



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 07:38 AM EDT

PDB ID : 3AYF / pdb_00003ayf
Title : Crystal structure of nitric oxide reductase
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Deposited on : 2011-05-06
Resolution : 2.50 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	:	2022.3.0, CSD as543be (2022)
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

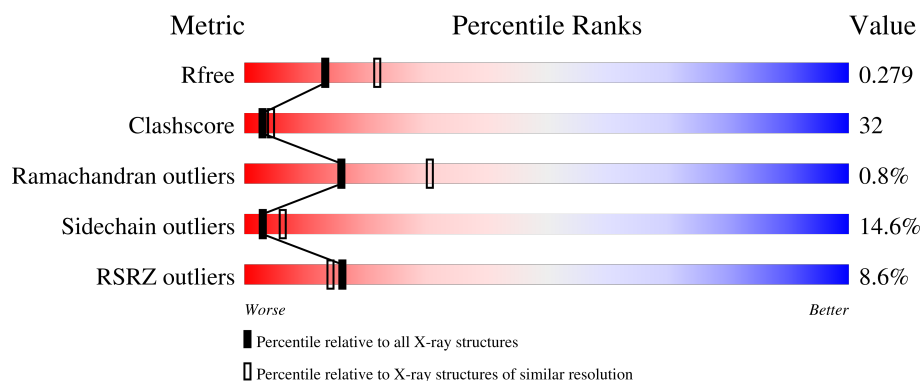
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	800	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	LOP	A	810	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6455 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.

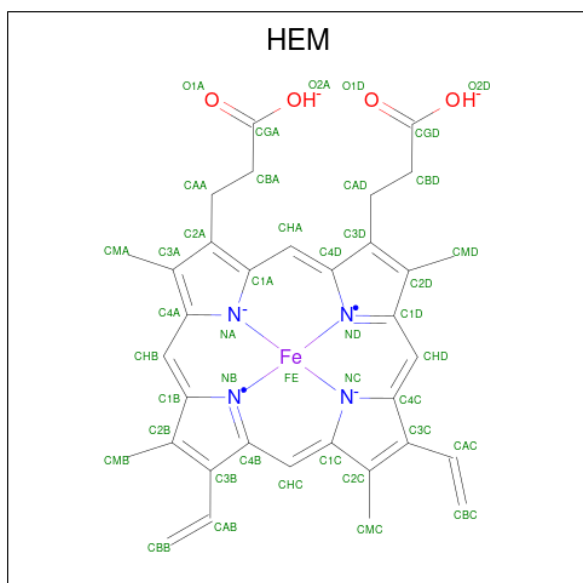
- Molecule 1 is a protein called Nitric oxide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	754	6078	4055	966	1034	23	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	793	LEU	-	expression tag	UNP B3Y963
A	794	GLU	-	expression tag	UNP B3Y963
A	795	HIS	-	expression tag	UNP B3Y963
A	796	HIS	-	expression tag	UNP B3Y963
A	797	HIS	-	expression tag	UNP B3Y963
A	798	HIS	-	expression tag	UNP B3Y963
A	799	HIS	-	expression tag	UNP B3Y963
A	800	HIS	-	expression tag	UNP B3Y963

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



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

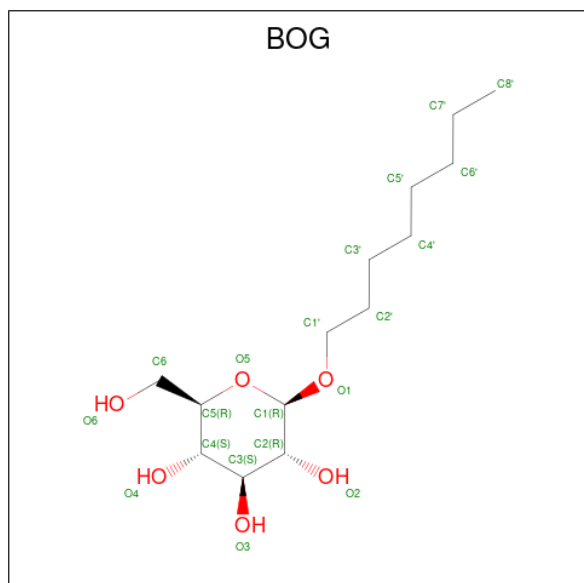
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn		
			1	1	0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

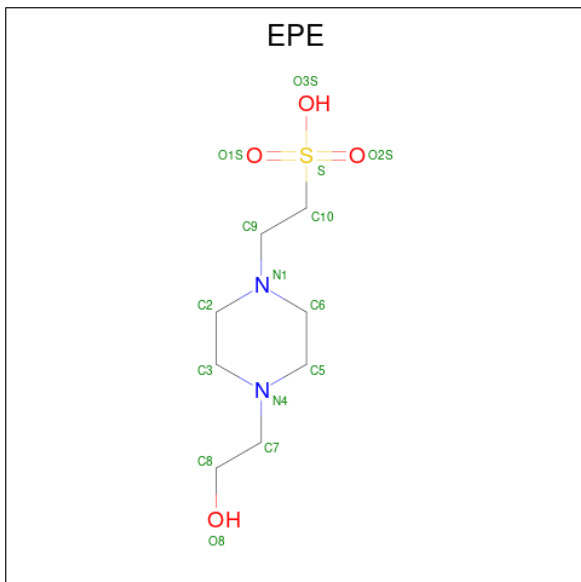
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca		
			1	1	0	0

- Molecule 5 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: C₁₄H₂₈O₆).



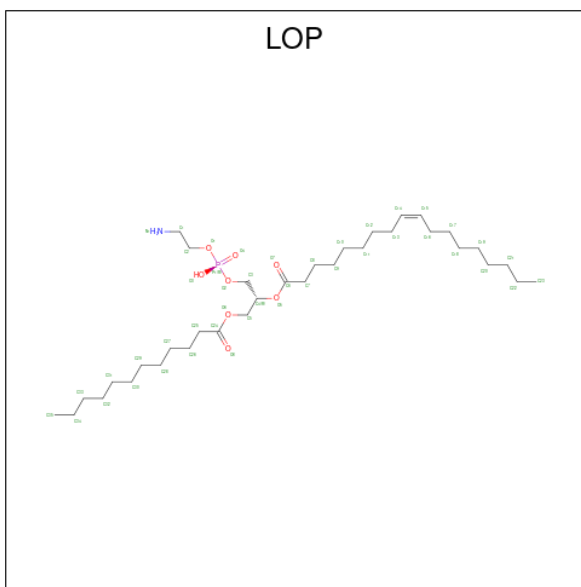
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O		
			20	14	6	0	0
5	A	1	Total	C	O		
			20	14	6	0	0
5	A	1	Total	C	O		
			20	14	6	0	0

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 7 is (1R)-2-{[(R)-(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(DODECANOYLOXY)METHYL]ETHYL (9Z)-OCTADEC-9-ENOATE (CCD ID: LOP) (formula: $C_{35}H_{68}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			45	35	1	8	1		
7	A	1	Total	C	N	O	P	0	0
			45	35	1	8	1		

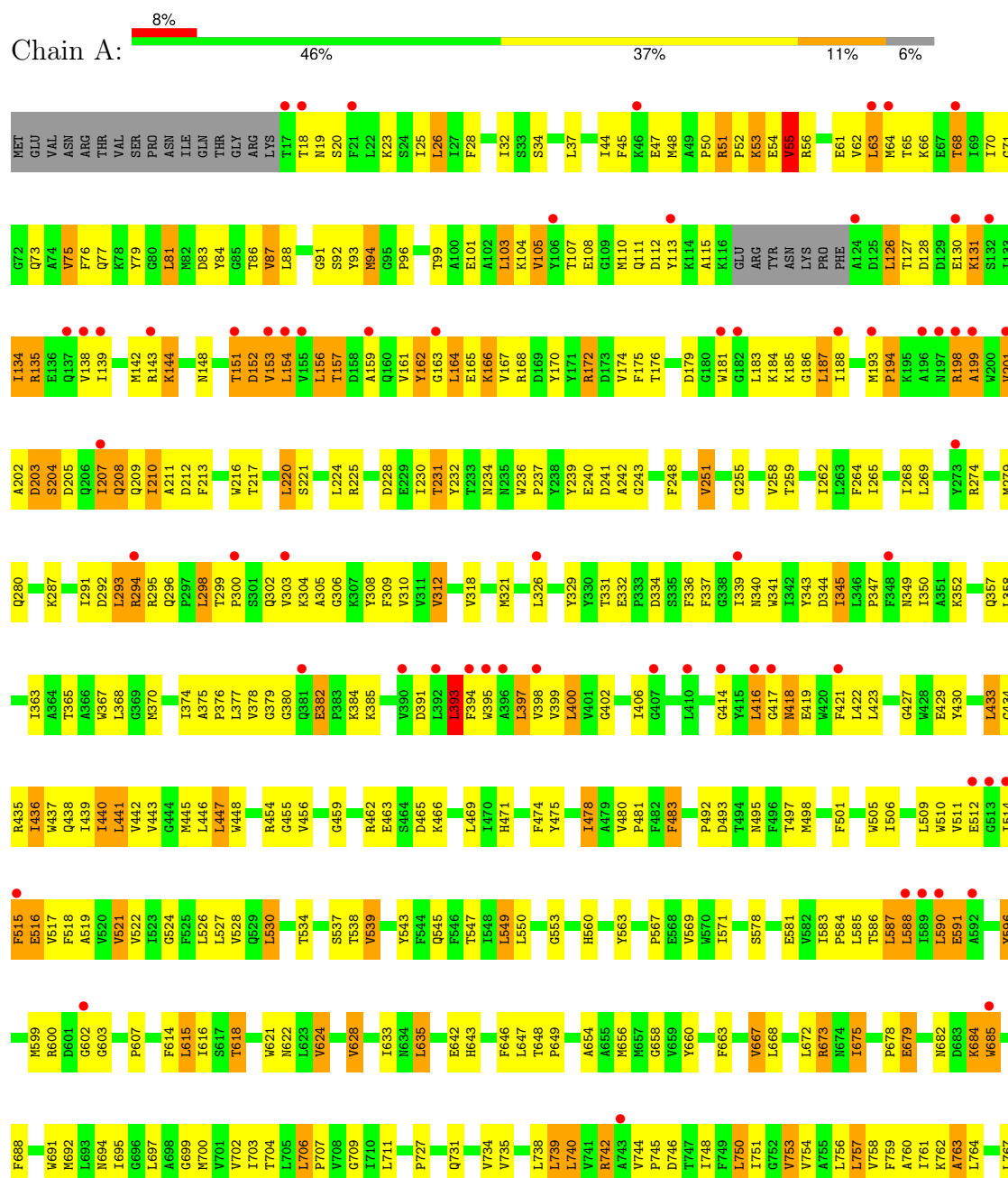
- Molecule 8 is water.

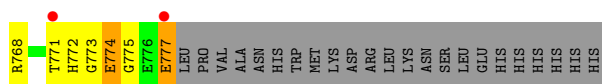
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	124	Total	O	0	0
			124	124		

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: Nitric oxide reductase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	110.41Å 149.65Å 151.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.78 – 2.50 19.78 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.78-2.50) 98.8 (19.78-2.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 2.51Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.244 , 0.282 0.241 , 0.279	Depositor DCC
R_{free} test set	2127 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6455	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, ZN, LOP, EPE, HEM, BOG

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	0.51	0/6262	1.02	31/8517 (0.4%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	332	GLU	CA-C-N	10.63	130.29	119.24
1	A	332	GLU	C-N-CA	10.63	130.29	119.24
1	A	18	THR	N-CA-C	10.19	123.45	111.02
1	A	208	GLN	N-CA-C	-9.61	102.06	113.88
1	A	172	ARG	N-CA-C	-7.51	103.03	111.14
1	A	763	ALA	N-CA-C	-7.50	105.03	114.56
1	A	624	VAL	N-CA-C	7.07	117.67	110.82
1	A	587	LEU	N-CA-C	-6.92	103.80	113.20
1	A	591	GLU	N-CA-C	-6.76	104.05	112.90
1	A	20	SER	N-CA-C	6.59	119.02	111.11
1	A	515	PHE	N-CA-C	6.51	121.36	113.41
1	A	684	LYS	N-CA-C	-6.51	103.81	111.03
1	A	538	THR	N-CA-C	6.42	117.94	111.07
1	A	702	VAL	N-CA-C	6.39	117.18	110.72
1	A	55	VAL	N-CA-C	-6.38	99.30	108.48
1	A	231	THR	N-CA-C	6.07	118.36	110.53
1	A	602	GLY	N-CA-C	-6.06	100.40	110.95
1	A	553	GLY	N-CA-C	5.99	121.40	113.37
1	A	642	GLU	N-CA-C	5.94	117.83	111.36
1	A	368	LEU	N-CA-C	-5.93	104.89	111.36
1	A	596	TYR	N-CA-C	-5.79	104.87	111.07
1	A	563	TYR	N-CA-C	5.76	120.13	112.30
1	A	675	ILE	N-CA-C	5.32	116.21	111.90
1	A	203	ASP	N-CA-C	-5.29	100.46	108.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	459	GLY	N-CA-C	-5.20	106.20	112.49
1	A	560	HIS	N-CA-C	-5.15	107.00	113.28
1	A	418	ASN	N-CA-C	-5.10	107.08	113.15
1	A	94	MET	N-CA-C	-5.04	105.69	111.14
1	A	162	TYR	N-CA-C	-5.01	105.81	111.28
1	A	393	LEU	N-CA-C	-5.01	105.82	111.28
1	A	87	VAL	N-CA-C	-5.00	101.42	108.27

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6078	0	6095	391	0
2	A	86	0	60	3	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	60	0	84	4	0
6	A	15	0	18	0	0
7	A	90	0	134	33	0
8	A	124	0	0	9	0
All	All	6455	0	6391	407	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 32.

All (407) 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:198:ARG:HG3	1:A:198:ARG:HH11	0.97	1.12
1:A:172:ARG:HG3	1:A:207:ILE:HD11	1.33	1.04
1:A:293:LEU:HD23	1:A:293:LEU:H	1.28	0.99
1:A:465:ASP:HA	7:A:809:LOP:H11	1.47	0.97
1:A:126:LEU:H	1:A:126:LEU:HD22	1.33	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ARG:HB3	1:A:62:VAL:HA	1.49	0.93
1:A:198:ARG:HG3	1:A:198:ARG:NH1	1.72	0.90
1:A:56:ARG:HA	1:A:63:LEU:HD22	1.54	0.88
1:A:585:LEU:HA	1:A:588:LEU:HD22	1.55	0.87
1:A:198:ARG:HH12	1:A:203:ASP:HA	1.41	0.85
1:A:75:VAL:CG2	1:A:210:ILE:HG12	2.07	0.85
1:A:742:ARG:HD2	1:A:746:ASP:OD2	1.77	0.85
7:A:810:LOP:H112	7:A:810:LOP:H272	1.59	0.84
1:A:441:LEU:HD22	1:A:445:MET:HE2	1.59	0.84
1:A:172:ARG:HA	1:A:207:ILE:HD12	1.61	0.82
1:A:422:LEU:O	1:A:436:ILE:HG23	1.81	0.81
1:A:543:TYR:O	1:A:547:THR:HG23	1.81	0.81
1:A:293:LEU:H	1:A:293:LEU:CD2	1.94	0.81
1:A:341:TRP:O	1:A:345:ILE:HG22	1.81	0.80
7:A:810:LOP:H132	7:A:810:LOP:H292	1.64	0.79
1:A:624:VAL:HA	1:A:628:VAL:HG13	1.65	0.78
1:A:255:GLY:O	1:A:259:THR:HG23	1.84	0.78
1:A:198:ARG:HH11	1:A:198:ARG:CG	1.87	0.77
1:A:55:VAL:HG13	1:A:64:MET:HB3	1.67	0.77
1:A:104:LYS:O	1:A:108:GLU:HG2	1.85	0.76
7:A:810:LOP:H91	7:A:810:LOP:O7	1.82	0.76
1:A:300:PRO:HD2	1:A:382:GLU:HG3	1.69	0.75
1:A:318:VAL:HG23	1:A:358:LEU:HD13	1.69	0.74
1:A:614:PHE:O	1:A:618:THR:HG22	1.88	0.74
1:A:164:LEU:O	1:A:168:ARG:HG3	1.88	0.73
1:A:126:LEU:HB3	1:A:130:GLU:HG2	1.71	0.73
1:A:517:VAL:O	1:A:521:VAL:HG12	1.89	0.73
1:A:175:PHE:HD1	1:A:187:LEU:HD11	1.52	0.72
1:A:104:LYS:HE2	1:A:108:GLU:OE2	1.90	0.72
1:A:585:LEU:O	1:A:588:LEU:HB2	1.90	0.71
1:A:599:MET:HE1	7:A:810:LOP:C7	2.21	0.70
1:A:735:VAL:HG12	1:A:739:LEU:HD22	1.72	0.70
1:A:64:MET:HE2	1:A:212:ASP:CG	2.16	0.70
1:A:624:VAL:HG11	7:A:810:LOP:H211	1.73	0.70
1:A:44:ILE:HG12	1:A:567:PRO:HD2	1.72	0.70
1:A:168:ARG:HD3	1:A:208:GLN:NE2	2.06	0.70
1:A:210:ILE:HG22	1:A:211:ALA:N	2.07	0.69
1:A:138:VAL:HG22	1:A:142:MET:HE2	1.73	0.69
7:A:810:LOP:H112	7:A:810:LOP:H251	1.73	0.69
7:A:810:LOP:C6	7:A:810:LOP:O6	2.40	0.69
1:A:51:ARG:HD2	1:A:495:ASN:ND2	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:THR:HB	1:A:382:GLU:HG2	1.74	0.69
1:A:466:LYS:HB2	7:A:809:LOP:O3	1.92	0.69
1:A:302:GLN:HE22	1:A:377:LEU:HD13	1.58	0.68
1:A:380:GLY:O	1:A:777:GLU:HG2	1.92	0.68
1:A:188:ILE:HG21	1:A:207:ILE:HG22	1.74	0.68
1:A:199:ALA:HB2	1:A:418:ASN:HB3	1.75	0.68
1:A:207:ILE:HG23	8:A:905:HOH:O	1.94	0.68
1:A:198:ARG:NH1	1:A:203:ASP:HA	2.07	0.67
1:A:216:TRP:O	1:A:220:LEU:HD13	1.94	0.67
1:A:194:PRO:O	1:A:198:ARG:HD3	1.94	0.67
1:A:599:MET:HE1	7:A:810:LOP:H71	1.77	0.67
1:A:375:ALA:HB3	1:A:376:PRO:HD3	1.76	0.66
1:A:110:MET:HG2	1:A:159:ALA:O	1.94	0.66
1:A:363:ILE:HG22	1:A:515:PHE:CE1	2.30	0.66
1:A:321:MET:HE2	1:A:750:LEU:HD21	1.77	0.66
1:A:334:ASP:HA	1:A:343:TYR:CD2	2.30	0.65
1:A:168:ARG:HD3	1:A:208:GLN:HE21	1.61	0.65
1:A:363:ILE:HG22	1:A:515:PHE:CZ	2.31	0.65
1:A:75:VAL:HG22	1:A:210:ILE:HG12	1.79	0.65
1:A:217:THR:HA	1:A:220:LEU:CD1	2.27	0.65
1:A:225:ARG:HE	1:A:232:TYR:HA	1.62	0.65
1:A:93:TYR:HE2	1:A:649:PRO:HG3	1.61	0.64
1:A:64:MET:HE2	1:A:212:ASP:CB	2.28	0.64
1:A:157:THR:O	1:A:161:VAL:HG23	1.97	0.64
1:A:135:ARG:O	1:A:139:ILE:HG12	1.97	0.64
1:A:621:TRP:CZ2	7:A:810:LOP:H192	2.33	0.64
1:A:648:THR:HB	1:A:649:PRO:HD3	1.80	0.63
7:A:809:LOP:O4	7:A:809:LOP:H12	1.97	0.63
1:A:646:PHE:C	1:A:649:PRO:HD2	2.23	0.63
1:A:65:THR:HG23	1:A:68:THR:H	1.63	0.63
1:A:393:LEU:HD22	1:A:397:LEU:HD21	1.80	0.63
1:A:293:LEU:HD23	1:A:293:LEU:N	2.07	0.63
1:A:331:THR:HG21	1:A:740:LEU:HD13	1.80	0.62
1:A:400:LEU:HB2	1:A:440:ILE:HD11	1.81	0.62
1:A:217:THR:HA	1:A:220:LEU:HD11	1.80	0.62
1:A:198:ARG:HH12	1:A:203:ASP:CA	2.12	0.62
1:A:302:GLN:NE2	1:A:377:LEU:HD13	2.15	0.62
1:A:347:PRO:HD2	1:A:350:ILE:HD12	1.81	0.62
1:A:436:ILE:O	1:A:440:ILE:HG23	2.00	0.61
1:A:771:THR:HG22	1:A:772:HIS:CD2	2.35	0.61
1:A:107:THR:O	1:A:111:GLN:HG3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:ARG:NE	1:A:232:TYR:HA	2.16	0.61
1:A:55:VAL:CG1	1:A:64:MET:HB3	2.31	0.61
1:A:274:ARG:O	1:A:274:ARG:HG3	2.00	0.61
7:A:809:LOP:O3	7:A:809:LOP:H4	2.00	0.61
1:A:588:LEU:HD23	1:A:622:ASN:HB3	1.81	0.61
1:A:607:PRO:O	1:A:673:ARG:HD2	2.01	0.61
1:A:298:LEU:CD1	1:A:303:VAL:HG13	2.31	0.61
1:A:581:GLU:O	1:A:584:PRO:HD2	2.00	0.61
7:A:810:LOP:H251	7:A:810:LOP:C11	2.31	0.61
1:A:480:VAL:HB	1:A:481:PRO:CD	2.31	0.60
1:A:569:VAL:HG23	5:A:807:BOG:H3'1	1.83	0.60
1:A:298:LEU:HD12	1:A:303:VAL:HG13	1.84	0.60
1:A:393:LEU:O	1:A:397:LEU:HD22	2.02	0.60
1:A:633:ILE:HD12	2:A:802:HEM:HBD2	1.82	0.60
1:A:309:PHE:HA	1:A:312:VAL:HG13	1.82	0.60
1:A:365:THR:HB	8:A:990:HOH:O	2.01	0.60
1:A:370:MET:HE2	1:A:526:LEU:HD21	1.83	0.60
1:A:516:GLU:HG2	1:A:549:LEU:HD21	1.83	0.60
1:A:34:SER:OG	7:A:809:LOP:H233	2.00	0.60
1:A:56:ARG:HB2	1:A:61:GLU:O	2.02	0.60
1:A:172:ARG:NH2	1:A:208:GLN:OE1	2.31	0.60
1:A:402:GLY:O	1:A:406:ILE:HG12	2.01	0.59
1:A:691:TRP:CE3	1:A:695:ILE:HD11	2.36	0.59
1:A:179:ASP:OD1	1:A:183:LEU:HB3	2.02	0.59
1:A:86:THR:HG23	1:A:92:SER:O	2.03	0.59
1:A:172:ARG:HG3	1:A:207:ILE:CD1	2.21	0.59
1:A:304:LYS:HG2	1:A:391:ASP:OD1	2.02	0.59
1:A:93:TYR:CE2	1:A:649:PRO:HG3	2.37	0.59
1:A:694:ASN:HB3	7:A:810:LOP:H312	1.84	0.58
1:A:113:TYR:HB2	1:A:162:TYR:CD2	2.38	0.58
1:A:164:LEU:O	1:A:164:LEU:HD22	2.02	0.58
1:A:599:MET:HE1	7:A:810:LOP:H72	1.86	0.58
1:A:101:GLU:O	1:A:105:VAL:HG23	2.04	0.57
1:A:692:MET:CE	1:A:748:ILE:HG23	2.34	0.57
1:A:151:THR:O	1:A:153:VAL:N	2.34	0.57
1:A:187:LEU:HD13	1:A:188:ILE:H	1.69	0.57
1:A:299:THR:HB	1:A:382:GLU:CG	2.33	0.57
1:A:704:THR:HG21	1:A:742:ARG:HG3	1.86	0.57
1:A:83:ASP:O	1:A:349:ASN:HA	2.04	0.57
1:A:692:MET:HE3	1:A:748:ILE:HG23	1.85	0.57
1:A:220:LEU:HD22	1:A:221:SER:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:GLU:O	1:A:430:TYR:HB2	2.04	0.57
1:A:291:ILE:CG2	1:A:607:PRO:HG3	2.35	0.57
1:A:148:ASN:O	1:A:151:THR:O	2.23	0.57
1:A:193:MET:HE3	1:A:198:ARG:HB3	1.87	0.56
1:A:421:PHE:CE1	1:A:492:PRO:HD3	2.40	0.56
1:A:156:LEU:H	1:A:156:LEU:HD23	1.71	0.56
1:A:198:ARG:NH1	1:A:202:ALA:O	2.38	0.56
1:A:395:TRP:HA	1:A:398:VAL:HG12	1.86	0.56
1:A:663:PHE:HB3	8:A:922:HOH:O	2.06	0.56
1:A:691:TRP:HE3	1:A:695:ILE:HD11	1.71	0.56
1:A:433:LEU:HD13	1:A:438:GLN:CG	2.35	0.56
1:A:675:ILE:CG2	1:A:767:LEU:HD22	2.36	0.56
1:A:94:MET:HE1	1:A:329:TYR:O	2.06	0.56
1:A:181:TRP:CG	1:A:727:PRO:HB3	2.41	0.55
1:A:511:VAL:O	1:A:515:PHE:CD2	2.58	0.55
1:A:139:ILE:HD13	1:A:142:MET:HE3	1.88	0.55
1:A:774:GLU:OE1	1:A:774:GLU:N	2.39	0.55
1:A:62:VAL:HG23	8:A:983:HOH:O	2.07	0.55
1:A:156:LEU:HD23	1:A:156:LEU:N	2.21	0.55
1:A:142:MET:CE	1:A:242:ALA:HA	2.37	0.55
1:A:299:THR:CB	1:A:382:GLU:HG2	2.37	0.55
1:A:395:TRP:HA	1:A:398:VAL:CG1	2.36	0.55
1:A:439:ILE:O	1:A:442:VAL:HG22	2.07	0.55
1:A:454:ARG:HG2	1:A:454:ARG:HH11	1.72	0.54
1:A:139:ILE:HD11	1:A:241:ASP:O	2.08	0.54
1:A:207:ILE:HG13	1:A:207:ILE:O	2.08	0.54
1:A:264:PHE:O	1:A:268:ILE:HG12	2.08	0.54
1:A:400:LEU:HG	1:A:440:ILE:CG1	2.38	0.54
1:A:688:PHE:O	1:A:692:MET:HG2	2.08	0.54
1:A:744:VAL:HB	1:A:745:PRO:CD	2.36	0.54
1:A:53:LYS:HE2	1:A:54:GLU:HG3	1.90	0.54
1:A:56:ARG:HB2	1:A:61:GLU:C	2.33	0.54
1:A:682:ASN:ND2	1:A:684:LYS:HB3	2.23	0.54
1:A:166:LYS:N	1:A:166:LYS:HE2	2.23	0.54
1:A:175:PHE:CE2	1:A:210:ILE:HG21	2.43	0.53
1:A:203:ASP:HB3	8:A:904:HOH:O	2.07	0.53
1:A:339:ILE:C	1:A:340:ASN:HD22	2.17	0.53
1:A:378:VAL:HG11	1:A:456:VAL:HG13	1.89	0.53
1:A:483:PHE:CZ	7:A:809:LOP:H222	2.43	0.53
1:A:682:ASN:HD21	1:A:684:LYS:HB3	1.73	0.53
1:A:539:VAL:HG22	8:A:984:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ILE:HG22	1:A:340:ASN:N	2.23	0.53
1:A:187:LEU:HD13	1:A:188:ILE:N	2.24	0.53
1:A:400:LEU:CG	1:A:440:ILE:HD11	2.39	0.53
1:A:685:TRP:CE3	1:A:685:TRP:HA	2.43	0.53
1:A:758:VAL:O	1:A:762:LYS:HG2	2.09	0.53
1:A:534:THR:OG1	1:A:537:SER:HB3	2.09	0.53
1:A:113:TYR:CD2	1:A:159:ALA:HA	2.44	0.53
1:A:400:LEU:HG	1:A:440:ILE:HD11	1.91	0.52
1:A:569:VAL:CG2	5:A:807:BOG:H3'1	2.39	0.52
1:A:131:LYS:O	1:A:131:LYS:HD3	2.10	0.52
1:A:760:ALA:O	1:A:763:ALA:HB3	2.09	0.52
1:A:110:MET:HE1	1:A:142:MET:HB3	1.91	0.52
1:A:586:THR:C	1:A:588:LEU:H	2.18	0.52
1:A:291:ILE:HG21	1:A:607:PRO:HG3	1.91	0.51
1:A:367:TRP:CZ3	1:A:667:VAL:HG21	2.45	0.51
1:A:378:VAL:HB	1:A:456:VAL:HG22	1.91	0.51
1:A:771:THR:HG22	1:A:772:HIS:HD2	1.74	0.51
1:A:203:ASP:O	1:A:204:SER:HB2	2.10	0.51
1:A:395:TRP:O	1:A:399:VAL:HG23	2.09	0.51
1:A:515:PHE:HB2	1:A:660:TYR:CE1	2.44	0.51
1:A:203:ASP:O	1:A:203:ASP:CG	2.52	0.51
1:A:172:ARG:HA	1:A:207:ILE:CD1	2.36	0.51
1:A:393:LEU:HD22	1:A:397:LEU:CD2	2.40	0.51
1:A:203:ASP:O	1:A:204:SER:CB	2.58	0.51
1:A:331:THR:CG2	1:A:740:LEU:HD13	2.41	0.51
1:A:434:GLY:O	1:A:437:TRP:HB2	2.11	0.51
1:A:480:VAL:HB	1:A:481:PRO:HD3	1.92	0.51
1:A:534:THR:OG1	1:A:537:SER:CB	2.59	0.51
1:A:55:VAL:HA	1:A:154:LEU:O	2.11	0.51
1:A:699:GLY:O	1:A:703:ILE:HB	2.10	0.51
1:A:76:PHE:HB2	1:A:210:ILE:HD11	1.93	0.51
1:A:201:VAL:CG2	1:A:209:GLN:HE22	2.24	0.50
1:A:19:ASN:O	1:A:23:LYS:HD2	2.11	0.50
1:A:65:THR:HG23	1:A:68:THR:N	2.25	0.50
1:A:382:GLU:HB2	1:A:773:GLY:O	2.11	0.50
1:A:583:ILE:HB	1:A:584:PRO:HD3	1.94	0.50
1:A:616:ILE:HD13	7:A:810:LOP:H82	1.93	0.50
1:A:52:PRO:HA	1:A:152:ASP:OD1	2.11	0.50
1:A:56:ARG:HA	1:A:63:LEU:CD2	2.35	0.50
1:A:110:MET:HE1	1:A:142:MET:CB	2.42	0.50
1:A:384:LYS:O	1:A:454:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:LYS:O	1:A:65:THR:HA	2.12	0.50
1:A:462:ARG:HG2	1:A:462:ARG:HH11	1.77	0.50
1:A:88:LEU:HA	1:A:236:TRP:HZ3	1.77	0.50
1:A:440:ILE:O	1:A:440:ILE:HD12	2.11	0.50
1:A:23:LYS:NZ	7:A:809:LOP:O4	2.37	0.50
1:A:25:ILE:HD13	5:A:806:BOG:H6'1	1.92	0.50
1:A:53:LYS:O	1:A:53:LYS:HD2	2.11	0.50
1:A:144:LYS:HZ2	1:A:144:LYS:HB3	1.77	0.50
1:A:188:ILE:CG2	1:A:207:ILE:HG22	2.40	0.50
1:A:209:GLN:O	1:A:212:ASP:HB2	2.12	0.50
1:A:217:THR:O	1:A:220:LEU:HD22	2.11	0.50
1:A:429:GLU:HG2	1:A:430:TYR:CD2	2.47	0.50
1:A:309:PHE:HB3	1:A:668:LEU:HG	1.93	0.49
1:A:518:PHE:O	1:A:522:VAL:HG23	2.12	0.49
1:A:395:TRP:C	1:A:398:VAL:HG12	2.37	0.49
1:A:55:VAL:HG22	1:A:64:MET:HB2	1.94	0.49
1:A:302:GLN:HE22	1:A:377:LEU:CD1	2.23	0.49
1:A:384:LYS:O	1:A:385:LYS:HB2	2.12	0.49
1:A:162:TYR:O	1:A:165:GLU:HB3	2.13	0.49
1:A:759:PHE:O	1:A:763:ALA:HB2	2.13	0.49
1:A:79:TYR:CE2	1:A:188:ILE:HG12	2.47	0.49
1:A:248:PHE:O	1:A:251:VAL:HG13	2.13	0.49
1:A:65:THR:H	1:A:68:THR:HG1	1.59	0.48
1:A:615:LEU:O	1:A:618:THR:HG23	2.13	0.48
1:A:440:ILE:HD12	1:A:440:ILE:C	2.38	0.48
1:A:56:ARG:CD	1:A:62:VAL:HG12	2.43	0.48
1:A:84:TYR:C	1:A:92:SER:HB2	2.37	0.48
1:A:163:GLY:O	1:A:167:VAL:HG23	2.12	0.48
1:A:240:GLU:HB2	8:A:918:HOH:O	2.13	0.48
1:A:475:TYR:CZ	7:A:809:LOP:H281	2.48	0.48
1:A:590:LEU:HD23	1:A:590:LEU:C	2.38	0.48
1:A:483:PHE:HZ	7:A:809:LOP:H222	1.78	0.48
1:A:55:VAL:HB	1:A:154:LEU:HD12	1.96	0.48
1:A:505:TRP:O	1:A:509:LEU:HB2	2.12	0.48
1:A:549:LEU:C	1:A:549:LEU:HD13	2.39	0.48
1:A:126:LEU:HD23	1:A:131:LYS:HG2	1.96	0.48
1:A:293:LEU:HA	1:A:296:GLN:CD	2.39	0.48
1:A:647:LEU:HG	1:A:709:GLY:HA3	1.94	0.48
1:A:184:LYS:NZ	1:A:344:ASP:O	2.46	0.47
1:A:293:LEU:HA	1:A:296:GLN:HG3	1.95	0.47
1:A:675:ILE:O	1:A:768:ARG:HD3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ALA:HB2	1:A:418:ASN:CB	2.44	0.47
1:A:265:ILE:O	1:A:269:LEU:HB2	2.14	0.47
1:A:305:ALA:O	1:A:308:TYR:HB2	2.14	0.47
1:A:751:ILE:O	1:A:754:VAL:HG22	2.15	0.47
1:A:675:ILE:HG22	1:A:767:LEU:HD22	1.97	0.47
1:A:26:LEU:HA	1:A:547:THR:HG22	1.97	0.47
1:A:280:GLN:N	1:A:537:SER:OG	2.46	0.47
1:A:515:PHE:CB	1:A:660:TYR:CE1	2.98	0.47
1:A:75:VAL:CG2	1:A:210:ILE:CG1	2.85	0.47
1:A:474:PHE:O	1:A:478:ILE:CG2	2.61	0.47
1:A:635:LEU:HB2	8:A:901:HOH:O	2.15	0.47
1:A:86:THR:HG22	1:A:91:GLY:C	2.40	0.47
1:A:139:ILE:CD1	1:A:241:ASP:O	2.63	0.47
1:A:599:MET:CE	7:A:810:LOP:H71	2.43	0.47
1:A:757:LEU:HD22	1:A:761:ILE:HG13	1.96	0.47
1:A:773:GLY:C	1:A:775:GLY:H	2.21	0.47
7:A:809:LOP:O7	7:A:809:LOP:O6	2.33	0.47
1:A:77:GLN:HB3	1:A:427:GLY:HA3	1.97	0.47
1:A:126:LEU:H	1:A:126:LEU:CD2	2.10	0.47
1:A:298:LEU:HB2	1:A:768:ARG:HH21	1.80	0.47
7:A:810:LOP:H181	7:A:810:LOP:C33	2.44	0.47
1:A:70:ILE:HG23	1:A:493:ASP:HA	1.97	0.46
1:A:379:GLY:HA3	1:A:455:GLY:O	2.16	0.46
1:A:445:MET:O	1:A:448:TRP:HB3	2.15	0.46
1:A:378:VAL:CB	1:A:456:VAL:HG22	2.46	0.46
1:A:400:LEU:CB	1:A:440:ILE:HD11	2.45	0.46
1:A:62:VAL:C	1:A:63:LEU:HD13	2.41	0.46
1:A:643:HIS:HA	2:A:802:HEM:O1D	2.16	0.46
1:A:73:GLN:HA	1:A:213:PHE:CD2	2.51	0.46
1:A:498:MET:O	1:A:501:PHE:HB3	2.16	0.46
1:A:70:ILE:HD13	1:A:493:ASP:HB2	1.98	0.46
1:A:510:TRP:CZ2	1:A:514:ILE:HD11	2.51	0.46
1:A:279:MET:HA	1:A:537:SER:OG	2.15	0.46
7:A:810:LOP:H181	7:A:810:LOP:H332	1.98	0.46
1:A:154:LEU:CD1	1:A:156:LEU:HD22	2.45	0.46
1:A:170:TYR:O	1:A:174:VAL:HG23	2.16	0.46
1:A:239:TYR:CZ	1:A:241:ASP:HB2	2.51	0.46
7:A:809:LOP:O6	7:A:809:LOP:C6	2.64	0.46
1:A:298:LEU:HD13	1:A:299:THR:H	1.80	0.46
1:A:292:ASP:OD2	1:A:295:ARG:HD2	2.17	0.45
1:A:321:MET:HE1	1:A:750:LEU:HD11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:GLY:C	1:A:419:GLU:H	2.23	0.45
1:A:54:GLU:HA	1:A:64:MET:O	2.16	0.45
1:A:675:ILE:C	1:A:768:ARG:HD3	2.42	0.45
1:A:217:THR:HA	1:A:220:LEU:HD13	1.96	0.45
1:A:463:GLU:OE2	1:A:471:HIS:HD2	1.99	0.45
1:A:225:ARG:HB2	1:A:228:ASP:CB	2.47	0.45
1:A:51:ARG:CZ	1:A:66:LYS:HZ2	2.30	0.45
1:A:81:LEU:HD21	1:A:175:PHE:CE1	2.52	0.45
1:A:111:GLN:CA	1:A:134:ILE:HD11	2.47	0.45
1:A:761:ILE:C	1:A:763:ALA:H	2.25	0.45
1:A:84:TYR:OH	1:A:179:ASP:OD2	2.35	0.45
1:A:99:THR:O	1:A:103:LEU:HB2	2.16	0.45
1:A:127:THR:HG22	1:A:128:ASP:N	2.32	0.45
1:A:148:ASN:C	1:A:148:ASN:HD22	2.25	0.45
1:A:549:LEU:HD13	1:A:549:LEU:O	2.17	0.45
1:A:126:LEU:HB3	1:A:130:GLU:CG	2.44	0.44
1:A:679:GLU:H	1:A:679:GLU:HG3	1.52	0.44
1:A:28:PHE:CZ	1:A:32:ILE:HG13	2.52	0.44
1:A:435:ARG:NH1	1:A:438:GLN:OE1	2.51	0.44
1:A:600:ARG:HA	1:A:600:ARG:HD3	1.55	0.44
1:A:94:MET:CE	1:A:329:TYR:HB3	2.46	0.44
1:A:506:ILE:O	1:A:510:TRP:HB3	2.18	0.44
1:A:526:LEU:O	1:A:530:LEU:HD13	2.18	0.44
1:A:306:GLY:HA3	1:A:675:ILE:HD13	2.00	0.44
1:A:363:ILE:CG2	1:A:515:PHE:CZ	2.99	0.44
1:A:423:LEU:CD2	1:A:436:ILE:HG12	2.48	0.44
1:A:56:ARG:HD3	1:A:62:VAL:HG12	1.99	0.44
1:A:112:ASP:O	1:A:115:ALA:HB3	2.16	0.44
1:A:522:VAL:O	1:A:526:LEU:HD13	2.18	0.44
1:A:706:LEU:HB3	1:A:707:PRO:CD	2.47	0.44
1:A:55:VAL:HG22	1:A:64:MET:CB	2.46	0.44
1:A:433:LEU:HD13	1:A:438:GLN:HG3	1.98	0.44
1:A:236:TRP:CG	1:A:237:PRO:HA	2.53	0.44
1:A:339:ILE:HG22	1:A:340:ASN:H	1.82	0.44
1:A:71:GLY:HA3	1:A:209:GLN:OE1	2.18	0.44
1:A:588:LEU:C	1:A:590:LEU:N	2.74	0.44
1:A:731:GLN:NE2	8:A:1006:HOH:O	2.51	0.44
1:A:154:LEU:HD13	1:A:154:LEU:C	2.43	0.44
1:A:50:PRO:C	1:A:52:PRO:HD3	2.43	0.43
1:A:56:ARG:CB	1:A:61:GLU:O	2.65	0.43
1:A:414:GLY:C	1:A:416:LEU:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:524:GLY:O	1:A:528:VAL:HG23	2.18	0.43
1:A:744:VAL:HB	1:A:745:PRO:HD3	1.99	0.43
1:A:442:VAL:HG23	1:A:443:VAL:N	2.32	0.43
1:A:646:PHE:O	1:A:649:PRO:HD2	2.17	0.43
1:A:294:ARG:NH2	1:A:678:PRO:HB2	2.33	0.43
1:A:19:ASN:C	1:A:23:LYS:HD2	2.43	0.43
1:A:131:LYS:HA	1:A:134:ILE:HG23	2.00	0.43
1:A:596:TYR:CD1	7:A:810:LOP:H81	2.54	0.43
1:A:668:LEU:HD23	1:A:668:LEU:C	2.44	0.43
1:A:762:LYS:O	1:A:762:LYS:HG3	2.17	0.43
1:A:51:ARG:CD	1:A:495:ASN:ND2	2.80	0.43
7:A:810:LOP:H112	7:A:810:LOP:C27	2.40	0.43
1:A:94:MET:HE1	1:A:329:TYR:C	2.43	0.43
1:A:298:LEU:HD11	1:A:303:VAL:HG13	2.01	0.43
1:A:44:ILE:CG1	1:A:567:PRO:HD2	2.46	0.42
1:A:181:TRP:CD1	1:A:181:TRP:O	2.72	0.42
1:A:578:SER:O	1:A:581:GLU:HB2	2.19	0.42
1:A:697:LEU:HA	1:A:700:MET:HE3	2.00	0.42
1:A:750:LEU:O	1:A:753:VAL:CG1	2.67	0.42
1:A:47:GLU:OE2	5:A:807:BOG:H62	2.19	0.42
1:A:185:LYS:O	1:A:186:GLY:C	2.62	0.42
1:A:433:LEU:HD13	1:A:438:GLN:HG2	2.01	0.42
1:A:143:ARG:HD2	1:A:243:GLY:HA3	2.00	0.42
1:A:685:TRP:HA	1:A:685:TRP:HE3	1.85	0.42
1:A:292:ASP:CG	1:A:295:ARG:HG2	2.44	0.42
1:A:258:VAL:O	1:A:262:ILE:HG12	2.19	0.42
1:A:331:THR:HG21	1:A:740:LEU:CD1	2.49	0.42
1:A:759:PHE:CD1	1:A:759:PHE:C	2.97	0.42
1:A:93:TYR:CE2	1:A:649:PRO:CG	3.02	0.42
1:A:646:PHE:HA	1:A:649:PRO:HD2	2.01	0.42
7:A:810:LOP:H251	7:A:810:LOP:C10	2.50	0.42
1:A:336:PHE:O	1:A:337:PHE:HB2	2.20	0.42
1:A:347:PRO:CD	1:A:350:ILE:HD12	2.48	0.42
1:A:367:TRP:CH2	1:A:519:ALA:HB1	2.55	0.42
1:A:370:MET:HE3	1:A:374:ILE:CG2	2.50	0.41
1:A:588:LEU:HD12	1:A:588:LEU:HA	1.87	0.41
1:A:691:TRP:CE2	7:A:810:LOP:H282	2.54	0.41
1:A:48:MET:SD	1:A:498:MET:HB2	2.61	0.41
1:A:176:THR:O	1:A:186:GLY:N	2.53	0.41
1:A:370:MET:CE	1:A:526:LEU:HD21	2.49	0.41
1:A:462:ARG:HG2	1:A:462:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:TRP:HE3	1:A:345:ILE:HG21	1.85	0.41
1:A:50:PRO:O	1:A:52:PRO:HD3	2.21	0.41
1:A:56:ARG:HB3	1:A:62:VAL:CA	2.36	0.41
1:A:198:ARG:NH2	1:A:204:SER:O	2.52	0.41
1:A:56:ARG:HD2	1:A:62:VAL:HG12	2.03	0.41
1:A:400:LEU:HG	1:A:440:ILE:CD1	2.50	0.41
1:A:113:TYR:HB2	1:A:162:TYR:HD2	1.83	0.41
1:A:586:THR:C	1:A:588:LEU:N	2.79	0.41
1:A:56:ARG:CB	1:A:62:VAL:HA	2.35	0.41
1:A:127:THR:N	1:A:130:GLU:HB3	2.35	0.41
1:A:187:LEU:CD1	1:A:187:LEU:H	2.34	0.41
1:A:204:SER:O	1:A:205:ASP:C	2.63	0.41
1:A:208:GLN:O	1:A:212:ASP:OD1	2.38	0.41
1:A:334:ASP:HA	1:A:343:TYR:CE2	2.55	0.41
1:A:391:ASP:O	1:A:394:PHE:HB3	2.20	0.41
1:A:654:ALA:O	1:A:658:GLY:HA3	2.21	0.41
1:A:750:LEU:O	1:A:753:VAL:HG13	2.20	0.41
7:A:810:LOP:O7	7:A:810:LOP:C9	2.59	0.41
2:A:801:HEM:HHA	2:A:801:HEM:HBA2	2.03	0.41
1:A:45:PHE:O	1:A:48:MET:HE2	2.20	0.40
1:A:81:LEU:HD21	1:A:175:PHE:HE1	1.85	0.40
1:A:230:ILE:HD12	1:A:234:ASN:HA	2.03	0.40
1:A:309:PHE:HA	1:A:312:VAL:CG1	2.50	0.40
1:A:310:VAL:HG21	1:A:764:LEU:HD21	2.03	0.40
1:A:139:ILE:HD11	1:A:241:ASP:C	2.46	0.40
1:A:239:TYR:CE1	1:A:241:ASP:HB2	2.57	0.40
1:A:326:LEU:HD11	1:A:352:LYS:HA	2.04	0.40
1:A:393:LEU:HG	1:A:447:LEU:HD13	2.03	0.40
1:A:63:LEU:HD13	1:A:63:LEU:N	2.36	0.40
1:A:142:MET:HE3	1:A:242:ALA:HA	2.04	0.40
1:A:596:TYR:CD1	7:A:810:LOP:C8	3.04	0.40
1:A:134:ILE:CG1	1:A:135:ARG:N	2.81	0.40
1:A:761:ILE:O	1:A:764:LEU:CD2	2.69	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	750/800 (94%)	695 (93%)	49 (6%)	6 (1%)	16	31

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	ASP
1	A	157	THR
1	A	199	ALA
1	A	204	SER
1	A	194	PRO
1	A	603	GLY

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	631/675 (94%)	539 (85%)	92 (15%)	3	6

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	37	LEU
1	A	51	ARG
1	A	53	LYS
1	A	55	VAL

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Mol	Chain	Res	Type
1	A	63	LEU
1	A	68	THR
1	A	75	VAL
1	A	81	LEU
1	A	87	VAL
1	A	96	PRO
1	A	103	LEU
1	A	105	VAL
1	A	126	LEU
1	A	131	LYS
1	A	134	ILE
1	A	135	ARG
1	A	144	LYS
1	A	151	THR
1	A	153	VAL
1	A	154	LEU
1	A	156	LEU
1	A	164	LEU
1	A	166	LYS
1	A	187	LEU
1	A	198	ARG
1	A	201	VAL
1	A	207	ILE
1	A	210	ILE
1	A	220	LEU
1	A	224	LEU
1	A	231	THR
1	A	251	VAL
1	A	287	LYS
1	A	293	LEU
1	A	294	ARG
1	A	298	LEU
1	A	312	VAL
1	A	345	ILE
1	A	357	GLN
1	A	382	GLU
1	A	393	LEU
1	A	397	LEU
1	A	400	LEU
1	A	416	LEU
1	A	433	LEU
1	A	436	ILE

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Mol	Chain	Res	Type
1	A	440	ILE
1	A	441	LEU
1	A	446	LEU
1	A	447	LEU
1	A	469	LEU
1	A	478	ILE
1	A	483	PHE
1	A	497	THR
1	A	512	GLU
1	A	516	GLU
1	A	521	VAL
1	A	527	LEU
1	A	530	LEU
1	A	539	VAL
1	A	545	GLN
1	A	549	LEU
1	A	550	LEU
1	A	571	ILE
1	A	587	LEU
1	A	588	LEU
1	A	590	LEU
1	A	591	GLU
1	A	615	LEU
1	A	618	THR
1	A	628	VAL
1	A	635	LEU
1	A	656	MET
1	A	667	VAL
1	A	672	LEU
1	A	673	ARG
1	A	679	GLU
1	A	685	TRP
1	A	706	LEU
1	A	711	LEU
1	A	734	VAL
1	A	738	LEU
1	A	739	LEU
1	A	740	LEU
1	A	742	ARG
1	A	750	LEU
1	A	753	VAL
1	A	756	LEU

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Mol	Chain	Res	Type
1	A	757	LEU
1	A	774	GLU
1	A	777	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	77	GLN
1	A	148	ASN
1	A	160	GLN
1	A	296	GLN
1	A	340	ASN
1	A	381	GLN
1	A	426	GLN
1	A	471	HIS
1	A	529	GLN
1	A	560	HIS
1	A	595	GLN
1	A	622	ASN
1	A	682	ASN
1	A	731	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	BOG	A	805	-	20,20,20	0.92	2 (10%)	25,25,25	0.89	0
2	HEM	A	802	1,4,8	50,50,50	1.78	9 (18%)	67,82,82	1.04	4 (5%)
5	BOG	A	807	-	20,20,20	0.90	2 (10%)	25,25,25	0.97	1 (4%)
7	LOP	A	810	-	44,44,44	0.72	1 (2%)	47,49,49	1.17	3 (6%)
5	BOG	A	806	-	20,20,20	1.01	2 (10%)	25,25,25	0.94	1 (4%)
6	EPE	A	808	-	15,15,15	1.35	1 (6%)	19,20,20	1.38	3 (15%)
2	HEM	A	801	1,4	50,50,50	1.67	7 (14%)	67,82,82	1.12	5 (7%)
7	LOP	A	809	-	44,44,44	0.70	0	47,49,49	1.21	4 (8%)

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
5	BOG	A	805	-	-	0/11/31/31	0/1/1/1
2	HEM	A	802	1,4,8	-	6/14/54/54	-
5	BOG	A	807	-	-	0/11/31/31	0/1/1/1
7	LOP	A	810	-	-	12/48/48/48	-
5	BOG	A	806	-	-	0/11/31/31	0/1/1/1
6	EPE	A	808	-	-	1/9/19/19	0/1/1/1
2	HEM	A	801	1,4	-	8/14/54/54	-
7	LOP	A	809	-	-	12/48/48/48	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	802	HEM	FE-NC	7.35	2.19	1.95
2	A	801	HEM	FE-NC	5.20	2.12	1.95
6	A	808	EPE	C10-S	3.99	1.83	1.77
2	A	801	HEM	FE-NB	3.94	2.07	1.94
2	A	801	HEM	FE-NA	3.49	2.06	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	806	BOG	O1-C1	3.07	1.45	1.40
2	A	802	HEM	FE-NA	2.68	2.04	1.95
2	A	802	HEM	CAC-C3C	-2.51	1.40	1.47
2	A	801	HEM	CBB-CAB	2.51	1.42	1.30
5	A	807	BOG	O1-C1	2.50	1.44	1.40
2	A	802	HEM	CBD-CGD	2.48	1.56	1.50
2	A	802	HEM	CBB-CAB	2.48	1.42	1.30
2	A	802	HEM	CMC-C2C	2.45	1.55	1.50
5	A	805	BOG	O1-C1	2.39	1.44	1.40
2	A	801	HEM	CMB-C2B	2.33	1.55	1.50
2	A	801	HEM	C1A-C2A	2.27	1.49	1.44
5	A	805	BOG	O5-C1	2.26	1.47	1.41
2	A	802	HEM	C4A-NA	-2.23	1.35	1.39
2	A	801	HEM	CMC-C2C	2.21	1.55	1.50
5	A	806	BOG	O5-C1	2.18	1.47	1.41
2	A	802	HEM	CMB-C2B	2.14	1.55	1.50
5	A	807	BOG	O5-C1	2.08	1.47	1.41
2	A	802	HEM	C1C-NC	-2.01	1.35	1.39
7	A	810	LOP	C16-C15	-2.00	1.39	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	809	LOP	C4-O5-C6	-4.20	107.76	117.80
6	A	808	EPE	O1S-S-C10	4.01	112.79	106.73
7	A	810	LOP	O5-C6-C7	4.01	120.15	111.48
7	A	809	LOP	O5-C6-C7	3.97	120.07	111.48
2	A	801	HEM	CBA-CAA-C2A	3.39	121.92	112.53
2	A	801	HEM	CAA-C2A-C1A	3.15	131.09	124.94
2	A	801	HEM	C3B-C4B-NB	3.02	111.64	109.47
2	A	802	HEM	C3B-C4B-NB	2.87	111.53	109.47
2	A	801	HEM	C4B-C3B-C2B	-2.80	104.70	107.28
5	A	807	BOG	C1'-O1-C1	-2.75	108.98	113.68
2	A	802	HEM	CBD-CAD-C3D	2.75	120.14	112.53
2	A	802	HEM	C4B-C3B-C2B	-2.70	104.80	107.28
5	A	806	BOG	C1'-O1-C1	-2.47	109.46	113.68
7	A	810	LOP	O6-C24-C25	2.44	119.28	111.83
6	A	808	EPE	O3S-S-O2S	-2.36	105.49	111.40
7	A	809	LOP	C5-O6-C24	-2.21	109.04	117.12
6	A	808	EPE	O3S-S-O1S	-2.16	105.98	111.40
2	A	801	HEM	C4C-C3C-C2C	-2.15	104.95	106.81
2	A	802	HEM	CAD-C3D-C4D	2.12	128.40	124.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	810	LOP	O6-C5-C4	-2.04	102.52	108.40
7	A	809	LOP	O6-C24-C25	2.00	117.94	111.83

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	802	HEM	C2C-C3C-CAC-CBC
2	A	802	HEM	C4C-C3C-CAC-CBC
7	A	809	LOP	C1-C2-O1-P1
7	A	809	LOP	C2-O1-P1-O2
7	A	809	LOP	C2-O1-P1-O4
7	A	809	LOP	C4-C3-O2-P1
7	A	810	LOP	N1-C1-C2-O1
7	A	810	LOP	C3-O2-P1-O3
7	A	810	LOP	C4-C3-O2-P1
2	A	801	HEM	C1A-C2A-CAA-CBA
2	A	801	HEM	C3A-C2A-CAA-CBA
6	A	808	EPE	N4-C7-C8-O8
7	A	809	LOP	C24-C25-C26-C27
7	A	810	LOP	C29-C30-C31-C32
2	A	801	HEM	C2C-C3C-CAC-CBC
7	A	810	LOP	C15-C16-C17-C18
7	A	810	LOP	O2-C3-C4-C5
7	A	809	LOP	C30-C31-C32-C33
7	A	809	LOP	C32-C33-C34-C35
7	A	810	LOP	C24-C25-C26-C27
7	A	810	LOP	O2-C3-C4-O5
2	A	801	HEM	C4C-C3C-CAC-CBC
2	A	801	HEM	C3D-CAD-CBD-CGD
7	A	809	LOP	C2-O1-P1-O3
7	A	809	LOP	C3-O2-P1-O4
7	A	810	LOP	C3-O2-P1-O1
7	A	810	LOP	C3-O2-P1-O4
2	A	802	HEM	CAA-CBA-CGA-O1A
7	A	809	LOP	C12-C13-C14-C15
7	A	810	LOP	C28-C29-C30-C31
2	A	801	HEM	CAD-CBD-CGD-O2D
2	A	802	HEM	CAD-CBD-CGD-O2D
7	A	809	LOP	C27-C28-C29-C30
2	A	801	HEM	CAD-CBD-CGD-O1D
2	A	802	HEM	CAA-CBA-CGA-O2A

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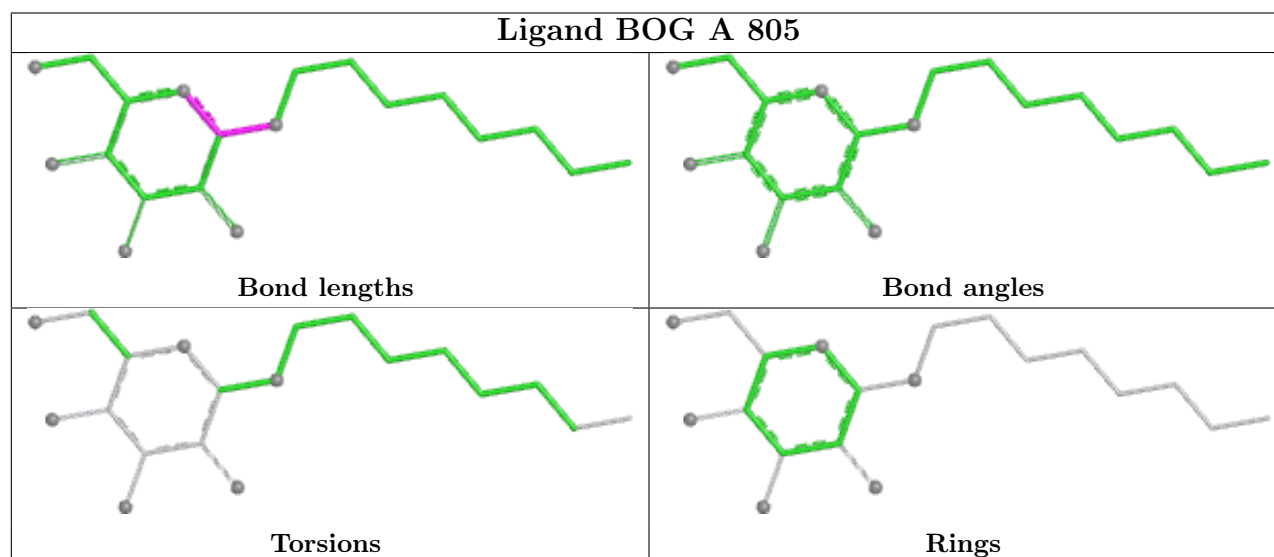
Mol	Chain	Res	Type	Atoms
2	A	802	HEM	CAD-CBD-CGD-O1D
7	A	810	LOP	C12-C13-C14-C15
7	A	809	LOP	C6-C7-C8-C9
2	A	801	HEM	CAA-CBA-CGA-O2A

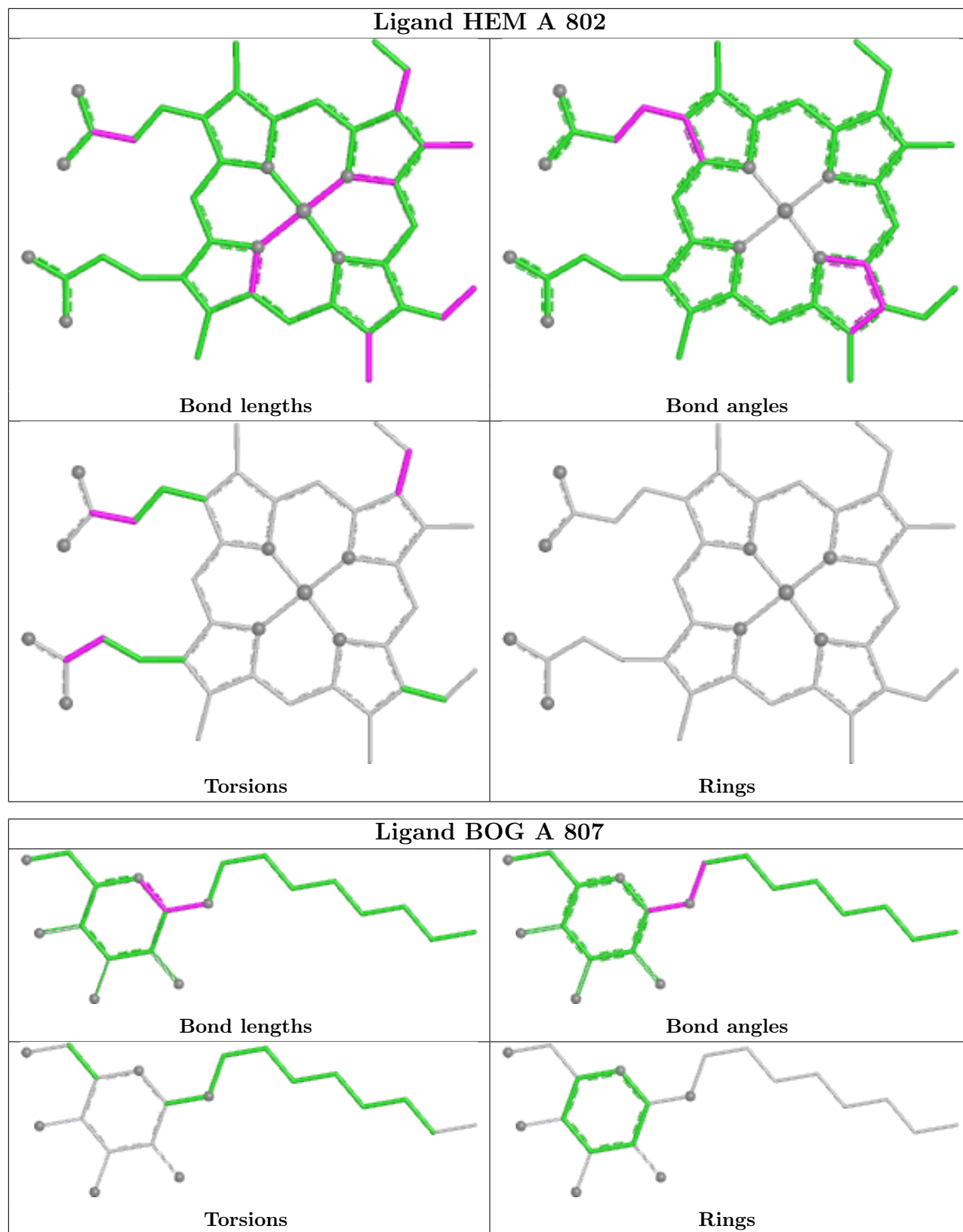
There are no ring outliers.

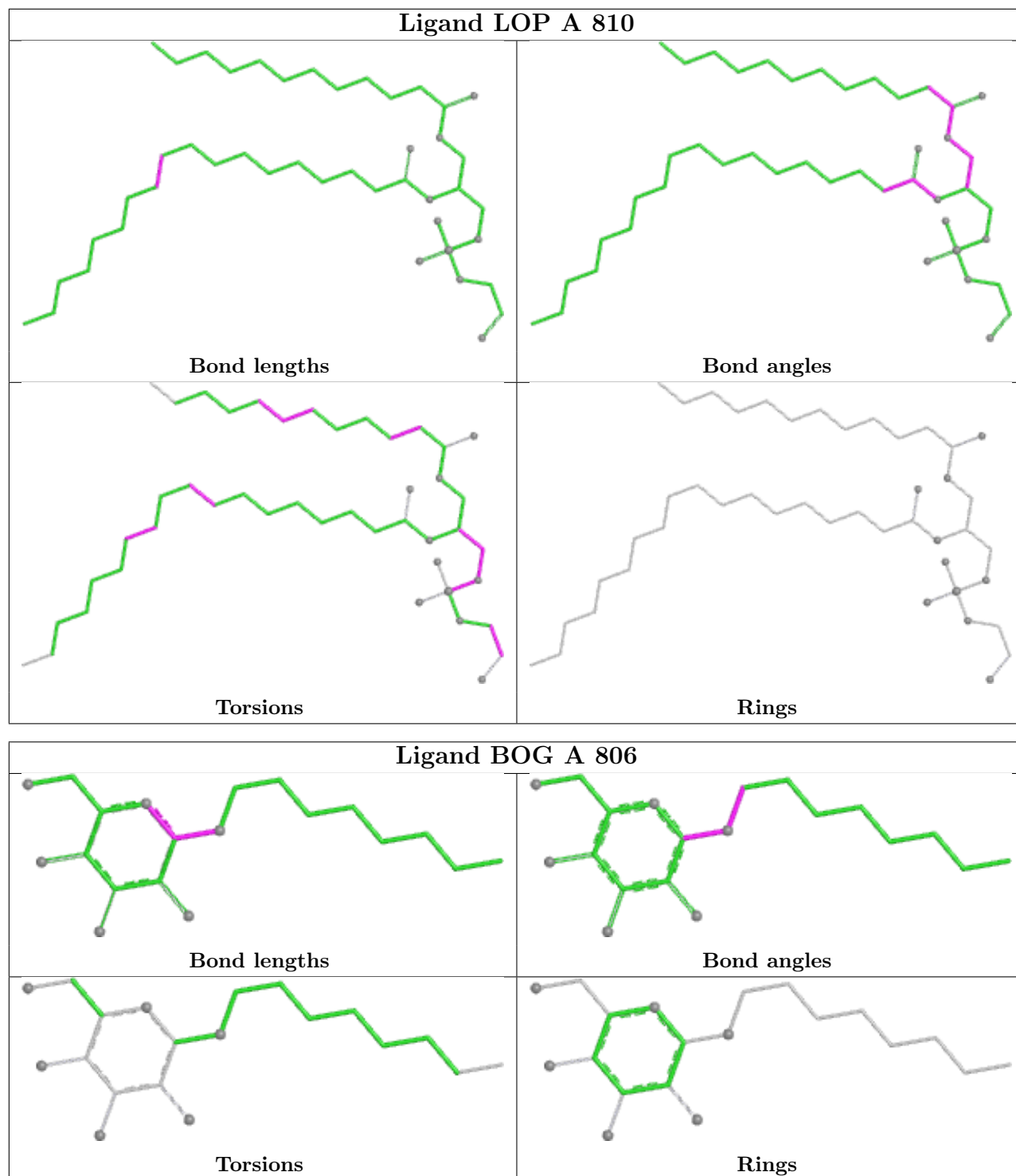
6 monomers are involved in 40 short contacts:

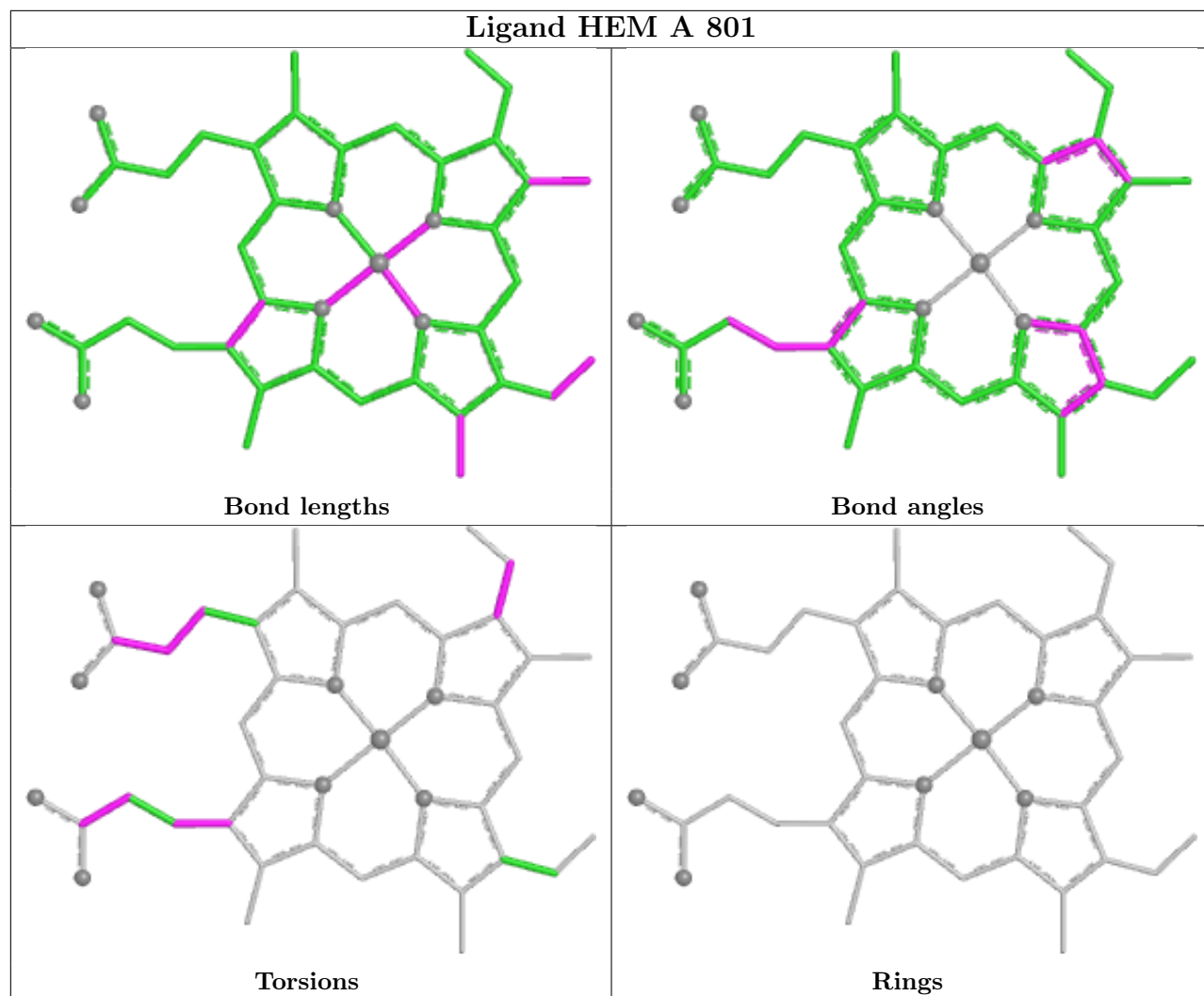
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	802	HEM	2	0
5	A	807	BOG	3	0
7	A	810	LOP	22	0
5	A	806	BOG	1	0
2	A	801	HEM	1	0
7	A	809	LOP	11	0

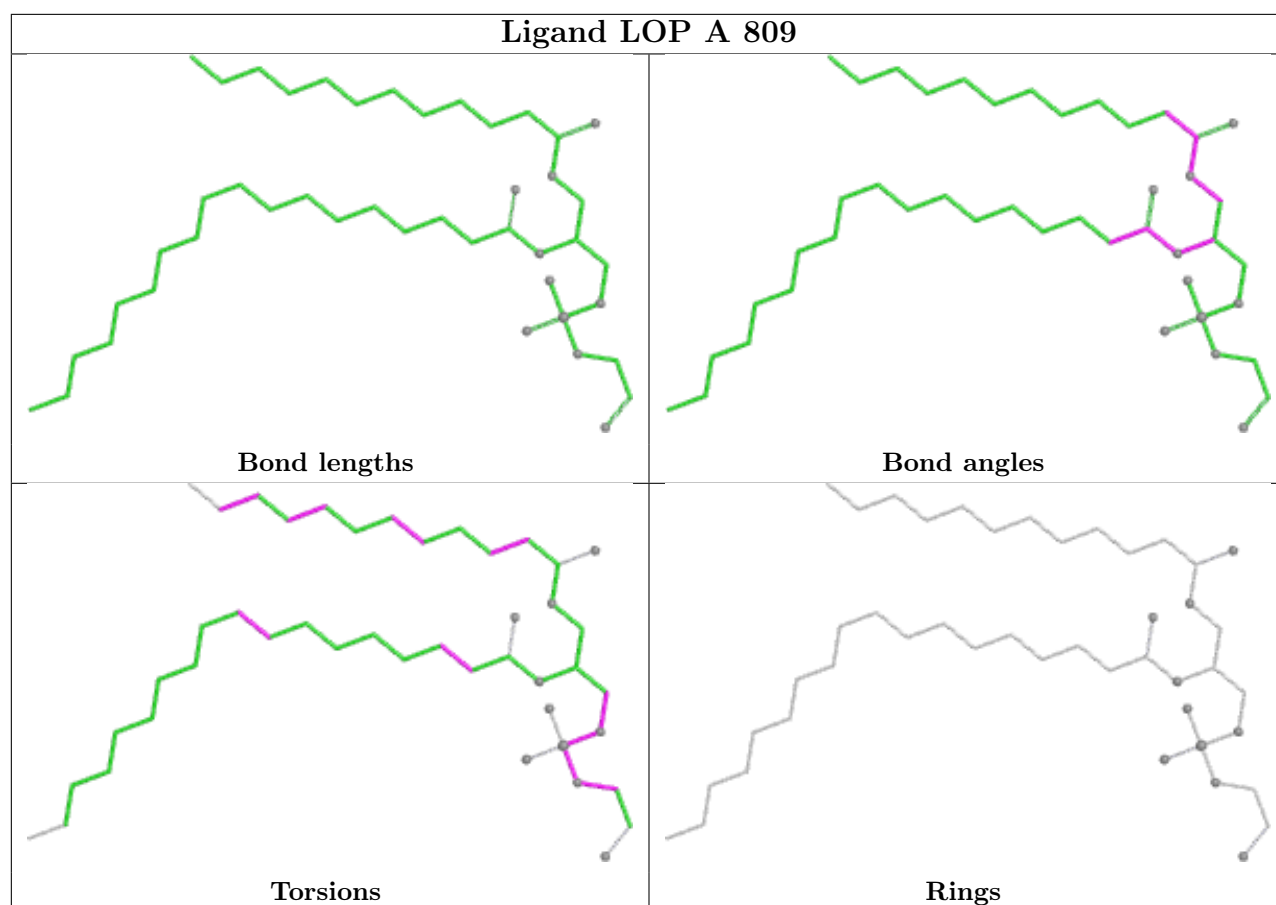
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	754/800 (94%)	0.63	65 (8%) 16 14	34, 62, 93, 104	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	394	PHE	5.8
1	A	154	LEU	4.7
1	A	513	GLY	4.5
1	A	416	LEU	4.4
1	A	514	ILE	4.4
1	A	207	ILE	4.1
1	A	18	THR	4.1
1	A	414	GLY	4.0
1	A	515	PHE	3.7
1	A	777	GLU	3.6
1	A	273	TYR	3.5
1	A	771	THR	3.2
1	A	589	ILE	3.1
1	A	196	ALA	3.1
1	A	390	VAL	3.1
1	A	17	THR	3.0
1	A	410	LEU	3.0
1	A	588	LEU	3.0
1	A	113	TYR	3.0
1	A	182	GLY	3.0
1	A	124	ALA	2.9
1	A	303	VAL	2.9
1	A	396	ALA	2.8
1	A	421	PHE	2.7
1	A	188	ILE	2.6
1	A	106	TYR	2.6
1	A	590	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	512	GLU	2.6
1	A	63	LEU	2.6
1	A	417	GLY	2.5
1	A	153	VAL	2.5
1	A	46	LYS	2.5
1	A	199	ALA	2.5
1	A	137	GLN	2.5
1	A	151	THR	2.5
1	A	294	ARG	2.5
1	A	300	PRO	2.5
1	A	159	ALA	2.5
1	A	392	LEU	2.4
1	A	163	GLY	2.4
1	A	197	ASN	2.4
1	A	181	TRP	2.4
1	A	602	GLY	2.3
1	A	685	TRP	2.3
1	A	21	PHE	2.3
1	A	592	ALA	2.3
1	A	381	GLN	2.3
1	A	339	ILE	2.3
1	A	139	ILE	2.2
1	A	130	GLU	2.2
1	A	348	PHE	2.2
1	A	138	VAL	2.2
1	A	743	ALA	2.2
1	A	193	MET	2.2
1	A	143	ARG	2.2
1	A	68	THR	2.2
1	A	155	VAL	2.1
1	A	398	VAL	2.1
1	A	132	SER	2.1
1	A	64	MET	2.1
1	A	201	VAL	2.1
1	A	198	ARG	2.1
1	A	407	GLY	2.1
1	A	395	TRP	2.0
1	A	326	LEU	2.0

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

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 [i](#)

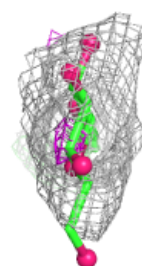
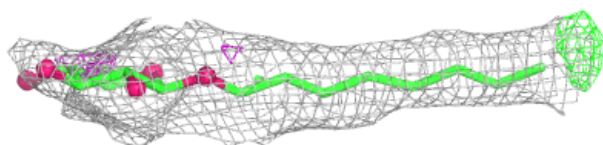
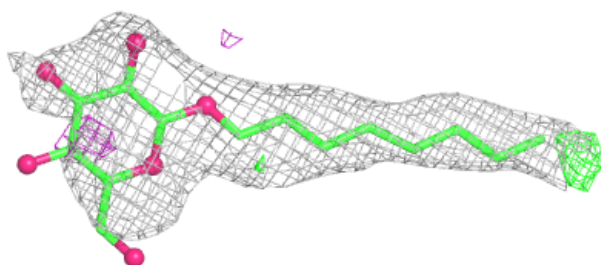
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EPE	A	808	15/15	0.45	0.29	88,93,109,109	0
5	BOG	A	805	20/20	0.61	0.15	75,89,93,95	0
7	LOP	A	809	45/45	0.72	0.18	73,85,101,104	0
5	BOG	A	807	20/20	0.73	0.18	73,85,88,90	0
5	BOG	A	806	20/20	0.75	0.16	76,87,90,91	0
7	LOP	A	810	45/45	0.78	0.18	59,70,102,104	0
2	HEM	A	801	43/43	0.96	0.11	38,46,52,54	0
2	HEM	A	802	43/43	0.97	0.08	29,38,50,54	0
4	CA	A	804	1/1	0.98	0.11	49,49,49,49	0
3	ZN	A	803	1/1	1.00	0.03	55,55,55,55	0

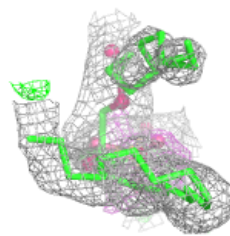
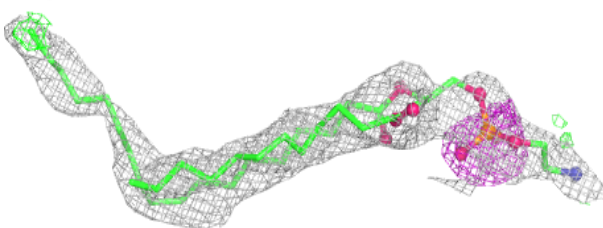
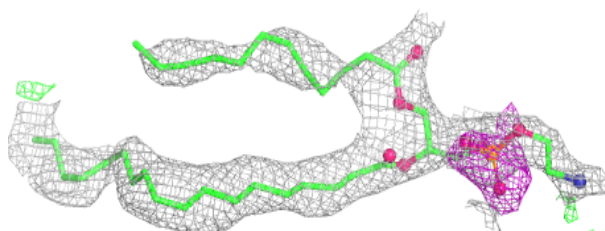
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BOG A 805:

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

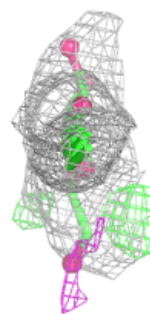
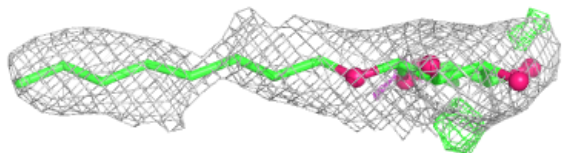
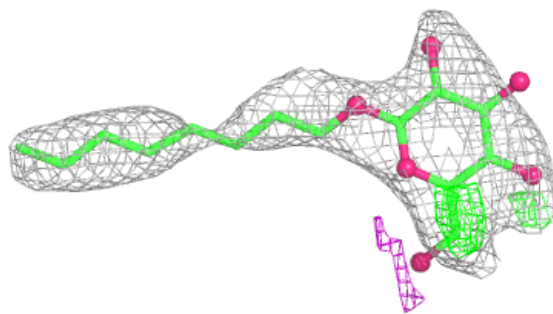
**Electron density around LOP A 809:**

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

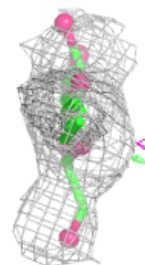
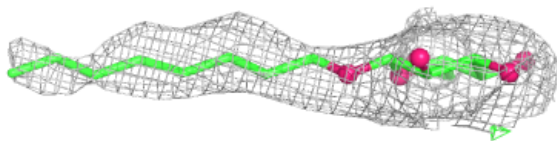
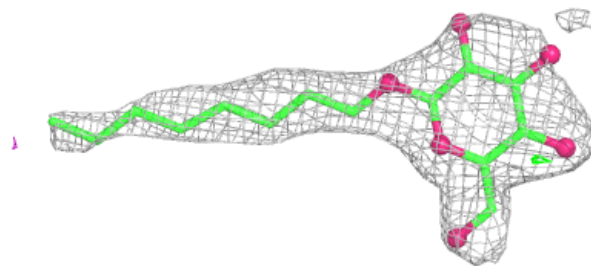


Electron density around BOG A 807:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

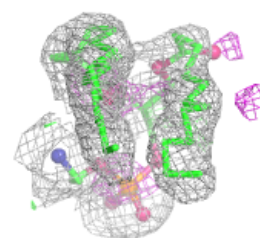
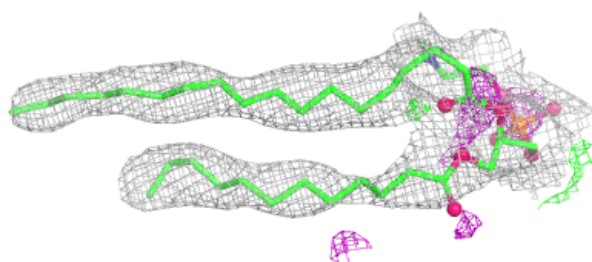
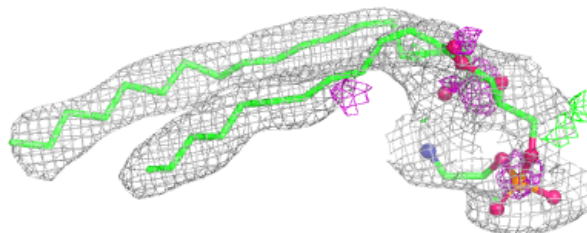
**Electron density around BOG A 806:**

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



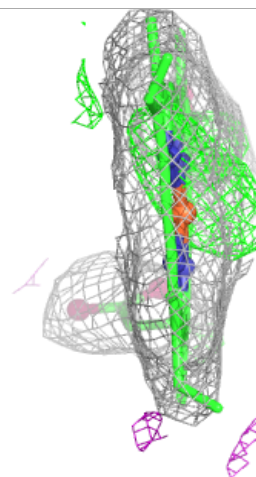
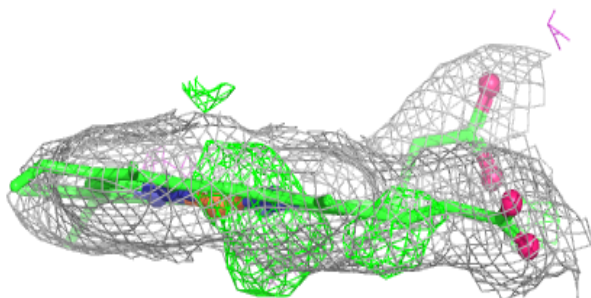
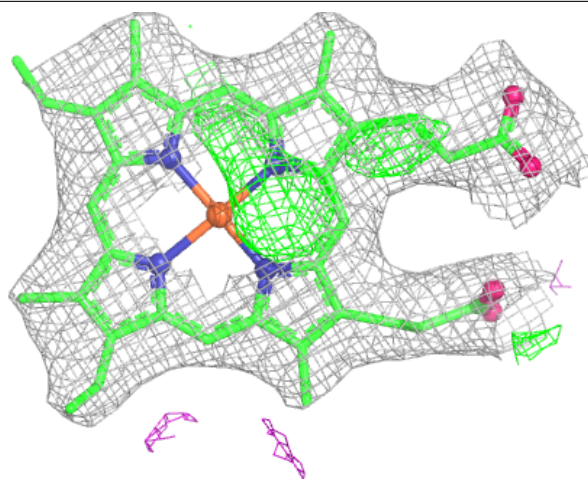
Electron density around LOP A 810:

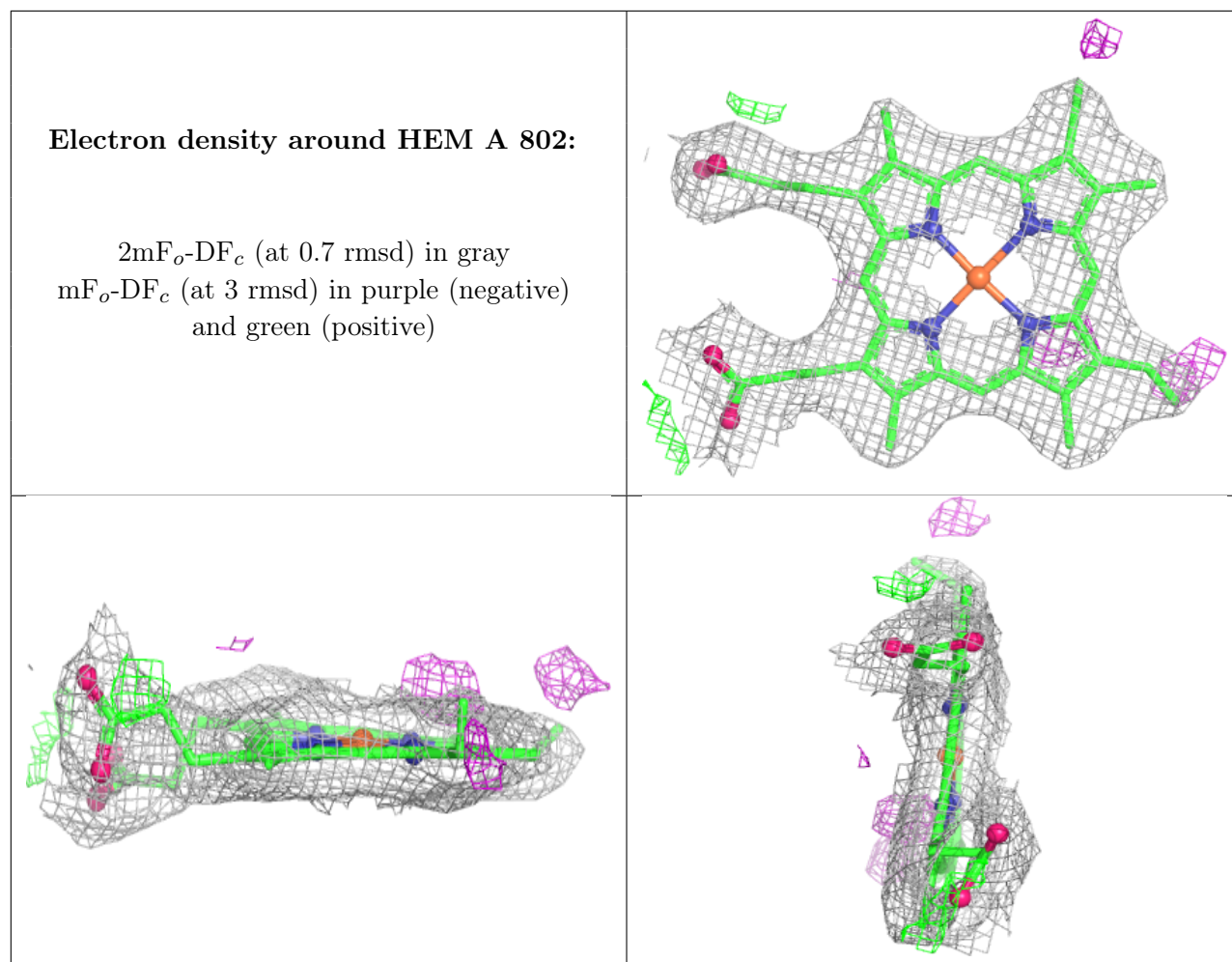
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 801:

$2mF_o-DF_c$ (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.