B:124:ARG:N	2.73	0.51
1:B:165:ILE:HD13	1:B:471:VAL:O	2.11	0.51
1:A:358:MET:CE	1:A:360:MET:CE	2.89	0.51
1:A:34:VAL:CG1	1:A:35:TYR:N	2.73	0.51
1:B:188:LEU:HD12	1:B:243:ILE:HG13	1.93	0.51
1:B:217:TRP:O	1:B:219:LEU:HD11	2.07	0.51
1:B:256:ASN:C	1:B:257:ASN:HD22	2.14	0.51
1:A:215:MET:N	1:A:216:PRO:HD3	2.26	0.50
1:A:237:GLN:HG2	1:A:278:LEU:HD13	1.92	0.50
1:B:86:HIS:CD2	1:B:382:CYS:SG	3.04	0.50
1:A:251:GLU:OE1	1:A:251:GLU:O	2.30	0.50
1:B:221:LEU:C	1:B:223:LEU:CD1	2.79	0.50
1:B:335:VAL:HA	1:B:339:MET:CG	2.41	0.50
1:B:412:PHE:CD1	1:B:412:PHE:C	2.84	0.50
1:A:216:PRO:O	1:A:219:LEU:HB2	2.12	0.50
1:A:384:PRO:HA	1:A:413:ILE:HG13	1.93	0.50
1:A:104:THR:C	1:A:106:MET:H	2.14	0.50
1:A:475:ARG:HD2	1:A:477:LYS:HE3	1.92	0.50
1:B:103:TYR:CE2	1:B:116:TYR:CE2	2.99	0.50
1:B:165:ILE:HD13	1:B:165:ILE:H	1.76	0.50
1:B:251:GLU:OE1	1:B:254:LYS:CE	2.54	0.50
1:B:309:HIS:CG	1:B:310:PRO:HD2	2.47	0.50
1:A:34:VAL:O	1:A:63:LEU:HD11	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:PRO:HB2	1:A:408:VAL:HG11	1.93	0.50
1:B:255:ASP:O	1:B:255:ASP:OD1	2.30	0.50
1:B:276:MET:HB3	1:B:281:VAL:HG22	1.93	0.50
1:A:192:LEU:HD12	1:A:192:LEU:C	2.33	0.49
1:B:145:ALA:HB1	1:B:181:GLN:HG3	1.92	0.49
1:B:230:ARG:HG3	1:B:231:GLU:N	2.27	0.49
1:A:348:GLU:OE2	1:A:401:ASP:N	2.37	0.49
1:B:217:TRP:CZ2	1:B:218:LEU:HD21	2.43	0.49
1:A:180:CYS:HB3	1:A:184:PHE:CD2	2.47	0.49
1:A:235:GLU:O	1:A:239:ILE:HG13	2.13	0.49
1:B:297:THR:HG23	1:B:298:ILE:N	2.27	0.49
1:A:204:MET:HG3	1:A:232:ALA:CB	2.42	0.49
1:A:97:LEU:HD13	1:A:380:ILE:HG21	1.95	0.49
1:A:245:VAL:HG12	1:A:249:LYS:HE2	1.94	0.49
1:A:269:VAL:HG12	1:A:270:TYR:O	2.12	0.49
1:B:257:ASN:N	1:B:257:ASN:ND2	2.60	0.49
1:A:233:ARG:NH1	1:A:279:HIS:HD2	1.93	0.49
1:B:335:VAL:HA	1:B:339:MET:SD	2.52	0.49
1:A:179:ALA:O	1:A:183:LEU:HG	2.12	0.49
1:A:233:ARG:HH22	1:A:279:HIS:CD2	2.31	0.49
1:B:389:HIS:ND1	1:B:397:PRO:HB2	2.28	0.49
2:B:1480:HEM:HMC2	2:B:1480:HEM:CBC	2.36	0.49
1:A:39:VAL:HG12	1:A:39:VAL:O	2.13	0.49
1:A:309:HIS:HD2	1:A:311:LYS:H	1.60	0.49
1:B:323:ILE:HA	1:B:326:PHE:CD2	2.48	0.49
1:A:120:TYR:HD1	1:A:123:MET:SD	2.35	0.49
1:B:221:LEU:C	1:B:221:LEU:CD2	2.80	0.49
1:B:133:GLU:OE2	1:B:264:GLY:HA3	2.13	0.48
1:A:146:ILE:CD1	1:A:182:CYS:SG	3.00	0.48
1:A:341:PHE:O	1:A:344:ARG:HB2	2.13	0.48
1:B:50:LYS:HB2	1:B:50:LYS:HZ2	1.78	0.48
1:B:352:ARG:NH1	1:B:398:ARG:NH2	2.61	0.48
1:A:180:CYS:HB3	1:A:184:PHE:HD2	1.78	0.48
1:B:207:SER:CA	1:B:225:GLN:CG	2.73	0.48
1:B:302:TRP:HA	1:B:305:LEU:HD12	1.95	0.48
1:A:204:MET:HG3	1:A:232:ALA:HB3	1.96	0.48
1:B:357:LEU:C	1:B:358:MET:HG2	2.33	0.48
1:B:366:GLU:HG2	1:B:373:VAL:HG13	1.96	0.48
1:A:191:ARG:NH1	1:A:242:GLU:CB	2.77	0.48
1:A:207:SER:OG	1:A:229:CYS:HB2	2.13	0.48
1:A:210:PRO:CB	3:A:1490:LFD:HAUA	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1480:HEM:HMB2	2:A:1480:HEM:CBB	2.33	0.48
1:B:59:CYS:O	1:B:63:LEU:HB2	2.14	0.48
1:B:103:TYR:HD2	1:B:116:TYR:HE2	1.50	0.48
1:B:129:PHE:HE2	1:B:270:TYR:CE1	2.31	0.48
1:B:143:VAL:HG22	1:B:430:LEU:HD11	1.94	0.48
1:B:116:TYR:HD1	1:B:123:MET:CE	2.27	0.48
1:B:293:GLN:O	1:B:297:THR:CG2	2.62	0.48
1:B:342:ALA:O	1:B:345:CYS:HB2	2.14	0.48
1:A:129:PHE:HE2	1:A:270:TYR:CE1	2.31	0.48
1:A:271:ARG:C	1:A:273:GLY:N	2.66	0.48
1:B:331:ASN:OD1	1:B:334:ASN:OD1	2.32	0.48
1:A:42:LEU:HB3	1:A:45:ILE:HG22	1.95	0.47
1:A:159:LYS:HB2	1:A:160:GLU:OE1	2.14	0.47
1:A:217:TRP:CE3	1:A:217:TRP:C	2.87	0.47
1:B:330:LEU:HA	1:B:334:ASN:ND2	2.29	0.47
1:B:426:LYS:HA	1:B:429:LEU:HD12	1.95	0.47
1:B:465:THR:CG2	1:B:468:GLN:HG3	2.44	0.47
1:A:153:PHE:CD1	1:A:153:PHE:C	2.88	0.47
1:A:200:LEU:HD13	1:A:236:LEU:HB2	1.95	0.47
1:A:423:ILE:C	1:A:425:GLN:H	2.17	0.47
1:B:238:LYS:O	1:B:240:LEU:N	2.47	0.47
1:A:166:ASN:HB3	1:A:169:GLU:HB2	1.96	0.47
1:A:101:GLU:HG3	1:A:362:MET:CB	2.43	0.47
1:A:155:ALA:O	1:A:159:LYS:HG2	2.14	0.47
1:A:176:ILE:HB	1:A:293:GLN:NE2	2.29	0.47
1:A:343:GLU:HB2	1:A:433:LYS:HE3	1.96	0.47
1:A:106:MET:HG2	1:A:110:PHE:CZ	2.49	0.47
1:A:351:ARG:HA	1:A:388:HIS:CD2	2.50	0.47
1:B:260:ASP:O	1:B:263:GLY:N	2.47	0.47
1:B:448:LEU:HD12	1:B:470:LEU:HB3	1.96	0.47
1:B:204:MET:HG3	1:B:232:ALA:HB3	1.96	0.47
1:A:422:CYS:HB2	2:A:1480:HEM:NA	2.30	0.47
1:A:217:TRP:CH2	1:A:218:LEU:HD23	2.50	0.47
1:A:255:ASP:OD1	1:A:256:ASN:N	2.45	0.47
1:A:357:LEU:HD11	1:A:462:VAL:HG21	1.96	0.47
1:B:42:LEU:HD23	1:B:42:LEU:HA	1.80	0.47
1:A:51:ASN:C	1:A:51:ASN:HD22	2.18	0.47
1:A:331:ASN:N	1:A:334:ASN:HD22	2.13	0.47
1:A:358:MET:HB3	1:A:360:MET:HE2	1.97	0.47
1:B:158:TRP:CD1	1:B:165:ILE:HG21	2.50	0.46
1:B:215:MET:C	1:B:217:TRP:N	2.65	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:VAL:HA	1:A:40:PRO:HD2	1.67	0.46
1:A:317:ASP:O	1:A:321:LYS:HE2	2.15	0.46
1:B:429:LEU:O	1:B:433:LYS:CG	2.50	0.46
1:A:447:LEU:HD13	1:A:449:ARG:CA	2.45	0.46
1:B:382:CYS:O	1:B:384:PRO:HD3	2.16	0.46
1:B:406:GLU:HG3	1:B:406:GLU:O	2.15	0.46
1:A:103:TYR:CD2	1:A:116:TYR:CD2	2.93	0.46
1:A:166:ASN:OD1	1:A:169:GLU:HG3	2.16	0.46
1:A:199:GLN:O	1:A:203:LYS:HB2	2.14	0.46
1:A:247:ARG:NH2	1:A:258:THR:HG21	2.31	0.46
1:B:158:TRP:CD1	1:B:473:TYR:CE2	3.04	0.46
1:B:460:MET:HE2	1:B:460:MET:HB3	1.71	0.46
1:A:210:PRO:HB3	3:A:1490:LFD:HAUA	1.97	0.46
1:B:51:ASN:C	1:B:51:ASN:ND2	2.69	0.46
1:B:210:PRO:CB	3:B:1490:LFD:HAV	2.31	0.46
1:B:240:LEU:O	1:B:244:ILE:HG13	2.15	0.46
1:A:193:ASN:N	1:A:193:ASN:OD1	2.49	0.46
1:A:216:PRO:HA	1:A:219:LEU:HD23	1.98	0.46
1:B:293:GLN:OE1	1:B:293:GLN:HA	2.14	0.46
1:B:359:VAL:HG13	2:B:1480:HEM:CGA	2.45	0.46
1:B:389:HIS:HA	1:B:397:PRO:HB3	1.98	0.46
1:B:460:MET:HE3	3:B:1490:LFD:HAH	1.76	0.46
1:A:154:MET:O	1:A:158:TRP:N	2.43	0.46
1:B:166:ASN:CG	1:B:169:GLU:HG3	2.36	0.46
1:A:233:ARG:CZ	1:A:279:HIS:CD2	2.98	0.46
1:A:320:HIS:C	1:A:322:GLU:H	2.19	0.46
1:A:331:ASN:OD1	1:A:331:ASN:N	2.48	0.46
1:A:373:VAL:CG1	1:A:374:VAL:N	2.77	0.46
1:A:99:PRO:HD2	1:A:120:TYR:OH	2.16	0.46
1:A:227:ALA:O	1:A:230:ARG:CA	2.64	0.46
1:B:133:GLU:CD	1:B:264:GLY:HA3	2.36	0.46
1:B:157:ASN:N	1:B:157:ASN:HD22	2.14	0.46
1:B:243:ILE:O	1:B:247:ARG:HG3	2.16	0.46
1:A:91:SER:N	1:A:92:PRO:CD	2.80	0.45
1:A:106:MET:CE	1:A:290:PHE:HE2	2.29	0.45
1:A:322:GLU:CD	1:A:339:MET:HA	2.36	0.45
1:B:103:TYR:CD2	1:B:116:TYR:CD2	3.02	0.45
1:B:431:GLN:O	1:B:435:ILE:HG13	2.16	0.45
1:B:247:ARG:NH2	1:B:258:THR:CG2	2.69	0.45
1:A:209:ILE:HD13	1:A:212:ALA:HB2	1.95	0.45
1:A:256:ASN:ND2	1:A:256:ASN:N	2.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ARG:HG2	1:B:243:ILE:HD11	1.98	0.45
1:A:41:PHE:O	1:A:41:PHE:CD1	2.69	0.45
1:A:236:LEU:O	1:A:239:ILE:HB	2.17	0.45
1:A:466:LEU:HD12	1:A:466:LEU:C	2.36	0.45
1:B:253:SER:CB	1:B:255:ASP:HB3	2.46	0.45
1:A:131:ALA:HB2	1:A:423:ILE:HG21	1.98	0.45
1:A:388:HIS:HA	1:A:394:PHE:CE2	2.51	0.45
1:B:321:LYS:HA	1:B:321:LYS:HD3	1.75	0.45
1:B:34:VAL:HG22	1:B:69:THR:HB	1.98	0.45
1:B:225:GLN:NE2	1:B:228:ARG:HB3	2.31	0.45
1:B:306:HIS:O	1:B:312:ASN:ND2	2.44	0.45
1:A:103:TYR:CD2	1:A:116:TYR:HE2	2.23	0.45
1:A:374:VAL:HA	1:A:375:PRO:HD3	1.86	0.45
1:B:102:VAL:HG11	1:B:360:MET:CB	2.46	0.45
1:B:207:SER:CB	1:B:225:GLN:HG3	2.44	0.45
1:B:213:VAL:O	1:B:213:VAL:CG1	2.65	0.45
1:B:420:HIS:C	2:B:1480:HEM:O2D	2.55	0.45
1:B:475:ARG:HH11	1:B:475:ARG:CG	2.28	0.45
1:A:100:ARG:HA	1:A:116:TYR:HB3	1.97	0.44
1:B:44:HIS:CD2	1:B:70:ILE:HB	2.52	0.44
1:A:116:TYR:CA	1:A:123:MET:HE3	2.45	0.44
1:A:120:TYR:N	1:A:121:PRO:CD	2.79	0.44
1:A:225:GLN:O	1:A:228:ARG:CB	2.61	0.44
1:A:228:ARG:CG	1:A:228:ARG:NH1	2.77	0.44
1:A:330:LEU:CA	1:A:334:ASN:HD22	2.30	0.44
1:A:406:GLU:O	1:A:406:GLU:CG	2.65	0.44
1:B:69:THR:HG21	1:B:76:ARG:NH1	2.32	0.44
1:B:305:LEU:HD13	1:B:453:PRO:HG2	1.98	0.44
1:B:348:GLU:OE1	1:B:348:GLU:CA	2.61	0.44
1:A:358:MET:HE2	1:A:360:MET:CE	2.48	0.44
1:A:205:GLU:O	1:A:208:LEU:HG	2.17	0.44
1:A:256:ASN:ND2	1:A:256:ASN:H	2.16	0.44
1:A:424:GLY:HA3	2:A:1480:HEM:C3C	2.53	0.44
1:B:158:TRP:CG	1:B:473:TYR:CE2	3.06	0.44
1:A:475:ARG:HG2	1:A:476:LYS:N	2.33	0.44
1:B:33:PRO:CB	1:B:63:LEU:CD1	2.60	0.44
1:A:320:HIS:O	1:A:322:GLU:N	2.51	0.44
1:A:352:ARG:NH1	1:A:352:ARG:HG2	2.33	0.44
1:B:299:THR:HG21	1:B:350:ILE:HD11	1.98	0.44
1:A:72:ILE:HG21	1:A:214:PHE:CD2	2.53	0.44
1:A:141:ASN:C	1:A:144:PRO:HD2	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:238:LYS:O	1:B:241:GLY:N	2.51	0.44
1:B:335:VAL:HA	1:B:339:MET:HG3	1.99	0.44
1:A:223:LEU:CA	1:A:226:SER:OG	2.66	0.44
1:A:309:HIS:CG	1:A:310:PRO:HD2	2.53	0.44
1:B:69:THR:HG21	1:B:76:ARG:CZ	2.48	0.44
1:B:221:LEU:C	1:B:223:LEU:CG	2.87	0.44
1:B:331:ASN:N	1:B:334:ASN:HD21	2.00	0.44
1:A:106:MET:CE	1:A:290:PHE:CE2	3.01	0.44
1:A:112:GLU:OE1	1:A:112:GLU:HA	2.17	0.44
1:A:476:LYS:C	1:A:477:LYS:HG3	2.38	0.44
1:B:91:SER:H	1:B:92:PRO:CD	2.29	0.44
1:B:207:SER:HB2	1:B:225:GLN:HB3	1.99	0.44
1:A:102:VAL:O	1:A:102:VAL:HG12	2.16	0.43
1:B:225:GLN:NE2	1:B:225:GLN:O	2.51	0.43
1:B:352:ARG:CZ	1:B:398:ARG:NH2	2.81	0.43
1:B:358:MET:SD	1:B:383:SER:HB2	2.58	0.43
1:A:227:ALA:O	1:A:231:GLU:N	2.48	0.43
1:A:471:VAL:HG12	1:A:472:LYS:N	2.33	0.43
1:B:323:ILE:HG22	1:B:339:MET:CE	2.48	0.43
1:A:146:ILE:O	1:A:150:VAL:HG23	2.18	0.43
1:A:223:LEU:C	1:A:226:SER:HG	2.22	0.43
1:A:308:MET:HE2	1:A:445:PHE:CB	2.47	0.43
1:B:447:LEU:C	1:B:449:ARG:N	2.72	0.43
1:B:396:ASN:O	1:B:398:ARG:N	2.52	0.43
1:A:309:HIS:CD2	1:A:310:PRO:CD	2.95	0.43
1:A:351:ARG:O	1:A:388:HIS:CD2	2.72	0.43
1:B:271:ARG:CB	1:B:271:ARG:HH11	2.32	0.43
1:A:139:PHE:HB2	1:A:332:TYR:HE1	1.84	0.43
1:B:449:ARG:HD3	1:B:468:GLN:O	2.19	0.43
1:A:32:PRO:O	1:A:33:PRO:C	2.54	0.43
1:A:356:LEU:HD12	2:A:1480:HEM:CHB	2.49	0.43
1:A:358:MET:HE3	1:A:360:MET:CE	2.45	0.43
1:B:226:SER:O	1:B:230:ARG:HG2	2.19	0.43
1:B:389:HIS:HE1	1:B:398:ARG:NH1	2.16	0.43
1:A:241:GLY:O	1:A:245:VAL:HG23	2.19	0.42
1:A:352:ARG:HG2	1:A:352:ARG:HH11	1.83	0.42
1:B:159:LYS:NZ	1:B:159:LYS:CB	2.80	0.42
1:B:250:GLU:HB3	1:B:255:ASP:OD2	2.19	0.42
1:B:426:LYS:O	1:B:429:LEU:HB2	2.19	0.42
1:A:143:VAL:N	1:A:144:PRO:CD	2.81	0.42
1:B:352:ARG:CZ	1:B:398:ARG:HH21	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ILE:HG13	1:A:182:CYS:SG	2.60	0.42
1:A:205:GLU:C	1:A:207:SER:N	2.73	0.42
1:A:290:PHE:HD2	3:A:1490:LFD:CLE	2.39	0.42
1:B:60:LYS:HB2	1:B:68:PHE:HE2	1.83	0.42
1:B:193:ASN:OD1	1:B:193:ASN:O	2.37	0.42
1:B:256:ASN:C	1:B:257:ASN:ND2	2.73	0.42
1:B:415:PHE:CG	1:B:425:GLN:HG3	2.55	0.42
1:B:33:PRO:CG	1:B:63:LEU:HD12	2.49	0.42
1:B:53:LEU:HG	1:B:57:GLN:OE1	2.20	0.42
1:B:146:ILE:HG13	1:B:182:CYS:SG	2.59	0.42
1:B:309:HIS:HE1	1:B:450:ASP:O	2.03	0.42
1:B:375:PRO:HG2	1:B:378:ASP:OD1	2.19	0.42
1:A:443:TYR:CD1	1:A:475:ARG:HA	2.53	0.42
1:B:103:TYR:HD2	1:B:116:TYR:CE2	2.24	0.42
1:A:120:TYR:N	1:A:121:PRO:HD2	2.34	0.42
1:A:460:MET:CG	3:A:1490:LFD:CAK	2.97	0.42
1:B:223:LEU:HD22	1:B:224:PRO:N	2.33	0.42
1:A:56:MET:SD	1:A:79:ILE:HD13	2.60	0.42
1:A:103:TYR:C	1:A:105:ILE:H	2.23	0.42
1:A:333:ASP:O	1:A:338:GLU:CG	2.67	0.42
1:B:101:GLU:C	1:B:103:TYR:H	2.22	0.42
1:B:326:PHE:HE1	1:B:338:GLU:OE1	2.02	0.42
1:B:330:LEU:HB3	1:B:334:ASN:HD22	1.85	0.42
1:A:191:ARG:NH1	1:A:242:GLU:HB3	2.35	0.42
1:A:344:ARG:NH1	1:A:403:GLU:HA	2.35	0.42
1:B:363:VAL:HG23	1:B:378:ASP:O	2.20	0.42
1:A:152:LYS:HE2	1:A:152:LYS:HB3	1.94	0.42
1:A:320:HIS:C	1:A:322:GLU:N	2.73	0.42
1:A:442:GLU:O	1:A:443:TYR:CG	2.72	0.42
1:B:99:PRO:HD2	1:B:120:TYR:OH	2.20	0.42
1:B:207:SER:CB	1:B:225:GLN:CG	2.98	0.42
1:B:225:GLN:OE1	1:B:228:ARG:CD	2.68	0.42
1:B:45:ILE:HD11	3:B:1490:LFD:CLD	2.57	0.41
1:B:106:MET:HE2	1:B:290:PHE:CE2	2.55	0.41
1:B:423:ILE:CD1	2:B:1480:HEM:CMD	2.91	0.41
1:B:233:ARG:NH1	1:B:279:HIS:NE2	2.68	0.41
1:B:271:ARG:HH11	1:B:271:ARG:CG	2.33	0.41
1:B:317:ASP:O	1:B:321:LYS:HE2	2.20	0.41
1:B:165:ILE:HB	1:B:170:ASP:OD2	2.21	0.41
1:B:297:THR:HG23	1:B:298:ILE:H	1.86	0.41
1:A:452:VAL:CG1	1:A:453:PRO:HD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:LEU:HD22	1:A:284:MET:CE	2.50	0.41
1:A:460:MET:HG3	3:A:1490:LFD:CAK	2.50	0.41
1:A:174:MET:O	1:A:178:THR:HG23	2.20	0.41
1:A:257:ASN:CB	4:A:2006:HOH:O	2.25	0.41
1:B:295:THR:HB	2:B:1480:HEM:C3B	2.56	0.41
1:B:420:HIS:CB	2:B:1480:HEM:O2D	2.69	0.41
1:A:348:GLU:HA	1:A:348:GLU:OE1	2.19	0.41
1:A:399:LEU:HD12	1:A:399:LEU:C	2.42	0.41
1:A:434:THR:O	1:A:437:ALA:HB3	2.21	0.41
1:A:359:VAL:O	1:A:381:ALA:HA	2.21	0.41
1:A:423:ILE:H	1:A:423:ILE:HG12	1.66	0.40
1:B:31:THR:HB	1:B:32:PRO:CD	2.49	0.40
1:A:116:TYR:HE1	1:A:123:MET:HE1	1.77	0.40
1:A:246:ALA:O	1:A:250:GLU:OE1	2.39	0.40
1:A:326:PHE:HB3	1:A:330:LEU:CD2	2.46	0.40
1:B:78:THR:OG1	1:B:378:ASP:OD2	2.38	0.40
1:B:191:ARG:HH21	1:B:242:GLU:CD	2.24	0.40
1:B:334:ASN:HA	1:B:338:GLU:CD	2.41	0.40
1:A:69:THR:HA	1:A:78:THR:HA	2.02	0.40
1:A:142:PHE:O	1:A:146:ILE:HD12	2.21	0.40
1:A:183:LEU:O	1:A:260:ASP:HB2	2.22	0.40
1:B:158:TRP:CD1	1:B:473:TYR:HE2	2.39	0.40
1:B:124:ARG:HD3	1:B:124:ARG:C	2.42	0.40
1:B:188:LEU:CD1	1:B:243:ILE:HG13	2.51	0.40
1:B:201:LEU:O	1:B:205:GLU:HB2	2.20	0.40
1:B:251:GLU:O	1:B:254:LYS:N	2.51	0.40
1:B:475:ARG:CG	1:B:475:ARG:NH1	2.84	0.40
1:A:62:ASP:C	1:A:64:LYS:H	2.25	0.40
1:A:221:LEU:N	1:A:221:LEU:HD12	2.37	0.40
1:B:52:PRO:HD2	1:B:457:TYR:CG	2.56	0.40
1:B:389:HIS:CE1	1:B:398:ARG:NH1	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	445/460 (97%)	408 (92%)	34 (8%)	3 (1%)	22	41
1	B	446/460 (97%)	411 (92%)	35 (8%)	0	100	100
All	All	891/920 (97%)	819 (92%)	69 (8%)	3 (0%)	41	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	SER
1	A	224	PRO
1	A	321	LYS

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 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	392/402 (98%)	353 (90%)	39 (10%)	8	14
1	B	392/402 (98%)	342 (87%)	50 (13%)	4	7
All	All	784/804 (98%)	695 (89%)	89 (11%)	5	9

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LYS
1	A	38	THR
1	A	51	ASN
1	A	63	LEU
1	A	87	SER
1	A	105	ILE
1	A	106	MET
1	A	107	THR
1	A	165	ILE
1	A	190	LYS

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Mol	Chain	Res	Type
1	A	191	ARG
1	A	192	LEU
1	A	193	ASN
1	A	209	ILE
1	A	219	LEU
1	A	220	ARG
1	A	223	LEU
1	A	226	SER
1	A	230	ARG
1	A	231	GLU
1	A	233	ARG
1	A	251	GLU
1	A	253	SER
1	A	254	LYS
1	A	256	ASN
1	A	257	ASN
1	A	278	LEU
1	A	297	THR
1	A	308	MET
1	A	331	ASN
1	A	336	MET
1	A	378	ASP
1	A	390	ASP
1	A	391	GLU
1	A	396	ASN
1	A	409	ASP
1	A	413	ILE
1	A	419	VAL
1	A	421	LYS
1	B	30	LYS
1	B	38	THR
1	B	45	ILE
1	B	51	ASN
1	B	54	GLU
1	B	63	LEU
1	B	83	PRO
1	B	101	GLU
1	B	106	MET
1	B	107	THR
1	B	122	ARG
1	B	123	MET
1	B	165	ILE

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Mol	Chain	Res	Type
1	B	192	LEU
1	B	193	ASN
1	B	208	LEU
1	B	209	ILE
1	B	213	VAL
1	B	215	MET
1	B	219	LEU
1	B	221	LEU
1	B	223	LEU
1	B	225	GLN
1	B	230	ARG
1	B	233	ARG
1	B	245	VAL
1	B	251	GLU
1	B	254	LYS
1	B	257	ASN
1	B	260	ASP
1	B	271	ARG
1	B	278	LEU
1	B	295	THR
1	B	308	MET
1	B	334	ASN
1	B	336	MET
1	B	337	ASP
1	B	339	MET
1	B	378	ASP
1	B	379	ILE
1	B	388	HIS
1	B	391	GLU
1	B	409	ASP
1	B	413	ILE
1	B	421	LYS
1	B	447	LEU
1	B	465	THR
1	B	466	LEU
1	B	473	TYR
1	B	475	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS

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Mol	Chain	Res	Type
1	A	51	ASN
1	A	256	ASN
1	A	257	ASN
1	A	279	HIS
1	A	293	GLN
1	A	306	HIS
1	A	309	HIS
1	A	334	ASN
1	A	388	HIS
1	A	389	HIS
1	A	396	ASN
1	A	446	GLN
1	A	458	HIS
1	B	44	HIS
1	B	51	ASN
1	B	157	ASN
1	B	257	ASN
1	B	279	HIS
1	B	309	HIS
1	B	329	GLN
1	B	334	ASN
1	B	388	HIS
1	B	389	HIS
1	B	431	GLN
1	B	446	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

4 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	B	1480	3,1	41,50,50	1.57	7 (17%)	45,82,82	2.49	12 (26%)
2	HEM	A	1480	3,1	41,50,50	1.63	7 (17%)	45,82,82	2.50	18 (40%)
3	LFD	A	1490	2	41,43,43	2.73	7 (17%)	56,60,60	2.37	10 (17%)
3	LFD	B	1490	2	41,43,43	3.17	8 (19%)	56,60,60	2.42	11 (19%)

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	B	1480	3,1	-	5/12/54/54	-
2	HEM	A	1480	3,1	-	7/12/54/54	-
3	LFD	A	1490	2	-	9/24/34/34	0/5/5/5
3	LFD	B	1490	2	-	9/24/34/34	0/5/5/5

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1490	LFD	CBB-CLB	-13.09	1.46	1.74
3	B	1490	LFD	CBF-CLE	-8.80	1.52	1.73
3	A	1490	LFD	CBB-CLB	-8.77	1.55	1.74
3	B	1490	LFD	CBE-CLD	-8.68	1.53	1.73
3	A	1490	LFD	CBE-CLD	-8.40	1.53	1.73
3	A	1490	LFD	CBF-CLE	-6.88	1.57	1.73
3	A	1490	LFD	CBI-CBJ	-5.39	1.38	1.52
3	A	1490	LFD	CAW-NBM	-4.95	1.43	1.48
3	B	1490	LFD	CBI-CBJ	-4.94	1.39	1.52
2	A	1480	HEM	C1B-NB	-4.90	1.31	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1480	HEM	C1B-NB	-4.44	1.32	1.40
3	A	1490	LFD	CAO-NBM	-4.39	1.29	1.37
2	A	1480	HEM	C4D-ND	-3.89	1.33	1.40
2	A	1480	HEM	C4B-NB	-3.68	1.31	1.38
2	B	1480	HEM	C4D-ND	-3.67	1.34	1.40
3	A	1490	LFD	CBC-NAY	-3.27	1.35	1.41
2	B	1480	HEM	C1D-ND	-3.21	1.32	1.38
3	B	1490	LFD	CAO-NBM	-3.13	1.31	1.37
3	B	1490	LFD	CBD-CLC	-2.96	1.66	1.73
2	A	1480	HEM	C1D-ND	-2.87	1.32	1.38
3	B	1490	LFD	CBC-NAY	-2.79	1.36	1.41
2	B	1480	HEM	FE-ND	-2.71	1.83	1.96
2	A	1480	HEM	FE-ND	-2.63	1.83	1.96
2	B	1480	HEM	C4B-NB	-2.54	1.33	1.38
2	A	1480	HEM	CAA-C2A	-2.28	1.48	1.52
2	B	1480	HEM	C1B-C2B	-2.25	1.40	1.44
2	A	1480	HEM	C1B-C2B	-2.16	1.40	1.44
2	B	1480	HEM	CAA-C2A	-2.13	1.48	1.52
3	B	1490	LFD	CBH-NBL	-2.07	1.33	1.38

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1490	LFD	OAZ-CBA-NAY	11.13	123.20	109.07
3	A	1490	LFD	OAZ-CBJ-CAW	8.94	117.59	106.02
3	A	1490	LFD	OAZ-CBA-NAY	8.56	119.94	109.07
3	B	1490	LFD	OAZ-CBJ-CAW	8.03	116.41	106.02
2	A	1480	HEM	CHC-C4B-NB	7.94	133.06	124.43
2	B	1480	HEM	CHC-C4B-NB	7.16	132.21	124.43
2	A	1480	HEM	CHD-C1D-ND	6.41	131.39	124.43
3	B	1490	LFD	OAZ-CBA-OAA	-6.00	115.49	124.53
3	A	1490	LFD	OAZ-CBJ-CBI	-5.75	102.01	108.92
2	B	1480	HEM	C1B-NB-C4B	5.62	110.88	105.07
2	B	1480	HEM	CHA-C4D-ND	5.45	131.11	124.38
2	B	1480	HEM	CHB-C1B-NB	5.21	130.82	124.38
2	B	1480	HEM	CHD-C1D-ND	5.09	129.96	124.43
2	B	1480	HEM	CBA-CAA-C2A	-4.78	104.46	112.62
2	A	1480	HEM	C1B-NB-C4B	4.76	109.99	105.07
2	B	1480	HEM	CHA-C4D-C3D	-4.18	117.49	125.33
2	A	1480	HEM	CHD-C1D-C2D	-3.94	118.82	124.98
2	B	1480	HEM	CAD-CBD-CGD	-3.81	105.41	113.60
3	A	1490	LFD	CAQ-CBF-CBI	-3.42	118.33	122.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1480	HEM	CHA-C4D-ND	3.40	128.58	124.38
3	A	1490	LFD	OAZ-CBA-OAA	-3.39	119.42	124.53
2	A	1480	HEM	CBA-CAA-C2A	-3.37	106.87	112.62
2	A	1480	HEM	CHB-C1B-NB	3.29	128.44	124.38
2	B	1480	HEM	CHD-C1D-C2D	-3.23	119.93	124.98
2	A	1480	HEM	CHC-C4B-C3B	-3.21	119.65	124.57
3	A	1490	LFD	CBF-CAQ-CBB	3.17	122.26	118.71
2	A	1480	HEM	C4D-ND-C1D	3.10	108.28	105.07
2	A	1480	HEM	CMC-C2C-C3C	3.08	130.43	124.68
2	A	1480	HEM	CAA-CBA-CGA	-3.07	105.14	113.76
3	B	1490	LFD	CAV-NBL-CAU	2.98	118.10	111.52
3	B	1490	LFD	CBC-NAY-CBA	-2.90	121.59	126.36
3	B	1490	LFD	CAL-CAI-CBC	2.85	123.59	120.30
2	A	1480	HEM	CMA-C3A-C4A	-2.76	124.22	128.46
3	A	1490	LFD	OAA-CBA-NAY	-2.63	120.39	126.11
3	B	1490	LFD	CAH-CAK-CBG	2.56	123.69	120.32
2	B	1480	HEM	CHB-C1B-C2B	-2.54	119.68	126.72
3	B	1490	LFD	CAU-NBL-CBH	2.50	124.86	118.09
3	A	1490	LFD	CAV-NBL-CAU	2.40	116.82	111.52
3	A	1490	LFD	CAT-NBK-CAS	2.39	116.78	111.52
2	A	1480	HEM	CAD-C3D-C4D	2.37	128.79	124.66
2	B	1480	HEM	CAA-CBA-CGA	-2.34	107.20	113.76
3	A	1490	LFD	CAI-CAL-CBG	2.33	123.39	120.32
3	B	1490	LFD	OAA-CBA-NAY	-2.33	121.04	126.11
2	A	1480	HEM	O2D-CGD-CBD	2.23	121.18	114.03
2	A	1480	HEM	CBB-CAB-C3B	-2.22	116.57	127.62
2	A	1480	HEM	CMA-C3A-C2A	2.18	129.05	124.94
3	B	1490	LFD	CAM-CBH-NBL	-2.16	118.40	121.38
2	B	1480	HEM	CBB-CAB-C3B	-2.15	116.94	127.62
3	B	1490	LFD	CAW-NBM-CAP	2.12	129.95	125.76
2	A	1480	HEM	C4C-CHD-C1D	-2.09	119.80	122.56
2	A	1480	HEM	O2A-CGA-CBA	2.01	120.50	114.03

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1490	LFD	OAA-CBA-OAZ-CBJ
3	A	1490	LFD	NAY-CBA-OAZ-CBJ
3	A	1490	LFD	CAW-CBJ-OAZ-CBA
3	A	1490	LFD	CAN-CBI-CBJ-OAZ
3	A	1490	LFD	CBF-CBI-CBJ-OAZ

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Mol	Chain	Res	Type	Atoms
3	B	1490	LFD	OAA-CBA-OAZ-CBJ
3	B	1490	LFD	NAY-CBA-OAZ-CBJ
3	B	1490	LFD	CAW-CBJ-OAZ-CBA
3	B	1490	LFD	CAN-CBI-CBJ-OAZ
3	B	1490	LFD	CBF-CBI-CBJ-OAZ
3	A	1490	LFD	CAH-CBC-NAY-CBA
3	A	1490	LFD	CAI-CBC-NAY-CBA
2	A	1480	HEM	C4D-C3D-CAD-CBD
2	A	1480	HEM	C2D-C3D-CAD-CBD
3	A	1490	LFD	NBM-CAW-CBJ-OAZ
3	B	1490	LFD	NBM-CAW-CBJ-OAZ
2	A	1480	HEM	C2A-CAA-CBA-CGA
3	B	1490	LFD	NBM-CAW-CBJ-CBI
2	B	1480	HEM	C2A-CAA-CBA-CGA
3	B	1490	LFD	CBI-CBJ-OAZ-CBA
2	A	1480	HEM	CAD-CBD-CGD-O2D
2	A	1480	HEM	CAD-CBD-CGD-O1D
2	B	1480	HEM	CAD-CBD-CGD-O2D
2	A	1480	HEM	CAA-CBA-CGA-O2A
2	B	1480	HEM	CAD-CBD-CGD-O1D
2	B	1480	HEM	CAA-CBA-CGA-O2A
2	A	1480	HEM	CAA-CBA-CGA-O1A
3	A	1490	LFD	NBM-CAW-CBJ-CBI
2	B	1480	HEM	CAA-CBA-CGA-O1A
3	B	1490	LFD	CAR-CBH-NBL-CAV

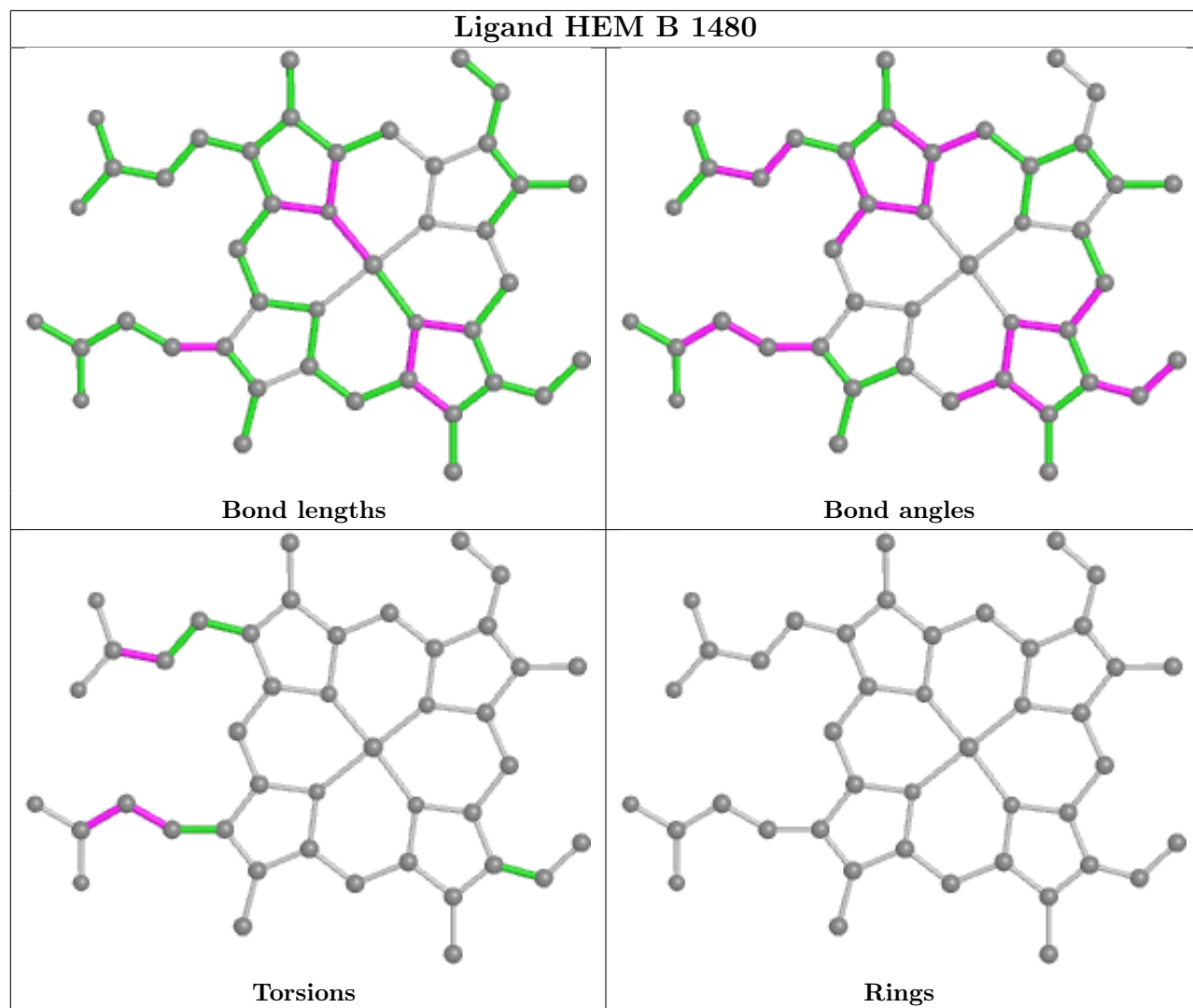
There are no ring outliers.

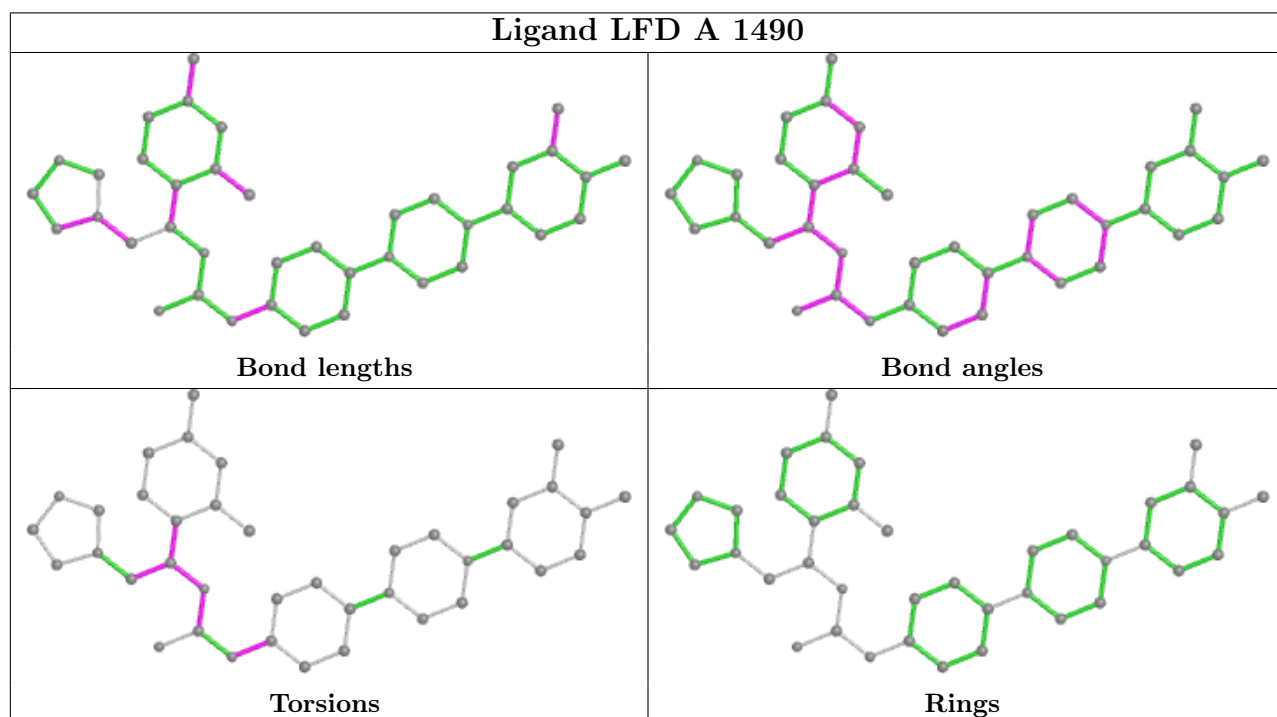
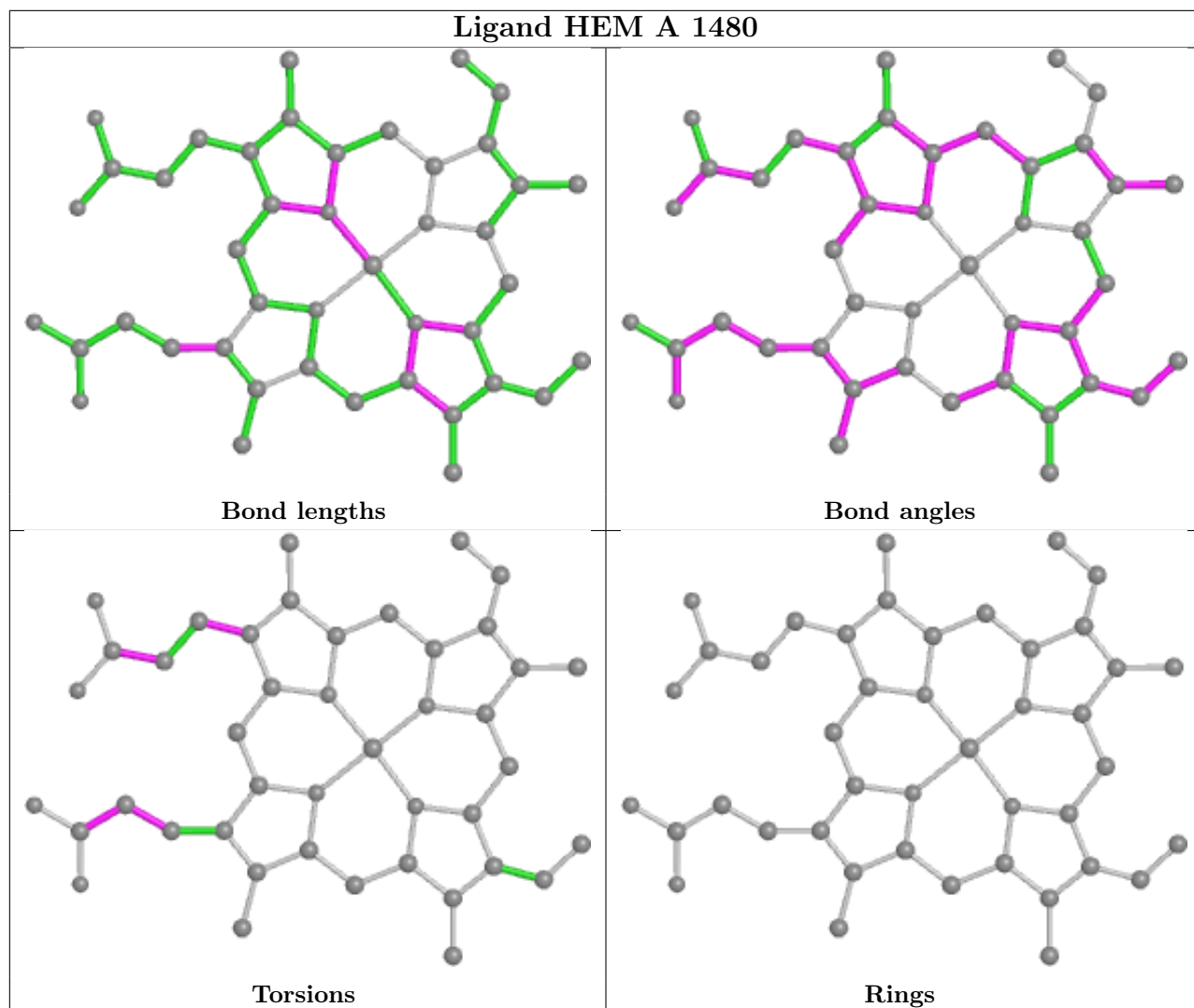
4 monomers are involved in 48 short contacts:

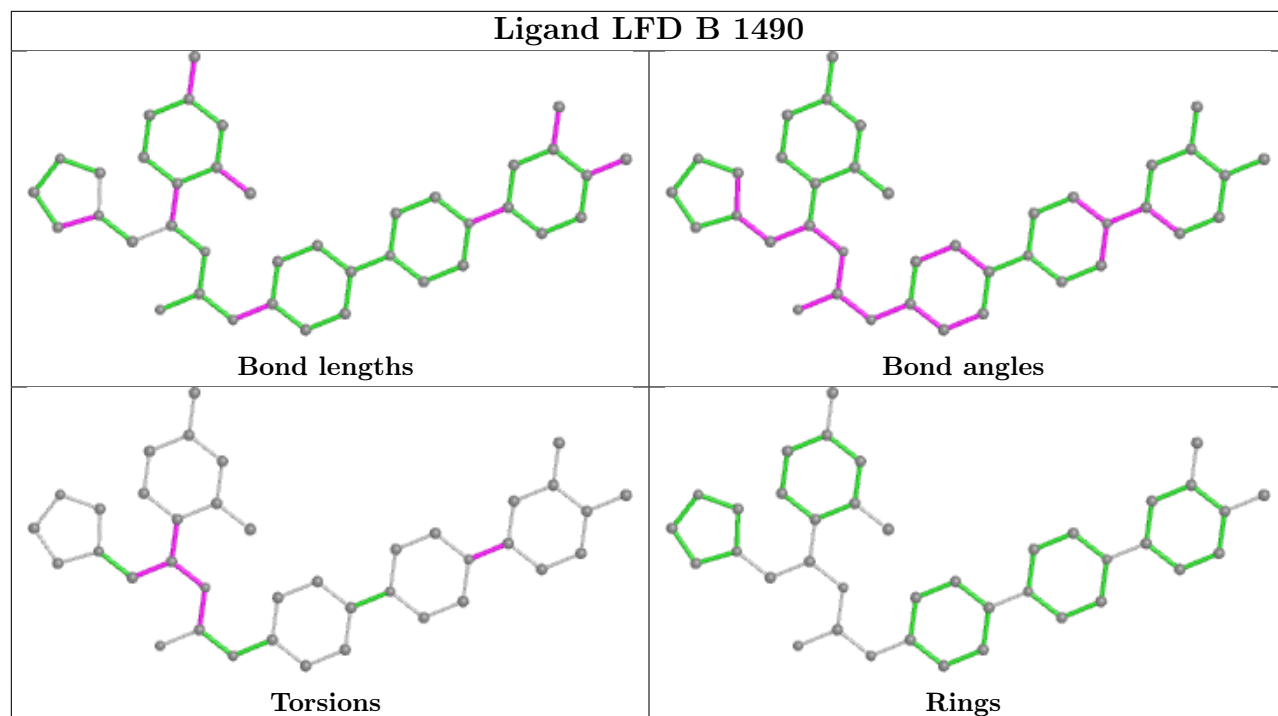
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1480	HEM	19	0
2	A	1480	HEM	8	0
3	A	1490	LFD	10	0
3	B	1490	LFD	11	0

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	449/460 (97%)	-0.16	14 (3%) 49 42	28, 64, 123, 185	0
1	B	450/460 (97%)	-0.05	25 (5%) 24 19	30, 64, 119, 170	0
All	All	899/920 (97%)	-0.11	39 (4%) 35 29	28, 64, 122, 185	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	252	ALA	6.0
1	B	28	ALA	5.5
1	A	251	GLU	5.1
1	B	253	SER	4.8
1	B	224	PRO	4.6
1	A	255	ASP	4.1
1	A	253	SER	3.9
1	B	255	ASP	3.8
1	B	228	ARG	3.3
1	B	225	GLN	3.3
1	B	256	ASN	3.3
1	A	252	ALA	3.1
1	B	251	GLU	3.0
1	B	257	ASN	2.9
1	A	246	ALA	2.9
1	B	221	LEU	2.8
1	B	478	LYS	2.8
1	B	246	ALA	2.8
1	B	190	LYS	2.8
1	B	223	LEU	2.7
1	A	250	GLU	2.7
1	B	300	THR	2.7
1	A	478	LYS	2.7
1	B	254	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	41	PHE	2.6
1	A	29	LYS	2.5
1	A	225	GLN	2.5
1	B	249	LYS	2.5
1	B	217	TRP	2.3
1	B	258	THR	2.3
1	B	159	LYS	2.2
1	A	273	GLY	2.2
1	A	257	ASN	2.2
1	A	224	PRO	2.1
1	A	256	ASN	2.1
1	B	208	LEU	2.1
1	A	274	THR	2.1
1	B	451	GLU	2.1
1	B	30	LYS	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 monosaccharides in this entry.

6.4 Ligands [i](#)

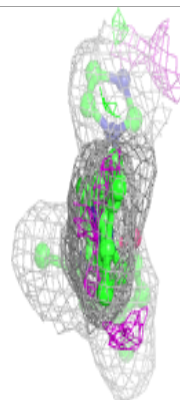
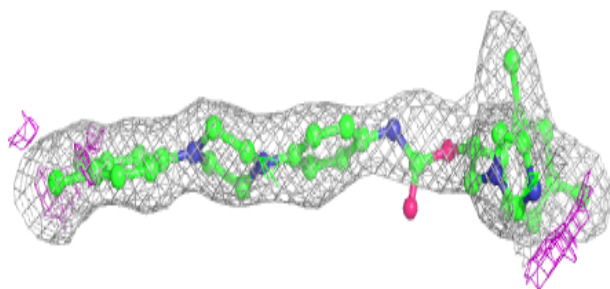
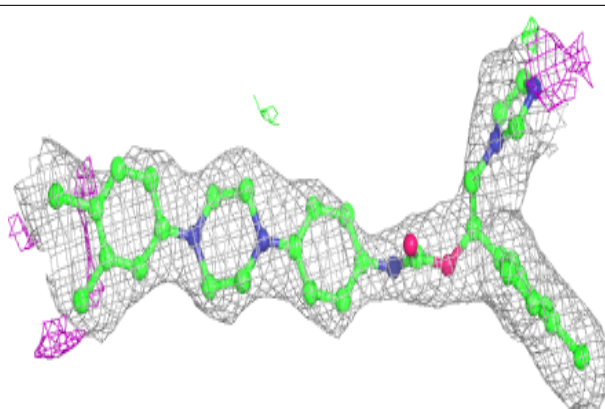
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	LFD	A	1490	39/39	0.89	0.19	60,74,96,135	0
3	LFD	B	1490	39/39	0.89	0.19	60,79,102,170	0
2	HEM	A	1480	43/43	0.95	0.14	22,29,38,41	0
2	HEM	B	1480	43/43	0.95	0.14	22,29,38,42	0

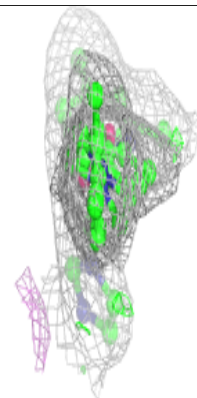
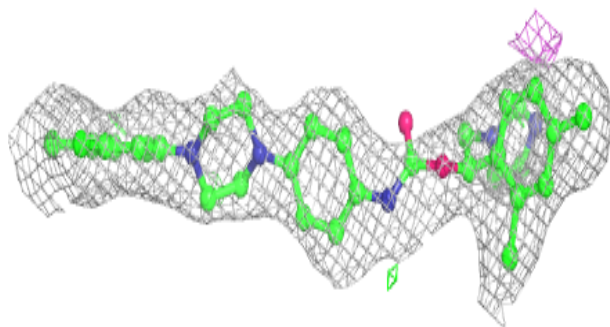
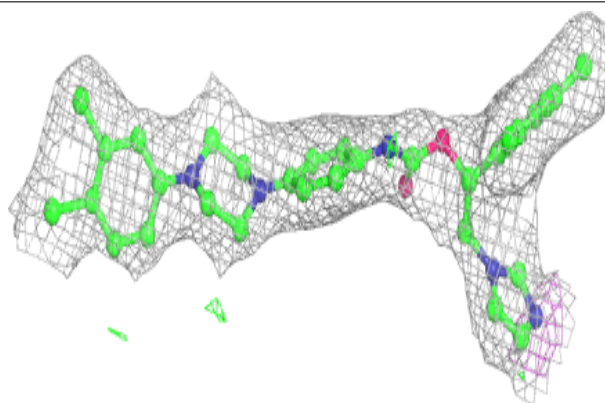
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LFD A 1490:

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

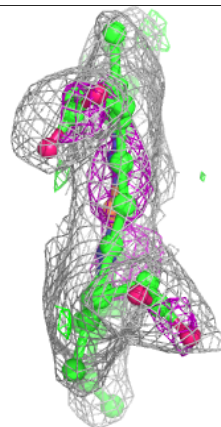
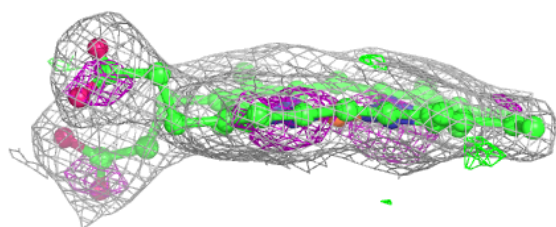
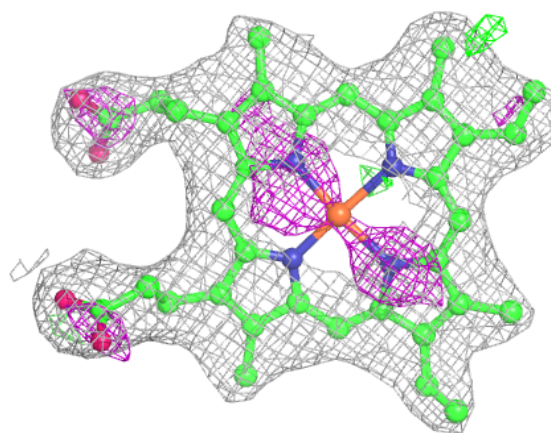
**Electron density around LFD B 1490:**

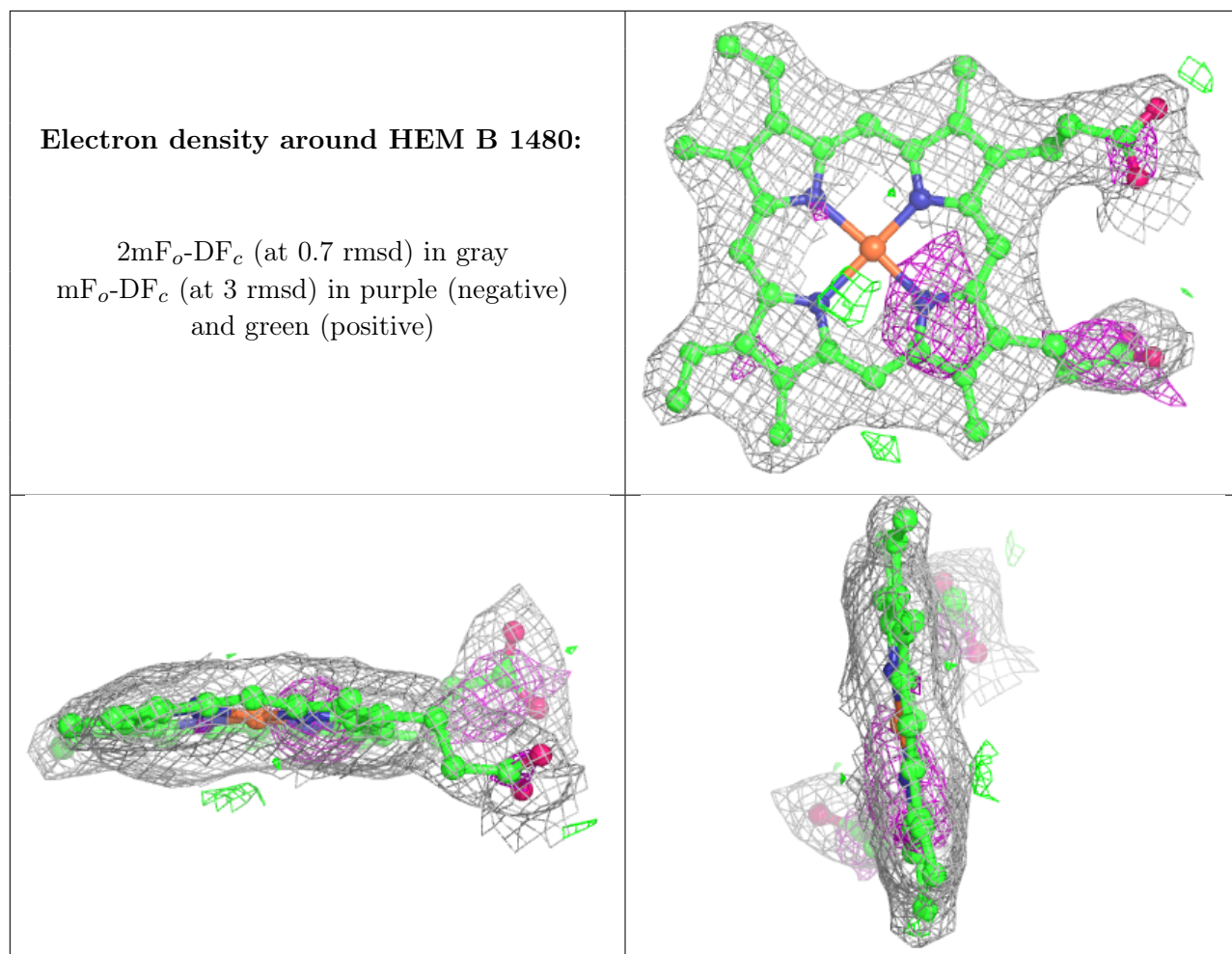
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 1480:

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





6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.