



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 11:49 AM JST

PDB ID : 5ZLH / pdb_00005zlh
Title : Crystal structure of Mn-ProtoporphyrinIX-reconstituted P450BM3
Authors : Omura, K.; Aiba, Y.; Onoda, H.; Sugimoto, H.; Shoji, O.; Watanabe, Y.
Deposited on : 2018-03-28
Resolution : 3.40 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 : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

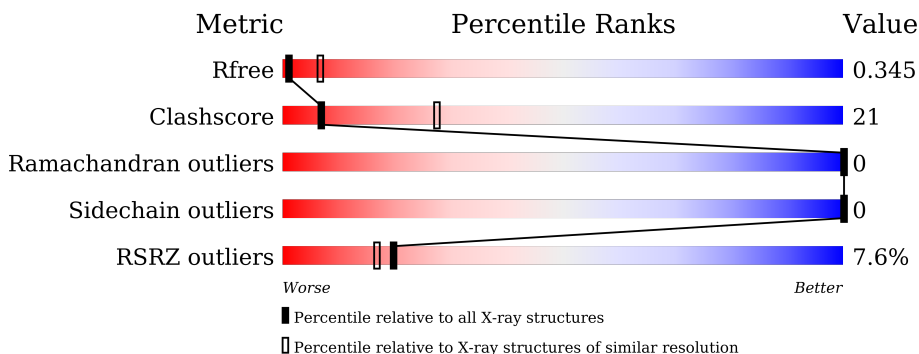
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	455	8% 56% 43% .
1	B	455	4% 64% 35% .
1	C	455	9% 57% 42% .
1	D	455	9% 58% 41% .

2 Entry composition [i](#)

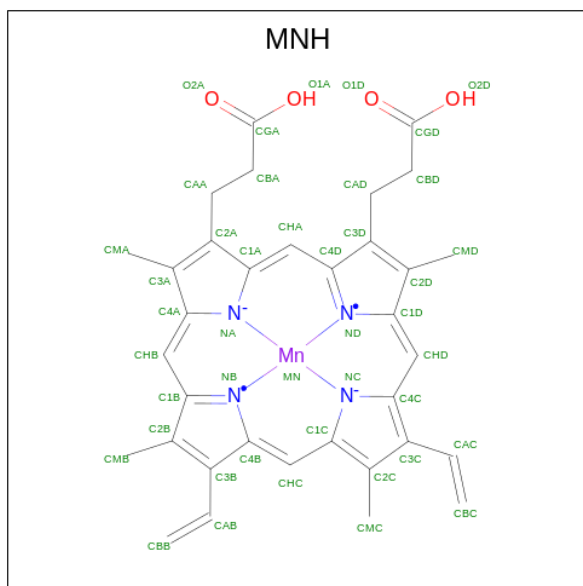
There are 2 unique types of molecules in this entry. The entry contains 14722 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional cytochrome P450/NADPH-P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3646	2329	619	681	17			
1	B	449	Total	C	N	O	S	0	0	0
			3621	2313	616	676	16			
1	C	452	Total	C	N	O	S	0	0	0
			3646	2329	619	681	17			
1	D	451	Total	C	N	O	S	0	0	0
			3637	2324	618	678	17			

- Molecule 2 is MANGANESE PROTOPORPHYRIN IX (CCD ID: MNH) (formula: $C_{34}H_{32}MnN_4O_4$).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	Mn	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Mn	N	O	0	0
			43	34	1	4	4		

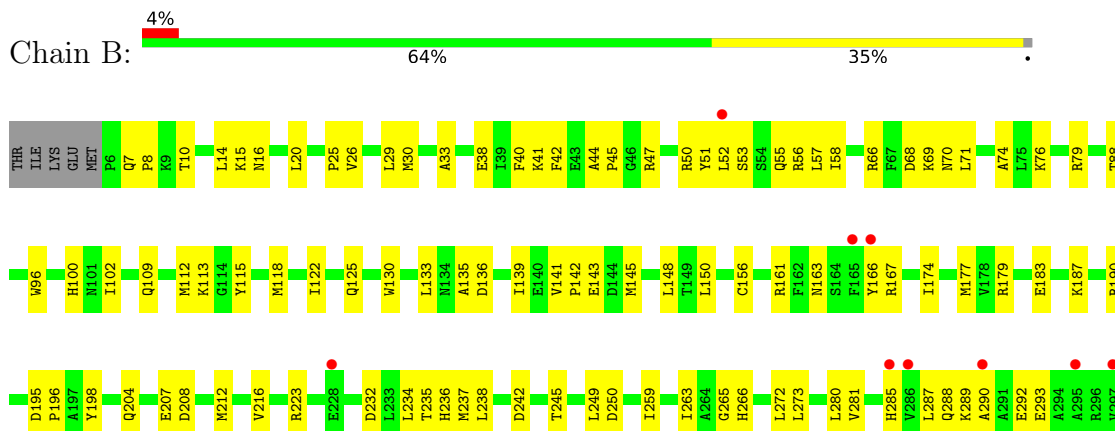
3 Residue-property plots

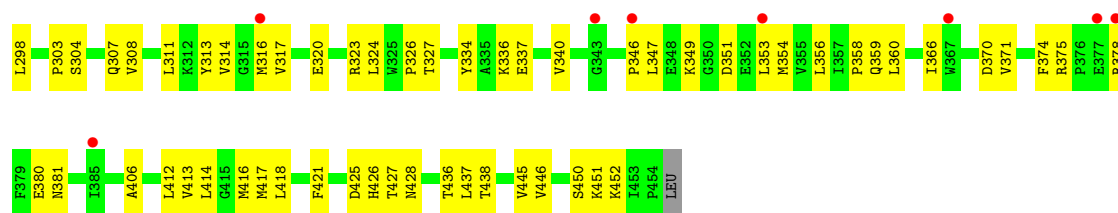
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Bifunctional cytochrome P450/NADPH-P450 reductase

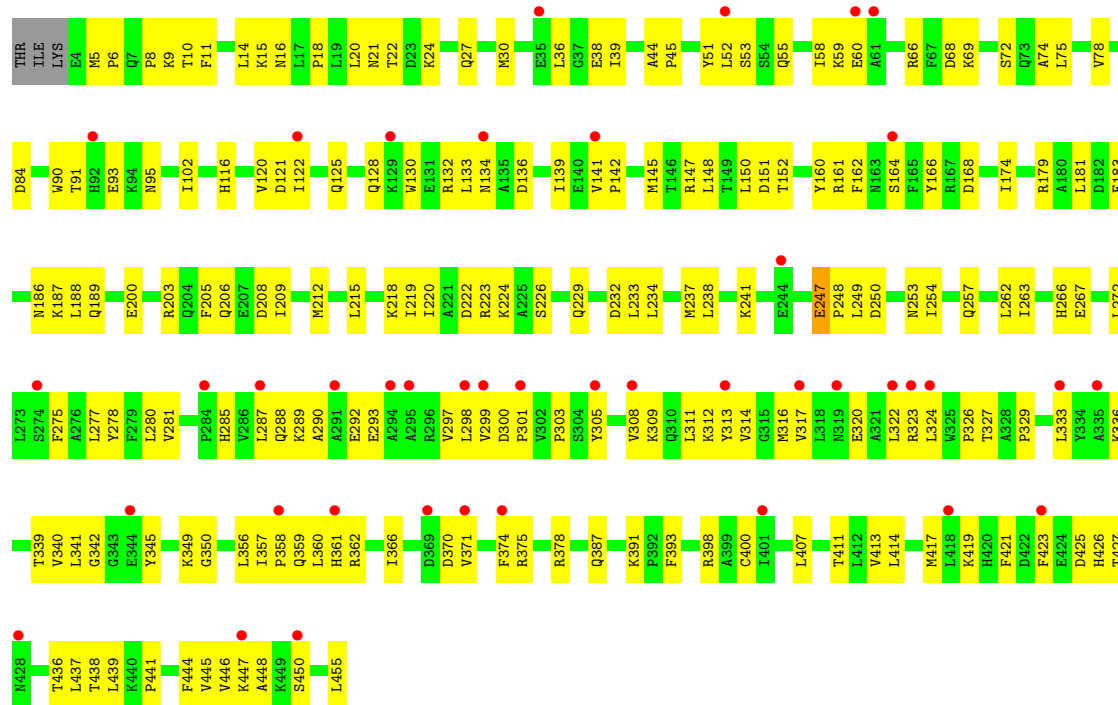


- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

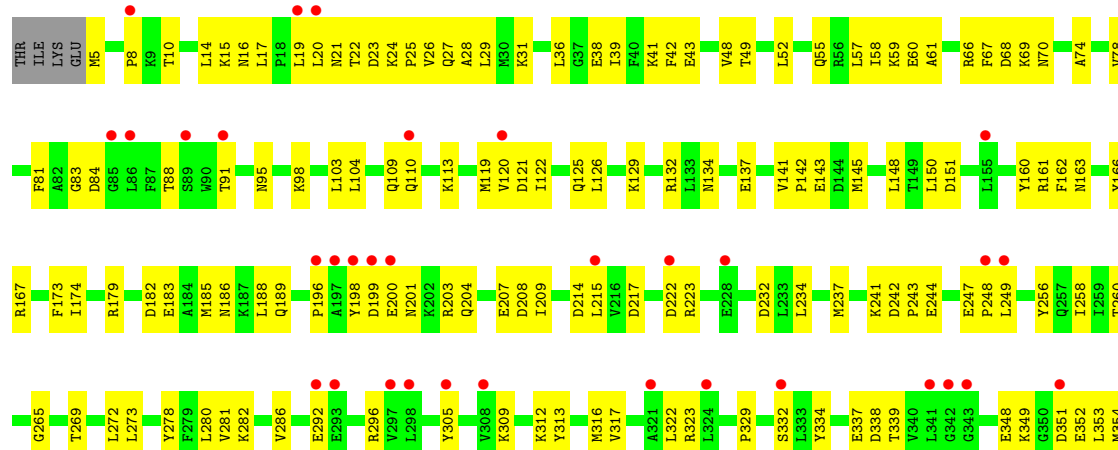


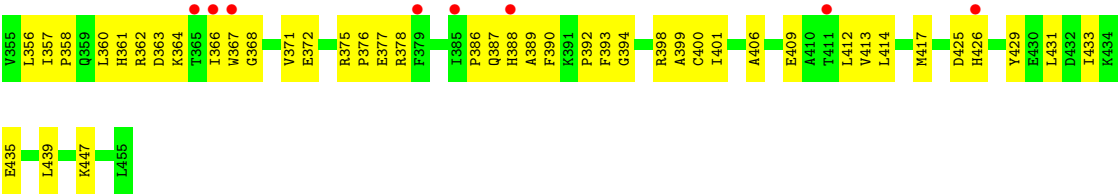


● Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



● Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	104.76Å 155.32Å 208.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 3.40 19.93 – 3.40	Depositor EDS
% Data completeness (in resolution range)	95.2 (19.93-3.40) 94.6 (19.93-3.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 3.44Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.310 , 0.346 0.309 , 0.345	Depositor DCC
R_{free} test set	1165 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 10.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	14722	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: MNH

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	0.21	0/3731	0.46	0/5045
1	B	0.20	0/3706	0.44	0/5011
1	C	0.27	0/3731	0.50	4/5045 (0.1%)
1	D	0.20	0/3722	0.42	0/5033
All	All	0.22	0/14890	0.45	4/20134 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	247	GLU	CA-C-N	9.70	129.64	120.03
1	C	247	GLU	C-N-CA	9.70	129.64	120.03
1	C	263	ILE	CB-CA-C	-5.10	105.44	111.97
1	C	263	ILE	N-CA-C	5.08	115.30	110.42

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	3646	0	3611	180	0
1	B	3621	0	3586	132	0
1	C	3646	0	3611	174	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3637	0	3605	167	0
2	A	43	0	30	9	0
2	B	43	0	30	6	0
2	C	43	0	30	1	0
2	D	43	0	30	6	0
All	All	14722	0	14533	621	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 21.

All (621) 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:A:69:LYS:HD3	1:A:398:ARG:HH11	1.14	1.12
1:C:128:GLN:HG2	1:C:132:ARG:HH12	1.17	1.06
1:C:128:GLN:CG	1:C:132:ARG:HH12	1.69	1.05
1:C:128:GLN:HG2	1:C:132:ARG:NH1	1.72	1.04
1:A:362:ARG:HA	1:A:371:VAL:HG11	1.47	0.93
1:A:69:LYS:HE3	2:A:500:MNH:O1A	1.71	0.91
1:A:69:LYS:HD3	1:A:398:ARG:NH1	1.85	0.90
1:D:387:GLN:O	1:D:388:HIS:ND1	2.08	0.85
1:B:421:PHE:HB3	1:B:450:SER:HA	1.64	0.80
1:D:16:ASN:HD21	1:D:42:PHE:HA	1.48	0.77
1:D:74:ALA:HB2	1:D:188:LEU:HD11	1.65	0.77
1:C:122:ILE:HG22	1:C:148:LEU:HD12	1.65	0.77
1:A:63:ASP:HB3	1:A:66:ARG:HB2	1.67	0.76
1:A:69:LYS:CD	1:A:398:ARG:HH11	1.94	0.76
1:C:329:PRO:HG3	1:C:439:LEU:HG	1.66	0.76
1:C:162:PHE:HZ	1:C:262:LEU:HD21	1.50	0.75
1:A:94:LYS:H	1:A:94:LYS:HD2	1.52	0.75
1:D:70:ASN:HB2	1:D:334:TYR:HB3	1.68	0.74
1:D:58:ILE:HD12	1:D:360:LEU:HD13	1.67	0.74
1:A:120:VAL:HG11	1:A:302:VAL:HG23	1.69	0.74
1:C:362:ARG:HA	1:C:371:VAL:HG11	1.67	0.73
1:A:102:ILE:HD11	1:A:249:LEU:HG	1.70	0.73
1:C:223:ARG:NH2	1:C:232:ASP:OD2	2.21	0.73
1:D:26:VAL:HG21	1:D:329:PRO:HB2	1.69	0.73
1:A:119:MET:HE1	1:A:408:HIS:HD2	1.53	0.73
1:A:183:GLU:HB2	1:A:205:PHE:CZ	2.25	0.72
1:C:311:LEU:HD13	1:C:314:VAL:HG21	1.71	0.72
1:A:24:LYS:HE3	1:C:250:ASP:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:LYS:HE3	2:A:500:MNH:CGA	2.19	0.71
1:B:323:ARG:HH22	1:B:371:VAL:HA	1.55	0.71
1:C:147:ARG:NH2	1:C:168:ASP:O	2.23	0.71
1:A:109:GLN:HG3	1:A:113:LYS:HE3	1.73	0.71
1:A:85:GLY:HA3	1:A:260:THR:HG21	1.72	0.71
1:D:69:LYS:HB2	1:D:398:ARG:HG3	1.72	0.71
1:B:223:ARG:NH2	1:B:232:ASP:OD2	2.25	0.70
1:A:329:PRO:HG3	1:A:439:LEU:HG	1.73	0.70
1:B:290:ALA:HB1	1:B:418:LEU:HD13	1.73	0.70
1:B:33:ALA:HB3	1:B:359:GLN:OE1	1.93	0.69
1:C:84:ASP:OD2	1:C:95:ASN:ND2	2.25	0.69
1:C:162:PHE:HZ	1:C:262:LEU:CD2	2.05	0.69
1:B:370:ASP:OD2	1:B:375:ARG:NH2	2.25	0.69
1:C:22:THR:HG23	1:C:24:LYS:H	1.58	0.68
1:C:128:GLN:HG3	1:C:132:ARG:HH12	1.56	0.68
1:C:370:ASP:OD2	1:C:375:ARG:NH1	2.25	0.68
1:C:414:LEU:HA	1:C:417:MET:HE2	1.75	0.68
1:C:301:PRO:HA	1:C:419:LYS:HE2	1.75	0.67
1:D:337:GLU:HG3	1:D:338:ASP:H	1.59	0.67
1:D:375:ARG:HE	1:D:377:GLU:HB2	1.60	0.67
1:C:285:HIS:O	1:C:288:GLN:NE2	2.27	0.67
1:D:121:ASP:OD2	1:D:161:ARG:NH2	2.25	0.67
1:A:79:ARG:HG2	1:A:88:THR:HG22	1.74	0.67
1:B:406:ALA:HB2	2:B:500:MNH:HMC1	1.76	0.67
1:D:84:ASP:OD2	1:D:95:ASN:ND2	2.27	0.67
1:D:59:LYS:HB2	1:D:388:HIS:CD2	2.29	0.67
1:D:98:LYS:HD2	1:D:249:LEU:HD23	1.77	0.67
1:A:10:THR:HB	1:A:15:LYS:HA	1.76	0.66
1:B:74:ALA:HB1	1:B:437:LEU:HD11	1.76	0.66
1:C:122:ILE:HA	1:C:125:GLN:HB2	1.75	0.66
1:A:122:ILE:HD12	1:A:151:ASP:HB3	1.78	0.66
1:D:414:LEU:HA	1:D:417:MET:HE2	1.78	0.66
1:B:281:VAL:HG11	1:B:425:ASP:HB2	1.78	0.66
1:C:222:ASP:OD1	1:C:223:ARG:N	2.28	0.66
1:C:280:LEU:HB3	1:C:287:LEU:HD21	1.77	0.66
1:D:49:THR:HG22	1:D:352:GLU:HG2	1.78	0.65
1:C:324:LEU:O	1:C:362:ARG:NH1	2.27	0.65
1:B:293:GLU:OE1	1:B:313:TYR:N	2.25	0.65
1:D:21:ASN:HA	1:D:189:GLN:HG2	1.79	0.65
1:A:119:MET:HE2	1:A:405:PHE:CE1	2.32	0.65
1:A:179:ARG:O	1:A:182:ASP:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:ARG:HD2	1:D:339:THR:HG21	1.79	0.64
1:B:33:ALA:HB2	1:B:40:PHE:HE1	1.61	0.64
1:C:148:LEU:HD21	1:C:413:VAL:HG21	1.78	0.64
1:A:90:TRP:HB2	1:A:93:GLU:HB2	1.79	0.64
1:B:356:LEU:HD23	1:B:358:PRO:HD2	1.79	0.64
1:C:179:ARG:NH1	1:C:208:ASP:OD1	2.31	0.64
1:A:112:MET:HE1	1:A:405:PHE:HB2	1.80	0.64
1:D:367:TRP:HD1	1:D:378:ARG:HD3	1.63	0.64
1:A:86:LEU:HB2	2:A:500:MNH:HAD1	1.78	0.63
1:C:249:LEU:HD23	1:C:253:ASN:OD1	1.97	0.63
1:C:121:ASP:OD2	1:D:132:ARG:NH1	2.29	0.63
1:D:247:GLU:HG2	1:D:248:PRO:HD2	1.81	0.63
1:A:86:LEU:HD12	1:A:96:TRP:CD1	2.34	0.63
1:C:139:ILE:HG12	1:C:446:VAL:O	1.98	0.63
1:A:190:ARG:HD3	1:A:198:TYR:CE2	2.34	0.62
1:B:232:ASP:O	1:B:236:HIS:ND1	2.33	0.62
1:C:128:GLN:CG	1:C:132:ARG:NH1	2.43	0.62
1:D:162:PHE:O	1:D:167:ARG:NH1	2.26	0.61
1:B:265:GLY:HA2	2:B:500:MNH:HMC2	1.82	0.61
1:C:44:ALA:HB1	1:C:45:PRO:HD2	1.81	0.61
1:C:233:LEU:HG	1:C:237:MET:HE3	1.82	0.61
1:D:8:PRO:HB2	1:D:19:LEU:HD11	1.83	0.61
1:D:137:GLU:O	1:D:447:LYS:NZ	2.34	0.61
1:A:85:GLY:O	1:A:89:SER:N	2.33	0.61
1:A:366:ILE:HG23	1:A:386:PRO:HG2	1.83	0.61
1:D:292:GLU:O	1:D:296:ARG:HG3	2.01	0.60
1:C:21:ASN:HA	1:C:189:GLN:OE1	2.02	0.60
1:D:59:LYS:HB2	1:D:388:HIS:NE2	2.17	0.60
1:D:27:GLN:HG3	1:D:435:GLU:OE2	2.02	0.60
1:B:30:MET:HA	1:B:359:GLN:OE1	2.01	0.59
1:A:327:THR:O	1:A:329:PRO:HD3	2.02	0.59
1:C:66:ARG:HH21	1:C:339:THR:HB	1.68	0.59
1:C:130:TRP:CE2	1:C:139:ILE:HD12	2.37	0.59
1:C:262:LEU:O	1:C:266:HIS:ND1	2.25	0.59
1:C:74:ALA:HB2	1:C:188:LEU:HD11	1.83	0.59
1:C:223:ARG:HA	1:C:226:SER:HB3	1.85	0.59
1:A:57:LEU:HD22	1:A:341:LEU:HG	1.84	0.59
1:B:187:LYS:HG2	1:B:190:ARG:HH12	1.67	0.59
1:B:375:ARG:HG3	1:B:378:ARG:HB2	1.85	0.59
1:D:55:GLN:OE1	1:D:360:LEU:HD11	2.03	0.59
1:B:122:ILE:HG22	1:B:148:LEU:HD12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:ILE:HD12	1:C:249:LEU:CD1	2.33	0.58
1:D:196:PRO:HA	1:D:199:ASP:HB3	1.85	0.58
1:A:69:LYS:CD	1:A:398:ARG:HE	2.17	0.58
1:A:86:LEU:CB	2:A:500:MNH:HAD1	2.33	0.58
1:A:153:ILE:HD12	1:A:265:GLY:HA3	1.86	0.58
1:A:320:GLU:OE2	1:A:323:ARG:NH2	2.29	0.58
1:C:393:PHE:O	1:C:400:CYS:N	2.36	0.58
1:D:280:LEU:HD21	1:D:317:VAL:HG11	1.84	0.58
1:A:52:LEU:HD12	1:A:353:LEU:HD13	1.85	0.58
1:B:356:LEU:HD22	1:B:359:GLN:HG3	1.84	0.58
1:C:141:VAL:HB	1:C:444:PHE:HD2	1.68	0.58
1:C:132:ARG:HG2	1:D:161:ARG:NH1	2.18	0.58
1:C:281:VAL:HG12	1:C:425:ASP:HB2	1.85	0.58
1:B:145:MET:HE2	1:B:273:LEU:HB2	1.85	0.58
1:D:305:TYR:HB2	1:D:309:LYS:NZ	2.19	0.58
1:A:86:LEU:HD12	1:A:96:TRP:HD1	1.69	0.57
1:B:38:GLU:OE1	1:B:56:ARG:NH2	2.37	0.57
1:B:421:PHE:HA	1:B:451:LYS:HG3	1.86	0.57
1:C:241:LYS:HG2	1:C:248:PRO:HG3	1.86	0.57
1:D:27:GLN:OE1	1:D:433:ILE:HB	2.04	0.57
1:C:39:ILE:HD11	1:C:345:TYR:CE2	2.40	0.57
1:C:142:PRO:HD3	1:C:444:PHE:HB3	1.87	0.57
1:D:241:LYS:HD2	1:D:248:PRO:HD3	1.87	0.57
1:D:348:GLU:N	1:D:351:ASP:OD2	2.38	0.57
1:A:70:ASN:HB2	1:A:334:TYR:HB3	1.87	0.56
1:C:223:ARG:HE	1:C:234:LEU:HD23	1.70	0.56
1:C:250:ASP:O	1:C:254:ILE:HG13	2.05	0.56
1:B:150:LEU:HD22	1:B:174:ILE:HD11	1.87	0.56
1:D:183:GLU:OE1	1:D:201:ASN:HB3	2.06	0.56
1:B:55:GLN:HG3	1:B:366:ILE:HD13	1.88	0.56
1:B:285:HIS:NE2	1:B:289:LYS:HE3	2.21	0.56
1:C:58:ILE:HD12	1:C:360:LEU:HD13	1.86	0.56
1:A:69:LYS:HD3	1:A:398:ARG:HE	1.69	0.56
1:B:52:LEU:HD11	1:B:57:LEU:HB2	1.88	0.56
1:C:55:GLN:HB3	1:C:366:ILE:HD11	1.87	0.56
1:D:60:GLU:HB3	1:D:66:ARG:NH2	2.20	0.56
1:D:179:ARG:NH1	1:D:208:ASP:OD1	2.39	0.56
1:A:86:LEU:HB3	2:A:500:MNH:CGD	2.35	0.56
1:C:421:PHE:HD1	1:C:450:SER:HA	1.71	0.56
1:B:320:GLU:OE1	1:B:323:ARG:HD3	2.07	0.55
1:C:320:GLU:OE1	1:C:323:ARG:NE	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:LYS:HD3	1:A:398:ARG:CZ	2.36	0.55
1:A:116:HIS:HA	1:A:119:MET:SD	2.46	0.55
1:A:79:ARG:HG2	1:A:88:THR:CG2	2.37	0.55
1:A:277:LEU:HD12	1:A:417:MET:HE1	1.87	0.55
1:C:125:GLN:C	1:C:128:GLN:HE22	2.15	0.55
1:C:297:VAL:HG11	1:C:311:LEU:HB3	1.88	0.55
1:C:417:MET:HB3	1:C:423:PHE:HZ	1.71	0.55
1:B:58:ILE:HG21	1:B:360:LEU:HD22	1.89	0.55
1:D:26:VAL:HG21	1:D:329:PRO:CB	2.35	0.55
1:A:157:GLY:O	1:A:233:LEU:HB2	2.07	0.55
1:D:329:PRO:HB3	1:D:439:LEU:HD13	1.89	0.55
1:A:119:MET:HE1	1:A:408:HIS:CD2	2.38	0.55
1:D:272:LEU:HD13	1:D:322:LEU:HG	1.89	0.55
1:D:361:HIS:HA	1:D:367:TRP:CZ3	2.41	0.54
1:B:71:LEU:O	1:B:76:LYS:NZ	2.37	0.54
1:B:10:THR:HG23	1:B:15:LYS:HA	1.90	0.54
1:C:132:ARG:CB	1:D:161:ARG:HD3	2.37	0.54
1:D:43:GLU:HB3	1:D:48:VAL:HG13	1.88	0.54
1:B:20:LEU:HD21	1:B:29:LEU:HD21	1.89	0.54
1:B:183:GLU:O	1:B:187:LYS:HG3	2.06	0.54
1:A:132:ARG:NH2	1:B:125:GLN:OE1	2.41	0.54
1:D:52:LEU:HD11	1:D:353:LEU:HD11	1.90	0.54
1:C:20:LEU:O	1:C:189:GLN:NE2	2.40	0.54
1:A:148:LEU:HA	1:A:165:PHE:HE1	1.71	0.54
1:A:293:GLU:OE2	1:A:312:LYS:N	2.38	0.54
1:D:60:GLU:HB3	1:D:66:ARG:HH22	1.72	0.54
1:B:427:THR:HG21	1:B:445:VAL:HG23	1.90	0.54
1:C:132:ARG:HG2	1:D:161:ARG:CZ	2.38	0.54
1:A:201:ASN:HB3	1:A:205:PHE:HE2	1.73	0.53
1:B:427:THR:O	1:B:428:ASN:OD1	2.26	0.53
1:C:181:LEU:HD22	1:C:437:LEU:HD12	1.90	0.53
1:A:24:LYS:HD3	1:A:27:GLN:OE1	2.09	0.53
1:A:108:SER:H	1:A:111:ALA:HB3	1.73	0.53
1:A:336:LYS:NZ	1:A:337:GLU:OE2	2.40	0.53
1:B:356:LEU:CD2	1:B:359:GLN:H	2.22	0.53
1:B:436:THR:C	1:B:438:THR:H	2.15	0.53
1:D:20:LEU:HD21	1:D:29:LEU:HG	1.90	0.53
1:D:60:GLU:OE1	1:D:66:ARG:NH2	2.41	0.53
1:A:133:LEU:HD23	1:B:163:ASN:ND2	2.24	0.53
1:B:190:ARG:HD3	1:B:198:TYR:CZ	2.44	0.53
1:C:74:ALA:O	1:C:78:VAL:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:ASN:N	1:A:399:ALA:HB2	2.24	0.53
1:A:413:VAL:O	1:A:417:MET:HG3	2.09	0.53
1:C:290:ALA:O	1:C:293:GLU:HB3	2.08	0.53
1:A:24:LYS:CE	1:C:250:ASP:HB3	2.38	0.53
1:C:298:LEU:HD22	1:C:303:PRO:HB3	1.89	0.53
1:C:134:ASN:OD1	1:D:160:TYR:CE1	2.62	0.53
1:C:220:ILE:O	1:C:224:LYS:HG2	2.09	0.53
1:A:82:ALA:HB1	1:A:260:THR:HG22	1.91	0.53
1:A:17:LEU:HD11	1:A:188:LEU:O	2.08	0.52
1:A:220:ILE:O	1:A:224:LYS:HB2	2.08	0.52
1:B:298:LEU:HD11	1:B:311:LEU:HD11	1.91	0.52
1:A:262:LEU:O	1:A:266:HIS:ND1	2.42	0.52
1:B:33:ALA:HB2	1:B:40:PHE:CE1	2.43	0.52
1:B:130:TRP:HA	1:B:133:LEU:HG	1.90	0.52
1:C:39:ILE:HG23	1:C:52:LEU:HD23	1.91	0.52
1:C:293:GLU:O	1:C:297:VAL:N	2.39	0.52
1:A:268:THR:HA	1:A:327:THR:HG21	1.91	0.52
1:B:288:GLN:O	1:B:292:GLU:HG3	2.09	0.52
1:C:10:THR:HG23	1:C:15:LYS:HA	1.90	0.52
1:A:54:SER:O	1:A:58:ILE:HG12	2.10	0.52
1:C:186:ASN:O	1:C:189:GLN:HB2	2.09	0.52
1:B:380:GLU:O	1:B:381:ASN:ND2	2.28	0.52
1:C:39:ILE:HA	1:C:51:TYR:O	2.09	0.52
1:A:85:GLY:HA2	1:A:257:GLN:OE1	2.10	0.52
1:A:177:MET:SD	1:A:266:HIS:NE2	2.83	0.52
1:A:228:GLU:N	1:A:228:GLU:OE1	2.43	0.52
1:A:86:LEU:HD11	1:A:99:ALA:HB3	1.92	0.51
1:A:251:ASP:HA	1:A:254:ILE:HD12	1.93	0.51
1:C:407:LEU:O	1:C:411:THR:HG23	2.10	0.51
1:A:69:LYS:HD3	1:A:398:ARG:NE	2.25	0.51
1:A:358:PRO:HB2	1:A:362:ARG:HH12	1.75	0.51
1:B:337:GLU:HA	1:B:349:LYS:HE2	1.91	0.51
1:C:68:ASP:OD2	1:C:91:THR:HG21	2.11	0.51
1:C:288:GLN:HG2	1:C:289:LYS:H	1.76	0.51
1:D:312:LYS:HG2	1:D:316:MET:HE2	1.92	0.51
1:B:96:TRP:O	1:B:100:HIS:HB3	2.11	0.51
1:D:242:ASP:OD1	1:D:243:PRO:HD2	2.10	0.51
1:A:74:ALA:O	1:A:78:VAL:HG23	2.10	0.51
1:B:450:SER:O	1:B:452:LYS:NZ	2.44	0.51
1:C:38:GLU:HA	1:C:53:SER:HB2	1.93	0.51
1:C:209:ILE:HA	1:C:212:MET:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:THR:OG1	1:D:398:ARG:NH1	2.42	0.51
1:D:199:ASP:OD1	1:D:200:GLU:N	2.43	0.51
1:A:219:ILE:HG22	1:A:234:LEU:HD22	1.93	0.51
1:D:214:ASP:O	1:D:217:ASP:HB2	2.11	0.51
1:A:14:LEU:HB3	1:A:18:PRO:HD3	1.90	0.51
1:D:366:ILE:HG23	1:D:386:PRO:HG2	1.93	0.51
1:A:183:GLU:HB2	1:A:205:PHE:CE1	2.45	0.51
1:D:126:LEU:HD22	1:D:148:LEU:HD13	1.91	0.51
1:B:187:LYS:HG2	1:B:190:ARG:NH1	2.25	0.51
1:C:132:ARG:HB3	1:D:161:ARG:HD3	1.92	0.51
1:D:323:ARG:HH22	1:D:371:VAL:HA	1.75	0.50
1:A:232:ASP:O	1:A:235:THR:OG1	2.24	0.50
1:A:388:HIS:ND1	1:A:391:LYS:HD2	2.26	0.50
1:C:39:ILE:HG23	1:C:52:LEU:HA	1.93	0.50
1:D:110:GLN:O	1:D:113:LYS:HE2	2.11	0.50
1:B:66:ARG:O	1:B:336:LYS:N	2.39	0.50
1:D:119:MET:SD	1:D:409:GLU:HB3	2.52	0.50
1:A:168:ASP:OD2	1:B:167:ARG:HB3	2.12	0.50
1:C:116:HIS:HE1	1:C:308:VAL:HG21	1.77	0.50
1:C:313:TYR:HA	1:C:316:MET:HG2	1.93	0.50
1:D:19:LEU:HB2	1:D:42:PHE:HE2	1.75	0.50
1:B:53:SER:HB3	1:B:359:GLN:NE2	2.26	0.50
1:C:324:LEU:HD11	1:C:374:PHE:HA	1.94	0.50
1:C:370:ASP:OD1	1:C:370:ASP:N	2.40	0.50
1:D:313:TYR:HD1	1:D:316:MET:HE3	1.76	0.50
1:B:380:GLU:C	1:B:381:ASN:HD22	2.14	0.50
1:C:151:ASP:OD1	1:C:162:PHE:HB2	2.12	0.50
1:A:68:ASP:HB3	1:A:334:TYR:CE1	2.47	0.50
1:B:68:ASP:OD1	1:B:69:LYS:N	2.45	0.50
1:C:121:ASP:CG	1:D:132:ARG:HH12	2.16	0.50
1:C:200:GLU:OE1	1:C:200:GLU:N	2.42	0.50
1:D:366:ILE:C	1:D:368:GLY:H	2.19	0.50
1:A:83:GLY:HA3	1:A:256:TYR:CE2	2.46	0.50
1:A:102:ILE:HG22	1:A:242:ASP:HA	1.93	0.50
1:C:417:MET:HB3	1:C:423:PHE:CZ	2.47	0.50
1:D:19:LEU:HD12	1:D:42:PHE:CE2	2.47	0.50
1:C:39:ILE:CG2	1:C:52:LEU:HD23	2.41	0.49
1:A:116:HIS:HB3	1:A:305:TYR:HD2	1.77	0.49
1:A:436:THR:C	1:A:438:THR:H	2.18	0.49
1:C:301:PRO:HB2	1:C:455:LEU:HD12	1.95	0.49
1:D:109:GLN:OE1	1:D:309:LYS:HE3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:375:ARG:HB3	1:D:378:ARG:NH1	2.28	0.49
1:B:265:GLY:HA2	2:B:500:MNH:CMC	2.43	0.49
1:A:168:ASP:OD1	1:B:167:ARG:HG2	2.13	0.49
1:A:367:TRP:CZ2	1:A:390:PHE:HB2	2.47	0.49
1:C:60:GLU:OE1	1:C:342:GLY:N	2.42	0.49
1:D:182:ASP:OD1	1:D:186:ASN:ND2	2.45	0.49
1:A:26:VAL:HG11	1:A:329:PRO:HB3	1.94	0.49
1:A:352:GLU:OE1	1:A:352:GLU:N	2.43	0.49
1:A:429:TYR:OH	1:A:442:GLU:O	2.28	0.49
1:B:29:LEU:HD13	1:B:51:TYR:CE2	2.47	0.49
1:C:341:LEU:O	1:C:345:TYR:HB2	2.13	0.49
1:A:168:ASP:CG	1:B:167:ARG:HB3	2.38	0.49
1:D:390:PHE:CZ	1:D:392:PRO:HG3	2.47	0.49
1:C:69:LYS:HA	1:C:333:LEU:HD23	1.94	0.49
1:B:109:GLN:O	1:B:113:LYS:HG3	2.13	0.49
1:B:320:GLU:HG3	1:B:374:PHE:CE1	2.48	0.49
1:C:426:HIS:CD2	1:C:447:LYS:HE3	2.47	0.49
1:D:256:TYR:O	1:D:260:THR:OG1	2.26	0.49
1:A:83:GLY:HA3	1:A:256:TYR:CD2	2.48	0.49
1:A:87:PHE:HA	2:A:500:MNH:HAD2	1.94	0.49
1:A:232:ASP:OD1	1:A:233:LEU:N	2.45	0.49
1:A:251:ASP:N	1:A:251:ASP:OD1	2.44	0.48
1:A:331:PHE:HE1	1:A:333:LEU:HD11	1.78	0.48
1:A:407:LEU:O	1:A:411:THR:OG1	2.27	0.48
1:C:166:TYR:HE2	1:D:129:LYS:HB2	1.78	0.48
1:A:115:TYR:O	1:A:119:MET:HG3	2.13	0.48
1:A:272:LEU:HD13	1:A:322:LEU:HD13	1.96	0.48
1:B:356:LEU:CD2	1:B:358:PRO:HD2	2.44	0.48
1:C:11:PHE:CD1	1:C:18:PRO:HG2	2.48	0.48
1:D:83:GLY:O	1:D:88:THR:OG1	2.32	0.48
1:B:216:VAL:HG21	1:B:259:ILE:HG13	1.94	0.48
1:D:141:VAL:O	1:D:145:MET:HG2	2.13	0.48
1:D:145:MET:HE1	1:D:417:MET:SD	2.54	0.48
1:C:122:ILE:HD13	1:C:152:THR:HA	1.96	0.48
1:C:298:LEU:HD23	1:C:298:LEU:HA	1.65	0.48
1:D:150:LEU:HD22	1:D:174:ILE:HD11	1.94	0.48
1:A:168:ASP:OD1	1:B:167:ARG:CG	2.62	0.48
1:A:209:ILE:HA	1:A:212:MET:HE3	1.95	0.48
1:A:367:TRP:HZ2	1:A:390:PHE:HB2	1.78	0.48
1:A:293:GLU:OE1	1:A:296:ARG:NH2	2.46	0.48
1:D:204:GLN:O	1:D:207:GLU:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ARG:HG2	1:C:164:SER:HB3	1.96	0.48
1:B:212:MET:HE1	1:B:263:ILE:HD11	1.96	0.48
1:D:357:ILE:HG22	1:D:361:HIS:HE1	1.79	0.48
1:A:66:ARG:HA	1:A:336:LYS:HE2	1.96	0.47
1:A:190:ARG:HD3	1:A:198:TYR:CZ	2.49	0.47
1:A:111:ALA:HB1	1:A:115:TYR:HE2	1.79	0.47
1:B:232:ASP:OD1	1:B:232:ASP:N	2.45	0.47
1:B:234:LEU:O	1:B:238:LEU:HG	2.13	0.47
1:C:125:GLN:HA	1:C:128:GLN:HE22	1.79	0.47
1:C:326:PRO:HG3	1:C:357:ILE:HG22	1.95	0.47
1:D:69:LYS:HD3	1:D:398:ARG:CZ	2.43	0.47
1:A:8:PRO:HG2	1:A:16:ASN:ND2	2.30	0.47
1:C:267:GLU:OE2	1:C:438:THR:OG1	2.31	0.47
1:D:313:TYR:HA	1:D:316:MET:HE3	1.96	0.47
1:D:337:GLU:HA	1:D:349:LYS:HB2	1.96	0.47
1:D:367:TRP:CD1	1:D:378:ARG:HD3	2.46	0.47
1:B:195:ASP:OD1	1:B:196:PRO:HD2	2.15	0.47
1:A:102:ILE:CD1	1:A:249:LEU:HG	2.44	0.47
1:B:324:LEU:HD12	1:B:374:PHE:HD1	1.79	0.47
1:D:223:ARG:NH2	1:D:232:ASP:OD2	2.47	0.47
1:A:141:VAL:O	1:A:145:MET:HG2	2.14	0.47
1:B:20:LEU:HG	1:B:42:PHE:CZ	2.50	0.47
1:C:90:TRP:HB2	1:C:93:GLU:HG3	1.97	0.47
1:D:392:PRO:HG2	1:D:393:PHE:CD2	2.50	0.47
1:D:429:TYR:HE2	1:D:431:LEU:HD12	1.80	0.47
1:B:130:TRP:CH2	1:B:417:MET:HE3	2.49	0.47
1:B:412:LEU:O	1:B:416:MET:HG3	2.14	0.47
1:C:222:ASP:O	1:C:226:SER:N	2.48	0.47
1:D:23:ASP:O	1:D:25:PRO:HD3	2.13	0.47
1:D:98:LYS:HG2	1:D:242:ASP:HB2	1.96	0.47
1:A:162:PHE:CE2	1:A:215:LEU:HD21	2.50	0.47
1:B:139:ILE:HG12	1:B:446:VAL:O	2.15	0.47
1:C:427:THR:HG21	1:C:445:VAL:HG23	1.96	0.47
1:A:218:LYS:HG2	1:B:136:ASP:OD2	2.15	0.47
1:A:303:PRO:HA	1:A:307:GLN:OE1	2.14	0.47
1:D:332:SER:HA	1:D:354:MET:HA	1.97	0.47
1:D:81:PHE:HB3	1:D:209:ILE:HG12	1.97	0.47
1:D:103:LEU:HD21	1:D:237:MET:HG2	1.97	0.47
1:D:148:LEU:HD21	1:D:413:VAL:HG21	1.96	0.47
1:A:422:ASP:OD1	1:A:451:LYS:NZ	2.49	0.46
1:B:51:TYR:CE2	1:B:354:MET:HG2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:LEU:HD22	1:A:257:GLN:HE22	1.80	0.46
1:C:66:ARG:NH2	1:C:340:VAL:O	2.46	0.46
1:D:25:PRO:HD2	1:D:435:GLU:OE1	2.15	0.46
1:A:61:ALA:HA	1:A:67:PHE:CD1	2.51	0.46
1:A:132:ARG:O	1:B:161:ARG:HD2	2.15	0.46
1:B:190:ARG:HD3	1:B:198:TYR:CE2	2.50	0.46
1:C:30:MET:O	1:C:359:GLN:NE2	2.48	0.46
1:C:58:ILE:HG21	1:C:360:LEU:HD22	1.97	0.46
1:C:278:TYR:HA	1:C:444:PHE:CZ	2.51	0.46
1:D:269:THR:OG1	2:D:500:MNH:HMC3	2.15	0.46
1:D:281:VAL:HG11	1:D:425:ASP:HB2	1.98	0.46
1:D:366:ILE:HB	1:D:367:TRP:CE3	2.50	0.46
1:A:58:ILE:HG13	1:A:360:LEU:HD13	1.97	0.46
1:B:326:PRO:HD2	1:B:358:PRO:HG3	1.98	0.46
1:C:8:PRO:HD2	1:C:16:ASN:HD21	1.81	0.46
1:D:14:LEU:O	1:D:14:LEU:HG	2.15	0.46
1:A:102:ILE:HD11	1:A:249:LEU:CG	2.44	0.46
1:B:356:LEU:HD22	1:B:359:GLN:CG	2.45	0.46
1:C:141:VAL:O	1:C:145:MET:HG2	2.15	0.46
1:C:288:GLN:O	1:C:292:GLU:HG3	2.14	0.46
1:D:426:HIS:ND1	1:D:447:LYS:HG3	2.31	0.46
1:B:58:ILE:HD12	1:B:360:LEU:HD13	1.98	0.46
1:B:96:TRP:NE1	2:B:500:MNH:O2D	2.31	0.46
1:C:24:LYS:HB2	1:C:27:GLN:HB3	1.98	0.46
1:D:20:LEU:HD22	1:D:25:PRO:CB	2.46	0.46
1:A:126:LEU:HA	1:A:165:PHE:CE2	2.50	0.46
1:A:158:PHE:HB3	1:A:219:ILE:HG21	1.98	0.46
1:A:263:ILE:HA	1:A:266:HIS:CE1	2.50	0.46
1:B:340:VAL:HG12	1:B:346:PRO:HA	1.97	0.46
1:B:204:GLN:HA	1:B:207:GLU:HB3	1.98	0.46
1:B:311:LEU:HB3	1:B:314:VAL:HG22	1.97	0.46
1:B:370:ASP:OD1	1:B:370:ASP:N	2.47	0.46
1:C:183:GLU:HG2	1:C:205:PHE:CD1	2.51	0.46
1:D:305:TYR:HB2	1:D:309:LYS:HZ3	1.79	0.46
1:C:162:PHE:CE2	1:C:215:LEU:HD21	2.50	0.46
1:A:171:HIS:H	1:A:174:ILE:HD12	1.82	0.45
1:B:428:ASN:OD1	1:B:428:ASN:O	2.35	0.45
1:D:185:MET:O	1:D:188:LEU:HB2	2.16	0.45
1:A:133:LEU:HD23	1:B:163:ASN:HD21	1.80	0.45
1:D:24:LYS:HD3	1:D:27:GLN:CD	2.42	0.45
1:D:332:SER:OG	1:D:352:GLU:OE2	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:414:LEU:HG	1:B:418:LEU:HD11	1.97	0.45
1:C:280:LEU:HD11	1:C:317:VAL:HG13	1.97	0.45
1:C:305:TYR:CE2	1:C:309:LYS:HD2	2.52	0.45
1:D:143:GLU:OE1	1:D:143:GLU:N	2.48	0.45
1:A:103:LEU:O	1:A:106:SER:OG	2.24	0.45
1:A:120:VAL:O	1:A:124:VAL:HG23	2.17	0.45
1:B:370:ASP:OD1	1:B:378:ARG:NH2	2.50	0.45
1:C:132:ARG:CA	1:D:161:ARG:HD3	2.46	0.45
1:C:436:THR:O	1:C:437:LEU:HB2	2.16	0.45
1:D:160:TYR:HD1	1:D:222:ASP:OD2	1.99	0.45
1:D:223:ARG:HH22	1:D:234:LEU:HB3	1.82	0.45
1:A:298:LEU:HD23	1:A:303:PRO:HG3	1.99	0.45
1:A:326:PRO:HD2	1:A:358:PRO:HB3	1.97	0.45
1:C:91:THR:HB	1:C:398:ARG:NH1	2.31	0.45
1:B:313:TYR:CD1	1:B:316:MET:HE2	2.52	0.45
1:C:166:TYR:CE2	1:D:129:LYS:HB2	2.51	0.45
1:C:203:ARG:HA	1:C:206:GLN:HE21	1.82	0.45
1:C:400:CYS:SG	2:C:500:MNH:C1C	3.00	0.45
1:A:104:LEU:HD13	1:A:401:ILE:HD12	1.97	0.45
1:D:244:GLU:OE1	1:D:244:GLU:N	2.49	0.45
1:A:102:ILE:CG2	1:A:242:ASP:HA	2.47	0.45
1:C:301:PRO:HG3	1:C:455:LEU:C	2.42	0.45
1:C:5:MET:HE3	1:C:39:ILE:HB	1.98	0.45
1:C:413:VAL:O	1:C:417:MET:HG3	2.16	0.45
1:A:147:ARG:HD3	1:A:165:PHE:HA	1.99	0.44
1:B:177:MET:HE1	1:B:266:HIS:CE1	2.52	0.44
1:B:234:LEU:HA	1:B:237:MET:HE2	1.98	0.44
1:C:132:ARG:NE	1:D:125:GLN:OE1	2.50	0.44
1:C:436:THR:C	1:C:438:THR:H	2.25	0.44
1:A:183:GLU:HB2	1:A:205:PHE:CE2	2.52	0.44
1:B:250:ASP:OD1	1:B:250:ASP:N	2.43	0.44
1:B:413:VAL:O	1:B:417:MET:HG3	2.18	0.44
1:D:20:LEU:HD22	1:D:25:PRO:HB2	2.00	0.44
1:A:108:SER:N	1:A:111:ALA:HB3	2.33	0.44
1:A:145:MET:HE1	1:A:417:MET:HE1	1.99	0.44
1:A:370:ASP:O	1:A:378:ARG:NH2	2.49	0.44
1:C:6:PRO:HB2	1:C:36:LEU:HB3	1.98	0.44
1:C:148:LEU:HD22	1:C:413:VAL:HG11	2.00	0.44
1:C:323:ARG:HA	1:C:361:HIS:ND1	2.32	0.44
1:D:16:ASN:HB2	1:D:19:LEU:HD11	1.99	0.44
1:D:27:GLN:O	1:D:31:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:406:ALA:HB2	2:D:500:MNH:HHC	2.00	0.44
1:A:222:ASP:OD2	1:B:135:ALA:HB3	2.16	0.44
1:B:50:ARG:NH2	1:B:351:ASP:OD2	2.50	0.44
1:B:179:ARG:NE	1:B:208:ASP:OD1	2.49	0.44
1:B:285:HIS:CE1	1:B:289:LYS:HE3	2.52	0.44
1:C:272:LEU:HD13	1:C:322:LEU:HG	2.00	0.44
1:C:288:GLN:HG2	1:C:289:LYS:N	2.32	0.44
1:D:223:ARG:NH2	1:D:234:LEU:HB3	2.33	0.44
1:A:320:GLU:HG3	1:A:374:PHE:CD1	2.53	0.44
1:C:312:LYS:HA	1:C:312:LYS:HD3	1.71	0.44
1:C:336:LYS:O	1:C:349:LYS:HG3	2.18	0.44
1:D:282:LYS:NZ	1:D:425:ASP:OD2	2.29	0.44
1:C:102:ILE:CD1	1:C:249:LEU:CD1	2.96	0.44
1:C:166:TYR:HA	1:D:166:TYR:HA	2.00	0.44
1:C:229:GLN:HA	1:C:229:GLN:OE1	2.18	0.44
1:D:357:ILE:HG21	1:D:392:PRO:HA	1.99	0.44
1:A:195:ASP:OD1	1:A:196:PRO:HD2	2.17	0.44
1:C:69:LYS:HD3	1:C:398:ARG:CZ	2.47	0.44
1:A:119:MET:HE2	1:A:405:PHE:HE1	1.80	0.43
1:C:161:ARG:HD3	1:D:132:ARG:HB3	2.00	0.43
1:A:278:TYR:OH	1:A:431:LEU:HB2	2.18	0.43
1:B:69:LYS:NZ	2:B:500:MNH:O1A	2.38	0.43
1:B:406:ALA:HB2	2:B:500:MNH:HHC	2.00	0.43
1:A:297:VAL:HG12	1:A:298:LEU:HD12	2.00	0.43
1:B:242:ASP:HB3	1:B:245:THR:OG1	2.19	0.43
1:B:336:LYS:HE3	1:B:336:LYS:HB2	1.88	0.43
1:B:426:HIS:CD2	1:B:427:THR:HG23	2.53	0.43
1:C:132:ARG:HA	1:D:161:ARG:CD	2.48	0.43
1:D:8:PRO:HB2	1:D:19:LEU:CD1	2.47	0.43
1:D:243:PRO:HG2	1:D:244:GLU:OE1	2.18	0.43
1:A:118:MET:HE3	1:A:156:CYS:HA	1.99	0.43
1:A:130:TRP:CD2	1:A:139:ILE:HD13	2.54	0.43
1:A:195:ASP:OD1	1:C:350:GLY:HA3	2.19	0.43
1:A:308:VAL:HG11	1:A:408:HIS:ND1	2.32	0.43
1:A:323:ARG:O	1:A:361:HIS:ND1	2.47	0.43
1:A:358:PRO:O	1:A:362:ARG:NH1	2.49	0.43
1:D:39:ILE:HD11	1:D:57:LEU:HB3	2.00	0.43
1:A:201:ASN:HB3	1:A:205:PHE:CE2	2.52	0.43
1:A:353:LEU:HD12	1:A:353:LEU:O	2.19	0.43
1:A:390:PHE:CZ	1:A:392:PRO:HG3	2.52	0.43
1:B:115:TYR:HD1	1:B:156:CYS:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:MET:HE1	1:B:273:LEU:HD22	2.01	0.43
1:B:356:LEU:HD22	1:B:359:GLN:H	1.82	0.43
1:C:224:LYS:NZ	1:C:238:LEU:HD13	2.33	0.43
1:D:55:GLN:CB	1:D:366:ILE:HD11	2.49	0.43
1:D:203:ARG:HG3	1:D:204:GLN:N	2.34	0.43
1:A:283:ASN:O	1:A:286:VAL:HG22	2.18	0.43
1:A:324:LEU:HD23	1:A:324:LEU:HA	1.74	0.43
1:B:14:LEU:O	1:B:45:PRO:HD3	2.19	0.43
1:B:272:LEU:N	1:B:327:THR:HG21	2.34	0.43
1:D:22:THR:HG21	1:D:28:ALA:HB2	1.99	0.43
1:A:50:ARG:HD2	1:A:352:GLU:O	2.19	0.43
1:A:233:LEU:HB3	1:A:237:MET:HE3	2.00	0.43
1:A:426:HIS:CD2	1:A:447:LYS:HG3	2.54	0.43
1:B:112:MET:HA	1:B:115:TYR:HD2	1.84	0.43
1:D:55:GLN:CD	1:D:389:ALA:HA	2.44	0.43
1:D:265:GLY:HA2	2:D:500:MNH:C2C	2.49	0.43
1:A:86:LEU:HD22	1:A:86:LEU:H	1.83	0.43
1:A:265:GLY:HA2	2:A:500:MNH:HMC1	2.01	0.43
1:B:8:PRO:HG2	1:B:16:ASN:ND2	2.34	0.43
1:B:26:VAL:O	1:B:30:MET:HG3	2.18	0.43
1:B:298:LEU:HD23	1:B:303:PRO:HB3	2.00	0.43
1:C:38:GLU:O	1:C:53:SER:N	2.51	0.43
1:D:173:PHE:HB2	1:D:215:LEU:HD22	1.99	0.43
1:B:347:LEU:HD21	1:B:353:LEU:HD11	2.01	0.42
1:C:215:LEU:O	1:C:219:ILE:HG13	2.19	0.42
1:D:120:VAL:HG12	1:D:412:LEU:HD21	2.01	0.42
1:D:122:ILE:HD12	1:D:151:ASP:HB3	2.01	0.42
1:D:196:PRO:HB3	1:D:199:ASP:OD2	2.19	0.42
1:D:413:VAL:O	1:D:417:MET:HG3	2.19	0.42
1:B:143:GLU:OE1	1:B:143:GLU:N	2.46	0.42
1:B:346:PRO:C	1:B:347:LEU:HD12	2.44	0.42
1:D:141:VAL:HB	1:D:142:PRO:HD3	2.01	0.42
1:D:145:MET:HE3	1:D:273:LEU:HB3	1.99	0.42
1:D:400:CYS:HB2	2:D:500:MNH:NA	2.33	0.42
1:A:21:ASN:HA	1:A:189:GLN:CD	2.44	0.42
1:A:280:LEU:HD21	1:A:317:VAL:HG11	2.01	0.42
1:D:38:GLU:OE1	1:D:38:GLU:N	2.51	0.42
1:A:149:THR:O	1:A:153:ILE:HG22	2.20	0.42
1:A:277:LEU:HD11	1:A:423:PHE:CE2	2.54	0.42
1:B:102:ILE:HD12	1:B:249:LEU:HD13	2.02	0.42
1:C:160:TYR:CE1	1:D:134:ASN:ND2	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:TYR:HB2	1:D:201:ASN:ND2	2.35	0.42
1:A:116:HIS:HB3	1:A:305:TYR:CD2	2.53	0.42
1:A:252:GLU:O	1:A:255:ARG:HG2	2.19	0.42
1:B:70:ASN:HB2	1:B:334:TYR:HD1	1.84	0.42
1:C:277:LEU:O	1:C:278:TYR:C	2.62	0.42
1:D:203:ARG:HG3	1:D:204:GLN:H	1.85	0.42
1:D:362:ARG:NH2	1:D:372:GLU:OE2	2.52	0.42
1:A:370:ASP:HB2	1:A:373:GLU:HG3	2.02	0.42
1:C:293:GLU:OE1	1:C:311:LEU:HB2	2.19	0.42
1:C:326:PRO:HD2	1:C:358:PRO:HG3	2.01	0.42
1:D:52:LEU:HD21	1:D:353:LEU:HD11	2.00	0.42
1:D:357:ILE:HD13	1:D:392:PRO:HA	2.02	0.42
1:A:126:LEU:HD22	1:A:148:LEU:HD13	2.02	0.42
1:B:289:LYS:HB2	1:B:313:TYR:CZ	2.55	0.42
1:B:308:VAL:HG21	1:B:412:LEU:HD12	2.02	0.42
1:C:72:SER:HB2	1:C:75:LEU:HD13	2.02	0.42
1:D:68:ASP:HB3	1:D:334:TYR:CE2	2.54	0.42
1:D:247:GLU:HG2	1:D:248:PRO:CD	2.48	0.42
1:D:278:TYR:CZ	1:D:431:LEU:HD13	2.54	0.42
1:A:111:ALA:HB1	1:A:115:TYR:CE2	2.54	0.42
1:B:280:LEU:HD22	1:B:287:LEU:HA	2.02	0.42
1:C:102:ILE:HD12	1:C:249:LEU:HD11	2.00	0.42
1:C:14:LEU:HG	1:C:18:PRO:HD3	2.02	0.42
1:C:133:LEU:HD23	1:D:163:ASN:HD21	1.85	0.42
1:C:316:MET:SD	1:C:316:MET:N	2.93	0.42
1:C:423:PHE:CD2	1:C:448:ALA:HB2	2.55	0.42
1:A:173:PHE:CD1	1:A:215:LEU:HD23	2.54	0.42
1:A:314:VAL:HG12	1:A:411:THR:HG22	2.02	0.42
1:B:44:ALA:HB3	1:B:47:ARG:HG3	2.02	0.42
1:C:51:TYR:HB3	1:C:356:LEU:HD11	2.02	0.42
1:C:247:GLU:HA	1:C:248:PRO:HD3	1.65	0.42
1:D:61:ALA:HA	1:D:67:PHE:CD2	2.55	0.42
1:D:272:LEU:HD22	2:D:500:MNH:HBB2	2.01	0.42
1:A:148:LEU:HD21	1:A:413:VAL:HG21	2.01	0.41
1:B:324:LEU:HD23	1:B:324:LEU:HA	1.77	0.41
1:C:120:VAL:O	1:C:121:ASP:C	2.62	0.41
1:C:183:GLU:O	1:C:187:LYS:HG3	2.19	0.41
1:C:253:ASN:O	1:C:257:GLN:HG2	2.20	0.41
1:D:8:PRO:HG3	1:D:36:LEU:HD11	2.02	0.41
1:D:20:LEU:HD23	1:D:20:LEU:HA	1.84	0.41
1:D:363:ASP:OD1	1:D:364:LYS:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:VAL:HG11	1:A:408:HIS:HD1	1.85	0.41
1:A:318:LEU:HD12	1:A:411:THR:HG23	2.02	0.41
1:C:58:ILE:HD13	1:C:360:LEU:HD22	2.02	0.41
1:C:60:GLU:HB3	1:C:66:ARG:NH1	2.36	0.41
1:C:387:GLN:O	1:C:391:LYS:HE2	2.20	0.41
1:D:74:ALA:O	1:D:78:VAL:HG23	2.19	0.41
1:D:281:VAL:CG1	1:D:425:ASP:HB2	2.50	0.41
1:C:398:ARG:HD2	1:C:398:ARG:HA	1.72	0.41
1:D:272:LEU:CD2	2:D:500:MNH:HBB2	2.49	0.41
1:A:166:TYR:HA	1:B:166:TYR:HA	2.02	0.41
1:A:186:ASN:O	1:A:189:GLN:HG2	2.21	0.41
1:D:5:MET:HG2	1:D:41:LYS:HE3	2.03	0.41
1:D:14:LEU:HG	1:D:17:LEU:HB3	2.03	0.41
1:D:366:ILE:HD13	1:D:389:ALA:HB1	2.02	0.41
1:A:24:LYS:HE3	1:C:250:ASP:CB	2.45	0.41
1:B:52:LEU:HG	1:B:58:ILE:CG1	2.51	0.41
1:C:55:GLN:O	1:C:59:LYS:HG2	2.20	0.41
1:C:234:LEU:O	1:C:238:LEU:HG	2.20	0.41
1:C:375:ARG:HD3	1:C:378:ARG:NH2	2.35	0.41
1:D:237:MET:HE1	1:D:258:ILE:HG12	2.01	0.41
1:A:104:LEU:N	1:A:105:PRO:HD2	2.34	0.41
1:C:132:ARG:HA	1:D:161:ARG:HD3	2.02	0.41
1:C:272:LEU:N	1:C:327:THR:HG21	2.34	0.41
1:C:299:VAL:HG23	1:C:300:ASP:OD1	2.21	0.41
1:A:268:THR:HB	2:A:500:MNH:CBB	2.50	0.41
1:B:79:ARG:HG3	1:B:88:THR:HB	2.03	0.41
1:B:304:SER:HB3	1:B:307:GLN:HG3	2.02	0.41
1:C:9:LYS:HD3	1:C:9:LYS:HA	1.90	0.41
1:D:16:ASN:HB2	1:D:19:LEU:CD1	2.51	0.41
1:D:38:GLU:HB3	1:D:57:LEU:HD12	2.03	0.41
1:B:141:VAL:HB	1:B:142:PRO:HD3	2.03	0.41
1:C:136:ASP:OD1	1:C:136:ASP:N	2.49	0.41
1:C:150:LEU:HD22	1:C:174:ILE:HD11	2.02	0.41
1:C:275:PHE:CE2	1:C:441:PRO:HD3	2.56	0.41
1:B:7:GLN:HG3	1:B:41:LYS:O	2.20	0.41
1:A:416:MET:HE3	1:A:416:MET:HB2	1.84	0.40
1:D:286:VAL:HG11	1:D:376:PRO:HG2	2.03	0.40
1:B:223:ARG:NH1	1:B:235:THR:OG1	2.55	0.40
1:D:10:THR:HG23	1:D:15:LYS:O	2.19	0.40
1:D:68:ASP:O	1:D:334:TYR:N	2.40	0.40
1:D:104:LEU:HA	1:D:401:ILE:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:356:LEU:HD12	1:D:358:PRO:HD2	2.02	0.40
1:A:69:LYS:CE	2:A:500:MNH:CGA	2.94	0.40
1:A:149:THR:HB	1:A:266:HIS:HA	2.02	0.40
1:A:324:LEU:O	1:A:362:ARG:NH2	2.55	0.40
1:B:118:MET:SD	1:B:156:CYS:HA	2.62	0.40
1:C:218:LYS:HA	1:C:218:LYS:HD3	1.83	0.40
1:A:81:PHE:O	1:A:259:ILE:HG21	2.21	0.40
1:A:375:ARG:HG3	1:A:378:ARG:HG3	2.03	0.40
1:A:422:ASP:O	1:A:448:ALA:HA	2.21	0.40
1:B:204:GLN:O	1:B:207:GLU:HB3	2.22	0.40
1:B:280:LEU:HB3	1:B:287:LEU:HD13	2.04	0.40
1:B:313:TYR:O	1:B:317:VAL:HG23	2.22	0.40
1:A:237:MET:HB3	1:A:254:ILE:HG23	2.03	0.40
1:A:357:ILE:HG22	1:A:361:HIS:CE1	2.57	0.40
1:B:20:LEU:HD22	1:B:25:PRO:HB2	2.04	0.40
1:C:162:PHE:CZ	1:C:262:LEU:CD2	2.94	0.40
1:C:249:LEU:CD2	1:C:253:ASN:OD1	2.67	0.40
1:D:55:GLN:HG2	1:D:366:ILE:HD11	2.04	0.40
1:D:394:GLY:HA3	1:D:399:ALA:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	450/455 (99%)	436 (97%)	14 (3%)	0	100	100
1	B	447/455 (98%)	439 (98%)	8 (2%)	0	100	100
1	C	450/455 (99%)	423 (94%)	27 (6%)	0	100	100
1	D	449/455 (99%)	421 (94%)	28 (6%)	0	100	100
All	All	1796/1820 (99%)	1719 (96%)	77 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	396/399 (99%)	396 (100%)	0	100	100
1	B	393/399 (98%)	393 (100%)	0	100	100
1	C	396/399 (99%)	396 (100%)	0	100	100
1	D	395/399 (99%)	395 (100%)	0	100	100
All	All	1580/1596 (99%)	1580 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	101	ASN
1	A	201	ASN
1	D	201	ASN
1	D	285	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 ⓘ

There are no oligosaccharides 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	MNH	C	500	1	46,50,50	2.44	21 (45%)	59,82,82	2.20	12 (20%)
2	MNH	B	500	1	46,50,50	2.50	22 (47%)	59,82,82	2.29	9 (15%)
2	MNH	A	500	1	46,50,50	2.47	22 (47%)	59,82,82	2.25	9 (15%)
2	MNH	D	500	1	46,50,50	2.46	21 (45%)	59,82,82	2.21	8 (13%)

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	MNH	C	500	1	-	4/14/94/94	-
2	MNH	B	500	1	-	5/14/94/94	-
2	MNH	A	500	1	-	2/14/94/94	-
2	MNH	D	500	1	-	2/14/94/94	-

All (86) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	MNH	CHA-C1A	4.79	1.47	1.38
2	B	500	MNH	CHA-C1A	4.78	1.47	1.38
2	C	500	MNH	CHA-C1A	4.73	1.47	1.38
2	A	500	MNH	CHB-C4A	4.67	1.47	1.38
2	C	500	MNH	CHB-C4A	4.59	1.47	1.38
2	B	500	MNH	CHB-C4A	4.58	1.47	1.38
2	D	500	MNH	CHC-C4B	4.58	1.47	1.38
2	B	500	MNH	CHC-C4B	4.52	1.47	1.38
2	D	500	MNH	CHA-C1A	4.51	1.47	1.38
2	C	500	MNH	CHC-C4B	4.46	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	MNH	CHD-C1D	4.42	1.47	1.38
2	A	500	MNH	CHD-C1D	4.42	1.47	1.38
2	D	500	MNH	CHB-C4A	4.42	1.47	1.38
2	D	500	MNH	CHD-C1D	4.35	1.47	1.38
2	A	500	MNH	CHC-C4B	4.33	1.47	1.38
2	C	500	MNH	CHD-C1D	4.33	1.47	1.38
2	A	500	MNH	CHB-C1B	3.95	1.48	1.39
2	C	500	MNH	CHB-C1B	3.93	1.48	1.39
2	D	500	MNH	CHB-C1B	3.87	1.48	1.39
2	D	500	MNH	CHC-C1C	3.84	1.48	1.39
2	D	500	MNH	C1B-C2B	-3.82	1.37	1.44
2	B	500	MNH	CHB-C1B	3.81	1.47	1.39
2	A	500	MNH	CHA-C4D	3.81	1.47	1.39
2	B	500	MNH	C1B-C2B	-3.78	1.37	1.44
2	C	500	MNH	C1B-C2B	-3.78	1.37	1.44
2	B	500	MNH	CHD-C4C	3.75	1.47	1.39
2	B	500	MNH	CHA-C4D	3.73	1.47	1.39
2	B	500	MNH	CHC-C1C	3.73	1.47	1.39
2	C	500	MNH	CHA-C4D	3.71	1.47	1.39
2	B	500	MNH	C4A-NA	-3.63	1.32	1.39
2	C	500	MNH	CHC-C1C	3.62	1.47	1.39
2	C	500	MNH	CHD-C4C	3.61	1.47	1.39
2	A	500	MNH	C1B-C2B	-3.58	1.37	1.44
2	D	500	MNH	CHD-C4C	3.58	1.47	1.39
2	A	500	MNH	CHD-C4C	3.57	1.47	1.39
2	D	500	MNH	CHA-C4D	3.54	1.47	1.39
2	A	500	MNH	CHC-C1C	3.53	1.47	1.39
2	A	500	MNH	O2A-CGA	3.49	1.33	1.22
2	D	500	MNH	O2A-CGA	3.47	1.33	1.22
2	A	500	MNH	C4A-NA	-3.47	1.33	1.39
2	D	500	MNH	O1D-CGD	3.46	1.33	1.22
2	D	500	MNH	C4D-C3D	-3.46	1.39	1.45
2	B	500	MNH	O2A-CGA	3.46	1.33	1.22
2	C	500	MNH	O2A-CGA	3.46	1.33	1.22
2	A	500	MNH	O1D-CGD	3.45	1.33	1.22
2	B	500	MNH	O1D-CGD	3.43	1.33	1.22
2	C	500	MNH	O1D-CGD	3.39	1.33	1.22
2	D	500	MNH	C1A-C2A	-3.38	1.39	1.45
2	B	500	MNH	C4D-C3D	-3.30	1.39	1.45
2	D	500	MNH	C4A-NA	-3.28	1.33	1.39
2	C	500	MNH	C4A-NA	-3.24	1.33	1.39
2	C	500	MNH	C1A-C2A	-3.21	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	MNH	C4A-C3A	-3.19	1.39	1.45
2	A	500	MNH	C4D-C3D	-3.15	1.39	1.45
2	C	500	MNH	C4D-C3D	-3.14	1.39	1.45
2	A	500	MNH	C4A-C3A	-3.11	1.39	1.45
2	B	500	MNH	C1A-C2A	-3.07	1.39	1.45
2	D	500	MNH	C4A-C3A	-3.05	1.39	1.45
2	A	500	MNH	C1A-C2A	-3.03	1.39	1.45
2	A	500	MNH	C1D-C2D	-3.03	1.38	1.44
2	B	500	MNH	C1A-NA	-3.01	1.33	1.39
2	A	500	MNH	C1A-NA	-2.95	1.33	1.39
2	D	500	MNH	C1A-NA	-2.91	1.33	1.39
2	A	500	MNH	C1C-NC	-2.91	1.33	1.39
2	B	500	MNH	C1D-C2D	-2.90	1.39	1.44
2	D	500	MNH	C4C-NC	-2.87	1.34	1.39
2	B	500	MNH	C1C-NC	-2.86	1.34	1.39
2	B	500	MNH	C4C-NC	-2.86	1.34	1.39
2	C	500	MNH	C4C-NC	-2.86	1.34	1.39
2	C	500	MNH	C4A-C3A	-2.84	1.39	1.45
2	D	500	MNH	C1D-C2D	-2.81	1.39	1.44
2	C	500	MNH	C1A-NA	-2.79	1.34	1.39
2	C	500	MNH	C1D-C2D	-2.78	1.39	1.44
2	C	500	MNH	C1C-NC	-2.78	1.34	1.39
2	A	500	MNH	C4C-NC	-2.75	1.34	1.39
2	D	500	MNH	C1C-NC	-2.70	1.34	1.39
2	C	500	MNH	O1A-CGA	-2.48	1.22	1.30
2	A	500	MNH	O2D-CGD	-2.47	1.22	1.30
2	B	500	MNH	O1A-CGA	-2.47	1.22	1.30
2	D	500	MNH	O1A-CGA	-2.43	1.22	1.30
2	B	500	MNH	O2D-CGD	-2.42	1.22	1.30
2	D	500	MNH	O2D-CGD	-2.42	1.22	1.30
2	C	500	MNH	O2D-CGD	-2.41	1.22	1.30
2	A	500	MNH	O1A-CGA	-2.35	1.22	1.30
2	B	500	MNH	C2A-C3A	2.04	1.41	1.36
2	A	500	MNH	C3B-C4B	-2.01	1.40	1.44

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	MNH	CHB-C1B-NB	-9.27	116.61	124.47
2	B	500	MNH	CHB-C1B-NB	-8.77	117.04	124.47
2	C	500	MNH	CHB-C1B-NB	-8.29	117.45	124.47
2	B	500	MNH	C3B-C2B-C1B	-7.98	100.56	106.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	MNH	C2B-C1B-NB	7.91	118.91	109.88
2	D	500	MNH	C3B-C2B-C1B	-7.86	100.66	106.49
2	A	500	MNH	C3B-C2B-C1B	-7.84	100.67	106.49
2	B	500	MNH	C2B-C1B-NB	7.84	118.83	109.88
2	C	500	MNH	C3B-C2B-C1B	-7.72	100.76	106.49
2	D	500	MNH	CHB-C1B-NB	-7.66	117.98	124.47
2	C	500	MNH	C2B-C1B-NB	7.56	118.50	109.88
2	A	500	MNH	C2B-C1B-NB	7.48	118.42	109.88
2	D	500	MNH	CHA-C4D-ND	3.87	127.75	124.47
2	B	500	MNH	CHA-C4D-ND	3.54	127.47	124.47
2	C	500	MNH	CHA-C4D-ND	3.28	127.25	124.47
2	A	500	MNH	CHD-C1D-ND	3.24	127.42	124.43
2	A	500	MNH	CHA-C4D-ND	2.98	127.00	124.47
2	B	500	MNH	CHD-C1D-ND	2.96	127.17	124.43
2	D	500	MNH	CHD-C1D-ND	2.85	127.06	124.43
2	B	500	MNH	CAA-C2A-C3A	2.78	133.06	127.88
2	C	500	MNH	CHD-C1D-ND	2.74	126.96	124.43
2	A	500	MNH	CAD-CBD-CGD	-2.66	107.88	113.60
2	B	500	MNH	CHB-C4A-NA	2.64	127.22	124.40
2	D	500	MNH	CHB-C4A-NA	2.62	127.20	124.40
2	D	500	MNH	CHA-C1A-NA	2.59	127.17	124.40
2	A	500	MNH	CHB-C4A-NA	2.35	126.91	124.40
2	A	500	MNH	CHC-C4B-NB	2.35	126.60	124.43
2	C	500	MNH	CHC-C4B-NB	2.34	126.59	124.43
2	C	500	MNH	CHB-C4A-NA	2.30	126.85	124.40
2	B	500	MNH	CMB-C2B-C1B	2.27	128.50	125.04
2	C	500	MNH	CHA-C1A-NA	2.26	126.82	124.40
2	C	500	MNH	O2D-CGD-CBD	2.23	121.18	114.03
2	C	500	MNH	CMB-C2B-C1B	2.22	128.41	125.04
2	B	500	MNH	CMA-C3A-C2A	2.14	131.94	126.12
2	A	500	MNH	CMB-C2B-C1B	2.14	128.30	125.04
2	C	500	MNH	CBA-CAA-C2A	-2.12	106.73	112.63
2	C	500	MNH	CBD-CAD-C3D	-2.04	106.96	112.63
2	D	500	MNH	CBA-CAA-C2A	-2.01	107.05	112.63

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	500	MNH	C1A-C2A-CAA-CBA
2	B	500	MNH	C3A-C2A-CAA-CBA
2	C	500	MNH	C2C-C3C-CAC-CBC

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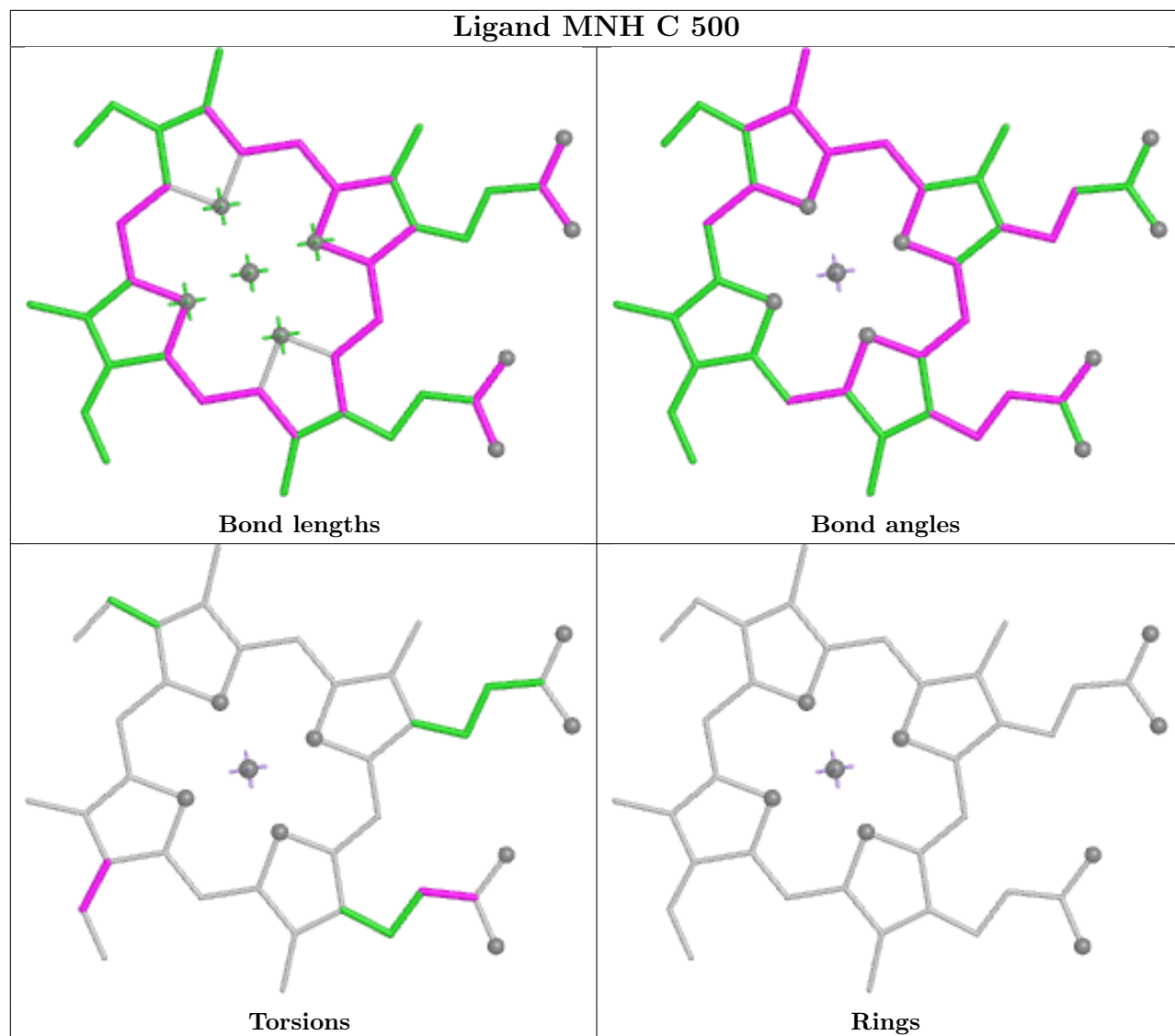
Mol	Chain	Res	Type	Atoms
2	C	500	MNH	C4C-C3C-CAC-CBC
2	B	500	MNH	CAA-CBA-CGA-O1A
2	B	500	MNH	CAA-CBA-CGA-O2A
2	A	500	MNH	CAD-CBD-CGD-O1D
2	D	500	MNH	CAD-CBD-CGD-O2D
2	A	500	MNH	CAD-CBD-CGD-O2D
2	D	500	MNH	CAD-CBD-CGD-O1D
2	B	500	MNH	C3D-CAD-CBD-CGD
2	C	500	MNH	CAD-CBD-CGD-O1D
2	C	500	MNH	CAD-CBD-CGD-O2D

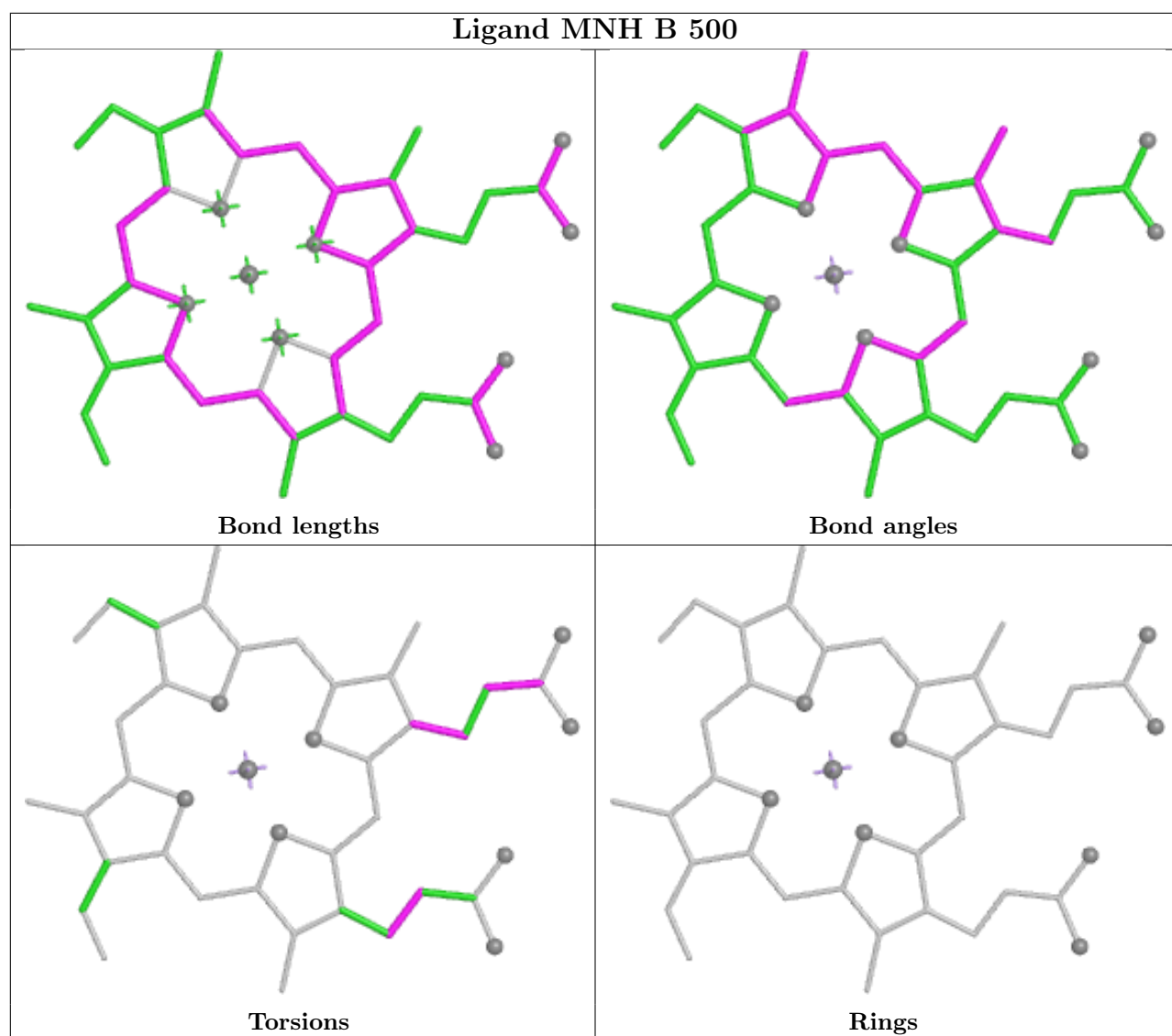
There are no ring outliers.

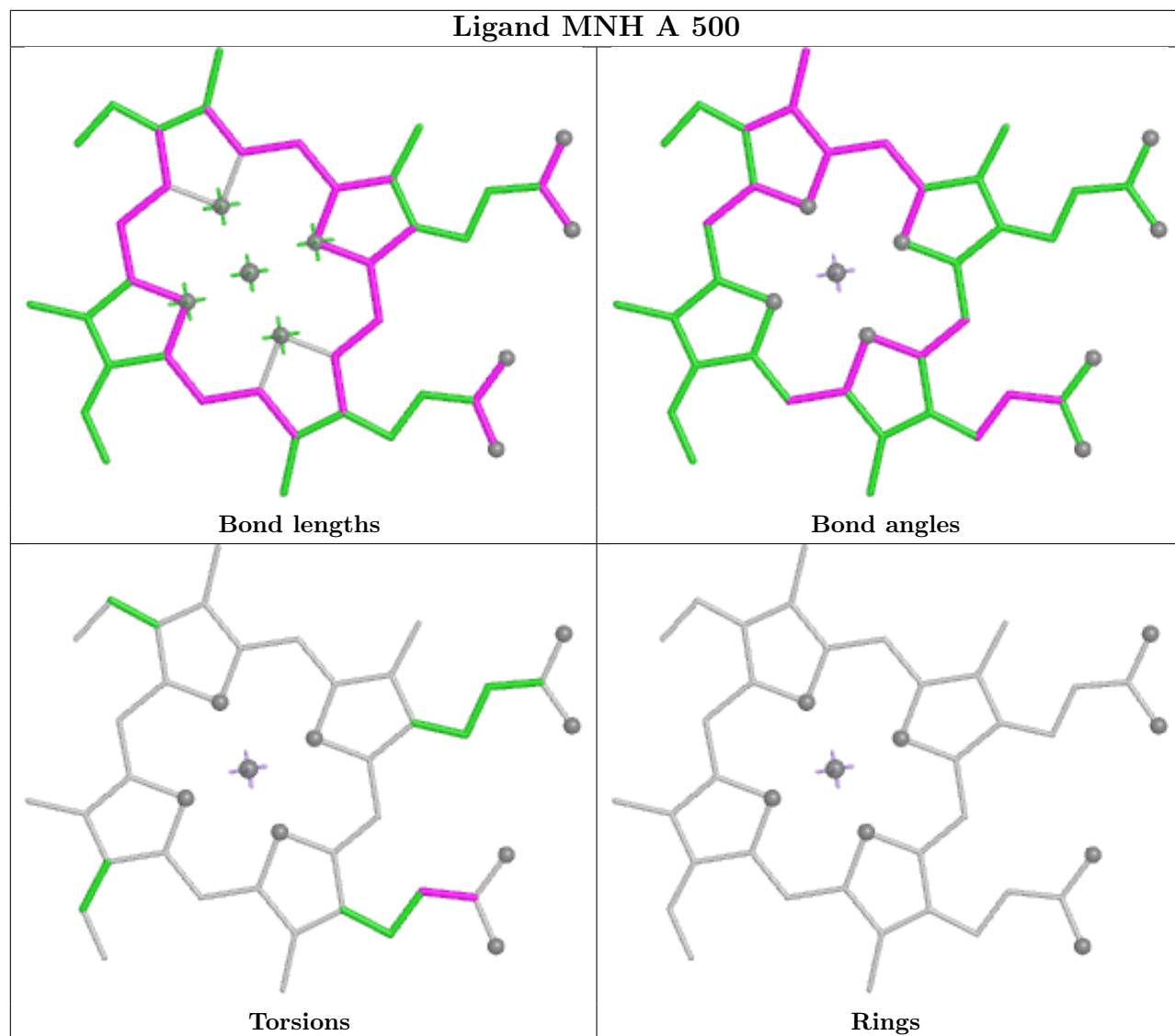
4 monomers are involved in 22 short contacts:

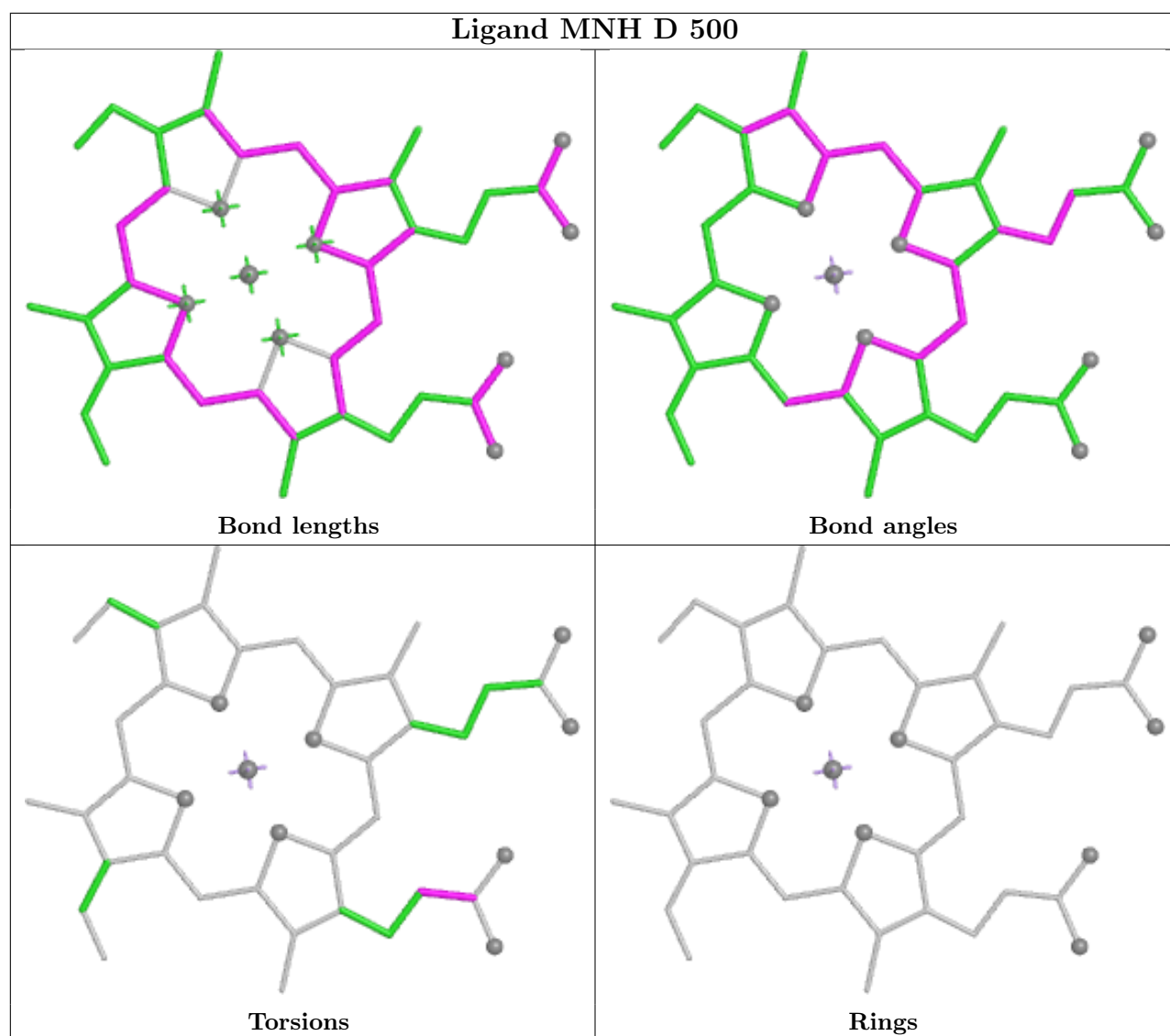
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	500	MNH	1	0
2	B	500	MNH	6	0
2	A	500	MNH	9	0
2	D	500	MNH	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	452/455 (99%)	0.99	37 (8%)	17	16	8, 39, 80, 117	0
1	B	449/455 (98%)	0.75	17 (3%)	44	31	8, 38, 74, 115	0
1	C	452/455 (99%)	0.90	42 (9%)	14	14	7, 40, 86, 145	0
1	D	451/455 (99%)	1.00	41 (9%)	15	14	6, 43, 86, 121	0
All	All	1804/1820 (99%)	0.91	137 (7%)	20	17	6, 40, 83, 145	0

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	ALA	4.6
1	A	64	GLU	4.4
1	C	323	ARG	4.4
1	A	248	PRO	4.3
1	C	344	GLU	4.0
1	C	294	ALA	3.9
1	D	19	LEU	3.8
1	D	110	GLN	3.7
1	C	324	LEU	3.6
1	D	379	PHE	3.5
1	B	343	GLY	3.5
1	D	198	TYR	3.4
1	C	52	LEU	3.4
1	C	295	ALA	3.4
1	A	239	ASN	3.4
1	C	423	PHE	3.4
1	A	189	GLN	3.3
1	D	86	LEU	3.2
1	A	191	ALA	3.2
1	B	295	ALA	3.2
1	A	257	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	316	MET	3.1
1	A	193	PRO	3.0
1	B	290	ALA	3.0
1	A	54	SER	3.0
1	B	297	VAL	3.0
1	A	20	LEU	2.9
1	D	343	GLY	2.9
1	A	297	VAL	2.9
1	C	313	TYR	2.9
1	D	324	LEU	2.9
1	A	250	ASP	2.7
1	C	35	GLU	2.7
1	D	308	VAL	2.7
1	A	229	GLN	2.6
1	D	200	GLU	2.6
1	D	20	LEU	2.6
1	D	120	VAL	2.6
1	D	297	VAL	2.6
1	D	321	ALA	2.6
1	D	351	ASP	2.6
1	B	286	VAL	2.6
1	A	198	TYR	2.6
1	A	21	ASN	2.6
1	C	298	LEU	2.6
1	A	128	GLN	2.6
1	C	291	ALA	2.6
1	C	274	SER	2.5
1	C	60	GLU	2.5
1	D	388	HIS	2.5
1	A	448	ALA	2.5
1	D	293	GLU	2.5
1	C	428	ASN	2.5
1	D	385	ILE	2.5
1	B	367	TRP	2.5
1	D	411	THR	2.5
1	A	103	LEU	2.5
1	B	285	HIS	2.5
1	B	165	PHE	2.4
1	D	222	ASP	2.4
1	C	61	ALA	2.4
1	A	194	ASP	2.4
1	C	305	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	67	PHE	2.4
1	D	292	GLU	2.4
1	C	322	LEU	2.4
1	D	341	LEU	2.4
1	D	305	TYR	2.4
1	D	197	ALA	2.4
1	D	332	SER	2.4
1	D	426	HIS	2.4
1	B	353	LEU	2.4
1	A	253	ASN	2.3
1	D	199	ASP	2.3
1	D	155	LEU	2.3
1	D	228	GLU	2.3
1	C	371	VAL	2.3
1	A	265	GLY	2.3
1	C	244	GLU	2.3
1	D	8	PRO	2.3
1	C	164	SER	2.3
1	D	367	TRP	2.3
1	C	308	VAL	2.3
1	B	378	ARG	2.3
1	C	450	SER	2.3
1	C	129	LYS	2.3
1	D	196	PRO	2.2
1	A	86	LEU	2.2
1	C	447	LYS	2.2
1	C	319	ASN	2.2
1	C	369	ASP	2.2
1	A	157	GLY	2.2
1	C	301	PRO	2.2
1	C	333	LEU	2.2
1	A	238	LEU	2.2
1	A	249	LEU	2.2
1	B	346	PRO	2.2
1	C	418	LEU	2.2
1	D	366	ILE	2.2
1	B	228	GLU	2.2
1	A	18	PRO	2.2
1	C	358	PRO	2.2
1	D	91	THR	2.2
1	C	401	ILE	2.2
1	C	335	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	284	PRO	2.2
1	A	68	ASP	2.2
1	A	84	ASP	2.2
1	A	310	GLN	2.1
1	C	287	LEU	2.1
1	D	89	SER	2.1
1	C	374	PHE	2.1
1	C	299	VAL	2.1
1	C	361	HIS	2.1
1	C	122	ILE	2.1
1	D	215	LEU	2.1
1	B	377	GLU	2.1
1	C	92	HIS	2.1
1	C	317	VAL	2.1
1	A	100	HIS	2.1
1	D	298	LEU	2.1
1	A	190	ARG	2.1
1	B	385	ILE	2.1
1	D	365	THR	2.1
1	A	165	PHE	2.1
1	A	178	VAL	2.0
1	B	52	LEU	2.0
1	D	249	LEU	2.0
1	A	182	ASP	2.0
1	D	85	GLY	2.0
1	D	342	GLY	2.0
1	D	248	PRO	2.0
1	A	207	GLU	2.0
1	A	453	ILE	2.0
1	C	134	ASN	2.0
1	B	166	TYR	2.0
1	C	141	VAL	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](#)

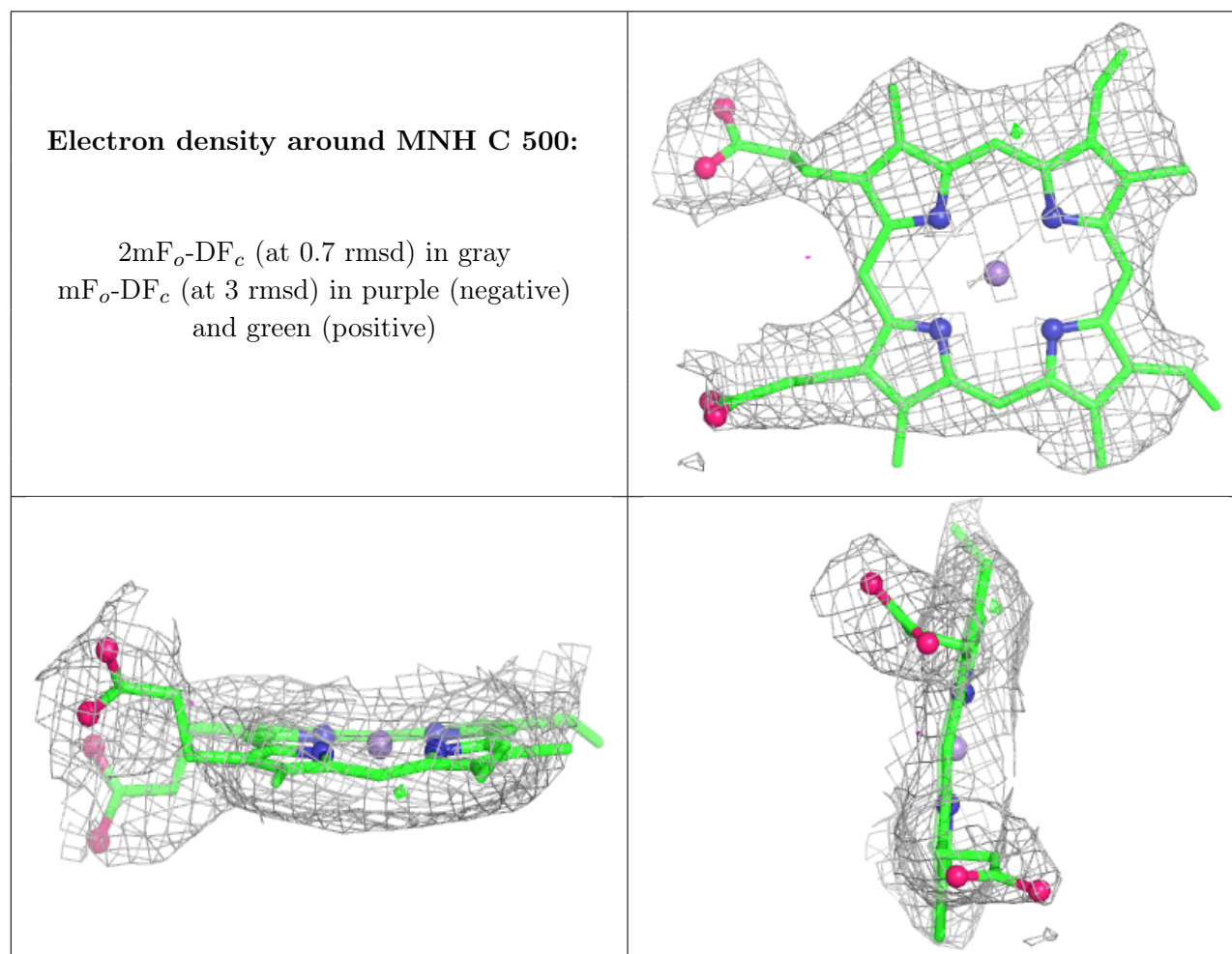
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

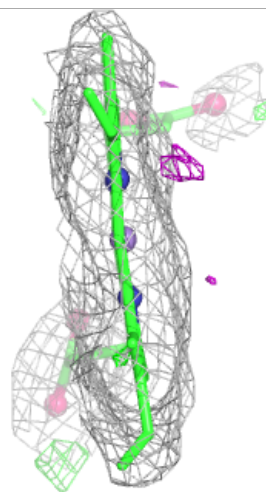
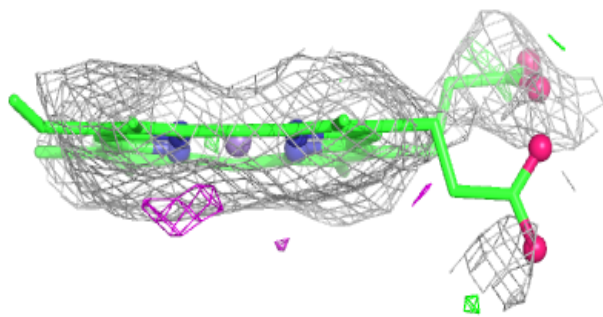
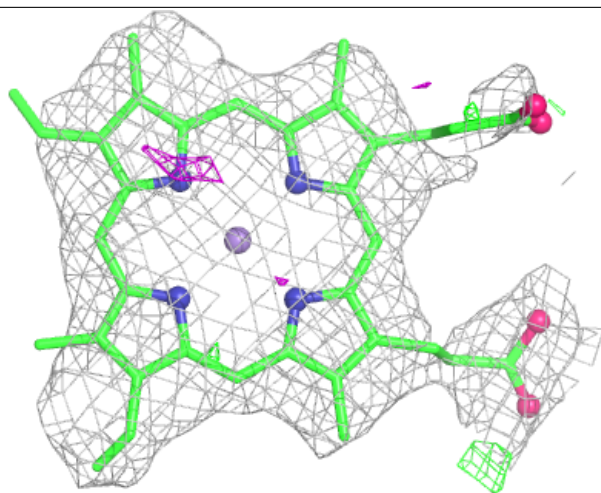
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MNH	C	500	43/43	0.89	0.14	7,18,35,41	0
2	MNH	D	500	43/43	0.89	0.16	11,19,41,59	0
2	MNH	A	500	43/43	0.90	0.13	7,19,36,58	0
2	MNH	B	500	43/43	0.90	0.14	10,18,25,32	0

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.



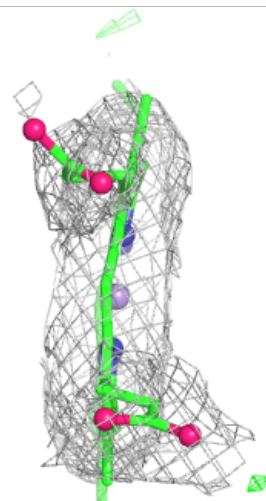
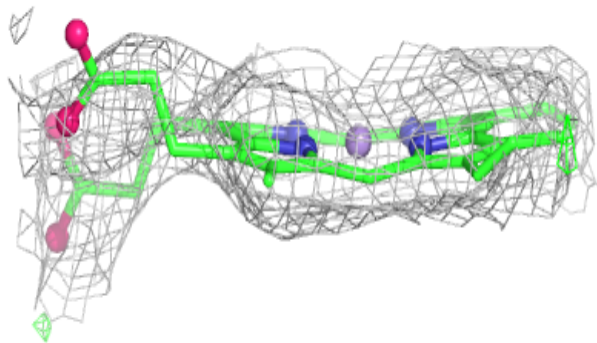
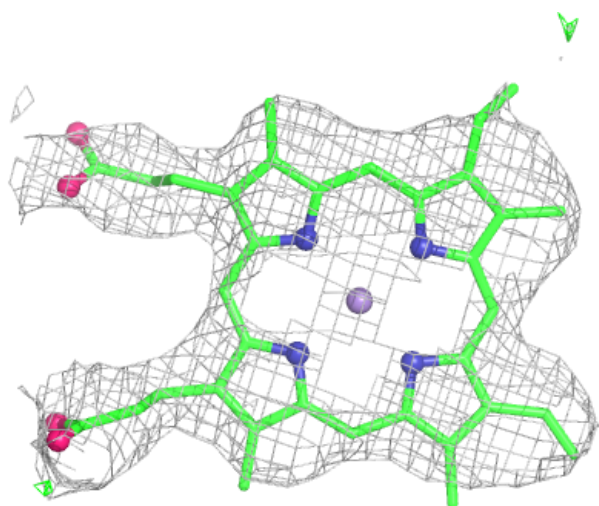
Electron density around MNH D 500:

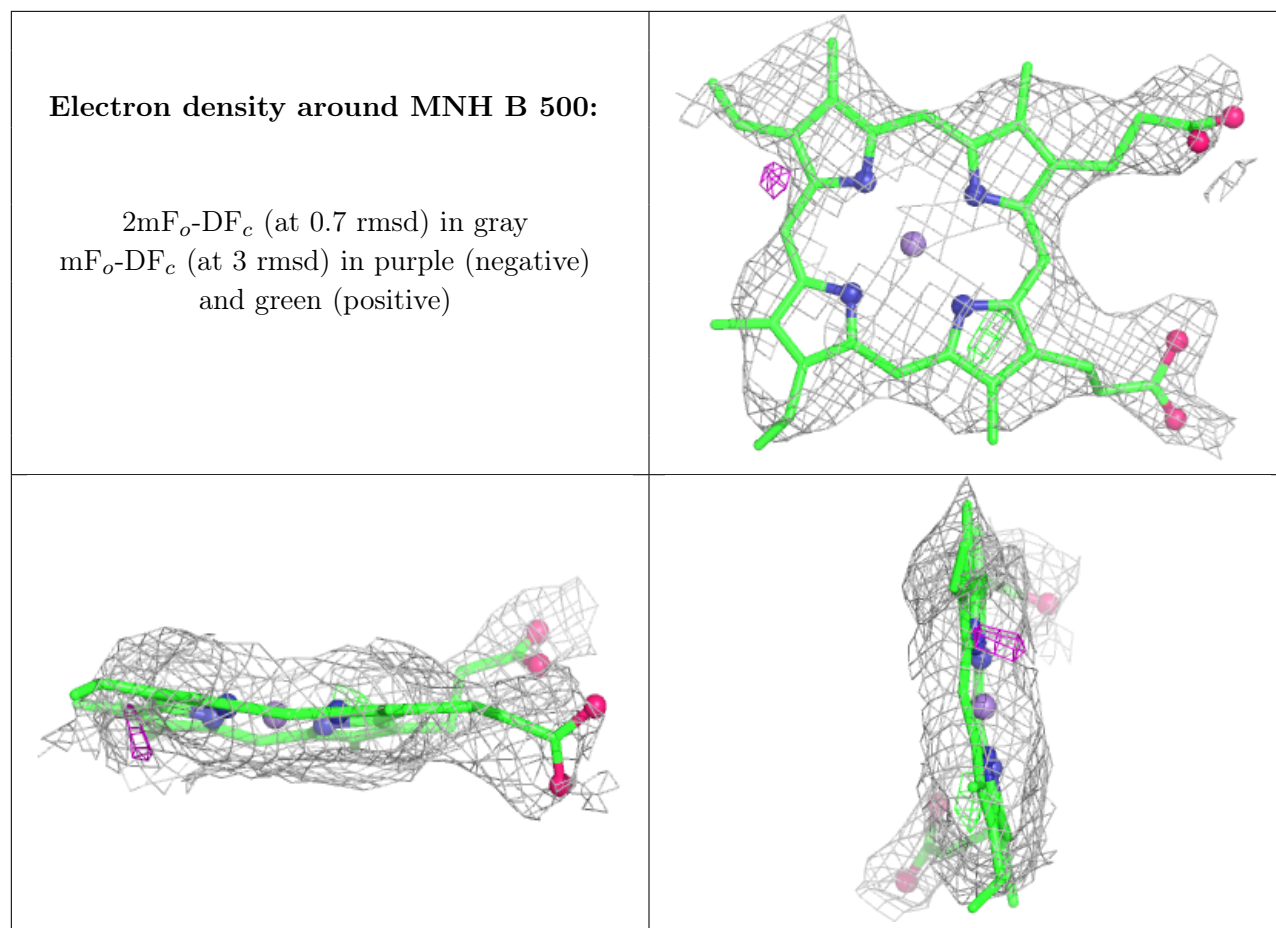
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MNH A 500:

$2mF_o-DF_c$ (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.