



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 09:35 PM BST

PDB ID : 2GMH  
Title : Structure of Porcine Electron Transfer Flavoprotein-Ubiquinone Oxidoreductase in Complexed with Ubiquinone  
Authors : Zhang, J.; Frerman, F.E.; Kim, J.-J.P.  
Deposited on : 2006-04-06  
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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

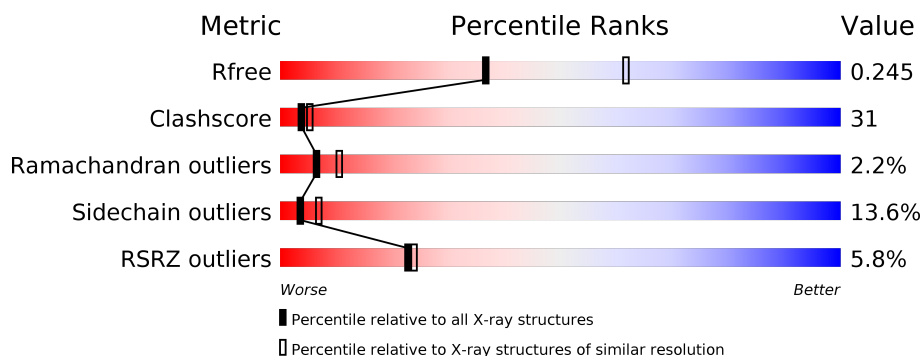
# 1 Overall quality at a glance

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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	584	
1	B	584	

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
2	BHG	A	616	X	-	-	-
2	BHG	A	617	X	-	-	X
2	BHG	B	618	X	-	-	-
7	EDO	A	623	-	-	X	-

## 2 Entry composition [i](#)

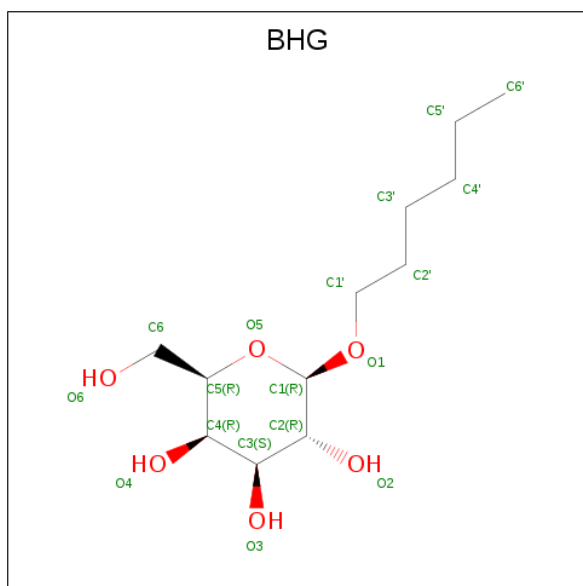
There are 8 unique types of molecules in this entry. The entry contains 9751 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Electron transfer flavoprotein-ubiquinone oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4558	2910	792	836	20			
1	B	578	Total	C	N	O	S	0	0	0
			4531	2893	787	832	19			

- Molecule 2 is hexyl beta-D-galactopyranoside (three-letter code: BHG) (formula: C<sub>12</sub>H<sub>24</sub>O<sub>6</sub>).

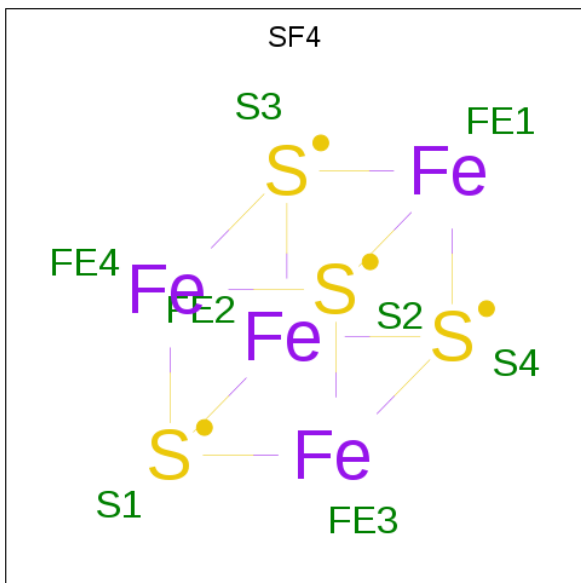


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			18	12	6		
2	A	1	Total	C	O	0	0
			18	12	6		
2	B	1	Total	C	O	0	0
			18	12	6		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula:  $\text{Fe}_4\text{S}_4$ ).



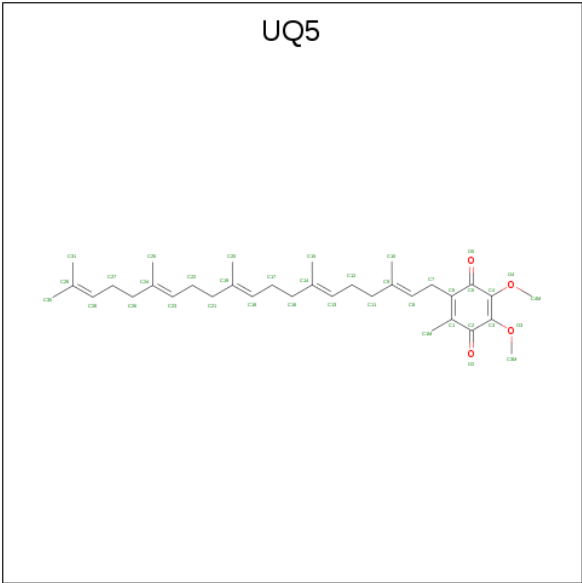
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0
			53	27	9	15	2	
5	B	1	Total	C	N	O	P	0
			53	27	9	15	2	

- Molecule 6 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (three-letter code: UQ5) (formula: C<sub>34</sub>H<sub>50</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			38	34	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			38	34	4		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



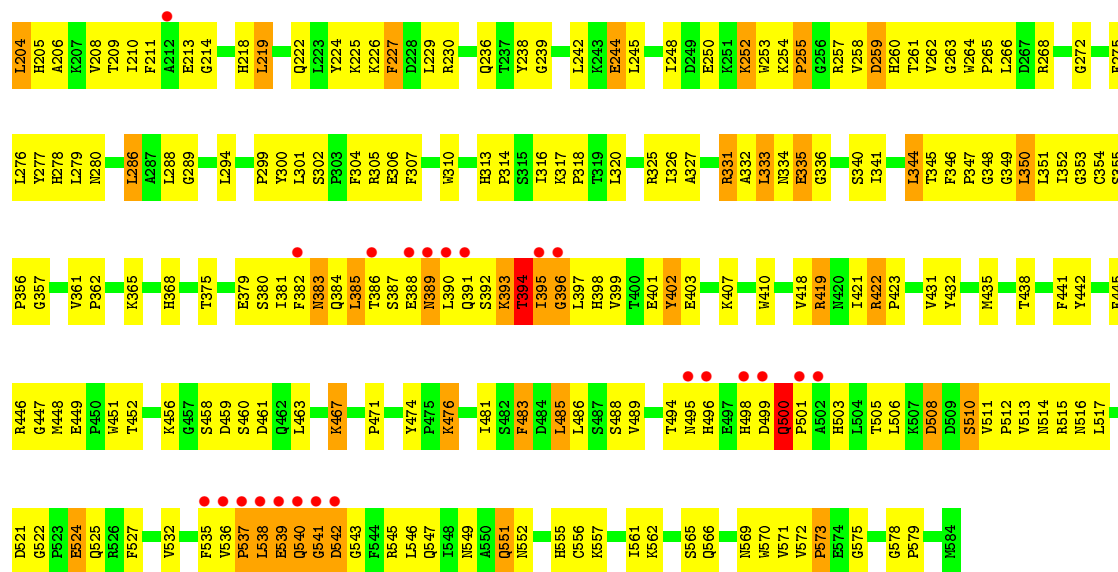
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	301	Total 301	O 301	0	0
8	B	68	Total 68	O 68	0	0







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	154.32Å 154.32Å 128.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.67 – 2.50 29.66 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.7 (29.67-2.50) 98.8 (29.66-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.94 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.221 , 0.254 0.214 , 0.245	Depositor DCC
$R_{free}$ test set	4358 reflections (8.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9751	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NA, SF4, EDO, BHG, UQ5, FAD

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	0.59	0/4687	0.96	18/6363 (0.3%)
1	B	0.50	0/4660	0.88	10/6326 (0.2%)
All	All	0.55	0/9347	0.92	28/12689 (0.2%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	VAL	C-N-CD	-15.72	86.01	120.60
1	A	542	ASP	N-CA-C	9.67	137.11	111.00
1	A	5	LYS	N-CA-C	8.39	133.65	111.00
1	A	6	VAL	C-N-CA	8.38	157.20	122.00
1	A	8	ARG	NE-CZ-NH1	-8.31	116.15	120.30
1	B	396	GLY	N-CA-C	-7.82	93.55	113.10
1	A	388	GLU	N-CA-C	-7.63	90.40	111.00
1	A	393	LYS	CA-C-N	-7.17	101.42	117.20
1	A	541	GLY	N-CA-C	6.87	130.27	113.10
1	B	394	THR	N-CA-C	-6.85	92.51	111.00
1	A	83	GLY	N-CA-C	-6.30	97.36	113.10
1	A	393	LYS	C-N-CA	6.17	137.12	121.70
1	A	394	THR	N-CA-C	-5.79	95.38	111.00
1	B	31	ARG	N-CA-C	5.67	126.32	111.00
1	A	6	VAL	N-CA-C	5.67	126.31	111.00
1	A	84	ALA	N-CA-C	5.61	126.15	111.00
1	B	65	LEU	CA-CB-CG	5.59	128.15	115.30
1	A	392	SER	CA-C-N	-5.54	105.02	117.20
1	B	8	ARG	N-CA-C	-5.51	96.13	111.00
1	B	541	GLY	N-CA-C	5.43	126.67	113.10
1	B	163	PRO	N-CA-C	5.36	126.03	112.10
1	B	508	ASP	N-CA-C	-5.22	96.90	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	SER	N-CA-C	5.16	124.94	111.00
1	B	7	PRO	C-N-CA	5.14	134.55	121.70
1	A	18	ARG	CG-CD-NE	-5.13	101.02	111.80
1	A	85	CYS	N-CA-C	-5.13	97.16	111.00
1	B	73	ALA	N-CA-C	5.11	124.79	111.00
1	A	86	LEU	CA-CB-CG	5.07	126.96	115.30

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	4558	0	4457	204	0
1	B	4531	0	4424	365	0
2	A	36	0	48	6	0
2	B	18	0	24	0	0
3	A	1	0	0	0	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
5	A	53	0	31	2	0
5	B	53	0	31	4	0
6	A	38	0	50	17	0
6	B	38	0	50	13	0
7	A	36	0	54	18	0
7	B	4	0	6	0	0
8	A	301	0	0	8	0
8	B	68	0	0	5	0
All	All	9751	0	9175	576	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 31.

All (576) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:VAL:HG12	1:B:67:VAL:HG12	1.26	1.13
1:B:55:LYS:HB2	1:B:157:LEU:HD12	1.30	1.08
1:B:351:LEU:HB3	1:B:356:PRO:HG3	1.43	1.00
1:B:510:SER:O	1:B:514:ASN:HB2	1.62	0.99
1:B:203:GLU:HG2	1:B:205:HIS:CE1	1.97	0.99
1:B:43:ALA:HB3	1:B:71:GLU:HG2	1.46	0.98
1:B:31:ARG:HE	1:B:200:ARG:NH1	1.61	0.98
1:B:34:GLU:HG3	1:B:66:ARG:HH22	1.28	0.98
1:B:12:HIS:ND1	1:B:14:THR:HG23	1.81	0.95
1:A:345:THR:HG22	1:A:398:HIS:CD2	2.03	0.94
1:B:31:ARG:NE	1:B:200:ARG:HH12	1.64	0.93
1:B:208:VAL:HG13	1:B:349:GLY:HA2	1.48	0.93
1:B:55:LYS:HB2	1:B:157:LEU:CD1	1.99	0.92
1:B:203:GLU:HG2	1:B:205:HIS:HE1	1.34	0.92
1:A:361:VAL:HG21	1:A:422:ARG:HG3	1.53	0.91
1:B:188:ILE:HG22	1:B:189:GLN:N	1.84	0.90
1:B:209:THR:CG2	1:B:211:PHE:HE1	1.84	0.90
1:B:325:ARG:HH12	1:B:488:SER:HA	1.37	0.90
1:B:38:VAL:HG12	1:B:67:VAL:CG1	2.03	0.89
1:A:5:LYS:HD3	1:A:6:VAL:HG12	1.53	0.89
1:B:325:ARG:HH21	1:B:483:PHE:HB2	1.39	0.88
1:B:508:ASP:HB3	1:B:511:VAL:CG1	2.03	0.88
1:B:209:THR:HG23	1:B:211:PHE:HE1	1.35	0.88
1:B:496:HIS:CD2	1:B:578:GLY:H	1.90	0.88
1:B:43:ALA:CB	1:B:71:GLU:HG2	2.04	0.88
1:B:40:ILE:HB	1:B:69:LEU:HD23	1.56	0.88
1:A:351:LEU:HB3	1:A:356:PRO:HG3	1.53	0.87
1:B:503:HIS:HB2	1:B:571:VAL:O	1.72	0.87
1:B:325:ARG:HH21	1:B:483:PHE:CB	1.87	0.86
1:A:355:SER:HB3	1:A:356:PRO:HD3	1.57	0.86
1:A:551:GLN:HE21	1:A:551:GLN:H	1.23	0.86
1:B:114:PHE:CE1	6:B:615:UQ5:H4M3	2.10	0.86
1:B:188:ILE:HG22	1:B:189:GLN:H	1.38	0.86
1:B:133:MET:HG2	6:B:615:UQ5:H4M1	1.57	0.86
1:B:39:VAL:HG23	1:B:206:ALA:HB2	1.56	0.86
1:B:392:SER:HB2	1:B:394:THR:OG1	1.74	0.86
1:B:72:LYS:HE2	1:B:555:HIS:CD2	2.11	0.86
1:B:248:ILE:HG21	1:B:286:LEU:HD22	1.56	0.85
1:B:188:ILE:CG2	1:B:189:GLN:H	1.89	0.85
1:B:173:HIS:CE1	1:B:179:LYS:HG2	2.12	0.85
1:B:248:ILE:HD13	1:B:286:LEU:HD22	1.55	0.85
1:B:541:GLY:O	1:B:542:ASP:HB2	1.74	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:PHE:HB3	1:A:449:GLU:OE2	1.76	0.84
1:B:508:ASP:O	1:B:511:VAL:HG13	1.78	0.84
1:B:361:VAL:HG11	1:B:422:ARG:HG3	1.58	0.83
1:A:353:GLY:O	1:A:356:PRO:HD2	1.77	0.83
1:B:114:PHE:HB2	1:B:127:ILE:HD11	1.61	0.83
1:B:325:ARG:NH2	1:B:483:PHE:HB2	1.94	0.82
1:B:209:THR:HG23	1:B:211:PHE:CE1	2.14	0.82
1:A:551:GLN:NE2	1:A:551:GLN:H	1.78	0.82
1:A:8:ARG:HE	1:A:8:ARG:H	1.28	0.81
1:A:490:ALA:HA	7:A:621:EDO:H21	1.62	0.81
1:B:21:ASP:HB3	1:B:24:TRP:HD1	1.46	0.81
1:B:72:LYS:HE2	1:B:555:HIS:HD2	1.45	0.81
1:B:171:LEU:HB2	1:B:179:LYS:HB2	1.63	0.81
1:A:117:LEU:CD2	1:A:122:ARG:HG3	2.11	0.80
1:B:498:HIS:CE1	1:B:551:GLN:HB3	2.16	0.80
1:B:81:LEU:HD22	1:B:331:ARG:HB2	1.64	0.80
7:A:621:EDO:H12	8:A:857:HOH:O	1.81	0.80
1:A:34:GLU:HG3	1:A:66:ARG:HH12	1.46	0.80
1:A:443:TRP:O	1:A:446:ARG:NH1	2.15	0.80
1:B:355:SER:HB3	1:B:356:PRO:HD3	1.63	0.79
1:B:15:ILE:HD13	1:B:506:LEU:O	1.83	0.79
1:B:132:PRO:HD3	1:B:442:TYR:CD2	2.18	0.79
1:B:127:ILE:HG22	1:B:127:ILE:O	1.83	0.79
1:A:114:PHE:HE1	6:A:612:UQ5:H4M2	1.48	0.79
1:B:353:GLY:O	1:B:356:PRO:HD2	1.84	0.78
1:B:275:PHE:CE2	1:B:289:GLY:HA3	2.18	0.78
1:B:517:LEU:HA	1:B:522:GLY:N	1.99	0.78
1:B:146:LEU:O	1:B:150:MET:HG3	1.83	0.78
1:A:445:PHE:O	1:A:448:MET:HG3	1.83	0.77
1:A:272:GLY:H	6:A:612:UQ5:H1M3	1.50	0.77
1:A:522:GLY:O	1:A:525:GLN:HG2	1.86	0.76
1:B:227:PHE:N	1:B:227:PHE:HD1	1.82	0.76
1:A:129:PRO:HG2	2:A:617:BHG:H62	1.66	0.76
1:B:73:ALA:CB	1:B:79:HIS:CE1	2.69	0.75
1:B:226:LYS:HB3	1:B:227:PHE:CD1	2.22	0.75
1:B:40:ILE:HB	1:B:69:LEU:CD2	2.16	0.75
1:B:15:ILE:CD1	1:B:505:THR:HB	2.17	0.74
1:B:132:PRO:HD3	1:B:442:TYR:CE2	2.23	0.74
1:B:84:ALA:HB3	1:B:141:VAL:O	1.87	0.73
1:B:334:ASN:HD21	1:B:354:CYS:HB3	1.54	0.73
1:A:361:VAL:HG22	1:A:362:PRO:HD3	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:512:PRO:CB	1:B:546:LEU:HD22	2.19	0.73
1:B:508:ASP:HB3	1:B:511:VAL:HG12	1.71	0.72
1:B:227:PHE:N	1:B:227:PHE:CD1	2.55	0.72
1:B:73:ALA:HB3	1:B:79:HIS:CE1	2.24	0.72
1:B:15:ILE:HD11	1:B:505:THR:HB	1.72	0.72
1:B:72:LYS:NZ	1:B:79:HIS:ND1	2.37	0.72
1:B:538:LEU:HB2	1:B:543:GLY:O	1.90	0.72
1:B:522:GLY:O	1:B:525:GLN:HG2	1.89	0.72
1:A:117:LEU:HD23	1:A:122:ARG:HG3	1.72	0.71
6:B:615:UQ5:H4M2	6:B:615:UQ5:H153	1.70	0.71
1:A:345:THR:CG2	1:A:398:HIS:CD2	2.73	0.71
1:A:65:LEU:HD11	1:A:385:LEU:HD13	1.71	0.71
1:A:345:THR:HG22	1:A:398:HIS:HD2	1.54	0.71
1:B:76:ILE:HD11	1:B:161:VAL:HG21	1.71	0.71
1:A:345:THR:CG2	1:A:398:HIS:HD2	2.04	0.70
1:B:173:HIS:ND1	1:B:179:LYS:HG2	2.05	0.70
1:B:393:LYS:HE3	1:B:393:LYS:HA	1.72	0.70
1:B:512:PRO:HB3	1:B:546:LEU:HD22	1.73	0.70
1:B:260:HIS:HB3	6:B:615:UQ5:H3M2	1.73	0.70
1:B:186:VAL:HG12	1:B:187:GLY:N	2.07	0.70
1:A:32:PHE:HA	7:A:628:EDO:H21	1.73	0.70
1:B:21:ASP:OD1	1:B:23:ARG:HD3	1.90	0.70
6:A:612:UQ5:H3M2	6:A:612:UQ5:H4M3	1.74	0.70
1:B:344:LEU:HD12	1:B:403:GLU:OE1	1.92	0.70
1:B:97:ASP:OD2	1:B:101:LYS:HD2	1.92	0.70
1:A:8:ARG:H	1:A:8:ARG:NE	1.90	0.69
1:A:5:LYS:HZ2	1:A:8:ARG:NH1	1.89	0.69
1:B:403:GLU:HG2	1:B:407:LYS:HE3	1.74	0.69
1:B:310:TRP:CZ2	1:B:316:ILE:HD13	2.28	0.69
1:B:210:ILE:HG12	1:B:350:LEU:HD21	1.75	0.69
1:B:272:GLY:C	6:B:615:UQ5:H1M3	2.12	0.69
1:B:334:ASN:ND2	1:B:354:CYS:HB3	2.08	0.69
1:A:5:LYS:NZ	1:A:8:ARG:NH1	2.40	0.68
1:B:230:ARG:NH2	8:B:1009:HOH:O	2.18	0.68
1:A:490:ALA:HA	7:A:621:EDO:C2	2.22	0.68
1:A:8:ARG:CD	1:A:8:ARG:N	2.56	0.68
1:A:505:THR:HA	7:A:623:EDO:H12	1.74	0.68
1:B:394:THR:C	1:B:396:GLY:H	1.96	0.68
1:A:53:ARG:NH1	1:A:57:LEU:HD13	2.09	0.68
1:A:260:HIS:HB3	6:A:612:UQ5:C4M	2.24	0.67
1:A:272:GLY:O	6:A:612:UQ5:H1M3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:ASP:O	1:B:101:LYS:HB2	1.95	0.67
1:B:214:GLY:O	1:B:355:SER:HA	1.96	0.66
1:B:432:TYR:HA	1:B:435:MET:HE3	1.77	0.66
1:A:31:ARG:HG2	1:A:200:ARG:HD3	1.78	0.66
1:B:498:HIS:HE1	1:B:551:GLN:HB3	1.60	0.65
1:B:40:ILE:O	1:B:70:VAL:HG23	1.96	0.65
1:B:189:GLN:HB3	1:B:499:ASP:OD2	1.96	0.65
1:B:503:HIS:CD2	1:B:573:PRO:HD3	2.32	0.65
1:A:8:ARG:HD2	1:A:8:ARG:N	2.11	0.65
1:B:227:PHE:HD2	1:B:346:PHE:HB2	1.60	0.65
1:B:208:VAL:HA	1:B:348:GLY:O	1.96	0.65
1:B:394:THR:O	1:B:396:GLY:N	2.28	0.65
1:B:498:HIS:CE1	1:B:551:GLN:CB	2.80	0.65
1:B:34:GLU:CG	1:B:66:ARG:HH22	2.06	0.65
1:B:18:ARG:HG3	1:B:29:MET:HE1	1.77	0.64
1:B:252:LYS:HE2	1:B:318:PRO:O	1.97	0.64
1:B:276:LEU:O	1:B:277:TYR:HD1	1.81	0.64
1:B:512:PRO:O	1:B:516:ASN:HB2	1.97	0.64
1:A:132:PRO:O	1:A:363:LYS:HG3	1.98	0.64
1:B:242:LEU:N	1:B:242:LEU:HD12	2.13	0.64
1:B:70:VAL:HG12	1:B:165:TYR:O	1.99	0.63
1:B:79:HIS:CD2	1:B:579:PRO:HD2	2.33	0.63
1:A:272:GLY:H	6:A:612:UQ5:C1M	2.11	0.63
1:B:257:ARG:HD3	1:B:259:ASP:OD1	1.98	0.63
1:B:52:THR:HG21	1:B:95:PHE:CZ	2.33	0.63
1:A:128:LEU:HD23	2:A:617:BHG:O3	1.99	0.63
1:A:9:ILE:HG22	1:A:548:ILE:HD12	1.81	0.63
1:A:5:LYS:HE3	1:A:8:ARG:HD3	1.80	0.63
1:B:244:GLU:HG2	1:B:307:PHE:HZ	1.63	0.63
1:B:310:TRP:CE2	1:B:316:ILE:HD13	2.34	0.63
1:B:117:LEU:HD22	1:B:313:HIS:CE1	2.34	0.62
1:B:347:PRO:HB3	1:B:394:THR:HG21	1.80	0.62
1:A:6:VAL:HG13	1:A:8:ARG:CZ	2.29	0.62
1:A:350:LEU:HD12	1:A:381:ILE:HD11	1.81	0.62
1:A:6:VAL:HG13	1:A:8:ARG:NH2	2.14	0.62
1:A:5:LYS:HE3	1:A:8:ARG:CD	2.30	0.62
1:B:382:PHE:O	1:B:386:THR:HG23	2.00	0.62
1:A:170:ILE:HD13	1:A:223:LEU:HD13	1.82	0.62
1:B:393:LYS:CE	1:B:393:LYS:HA	2.29	0.62
1:B:242:LEU:HD22	1:B:304:PHE:HA	1.82	0.61
1:B:31:ARG:HE	1:B:200:ARG:HH12	0.79	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:GLY:HA3	1:B:204:LEU:O	2.00	0.61
1:B:242:LEU:CD2	1:B:304:PHE:HA	2.31	0.61
1:A:128:LEU:HD23	2:A:617:BHG:HO3	1.65	0.61
1:B:248:ILE:HD13	1:B:286:LEU:CD2	2.27	0.61
1:B:483:PHE:HD2	1:B:483:PHE:N	1.98	0.61
1:A:5:LYS:HD3	1:A:6:VAL:CG1	2.27	0.61
1:A:517:LEU:HA	1:A:522:GLY:H	1.66	0.61
1:A:39:VAL:HG23	1:A:206:ALA:HB2	1.81	0.61
1:B:365:LYS:HB3	1:B:368:HIS:CE1	2.36	0.61
1:B:352:ILE:HG22	1:B:402:TYR:OH	2.00	0.61
1:B:14:THR:HG21	1:B:571:VAL:HG11	1.82	0.60
1:B:485:LEU:O	1:B:489:VAL:HG23	2.01	0.60
1:A:173:HIS:CE1	1:A:179:LYS:HG3	2.36	0.60
1:B:517:LEU:O	1:B:521:ASP:HA	2.01	0.60
1:B:226:LYS:HB3	1:B:227:PHE:HD1	1.63	0.60
1:B:447:GLY:HA2	1:B:449:GLU:OE2	2.01	0.60
1:B:517:LEU:HA	1:B:522:GLY:H	1.65	0.60
1:A:426:HIS:CE1	1:A:456:LYS:HD2	2.36	0.59
1:B:299:PRO:HG3	1:B:463:LEU:HD22	1.84	0.59
1:B:483:PHE:CD2	1:B:483:PHE:N	2.68	0.59
1:A:401:GLU:H	1:A:401:GLU:CD	2.04	0.59
1:B:22:LYS:O	1:B:25:GLU:OE2	2.20	0.59
1:A:8:ARG:NE	1:A:8:ARG:N	2.51	0.59
1:B:244:GLU:HG2	1:B:307:PHE:CZ	2.38	0.59
1:B:325:ARG:NH2	1:B:483:PHE:CB	2.57	0.59
1:B:61:HIS:C	1:B:63:LYS:H	2.05	0.59
1:A:335:GLU:HA	1:A:361:VAL:CG1	2.33	0.59
1:B:276:LEU:C	1:B:277:TYR:HD1	2.07	0.59
1:B:84:ALA:CB	1:B:141:VAL:O	2.50	0.59
1:A:497:GLU:H	7:A:619:EDO:H12	1.68	0.59
1:B:375:THR:HG22	1:B:379:GLU:OE2	2.03	0.59
1:B:218:HIS:CD2	1:B:572:VAL:HG13	2.38	0.58
1:A:335:GLU:HA	1:A:361:VAL:HG11	1.84	0.58
1:B:160:GLU:HB3	1:B:162:TYR:CE1	2.39	0.58
1:B:499:ASP:O	1:B:500:GLN:HB3	2.01	0.58
1:A:352:ILE:HG22	1:A:402:TYR:OH	2.04	0.58
1:B:345:THR:HB	1:B:398:HIS:NE2	2.18	0.58
1:B:186:VAL:CG1	1:B:187:GLY:N	2.66	0.58
1:B:72:LYS:NZ	1:B:72:LYS:HB3	2.18	0.58
1:B:86:LEU:HD22	1:B:87:ASP:N	2.18	0.58
1:B:99:LYS:HD2	1:B:99:LYS:H	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:476:LYS:H	1:B:476:LYS:CE	2.17	0.58
1:A:15:ILE:HD13	1:A:506:LEU:O	2.04	0.57
1:B:25:GLU:HG2	1:B:26:GLY:N	2.18	0.57
1:A:517:LEU:HA	1:A:522:GLY:N	2.19	0.57
1:B:60:GLN:HG3	1:B:61:HIS:CE1	2.40	0.57
1:A:40:ILE:HB	1:A:69:LEU:HD22	1.86	0.57
1:A:538:LEU:HB2	1:A:543:GLY:O	2.04	0.57
1:A:10:THR:HA	7:A:623:EDO:C2	2.34	0.57
1:B:348:GLY:N	1:B:397:LEU:O	2.34	0.57
1:A:107:THR:HG23	1:A:280:ASN:HB3	1.87	0.57
1:B:209:THR:CG2	1:B:211:PHE:CE1	2.75	0.56
1:B:226:LYS:HD2	1:B:227:PHE:CE1	2.39	0.56
1:B:294:LEU:O	1:B:459:ASP:HB3	2.06	0.56
1:B:224:TYR:HA	1:B:229:LEU:HD12	1.88	0.56
1:B:300:TYR:CE2	1:B:471:PRO:HG3	2.41	0.56
1:A:497:GLU:H	7:A:619:EDO:C1	2.17	0.56
1:B:317:LYS:HG3	1:B:481:ILE:HD13	1.87	0.56
1:B:300:TYR:CZ	1:B:471:PRO:HG3	2.41	0.56
1:A:107:THR:HB	1:A:140:VAL:HB	1.86	0.56
1:A:372:LYS:HE3	1:A:376:LEU:HD21	1.86	0.56
1:B:499:ASP:O	1:B:500:GLN:CB	2.53	0.56
1:B:260:HIS:HB3	6:B:615:UQ5:C3M	2.34	0.56
1:B:335:GLU:OE2	1:B:422:ARG:NH1	2.36	0.56
1:B:333:LEU:HD22	5:B:614:FAD:HM83	1.88	0.56
1:B:202:LEU:HD12	1:B:204:LEU:HG	1.88	0.55
1:B:85:CYS:HB3	1:B:365:LYS:HE3	1.89	0.55
1:A:260:HIS:HB3	6:A:612:UQ5:H4M1	1.89	0.55
1:B:317:LYS:HE3	1:B:481:ILE:HD12	1.87	0.55
1:B:218:HIS:NE2	1:B:219:LEU:HD13	2.21	0.55
1:B:25:GLU:HG2	1:B:26:GLY:H	1.72	0.55
1:B:83:GLY:O	1:B:84:ALA:HB3	2.06	0.55
1:A:551:GLN:HE21	1:A:551:GLN:N	1.98	0.55
1:B:422:ARG:N	1:B:423:PRO:HD2	2.21	0.55
1:B:445:PHE:O	1:B:448:MET:HG2	2.07	0.55
1:B:127:ILE:CG2	1:B:127:ILE:O	2.54	0.55
1:B:171:LEU:O	1:B:179:LYS:N	2.33	0.55
1:B:248:ILE:HG21	1:B:286:LEU:CD2	2.34	0.55
1:B:275:PHE:CZ	1:B:289:GLY:HA3	2.41	0.55
1:A:15:ILE:HD12	1:A:505:THR:HB	1.89	0.55
1:A:508:ASP:HB3	1:A:511:VAL:CG1	2.37	0.55
1:A:272:GLY:N	6:A:612:UQ5:H1M3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:PHE:CE2	1:B:219:LEU:HD23	2.42	0.55
1:B:326:ILE:O	1:B:327:ALA:HB2	2.06	0.54
1:B:173:HIS:HB2	1:B:175:ASP:OD1	2.07	0.54
1:B:476:LYS:H	1:B:476:LYS:HE2	1.73	0.54
1:A:6:VAL:O	1:A:6:VAL:HG22	2.07	0.54
1:B:209:THR:HG21	1:B:211:PHE:HE1	1.67	0.54
1:B:272:GLY:O	6:B:615:UQ5:H1M3	2.08	0.54
1:A:218:HIS:CE1	1:A:219:LEU:HD13	2.43	0.54
1:A:31:ARG:CG	1:A:200:ARG:HD3	2.37	0.54
1:B:245:LEU:HB2	1:B:327:ALA:HB3	1.90	0.54
1:A:202:LEU:HD12	1:A:203:GLU:N	2.22	0.54
1:B:178:VAL:HG22	1:B:348:GLY:HA3	1.89	0.54
1:B:545:ARG:HH11	1:B:545:ARG:HG3	1.72	0.54
1:B:98:TRP:HB2	1:B:103:ALA:CB	2.38	0.54
1:B:226:LYS:HB3	1:B:227:PHE:CE1	2.42	0.54
1:B:389:ASN:H	1:B:389:ASN:ND2	2.04	0.54
1:B:347:PRO:HB3	1:B:394:THR:CG2	2.38	0.54
1:B:227:PHE:CD2	1:B:346:PHE:HB2	2.43	0.54
1:B:498:HIS:HE1	1:B:551:GLN:CB	2.19	0.54
1:B:73:ALA:HB2	1:B:79:HIS:CE1	2.42	0.54
1:B:81:LEU:CD2	1:B:331:ARG:HB2	2.36	0.53
1:B:341:ILE:HG12	1:B:357:GLY:O	2.08	0.53
1:B:38:VAL:CG1	1:B:67:VAL:CG1	2.84	0.53
1:B:151:GLY:O	1:B:154:ALA:HB3	2.07	0.53
1:B:344:LEU:HD12	1:B:403:GLU:CD	2.27	0.53
1:B:210:ILE:HD11	1:B:381:ILE:CD1	2.38	0.53
1:B:387:SER:O	1:B:388:GLU:HB2	2.07	0.53
1:A:350:LEU:CD1	1:A:381:ILE:HD11	2.38	0.53
1:B:55:LYS:NZ	1:B:158:GLY:O	2.42	0.53
1:B:177:SER:HB3	1:B:394:THR:HG22	1.90	0.53
1:B:435:MET:HG3	6:B:615:UQ5:H112	1.90	0.53
1:B:301:LEU:HD23	1:B:302:SER:N	2.23	0.53
1:B:43:ALA:HB3	1:B:71:GLU:CG	2.29	0.53
1:A:500:GLN:OE1	1:A:574:GLU:HG3	2.09	0.53
1:B:441:PHE:CD2	1:B:449:GLU:HG2	2.43	0.53
1:B:208:VAL:CG2	1:B:397:LEU:HB2	2.39	0.53
1:A:271:TYR:HE1	6:A:612:UQ5:H103	1.74	0.53
1:B:114:PHE:HD2	1:B:125:VAL:HB	1.75	0.52
1:B:15:ILE:HD12	1:B:505:THR:HB	1.90	0.52
1:B:385:LEU:HD21	1:B:397:LEU:CD1	2.39	0.52
1:A:230:ARG:HA	1:A:233:CYS:SG	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:THR:HG22	1:A:398:HIS:NE2	2.25	0.52
1:A:355:SER:HB3	1:A:356:PRO:CD	2.35	0.52
1:B:335:GLU:HA	1:B:361:VAL:CG2	2.39	0.52
1:A:497:GLU:N	7:A:619:EDO:H12	2.24	0.52
1:B:85:CYS:H	5:B:614:FAD:C4	2.22	0.52
1:B:188:ILE:CG2	1:B:189:GLN:N	2.46	0.52
1:B:276:LEU:C	1:B:277:TYR:CD1	2.82	0.52
1:B:254:LYS:H	1:B:278:HIS:CE1	2.28	0.52
1:B:517:LEU:HD22	1:B:535:PHE:CD2	2.43	0.52
1:B:38:VAL:CG1	1:B:67:VAL:HG12	2.19	0.52
1:A:246:TRP:O	1:A:285:LEU:HD12	2.10	0.52
1:A:29:MET:CA	1:A:200:ARG:HD2	2.40	0.52
1:A:335:GLU:OE2	1:A:422:ARG:NH1	2.43	0.52
1:B:262:VAL:HG12	1:B:263:GLY:H	1.75	0.51
1:B:61:HIS:C	1:B:63:LYS:N	2.64	0.51
1:B:72:LYS:HZ3	1:B:72:LYS:HB3	1.74	0.51
1:B:76:ILE:HD11	1:B:161:VAL:CG2	2.40	0.51
1:A:8:ARG:C	1:A:10:THR:N	2.61	0.51
1:B:300:TYR:CD2	1:B:471:PRO:HA	2.46	0.51
1:B:302:SER:HB3	1:B:305:ARG:HB2	1.92	0.51
1:B:208:VAL:HG23	1:B:397:LEU:HB2	1.90	0.51
1:A:539:GLU:OE1	1:A:539:GLU:N	2.38	0.51
1:A:10:THR:HG23	7:A:623:EDO:H11	1.92	0.51
1:A:117:LEU:HD21	1:A:122:ARG:HG3	1.92	0.51
1:A:43:ALA:HB2	1:A:69:LEU:HD11	1.92	0.51
1:B:262:VAL:HG12	1:B:263:GLY:N	2.25	0.51
1:B:13:TYR:HB2	1:B:18:ARG:HD2	1.93	0.50
1:A:29:MET:HA	1:A:200:ARG:HD2	1.94	0.50
1:B:12:HIS:ND1	1:B:14:THR:CG2	2.65	0.50
1:B:40:ILE:O	1:B:69:LEU:CD2	2.60	0.50
1:A:393:LYS:O	1:A:394:THR:HG23	2.10	0.50
1:B:98:TRP:CZ3	1:B:105:LEU:HB2	2.46	0.50
1:B:335:GLU:HA	1:B:361:VAL:HG22	1.94	0.50
1:B:48:LEU:HD13	1:B:150:MET:HB2	1.93	0.50
1:B:143:LEU:O	1:B:144:GLY:C	2.50	0.50
1:A:420:ASN:ND2	1:A:449:GLU:OE1	2.45	0.50
1:B:33:ALA:HA	1:B:203:GLU:O	2.11	0.50
1:B:257:ARG:HG2	1:B:258:VAL:N	2.25	0.50
1:B:43:ALA:HB2	1:B:69:LEU:HD13	1.94	0.50
1:B:43:ALA:HB1	1:B:71:GLU:HG2	1.92	0.50
1:B:107:THR:OG1	1:B:280:ASN:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:538:LEU:O	1:B:540:GLN:N	2.45	0.50
1:A:282:GLY:HA2	7:A:627:EDO:H21	1.94	0.49
1:B:213:GLU:OE2	1:B:219:LEU:HB2	2.12	0.49
1:B:86:LEU:O	1:B:88:PRO:HD3	2.11	0.49
1:A:29:MET:C	1:A:200:ARG:HD2	2.33	0.49
1:A:34:GLU:HG3	1:A:66:ARG:NH1	2.23	0.49
1:A:5:LYS:HZ2	1:A:6:VAL:CG1	2.25	0.49
1:B:375:THR:O	1:B:379:GLU:HG3	2.12	0.49
1:B:505:THR:C	1:B:506:LEU:HD12	2.32	0.49
1:A:299:PRO:O	1:A:526:ARG:HD2	2.13	0.49
1:B:399:VAL:HG13	1:B:401:GLU:OE1	2.12	0.49
1:A:557:LYS:HE2	1:A:570:TRP:CE3	2.47	0.49
1:B:210:ILE:HA	1:B:350:LEU:HD23	1.95	0.49
1:B:545:ARG:NH1	1:B:545:ARG:HG3	2.27	0.49
1:B:203:GLU:CG	1:B:205:HIS:HE1	2.17	0.49
1:A:213:GLU:OE2	1:A:219:LEU:HB2	2.12	0.49
1:B:151:GLY:O	1:B:155:GLU:HG3	2.12	0.49
1:B:494:THR:HA	1:B:578:GLY:O	2.13	0.49
1:B:55:LYS:O	1:B:58:ALA:HB3	2.12	0.49
1:B:75:HIS:ND1	1:B:76:ILE:N	2.60	0.49
1:A:129:PRO:HG2	2:A:617:BHG:C6	2.42	0.49
1:A:333:LEU:H	1:A:333:LEU:HD23	1.76	0.49
1:A:333:LEU:N	1:A:333:LEU:HD23	2.27	0.49
1:A:65:LEU:HD11	1:A:385:LEU:CD1	2.39	0.49
1:B:24:TRP:CE2	1:B:194:PRO:HD3	2.48	0.49
1:B:31:ARG:HD2	1:B:203:GLU:OE1	2.13	0.48
1:B:257:ARG:NH1	8:B:1039:HOH:O	2.44	0.48
1:A:511:VAL:N	1:A:512:PRO:HD2	2.29	0.48
1:B:438:THR:CB	6:B:615:UQ5:H13	2.43	0.48
1:A:227:PHE:HB2	1:A:229:LEU:HD21	1.94	0.48
1:B:419:ARG:NH1	1:B:451:TRP:O	2.46	0.48
1:B:85:CYS:SG	1:B:258:VAL:HG11	2.53	0.48
1:A:5:LYS:HD2	1:A:7:PRO:HA	1.94	0.48
1:B:174:GLU:HA	1:B:174:GLU:OE1	2.13	0.48
1:B:557:LYS:HE2	1:B:570:TRP:CE3	2.49	0.48
1:B:161:VAL:HG23	1:B:163:PRO:HD3	1.94	0.48
1:B:385:LEU:HD21	1:B:397:LEU:HD11	1.95	0.48
1:A:72:LYS:HE3	5:A:611:FAD:O2B	2.14	0.48
1:A:5:LYS:NZ	1:A:6:VAL:HG12	2.28	0.48
1:B:61:HIS:O	1:B:63:LYS:N	2.47	0.48
1:A:73:ALA:HB1	1:A:78:ALA:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:TRP:CG	1:B:265:PRO:HA	2.49	0.48
1:B:236:GLN:OE1	1:B:336:GLY:HA3	2.14	0.48
1:B:362:PRO:HG3	1:B:418:VAL:HB	1.95	0.48
1:A:438:THR:CB	6:A:612:UQ5:H13	2.43	0.47
1:A:438:THR:OG1	6:A:612:UQ5:H13	2.14	0.47
1:B:210:ILE:HG12	1:B:350:LEU:CD2	2.43	0.47
1:A:46:ALA:HB1	1:A:352:ILE:HD12	1.96	0.47
1:B:160:GLU:HB3	1:B:162:TYR:HE1	1.78	0.47
1:A:243:LYS:HG2	1:A:244:GLU:N	2.29	0.47
1:A:186:VAL:HG12	1:A:199:GLU:HB2	1.96	0.47
1:B:494:THR:HG21	1:B:552:ASN:O	2.15	0.47
1:A:258:VAL:HG13	1:A:277:TYR:CE2	2.49	0.47
1:A:299:PRO:HG3	1:A:464:LYS:O	2.14	0.47
1:B:40:ILE:CG2	1:B:69:LEU:HD21	2.45	0.47
1:B:316:ILE:O	1:B:316:ILE:HG22	2.15	0.47
1:B:362:PRO:HG3	1:B:421:ILE:HD12	1.96	0.47
1:B:456:LYS:HE3	8:B:918:HOH:O	2.15	0.47
1:A:252:LYS:HD3	1:A:319:THR:HA	1.97	0.47
1:A:7:PRO:HD2	1:A:9:ILE:CG1	2.44	0.47
1:B:53:ARG:HD2	1:B:375:THR:HG23	1.97	0.47
1:A:515:ARG:HG3	8:A:1020:HOH:O	2.14	0.47
1:B:40:ILE:O	1:B:69:LEU:HD22	2.15	0.47
1:B:114:PHE:CZ	6:B:615:UQ5:H4M3	2.49	0.46
1:B:149:TRP:O	1:B:153:GLN:HG2	2.14	0.46
1:B:317:LYS:HB3	1:B:318:PRO:HD3	1.97	0.46
1:B:244:GLU:HA	1:B:327:ALA:O	2.15	0.46
1:A:29:MET:O	1:A:200:ARG:HD2	2.15	0.46
1:B:384:GLN:OE1	1:B:397:LEU:HD22	2.16	0.46
1:A:31:ARG:HG2	1:A:200:ARG:HB3	1.98	0.46
1:B:202:LEU:HD13	1:B:203:GLU:N	2.29	0.46
1:B:549:ASN:HB3	1:B:551:GLN:OE1	2.15	0.46
1:B:394:THR:C	1:B:396:GLY:N	2.65	0.46
1:B:538:LEU:HG	1:B:543:GLY:C	2.36	0.46
1:B:80:THR:HG21	1:B:147:VAL:HG21	1.98	0.46
1:A:181:ILE:HD12	1:A:181:ILE:C	2.36	0.46
1:A:239:GLY:O	1:A:333:LEU:HD23	2.16	0.46
1:A:40:ILE:HD12	1:A:51:ALA:HB2	1.98	0.46
1:B:505:THR:O	1:B:506:LEU:HD12	2.15	0.46
1:A:185:ASP:OD1	1:A:201:GLY:N	2.40	0.46
1:B:388:GLU:HA	1:B:388:GLU:OE1	2.16	0.46
1:B:72:LYS:CE	1:B:555:HIS:HD2	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:615:UQ5:H203	6:B:615:UQ5:H162	1.98	0.46
1:B:97:ASP:OD2	1:B:101:LYS:CD	2.63	0.46
1:B:186:VAL:CG1	1:B:187:GLY:H	2.29	0.46
1:B:210:ILE:HA	1:B:350:LEU:CD2	2.46	0.46
1:B:34:GLU:HG3	1:B:66:ARG:NH2	2.12	0.46
1:B:383:ASN:HA	1:B:383:ASN:HD22	1.51	0.46
1:A:399:VAL:HA	1:A:401:GLU:OE1	2.15	0.45
1:B:95:PHE:O	1:B:98:TRP:HD1	1.99	0.45
1:A:21:ASP:OD1	1:A:24:TRP:HD1	1.99	0.45
1:A:211:PHE:HB2	1:A:351:LEU:HD23	1.97	0.45
1:B:118:THR:O	1:B:119:GLU:C	2.55	0.45
1:A:182:ALA:HA	1:A:202:LEU:O	2.16	0.45
1:A:5:LYS:HE3	1:A:8:ARG:HD2	1.99	0.45
1:A:502:ALA:HB3	7:A:623:EDO:H21	1.98	0.45
1:A:97:ASP:OD2	1:A:101:LYS:HE3	2.15	0.45
1:B:175:ASP:OD2	1:B:394:THR:HA	2.16	0.45
1:A:72:LYS:HD3	1:A:572:VAL:HG12	1.98	0.45
6:A:612:UQ5:H272	6:A:612:UQ5:H251	1.45	0.45
1:B:261:THR:HG23	8:B:719:HOH:O	2.15	0.45
1:A:114:PHE:CE1	6:A:612:UQ5:H4M2	2.39	0.45
1:A:87:ASP:HA	1:A:138:ASN:OD1	2.16	0.45
1:B:210:ILE:HD11	1:B:381:ILE:HD12	1.98	0.45
1:B:460:SER:OG	1:B:566:GLN:HG2	2.17	0.45
1:B:344:LEU:HD12	1:B:344:LEU:H	1.82	0.45
1:B:361:VAL:HG11	1:B:422:ARG:CG	2.38	0.45
1:B:260:HIS:CD2	6:B:615:UQ5:H3M1	2.52	0.45
1:A:107:THR:HG23	1:A:280:ASN:CB	2.46	0.44
1:A:388:GLU:O	1:A:389:ASN:C	2.56	0.44
1:A:218:HIS:NE2	7:A:622:EDO:O1	2.49	0.44
1:B:188:ILE:HG21	1:B:501:PRO:HG3	1.99	0.44
1:A:407:LYS:NZ	8:A:806:HOH:O	2.50	0.44
1:A:502:ALA:O	7:A:623:EDO:H21	2.17	0.44
1:B:392:SER:CB	1:B:394:THR:OG1	2.56	0.44
1:A:230:ARG:HB3	8:A:1015:HOH:O	2.16	0.44
1:A:126:PRO:HB3	1:B:123:ILE:CG2	2.47	0.44
1:B:198:PHE:HZ	1:B:200:ARG:HD3	1.82	0.44
1:A:272:GLY:N	6:A:612:UQ5:C1M	2.79	0.44
1:A:443:TRP:HE1	2:A:617:BHG:HO3	1.65	0.44
1:B:189:GLN:NE2	1:B:191:ASP:OD1	2.41	0.44
1:B:182:ALA:HA	1:B:202:LEU:O	2.18	0.44
1:B:238:TYR:CG	1:B:561:ILE:HD13	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:LEU:HB2	1:B:402:TYR:HE1	1.80	0.44
1:B:52:THR:HG21	1:B:95:PHE:HZ	1.82	0.44
1:A:360:ASN:ND2	1:A:363:LYS:HD3	2.32	0.44
1:B:307:PHE:O	1:B:307:PHE:CD1	2.70	0.44
1:A:273:GLY:C	6:A:612:UQ5:H3M3	2.38	0.44
1:B:394:THR:O	1:B:395:ILE:HG23	2.17	0.44
1:A:15:ILE:CD1	1:A:506:LEU:O	2.65	0.44
1:A:557:LYS:HE2	1:A:570:TRP:CZ3	2.53	0.44
1:A:391:GLN:HB3	8:A:805:HOH:O	2.18	0.44
1:A:8:ARG:HD3	1:A:8:ARG:HH11	1.55	0.44
1:B:214:GLY:O	1:B:355:SER:CA	2.65	0.44
1:B:331:ARG:HD2	1:B:332:ALA:H	1.83	0.44
1:A:5:LYS:HD3	1:A:6:VAL:N	2.32	0.44
1:B:129:PRO:HA	1:B:134:ASN:ND2	2.33	0.44
1:B:239:GLY:O	1:B:333:LEU:HD23	2.17	0.44
1:A:5:LYS:NZ	1:A:8:ARG:HH11	2.15	0.43
1:B:55:LYS:HA	1:B:58:ALA:CB	2.48	0.43
1:B:165:TYR:HD2	1:B:165:TYR:HA	1.49	0.43
1:B:390:LEU:HA	1:B:390:LEU:HD13	1.56	0.43
1:B:516:ASN:HB3	1:B:524:GLU:OE2	2.18	0.43
1:A:113:ARG:HB2	1:A:259:ASP:OD1	2.19	0.43
1:A:161:VAL:HG12	1:A:163:PRO:HD3	2.00	0.43
1:A:214:GLY:O	1:A:355:SER:HA	2.18	0.43
1:B:325:ARG:NH2	1:B:483:PHE:CD1	2.87	0.43
1:B:547:GLN:HG2	1:B:547:GLN:O	2.19	0.43
1:B:556:CYS:O	1:B:557:LYS:HB2	2.18	0.43
1:A:361:VAL:CG2	1:A:362:PRO:HD3	2.46	0.43
1:A:572:VAL:HG23	7:A:622:EDO:O2	2.18	0.43
1:B:181:ILE:HG23	1:B:182:ALA:N	2.33	0.43
1:A:29:MET:HG3	1:A:200:ARG:NE	2.32	0.43
1:A:419:ARG:HG2	1:A:420:ASN:N	2.34	0.43
1:B:157:LEU:HD22	1:B:157:LEU:HA	1.78	0.43
1:B:181:ILE:HD11	1:B:211:PHE:CZ	2.54	0.43
1:B:236:GLN:NE2	1:B:340:SER:CB	2.82	0.43
1:B:387:SER:OG	1:B:389:ASN:ND2	2.51	0.43
1:A:245:LEU:HD23	1:A:245:LEU:HA	1.90	0.43
1:A:403:GLU:HG2	1:A:407:LYS:NZ	2.34	0.43
1:B:253:TRP:CD2	1:B:255:PRO:HD3	2.54	0.43
1:A:81:LEU:CD1	1:A:329:GLY:HA3	2.49	0.43
1:A:432:TYR:CD2	1:A:435:MET:CE	3.02	0.42
1:A:128:LEU:CD2	2:A:617:BHG:O3	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:LYS:HZ1	1:A:8:ARG:NH1	2.15	0.42
1:B:130:GLY:O	1:B:446:ARG:NH1	2.46	0.42
1:A:13:TYR:OH	7:A:622:EDO:H22	2.18	0.42
1:B:99:LYS:C	1:B:101:LYS:H	2.22	0.42
1:B:365:LYS:HA	5:B:614:FAD:C2	2.49	0.42
1:A:241:GLY:O	1:A:330:ALA:HA	2.20	0.42
1:A:503:HIS:HB2	1:A:571:VAL:O	2.20	0.42
1:A:5:LYS:CE	1:A:8:ARG:HD3	2.46	0.42
1:B:387:SER:O	1:B:388:GLU:CB	2.68	0.42
1:A:300:TYR:CG	1:A:471:PRO:HA	2.54	0.42
1:A:552:ASN:ND2	8:A:857:HOH:O	2.52	0.42
1:B:120:LYS:HE3	8:B:913:HOH:O	2.18	0.42
1:B:7:PRO:HG2	1:B:9:ILE:HD11	2.02	0.42
1:A:533:TYR:HB3	1:A:546:LEU:HD11	2.01	0.42
1:A:555:HIS:N	1:A:555:HIS:CD2	2.88	0.42
1:B:31:ARG:NH1	1:B:203:GLU:OE1	2.49	0.42
1:A:325:ARG:HD3	1:A:483:PHE:CE1	2.55	0.42
6:A:612:UQ5:H203	6:A:612:UQ5:H162	2.01	0.42
1:B:395:ILE:CG1	1:B:395:ILE:O	2.68	0.42
1:A:5:LYS:HZ2	1:A:8:ARG:CZ	2.33	0.42
1:A:7:PRO:HD2	1:A:9:ILE:HG13	2.02	0.42
1:B:99:LYS:C	1:B:101:LYS:N	2.71	0.42
1:A:96:PRO:HD2	1:A:97:ASP:OD1	2.20	0.42
1:B:155:GLU:HG2	1:B:161:VAL:HG11	2.01	0.42
1:B:268:ARG:O	1:B:431:VAL:HG13	2.19	0.42
1:A:220:ALA:HA	1:A:223:LEU:HB2	2.02	0.41
1:B:103:ALA:HA	1:B:104:PRO:HD2	1.87	0.41
1:B:128:LEU:HB3	1:B:129:PRO:HD2	2.01	0.41
1:A:539:GLU:CD	1:A:539:GLU:H	2.09	0.41
1:B:306:GLU:CD	1:B:474:TYR:HE2	2.23	0.41
1:A:449:GLU:H	1:A:449:GLU:HG2	1.51	0.41
1:B:111:GLU:HG2	1:B:257:ARG:HG3	2.02	0.41
1:A:335:GLU:CA	1:A:361:VAL:HG11	2.48	0.41
1:B:188:ILE:CG2	1:B:501:PRO:HG3	2.50	0.41
1:B:226:LYS:C	1:B:227:PHE:HD1	2.23	0.41
1:B:224:TYR:OH	1:B:355:SER:O	2.38	0.41
1:B:89:ARG:HD3	1:B:410:TRP:CE2	2.55	0.41
1:A:86:LEU:HD22	1:A:87:ASP:N	2.36	0.41
1:A:573:PRO:HA	8:A:1028:HOH:O	2.21	0.41
6:A:612:UQ5:H71	6:A:612:UQ5:H1M1	1.72	0.41
1:A:10:THR:HA	7:A:623:EDO:H22	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:VAL:HG23	1:A:138:ASN:O	2.21	0.41
1:A:21:ASP:OD1	1:A:24:TRP:CD1	2.73	0.41
1:A:538:LEU:HD12	1:A:538:LEU:HA	1.91	0.41
1:B:200:ARG:HB3	1:B:201:GLY:H	1.57	0.41
1:B:516:ASN:ND2	1:B:565:SER:OG	2.48	0.41
1:B:569:ASN:O	1:B:571:VAL:HG23	2.20	0.41
1:A:84:ALA:HB3	1:A:141:VAL:O	2.21	0.41
1:B:536:VAL:HA	1:B:537:PRO:HD3	1.68	0.41
1:B:184:ASN:ND2	1:B:575:GLY:H	2.19	0.41
6:B:615:UQ5:H251	6:B:615:UQ5:H272	1.73	0.41
1:B:69:LEU:HD23	1:B:69:LEU:HA	1.72	0.41
1:B:236:GLN:NE2	1:B:340:SER:HB2	2.36	0.41
1:B:355:SER:N	1:B:356:PRO:CD	2.83	0.41
1:B:99:LYS:O	1:B:101:LYS:N	2.54	0.41
1:A:495:ASN:HD22	1:A:495:ASN:C	2.25	0.41
1:A:5:LYS:HZ2	1:A:6:VAL:HG12	1.85	0.41
1:A:8:ARG:HE	1:A:8:ARG:N	2.01	0.41
1:B:294:LEU:O	1:B:562:LYS:NZ	2.43	0.41
1:B:392:SER:HB2	1:B:394:THR:HG1	1.80	0.41
1:A:305:ARG:O	1:A:309:ARG:HB3	2.20	0.40
1:A:388:GLU:HB3	1:A:389:ASN:H	1.63	0.40
1:A:5:LYS:HD3	1:A:6:VAL:H	1.87	0.40
1:B:258:VAL:HG12	1:B:277:TYR:CD1	2.57	0.40
1:B:42:GLY:O	1:B:43:ALA:HB3	2.21	0.40
1:B:562:LYS:O	1:B:562:LYS:HG3	2.21	0.40
1:B:94:LEU:HD13	1:B:95:PHE:CE1	2.56	0.40
1:A:5:LYS:HZ1	1:A:8:ARG:HH11	1.69	0.40
1:B:56:GLN:O	1:B:60:GLN:HG2	2.21	0.40
1:B:72:LYS:HB2	5:B:614:FAD:C4A	2.50	0.40
1:A:294:LEU:O	1:A:459:ASP:HB3	2.21	0.40
1:A:365:LYS:HA	5:A:611:FAD:C2	2.52	0.40
1:B:129:PRO:HA	1:B:134:ASN:HD22	1.85	0.40
1:B:200:ARG:HH11	1:B:200:ARG:HB3	1.87	0.40
1:B:21:ASP:HB3	1:B:24:TRP:CD1	2.37	0.40
1:A:133:MET:HA	8:A:710:HOH:O	2.20	0.40
1:A:15:ILE:CD1	1:A:505:THR:HB	2.52	0.40
1:A:538:LEU:N	1:A:543:GLY:O	2.43	0.40
1:B:198:PHE:CZ	1:B:200:ARG:HD3	2.56	0.40
1:B:244:GLU:CG	1:B:307:PHE:HZ	2.32	0.40
1:A:10:THR:OG1	7:A:623:EDO:H11	2.22	0.40
1:B:195:LYS:HB3	1:B:197:THR:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:467:LYS:H	1:B:467:LYS:HG2	1.58	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	579/584 (99%)	544 (94%)	31 (5%)	4 (1%)	22	39
1	B	576/584 (99%)	493 (86%)	62 (11%)	21 (4%)	3	4
All	All	1155/1168 (99%)	1037 (90%)	93 (8%)	25 (2%)	6	10

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	8	ARG
1	B	74	ALA
1	B	84	ALA
1	B	99	LYS
1	B	391	GLN
1	B	395	ILE
1	B	500	GLN
1	B	532	VAL
1	B	539	GLU
1	B	62	GLU
1	B	187	GLY
1	B	385	LEU
1	A	6	VAL
1	A	394	THR
1	A	541	GLY
1	B	314	PRO
1	A	7	PRO

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Mol	Chain	Res	Type
1	B	23	ARG
1	B	164	GLY
1	B	542	ASP
1	B	17	PRO
1	B	133	MET
1	B	573	PRO
1	B	537	PRO
1	B	194	PRO

### 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	483/486 (99%)	428 (89%)	55 (11%)	5	11
1	B	479/486 (99%)	403 (84%)	76 (16%)	2	4
All	All	962/972 (99%)	831 (86%)	131 (14%)	3	7

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	CYS
1	A	5	LYS
1	A	8	ARG
1	A	18	ARG
1	A	19	ASP
1	A	21	ASP
1	A	22	LYS
1	A	29	MET
1	A	57	LEU
1	A	62	GLU
1	A	69	LEU
1	A	75	HIS
1	A	81	LEU
1	A	85	CYS
1	A	86	LEU

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Mol	Chain	Res	Type
1	A	121	TYR
1	A	128	LEU
1	A	133	MET
1	A	157	LEU
1	A	174	GLU
1	A	200	ARG
1	A	202	LEU
1	A	219	LEU
1	A	223	LEU
1	A	225	LYS
1	A	244	GLU
1	A	266	LEU
1	A	279	LEU
1	A	320	LEU
1	A	321	GLU
1	A	331	ARG
1	A	333	LEU
1	A	342	PRO
1	A	359	MET
1	A	361	VAL
1	A	363	LYS
1	A	383	ASN
1	A	390	LEU
1	A	391	GLN
1	A	393	LYS
1	A	419	ARG
1	A	422	ARG
1	A	449	GLU
1	A	456	LYS
1	A	461	ASP
1	A	462	GLN
1	A	467	LYS
1	A	495	ASN
1	A	515	ARG
1	A	526	ARG
1	A	527	PHE
1	A	529	PRO
1	A	539	GLU
1	A	545	ARG
1	A	551	GLN
1	B	8	ARG
1	B	11	THR

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Mol	Chain	Res	Type
1	B	18	ARG
1	B	25	GLU
1	B	27	VAL
1	B	30	GLU
1	B	31	ARG
1	B	64	ASP
1	B	65	LEU
1	B	69	LEU
1	B	70	VAL
1	B	71	GLU
1	B	72	LYS
1	B	80	THR
1	B	85	CYS
1	B	86	LEU
1	B	94	LEU
1	B	99	LYS
1	B	112	ASP
1	B	133	MET
1	B	152	GLU
1	B	157	LEU
1	B	161	VAL
1	B	165	TYR
1	B	171	LEU
1	B	174	GLU
1	B	197	THR
1	B	200	ARG
1	B	202	LEU
1	B	204	LEU
1	B	219	LEU
1	B	222	GLN
1	B	225	LYS
1	B	227	PHE
1	B	244	GLU
1	B	250	GLU
1	B	252	LYS
1	B	255	PRO
1	B	259	ASP
1	B	266	LEU
1	B	279	LEU
1	B	286	LEU
1	B	288	LEU
1	B	320	LEU

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Mol	Chain	Res	Type
1	B	331	ARG
1	B	333	LEU
1	B	335	GLU
1	B	344	LEU
1	B	350	LEU
1	B	380	SER
1	B	383	ASN
1	B	389	ASN
1	B	393	LYS
1	B	394	THR
1	B	402	TYR
1	B	419	ARG
1	B	422	ARG
1	B	452	THR
1	B	458	SER
1	B	461	ASP
1	B	467	LYS
1	B	476	LYS
1	B	483	PHE
1	B	485	LEU
1	B	486	LEU
1	B	495	ASN
1	B	500	GLN
1	B	510	SER
1	B	513	VAL
1	B	515	ARG
1	B	524	GLU
1	B	527	PHE
1	B	538	LEU
1	B	539	GLU
1	B	540	GLN
1	B	551	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	106	ASN
1	A	173	HIS
1	A	222	GLN
1	A	384	GLN
1	A	495	ASN

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Mol	Chain	Res	Type
1	A	525	GLN
1	A	551	GLN
1	B	106	ASN
1	B	205	HIS
1	B	383	ASN
1	B	389	ASN
1	B	462	GLN
1	B	498	HIS
1	B	516	ASN
1	B	525	GLN
1	B	582	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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	$\# Z  > 2$
7	EDO	A	621	-	3,3,3	0.62	0	2,2,2	0.42	0
4	SF4	A	610	1	0,12,12	0.00	-	-		
5	FAD	B	614	-	51,58,58	2.59	17 (33%)	60,89,89	3.10	17 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	EDO	A	625	-	3,3,3	0.72	0	2,2,2	0.45	0
6	UQ5	B	615	-	38,38,38	2.65	17 (44%)	46,49,49	2.35	21 (45%)
2	BHG	B	618	-	18,18,18	1.04	1 (5%)	23,23,23	2.87	3 (13%)
7	EDO	A	622	-	3,3,3	0.73	0	2,2,2	0.06	0
6	UQ5	A	612	-	38,38,38	2.61	15 (39%)	46,49,49	2.49	16 (34%)
7	EDO	A	623	-	3,3,3	0.52	0	2,2,2	0.61	0
7	EDO	A	626	-	3,3,3	0.78	0	2,2,2	0.50	0
7	EDO	A	628	-	3,3,3	0.85	0	2,2,2	0.32	0
7	EDO	A	627	-	3,3,3	0.84	0	2,2,2	0.44	0
2	BHG	A	616	-	18,18,18	1.08	2 (11%)	23,23,23	3.64	4 (17%)
7	EDO	B	620	-	3,3,3	0.64	0	2,2,2	0.56	0
7	EDO	A	619	-	3,3,3	0.61	0	2,2,2	0.42	0
5	FAD	A	611	-	51,58,58	2.78	22 (43%)	60,89,89	2.80	15 (25%)
4	SF4	B	613	1	0,12,12	0.00	-	-	-	-
2	BHG	A	617	-	18,18,18	1.39	4 (22%)	23,23,23	2.38	5 (21%)
7	EDO	A	624	-	3,3,3	0.65	0	2,2,2	0.59	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	A	621	-	-	1/1/1/1	-
4	SF4	A	610	1	-	-	0/6/5/5
5	FAD	B	614	-	-	6/30/50/50	0/6/6/6
7	EDO	A	625	-	-	1/1/1/1	-
6	UQ5	B	615	-	-	18/33/57/57	0/1/1/1
2	BHG	B	618	-	1/1/5/5	5/9/29/29	0/1/1/1
7	EDO	A	622	-	-	1/1/1/1	-
6	UQ5	A	612	-	-	19/33/57/57	0/1/1/1
7	EDO	A	623	-	-	1/1/1/1	-
7	EDO	A	626	-	-	0/1/1/1	-
7	EDO	A	628	-	-	0/1/1/1	-
7	EDO	A	627	-	-	0/1/1/1	-
2	BHG	A	616	-	1/1/5/5	7/9/29/29	0/1/1/1
7	EDO	B	620	-	-	0/1/1/1	-
7	EDO	A	619	-	-	1/1/1/1	-
5	FAD	A	611	-	-	2/30/50/50	0/6/6/6
7	EDO	A	624	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BHG	A	617	-	1/1/5/5	5/9/29/29	0/1/1/1
4	SF4	B	613	1	-	-	0/6/5/5

All (78) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	611	FAD	C1'-N10	-9.86	1.38	1.48
6	B	615	UQ5	C28-C29	7.69	1.54	1.32
6	A	612	UQ5	C28-C29	7.37	1.53	1.32
5	B	614	FAD	C4X-C10	7.18	1.46	1.38
5	B	614	FAD	C4X-N5	6.39	1.42	1.33
5	A	611	FAD	C4-N3	6.30	1.44	1.33
5	B	614	FAD	C1'-N10	-6.29	1.41	1.48
5	B	614	FAD	C9A-N10	5.78	1.46	1.38
6	A	612	UQ5	C8-C9	5.47	1.46	1.33
6	A	612	UQ5	C18-C19	5.31	1.45	1.33
6	A	612	UQ5	O3-C3	5.19	1.49	1.36
6	B	615	UQ5	C18-C19	5.17	1.45	1.33
6	B	615	UQ5	C7-C8	-5.13	1.43	1.50
5	A	611	FAD	O4B-C1B	5.11	1.48	1.41
6	B	615	UQ5	C8-C9	5.07	1.45	1.33
5	A	611	FAD	C6-C5X	5.00	1.49	1.41
5	B	614	FAD	C4-N3	4.80	1.41	1.33
5	B	614	FAD	C4A-N3A	4.68	1.42	1.35
5	A	611	FAD	C4X-N5	4.41	1.39	1.33
5	A	611	FAD	C10-N1	4.29	1.38	1.33
6	B	615	UQ5	C25-C24	4.14	1.61	1.50
5	B	614	FAD	C5'-C4'	4.02	1.57	1.51
5	A	611	FAD	C8-C7	3.96	1.50	1.40
6	A	612	UQ5	C21-C19	3.82	1.59	1.51
6	A	612	UQ5	C7-C8	-3.81	1.45	1.50
5	A	611	FAD	C5X-N5	3.77	1.41	1.35
5	B	614	FAD	C6-C5X	3.65	1.47	1.41
5	A	611	FAD	C9A-N10	3.64	1.43	1.38
6	B	615	UQ5	C22-C23	-3.62	1.38	1.50
5	B	614	FAD	C8A-N7A	-3.61	1.28	1.34
5	A	611	FAD	C4-C4X	3.55	1.47	1.41
6	A	612	UQ5	C23-C24	3.52	1.41	1.33
5	B	614	FAD	C2-N1	-3.52	1.31	1.38
5	A	611	FAD	C5'-C4'	-3.51	1.46	1.51
5	A	611	FAD	P-O5'	-3.36	1.45	1.59
6	B	615	UQ5	C6-C5	3.27	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	615	UQ5	C13-C14	3.23	1.40	1.33
5	B	614	FAD	O4B-C1B	3.22	1.45	1.41
6	A	612	UQ5	C13-C14	3.17	1.40	1.33
5	A	611	FAD	C2A-N3A	3.14	1.37	1.32
6	A	612	UQ5	C22-C23	-3.14	1.40	1.50
6	B	615	UQ5	C21-C19	2.90	1.57	1.51
5	B	614	FAD	C8-C7	2.90	1.48	1.40
2	A	617	BHG	O5-C1	2.88	1.49	1.41
6	B	615	UQ5	O3-C3	2.88	1.43	1.36
5	B	614	FAD	C9A-C5X	2.87	1.48	1.42
6	A	612	UQ5	O3-C3M	-2.82	1.38	1.45
6	A	612	UQ5	C20-C19	-2.81	1.43	1.50
6	B	615	UQ5	C20-C19	-2.73	1.43	1.50
2	A	617	BHG	O1-C1'	2.67	1.50	1.43
6	B	615	UQ5	O4-C4	2.67	1.43	1.36
6	B	615	UQ5	C7-C6	2.57	1.55	1.51
5	A	611	FAD	C8A-N7A	-2.55	1.30	1.34
5	A	611	FAD	C2-N3	2.55	1.43	1.38
5	A	611	FAD	O4B-C4B	-2.55	1.39	1.45
5	A	611	FAD	C4X-C10	2.50	1.41	1.38
5	B	614	FAD	C2-N3	2.47	1.43	1.38
2	A	617	BHG	O5-C5	2.44	1.50	1.44
6	A	612	UQ5	C11-C9	-2.40	1.46	1.51
6	A	612	UQ5	C6-C5	2.38	1.53	1.46
6	B	615	UQ5	C11-C9	-2.35	1.46	1.51
2	A	616	BHG	O1-C1	-2.32	1.36	1.40
5	B	614	FAD	P-O5'	-2.28	1.50	1.59
2	B	618	BHG	O5-C1	2.28	1.47	1.41
5	A	611	FAD	C9-C9A	2.28	1.45	1.40
5	B	614	FAD	C10-N1	2.27	1.36	1.33
6	B	615	UQ5	C23-C24	2.25	1.38	1.33
5	A	611	FAD	C4A-N3A	2.22	1.38	1.35
6	B	615	UQ5	C30-C29	2.15	1.56	1.50
5	A	611	FAD	C2B-C1B	-2.14	1.50	1.53
6	B	615	UQ5	O3-C3M	-2.10	1.40	1.45
5	B	614	FAD	C9-C9A	2.09	1.44	1.40
6	A	612	UQ5	C25-C24	2.07	1.56	1.50
5	A	611	FAD	C2-N1	-2.05	1.34	1.38
2	A	616	BHG	C1-C2	2.05	1.58	1.52
6	A	612	UQ5	C7-C6	2.05	1.54	1.51
2	A	617	BHG	O1-C1	-2.02	1.36	1.40
5	A	611	FAD	PA-O2A	-2.02	1.45	1.55

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	614	FAD	C4-N3-C2	13.64	126.66	115.14
5	A	611	FAD	C4-N3-C2	13.25	126.33	115.14
2	B	618	BHG	O1-C1'-C2'	11.74	150.73	109.56
2	A	616	BHG	C1'-O1-C1	11.42	132.78	113.84
2	A	616	BHG	O1-C1'-C2'	10.04	144.74	109.56
2	A	617	BHG	O1-C1'-C2'	9.48	142.78	109.56
5	B	614	FAD	C10-C4X-N5	8.33	127.02	121.26
5	B	614	FAD	C4X-C4-N3	-7.77	112.80	123.43
5	A	611	FAD	C4X-C4-N3	-7.33	113.40	123.43
6	A	612	UQ5	C8-C7-C6	6.99	130.88	112.05
5	A	611	FAD	C10-C4X-N5	6.98	126.09	121.26
5	B	614	FAD	O3'-C3'-C2'	6.93	125.55	108.81
2	A	616	BHG	O1-C1-C2	6.87	119.03	108.30
5	B	614	FAD	O4B-C1B-C2B	-6.78	97.02	106.93
2	B	618	BHG	C1'-O1-C1	5.95	123.71	113.84
5	A	611	FAD	O4B-C1B-C2B	-5.71	98.58	106.93
6	A	612	UQ5	C12-C11-C9	-5.25	95.72	112.98
6	B	615	UQ5	C11-C12-C13	5.06	128.50	111.88
6	B	615	UQ5	C12-C11-C9	-4.94	96.73	112.98
5	B	614	FAD	P-O5'-C5'	4.86	150.18	121.68
5	B	614	FAD	C4X-C10-N10	-4.43	115.75	120.30
5	B	614	FAD	O4'-C4'-C3'	4.12	119.12	109.10
5	A	611	FAD	C4-C4X-C10	-4.11	117.23	119.95
5	A	611	FAD	O3'-C3'-C2'	4.01	118.50	108.81
6	A	612	UQ5	C15-C14-C16	3.98	121.97	115.27
6	A	612	UQ5	C16-C17-C18	3.94	124.82	111.88
6	B	615	UQ5	C1-C6-C5	-3.85	115.96	119.58
6	A	612	UQ5	C1M-C1-C6	-3.83	118.16	124.40
6	B	615	UQ5	C20-C19-C21	3.75	121.58	115.27
6	A	612	UQ5	C6-C1-C2	3.61	122.03	119.18
6	A	612	UQ5	O2-C2-C3	-3.59	113.31	120.93
6	A	612	UQ5	C20-C19-C21	3.58	121.29	115.27
6	A	612	UQ5	C11-C12-C13	3.54	123.52	111.88
6	B	615	UQ5	C6-C1-C2	3.54	121.98	119.18
6	B	615	UQ5	C1M-C1-C6	-3.52	118.65	124.40
6	B	615	UQ5	C8-C7-C6	3.52	121.54	112.05
6	B	615	UQ5	C26-C27-C28	3.49	123.34	111.88
5	A	611	FAD	P-O5'-C5'	3.48	142.10	121.68
5	A	611	FAD	C3B-C2B-C1B	3.47	106.20	100.98
6	B	615	UQ5	O2-C2-C3	-3.47	113.57	120.93
2	A	616	BHG	O5-C1-O1	-3.46	101.78	109.97
6	A	612	UQ5	C10-C9-C11	3.41	121.01	115.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	611	FAD	C4X-C10-N10	-3.37	116.84	120.30
5	A	611	FAD	C1'-N10-C9A	3.30	120.89	118.29
6	A	612	UQ5	C26-C27-C28	3.27	122.63	111.88
6	B	615	UQ5	C16-C17-C18	3.26	122.61	111.88
6	B	615	UQ5	C15-C14-C16	3.25	120.74	115.27
6	B	615	UQ5	C10-C9-C11	3.24	120.72	115.27
5	A	611	FAD	P-O3P-PA	3.23	143.92	132.83
5	B	614	FAD	C4-C4X-C10	-3.22	117.82	119.95
6	A	612	UQ5	O5-C5-C6	-3.14	116.04	121.55
5	B	614	FAD	C4-C4X-N5	-3.05	115.11	118.60
5	A	611	FAD	C5X-C9A-N10	-3.01	115.53	117.72
6	B	615	UQ5	O4-C4-C5	3.01	126.75	116.56
2	A	617	BHG	O1-C1-C2	2.97	112.94	108.30
5	B	614	FAD	C3B-C2B-C1B	2.86	105.29	100.98
5	B	614	FAD	C9A-C5X-N5	2.85	126.83	122.36
5	B	614	FAD	C4A-C5A-N7A	2.83	112.35	109.40
5	B	614	FAD	C4X-N5-C5X	-2.82	113.96	116.77
6	A	612	UQ5	C31-C29-C30	-2.79	108.44	114.60
6	B	615	UQ5	C25-C24-C26	2.77	119.92	115.27
6	B	615	UQ5	C10-C9-C8	-2.76	116.60	123.68
2	A	617	BHG	C1'-O1-C1	-2.72	109.33	113.84
6	A	612	UQ5	C17-C18-C19	2.71	134.19	127.66
5	B	614	FAD	C6-C5X-N5	-2.71	116.06	119.05
5	A	611	FAD	O4'-C4'-C3'	2.64	115.51	109.10
6	A	612	UQ5	C1-C6-C5	-2.59	117.14	119.58
5	B	614	FAD	C1'-N10-C9A	2.52	120.28	118.29
2	B	618	BHG	C4'-C3'-C2'	2.48	127.01	114.42
5	A	611	FAD	C4A-C5A-N7A	2.41	111.91	109.40
6	B	615	UQ5	O5-C5-C6	-2.39	117.35	121.55
6	A	612	UQ5	O4-C4-C5	2.37	124.59	116.56
6	B	615	UQ5	C31-C29-C30	-2.36	109.38	114.60
2	A	617	BHG	O5-C1-O1	2.34	115.51	109.97
5	A	611	FAD	O3B-C3B-C4B	-2.19	104.73	111.05
2	A	617	BHG	C4'-C3'-C2'	2.17	125.46	114.42
6	B	615	UQ5	O4-C4-C3	-2.17	115.44	123.64
5	B	614	FAD	P-O3P-PA	2.13	140.15	132.83
6	B	615	UQ5	C4M-O4-C4	2.11	123.94	116.47
6	B	615	UQ5	C25-C24-C23	-2.09	118.31	123.68
6	B	615	UQ5	C7-C6-C5	2.01	120.90	118.48

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	618	BHG	C4
2	A	616	BHG	C4
2	A	617	BHG	C4

All (68) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	614	FAD	C5'-O5'-P-O2P
6	B	615	UQ5	C1-C6-C7-C8
6	B	615	UQ5	C5-C6-C7-C8
6	B	615	UQ5	C14-C16-C17-C18
6	B	615	UQ5	C16-C17-C18-C19
6	B	615	UQ5	C18-C19-C21-C22
6	B	615	UQ5	C20-C19-C21-C22
6	B	615	UQ5	C19-C21-C22-C23
6	B	615	UQ5	C26-C27-C28-C29
6	B	615	UQ5	C27-C28-C29-C31
6	A	612	UQ5	C1-C6-C7-C8
6	A	612	UQ5	C5-C6-C7-C8
6	A	612	UQ5	C6-C7-C8-C9
6	A	612	UQ5	C16-C17-C18-C19
6	A	612	UQ5	C23-C24-C26-C27
6	A	612	UQ5	C25-C24-C26-C27
6	A	612	UQ5	C26-C27-C28-C29
6	A	612	UQ5	C27-C28-C29-C30
2	A	616	BHG	C2-C1-O1-C1'
2	A	616	BHG	O5-C1-O1-C1'
2	A	617	BHG	C2-C1-O1-C1'
2	A	617	BHG	O5-C1-O1-C1'
2	A	617	BHG	C2'-C1'-O1-C1
6	B	615	UQ5	C27-C28-C29-C30
6	A	612	UQ5	C27-C28-C29-C31
6	A	612	UQ5	C20-C19-C21-C22
6	B	615	UQ5	C25-C24-C26-C27
6	B	615	UQ5	C23-C24-C26-C27
6	A	612	UQ5	C9-C11-C12-C13
6	A	612	UQ5	C14-C16-C17-C18
6	A	612	UQ5	C18-C19-C21-C22
2	A	617	BHG	C4-C5-C6-O6
2	B	618	BHG	C1'-C2'-C3'-C4'
6	B	615	UQ5	C15-C14-C16-C17
2	A	616	BHG	C2'-C3'-C4'-C5'
6	A	612	UQ5	C19-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
2	B	618	BHG	C2'-C3'-C4'-C5'
7	A	624	EDO	O1-C1-C2-O2
2	A	616	BHG	C3'-C4'-C5'-C6'
6	B	615	UQ5	C3-C4-O4-C4M
2	B	618	BHG	C3'-C4'-C5'-C6'
2	A	616	BHG	O1-C1'-C2'-C3'
6	A	612	UQ5	C15-C14-C16-C17
6	B	615	UQ5	C13-C14-C16-C17
6	A	612	UQ5	C13-C14-C16-C17
2	B	618	BHG	O1-C1'-C2'-C3'
2	A	617	BHG	O5-C5-C6-O6
2	A	616	BHG	C1'-C2'-C3'-C4'
2	A	616	BHG	C2'-C1'-O1-C1
7	A	621	EDO	O1-C1-C2-O2
5	B	614	FAD	PA-O3P-P-O5'
5	B	614	FAD	C5'-O5'-P-O3P
5	B	614	FAD	C5'-O5'-P-O1P
6	B	615	UQ5	C6-C7-C8-C9
2	B	618	BHG	O5-C1-O1-C1'
6	A	612	UQ5	C24-C26-C27-C28
7	A	623	EDO	O1-C1-C2-O2
6	A	612	UQ5	C5-C4-O4-C4M
6	B	615	UQ5	C9-C11-C12-C13
7	A	622	EDO	O1-C1-C2-O2
5	A	611	FAD	O4B-C4B-C5B-O5B
6	B	615	UQ5	C24-C26-C27-C28
5	A	611	FAD	PA-O3P-P-O5'
5	B	614	FAD	O4B-C4B-C5B-O5B
7	A	619	EDO	O1-C1-C2-O2
6	A	612	UQ5	C3-C4-O4-C4M
7	A	625	EDO	O1-C1-C2-O2
5	B	614	FAD	O4'-C4'-C5'-O5'

There are no ring outliers.

11 monomers are involved in 60 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	621	EDO	3	0
5	B	614	FAD	4	0
6	B	615	UQ5	13	0
7	A	622	EDO	3	0
6	A	612	UQ5	17	0

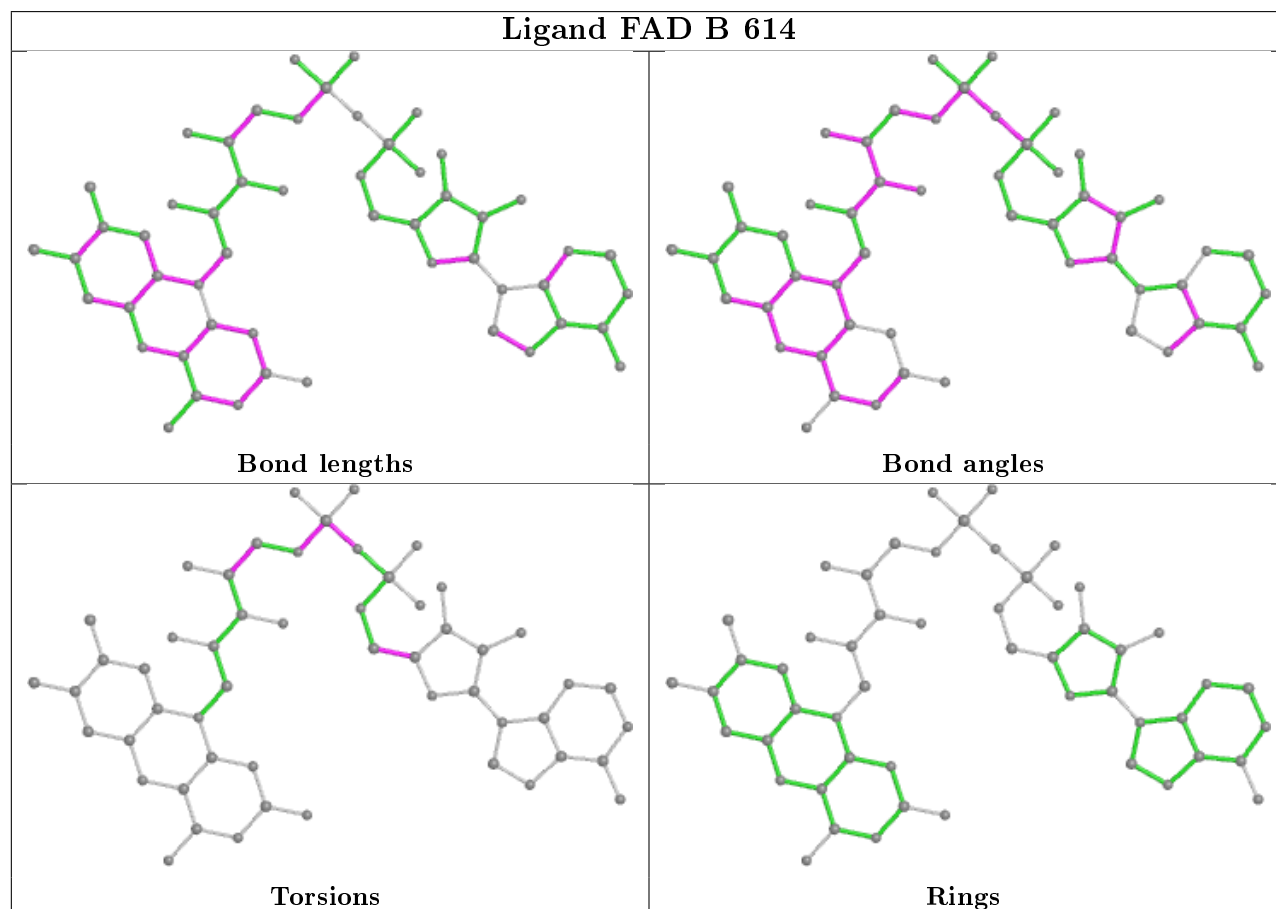
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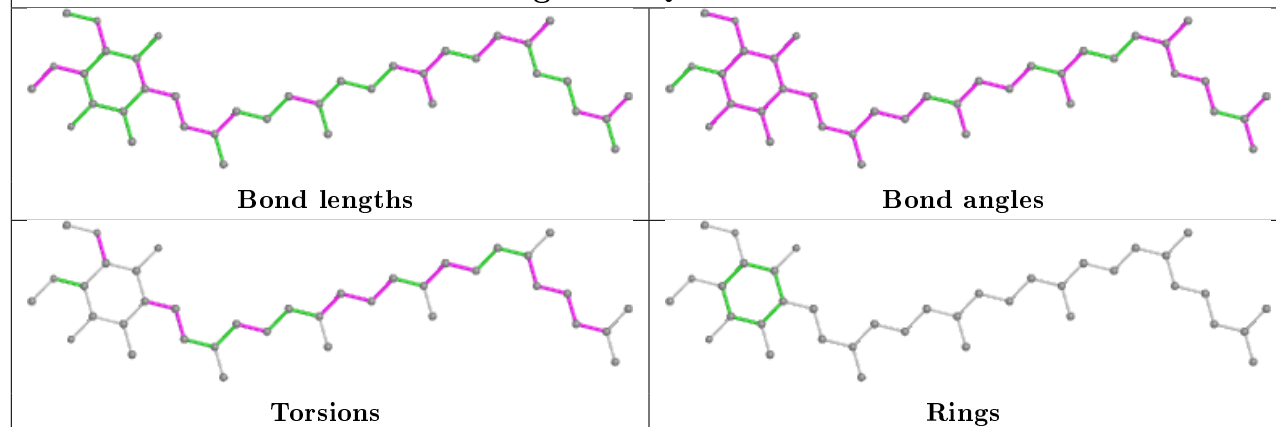
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	623	EDO	7	0
7	A	628	EDO	1	0
7	A	627	EDO	1	0
7	A	619	EDO	3	0
5	A	611	FAD	2	0
2	A	617	BHG	6	0

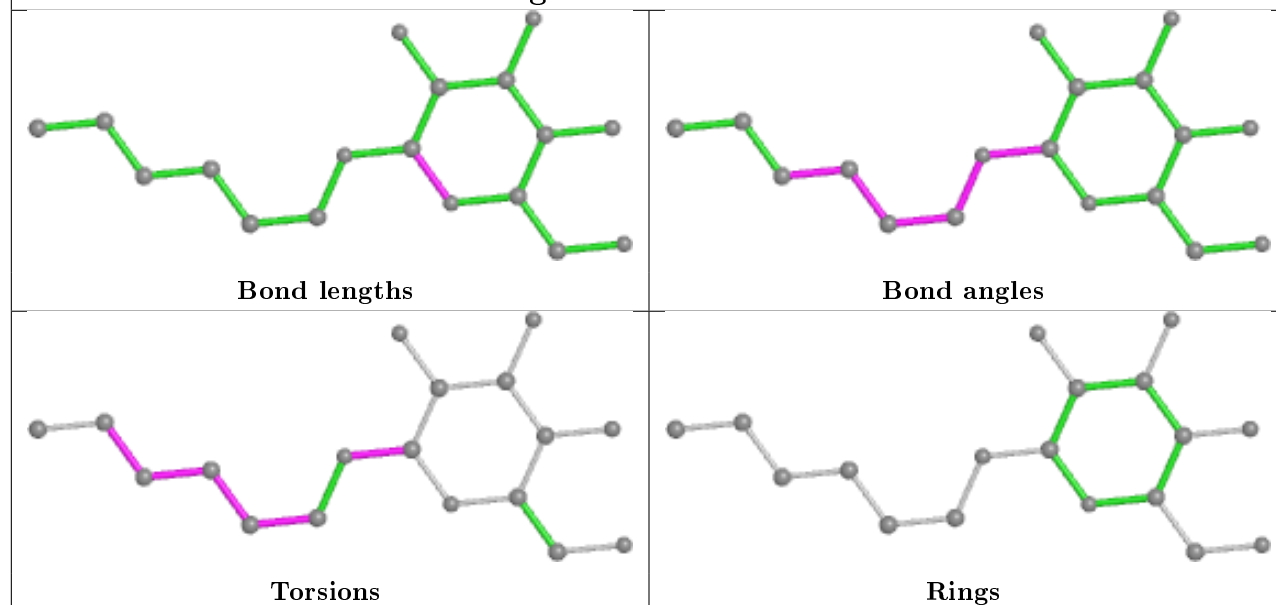
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



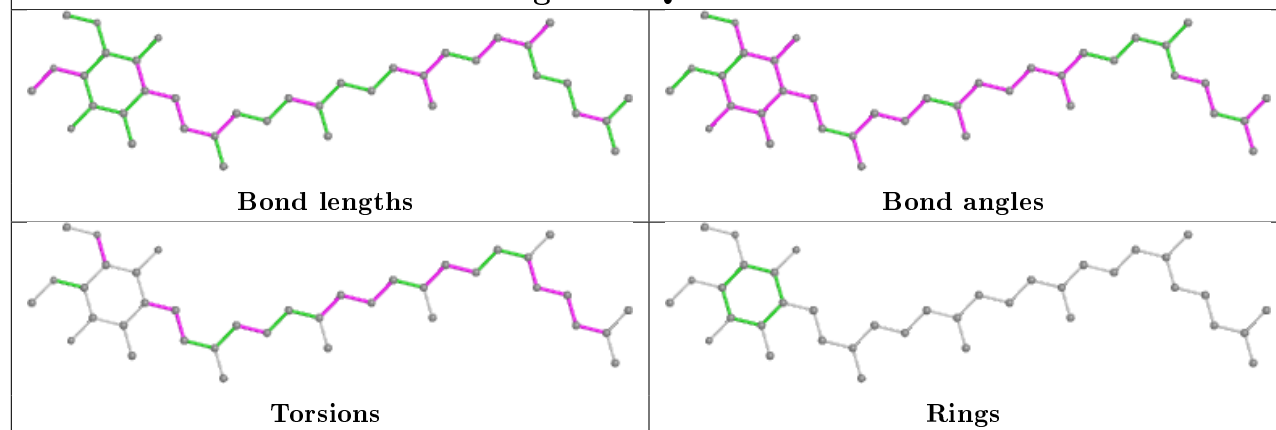
## Ligand UQ5 B 615

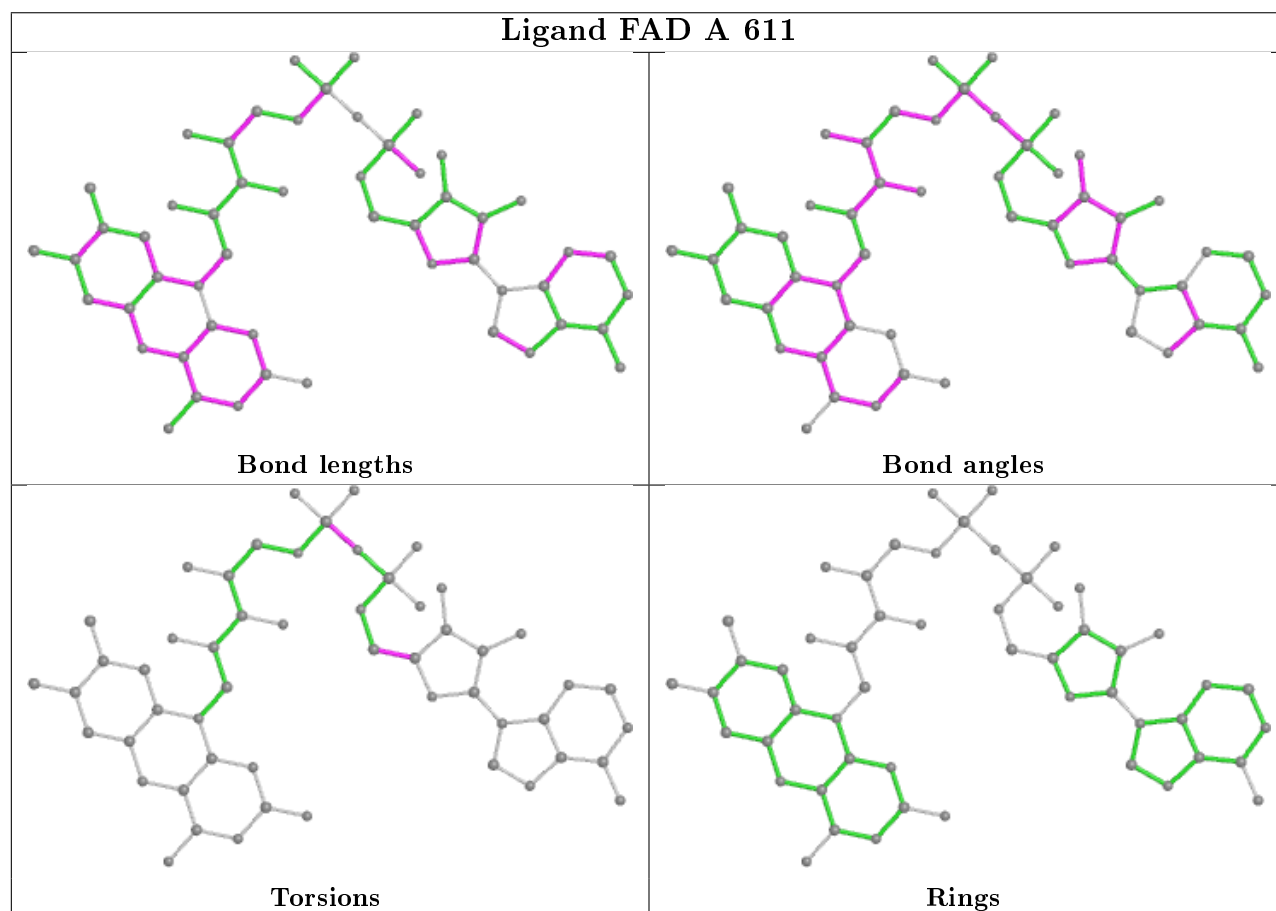
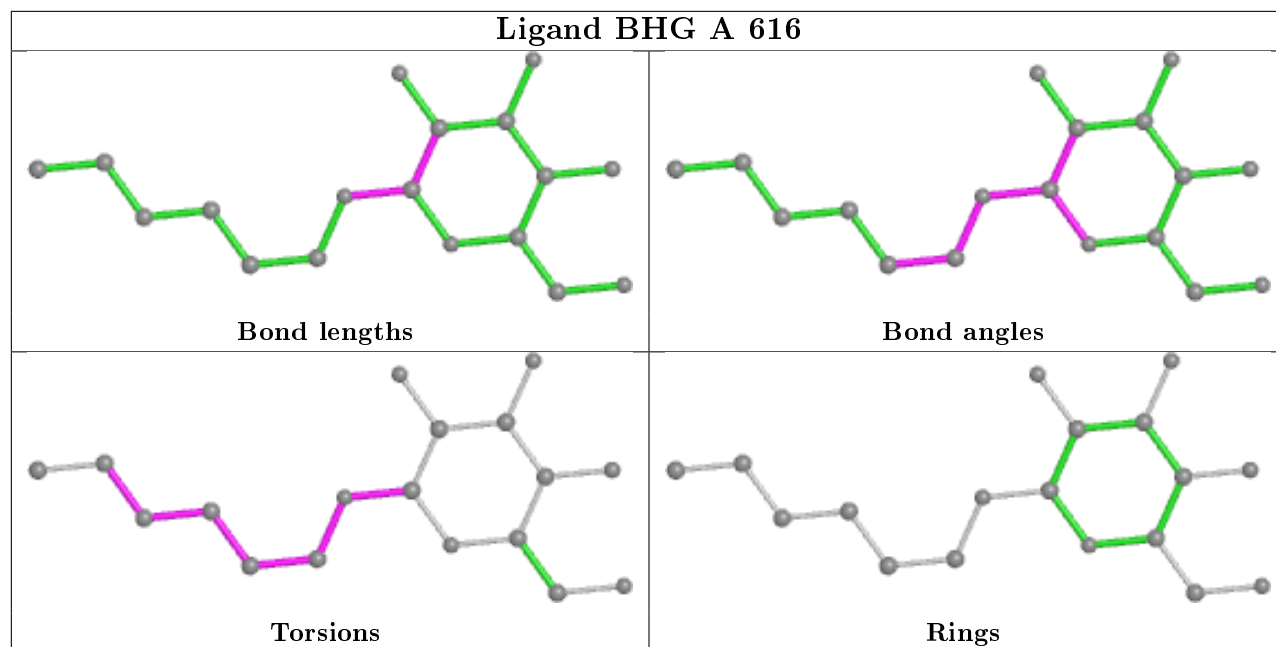


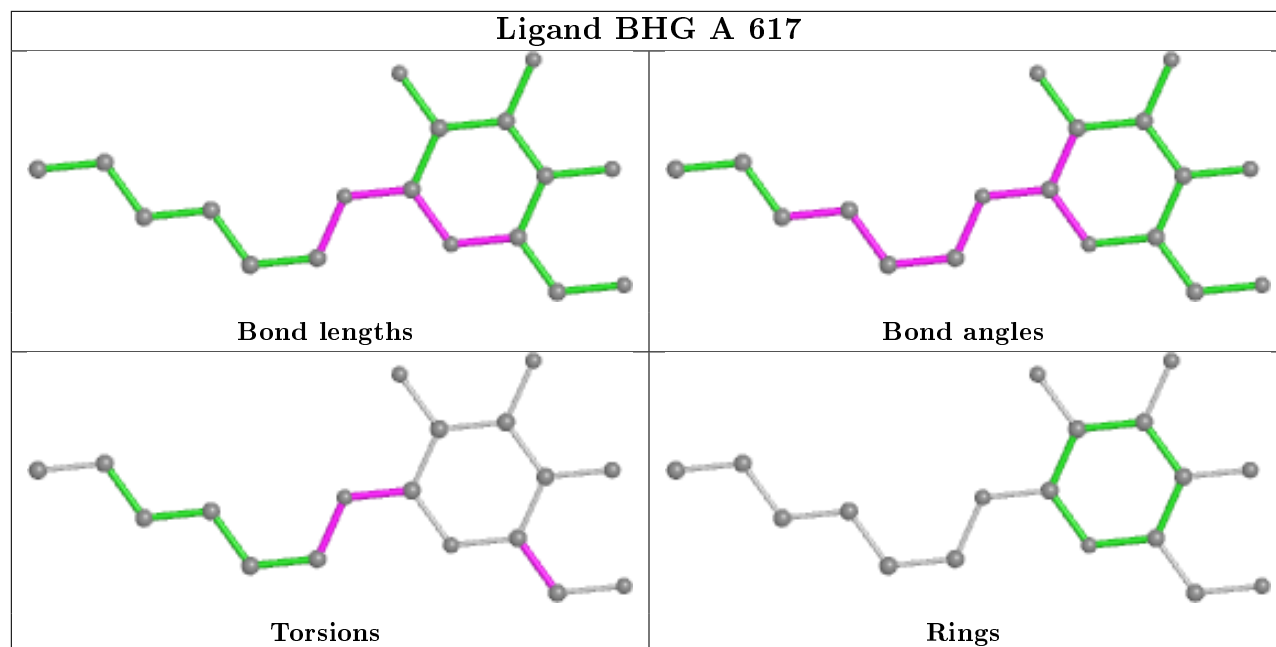
## Ligand BHG B 618



## Ligand UQ5 A 612







## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	581/584 (99%)	-0.25	10 (1%) 70 72	13, 30, 57, 84	0
1	B	578/584 (98%)	0.62	57 (9%) 7 7	38, 64, 79, 86	0
All	All	1159/1168 (99%)	0.18	67 (5%) 23 24	13, 49, 77, 86	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	CYS	7.9
1	B	176	GLY	5.6
1	B	540	GLN	5.4
1	A	540	GLN	5.4
1	B	390	LEU	5.1
1	A	7	PRO	4.9
1	A	389	ASN	4.6
1	B	7	PRO	4.6
1	A	6	VAL	4.5
1	B	502	ALA	4.5
1	B	389	ASN	4.3
1	B	27	VAL	4.3
1	B	388	GLU	3.8
1	B	538	LEU	3.7
1	B	61	HIS	3.7
1	B	382	PHE	3.7
1	B	499	ASP	3.7
1	A	5	LYS	3.7
1	B	537	PRO	3.6
1	B	26	GLY	3.5
1	B	8	ARG	3.4
1	B	100	GLU	3.4
1	B	32	PHE	3.3
1	B	24	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	539	GLU	3.2
1	B	22	LYS	3.2
1	B	498	HIS	3.0
1	B	30	GLU	3.0
1	B	535	PHE	2.9
1	B	212	ALA	2.9
1	B	541	GLY	2.8
1	B	536	VAL	2.8
1	A	8	ARG	2.7
1	B	43	ALA	2.7
1	B	395	ILE	2.7
1	B	20	GLN	2.7
1	B	396	GLY	2.6
1	B	19	ASP	2.6
1	B	174	GLU	2.6
1	B	165	TYR	2.6
1	A	388	GLU	2.6
1	B	191	ASP	2.6
1	B	28	ASN	2.5
1	B	172	PHE	2.5
1	B	386	THR	2.5
1	B	391	GLN	2.5
1	A	391	GLN	2.5
1	B	16	TYR	2.4
1	B	15	ILE	2.4
1	B	161	VAL	2.4
1	B	62	GLU	2.4
1	B	501	PRO	2.4
1	B	496	HIS	2.4
1	B	155	GLU	2.3
1	B	495	ASN	2.3
1	B	75	HIS	2.3
1	B	41	VAL	2.2
1	B	33	ALA	2.2
1	A	539	GLU	2.2
1	B	542	ASP	2.1
1	B	97	ASP	2.1
1	B	23	ARG	2.1
1	B	188	ILE	2.1
1	B	177	SER	2.1
1	B	50	ALA	2.1
1	B	68	CYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	58	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

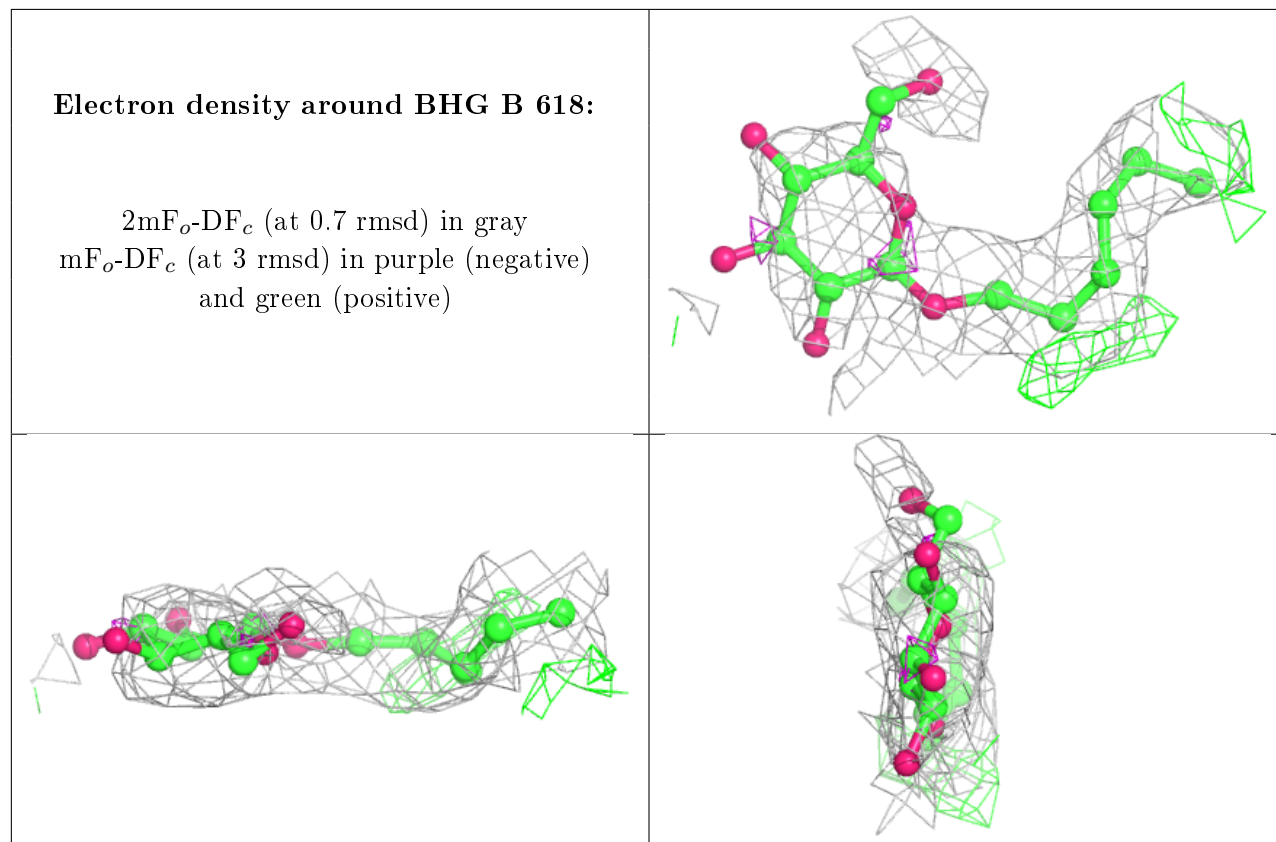
## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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
2	BHG	B	618	18/18	0.53	0.37	61,76,78,78	0
2	BHG	A	616	18/18	0.58	0.39	52,76,78,79	0
2	BHG	A	617	18/18	0.59	0.58	55,75,78,79	0
7	EDO	A	628	4/4	0.77	0.33	53,54,55,55	0
7	EDO	A	627	4/4	0.81	0.52	57,58,58,58	0
7	EDO	A	622	4/4	0.82	0.40	51,55,55,57	0
6	UQ5	B	615	38/38	0.86	0.26	51,56,68,71	0
7	EDO	B	620	4/4	0.88	0.16	49,53,54,56	0
6	UQ5	A	612	38/38	0.88	0.26	39,48,62,63	0
7	EDO	A	626	4/4	0.89	0.14	43,45,45,46	0
7	EDO	A	619	4/4	0.90	0.21	37,37,38,43	0
7	EDO	A	625	4/4	0.90	0.15	49,55,55,57	0
7	EDO	A	623	4/4	0.92	0.49	48,49,49,53	0
5	FAD	B	614	53/53	0.93	0.19	44,60,68,69	0
7	EDO	A	621	4/4	0.94	0.26	45,47,48,49	0
3	NA	A	1070	1/1	0.95	0.08	37,37,37,37	0
7	EDO	A	624	4/4	0.95	0.31	35,41,42,42	0
5	FAD	A	611	53/53	0.98	0.17	16,20,24,26	0
4	SF4	B	613	8/8	0.98	0.09	55,58,59,59	0
4	SF4	A	610	8/8	0.99	0.12	16,19,22,22	0

The following is a graphical depiction of the model fit to experimental electron density of all

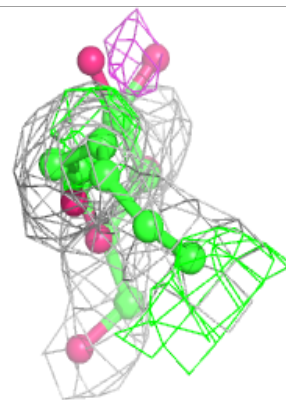
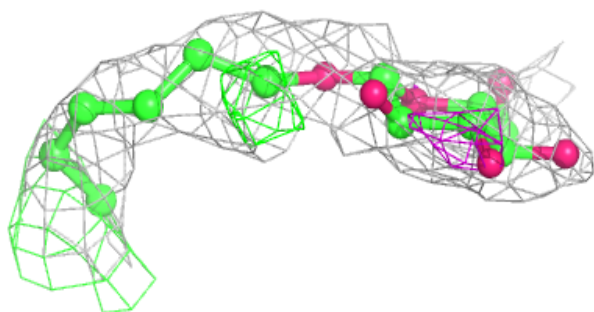
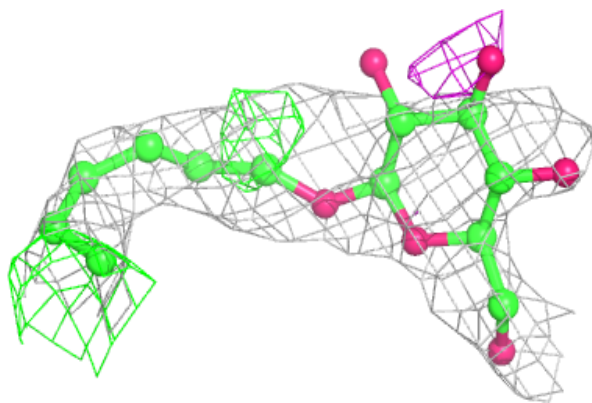
instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



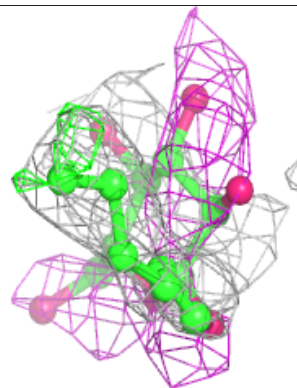
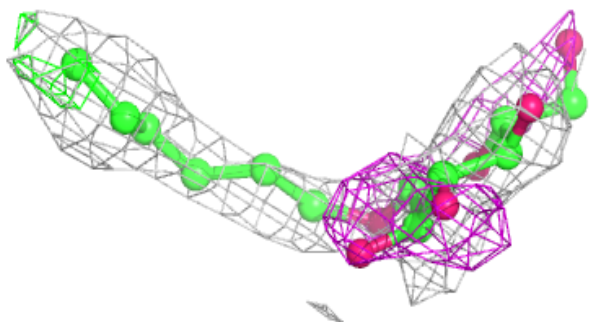
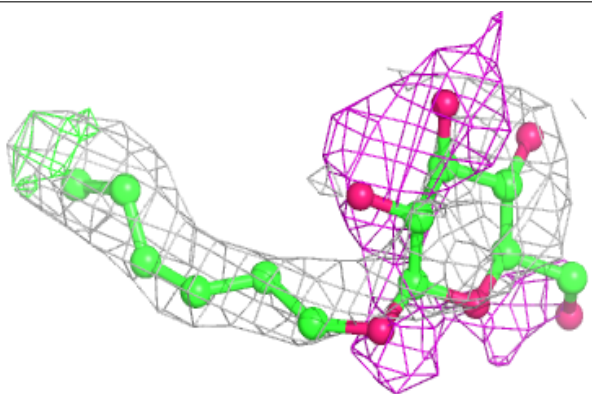


**Electron density around BHG A 616:**

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

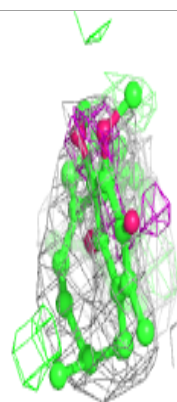
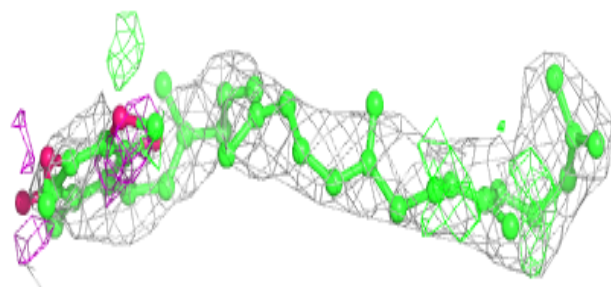
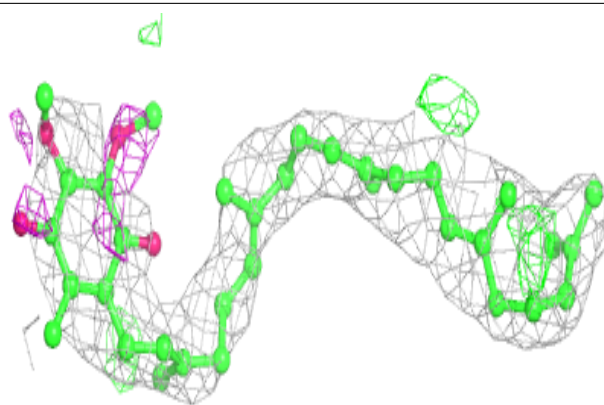
**Electron density around BHG A 617:**

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

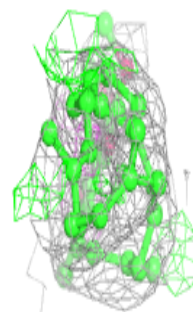
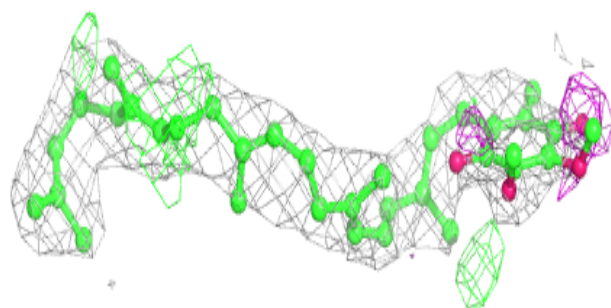
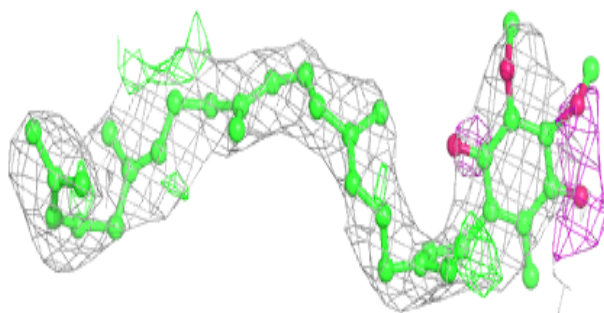


**Electron density around UQ5 B 615:**

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

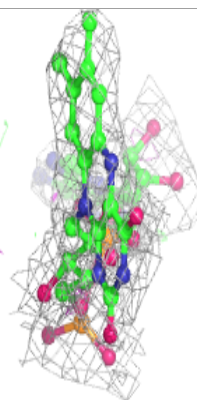
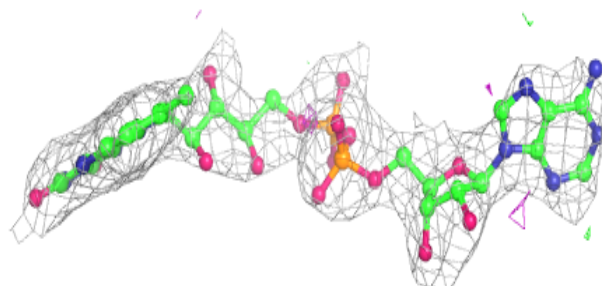
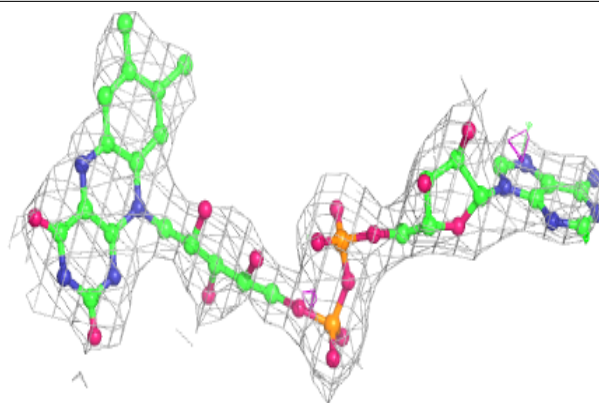
**Electron density around UQ5 A 612:**

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

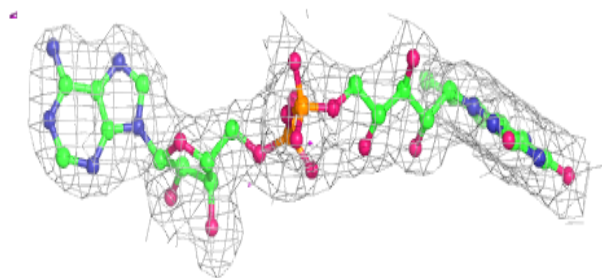
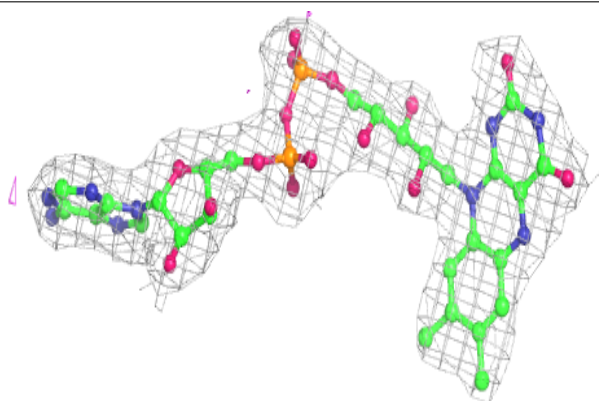


**Electron density around FAD B 614:**

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

**Electron density around FAD A 611:**

$2mF_o-DF_c$  (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.