



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 02:46 am BST

PDB ID : 5TT3  
Title : Crystal structure of the complex of Helicobacter pylori alpha-carbonic anhydrase with ethoxzolamide  
Authors : Modak, J.K.; Roujeinikova, A.  
Deposited on : 2016-11-01  
Resolution : 2.20 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 : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

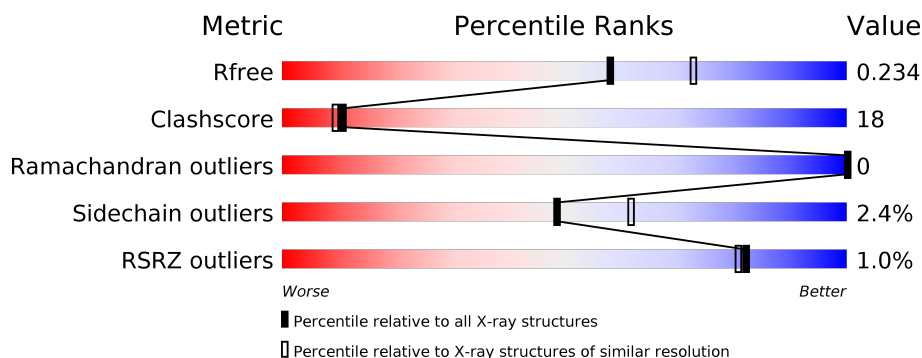
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	234	<div> <div>%</div> <div> <div></div> <div>64%</div> <div>30%</div> <div>• 5%</div> </div> </div>
1	B	234	<div> <div>2%</div> <div> <div></div> <div>53%</div> <div>36%</div> <div>• 9%</div> </div> </div>
1	C	234	<div> <div>%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>• •</div> </div> </div>
1	D	234	<div> <div>2%</div> <div> <div></div> <div>51%</div> <div>33%</div> <div>• 14%</div> </div> </div>
1	E	234	<div> <div></div> <div> <div></div> <div>66%</div> <div>30%</div> <div>• •</div> </div> </div>
1	F	234	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>• 6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	234	
1	H	234	

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
3	CL	B	302	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 15076 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 Alpha-carbonic anhydrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	3	0
			1835	1180	319	332	4			
1	B	212	Total	C	N	O	S	0	2	0
			1746	1125	303	314	4			
1	C	227	Total	C	N	O	S	0	2	0
			1864	1196	326	338	4			
1	D	202	Total	C	N	O	S	0	2	0
			1656	1068	286	299	3			
1	E	226	Total	C	N	O	S	0	2	0
			1857	1192	325	336	4			
1	F	220	Total	C	N	O	S	0	2	0
			1803	1158	314	327	4			
1	G	218	Total	C	N	O	S	0	2	0
			1793	1151	314	324	4			
1	H	223	Total	C	N	O	S	0	1	0
			1831	1175	320	332	4			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	H	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

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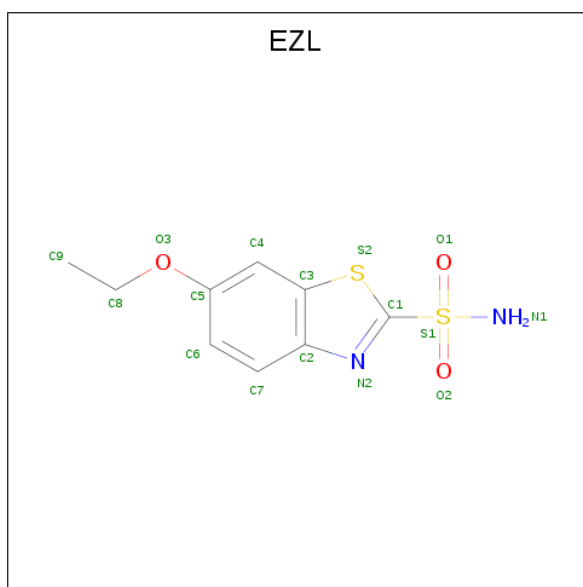
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Cl	0	0
			1	1		
3	E	1	Total	Cl	0	0
			1	1		
3	H	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is 6-ethoxy-1,3-benzothiazole-2-sulfonamide (three-letter code: EZL) (formula: C<sub>9</sub>H<sub>10</sub>N<sub>2</sub>O<sub>3</sub>S<sub>2</sub>).



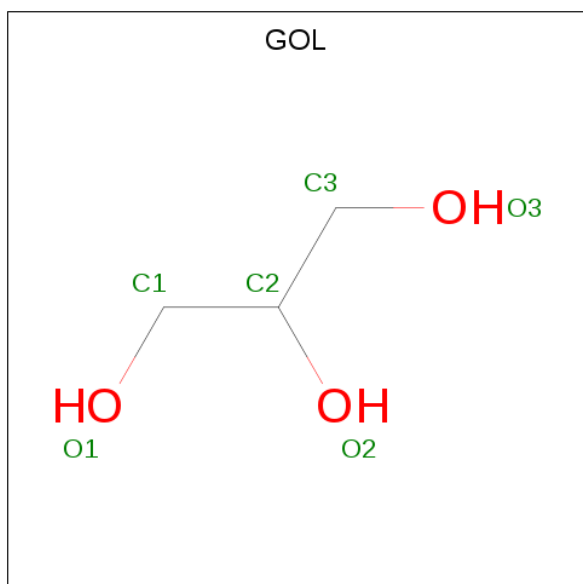
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			16	9	2	3	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			16	9	2	3	2		
4	C	1	Total	C	N	O	S	0	0
			16	9	2	3	2		
4	E	1	Total	C	N	O	S	0	0
			16	9	2	3	2		
4	F	1	Total	C	N	O	S	0	0
			16	9	2	3	2		
4	G	1	Total	C	N	O	S	0	0
			16	9	2	3	2		
4	H	1	Total	C	N	O	S	0	0
			16	9	2	3	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	H	1	Total	C	O	0	0
			6	3	3		

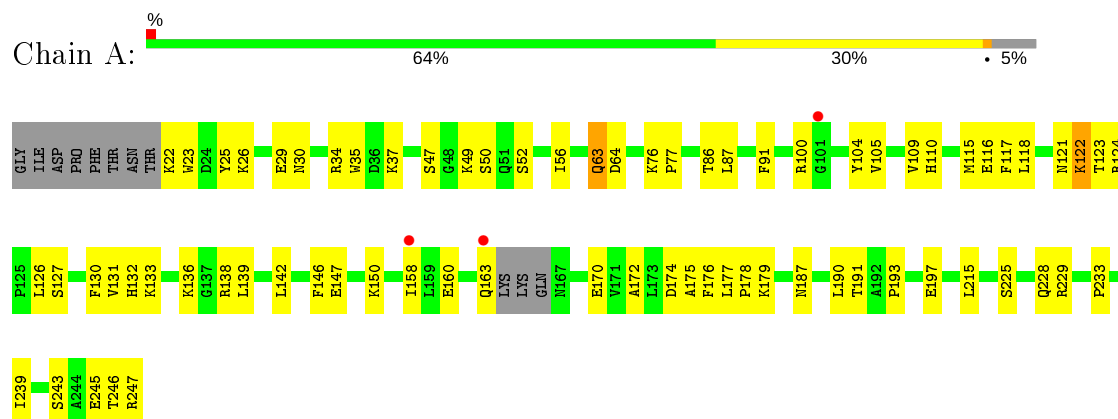
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	56	Total 56	O 56	0	0
6	B	46	Total 46	O 46	0	0
6	C	110	Total 110	O 110	0	0
6	D	38	Total 38	O 38	0	0
6	E	125	Total 125	O 125	0	0
6	F	41	Total 41	O 41	0	0
6	G	65	Total 65	O 65	0	0
6	H	54	Total 54	O 54	0	0

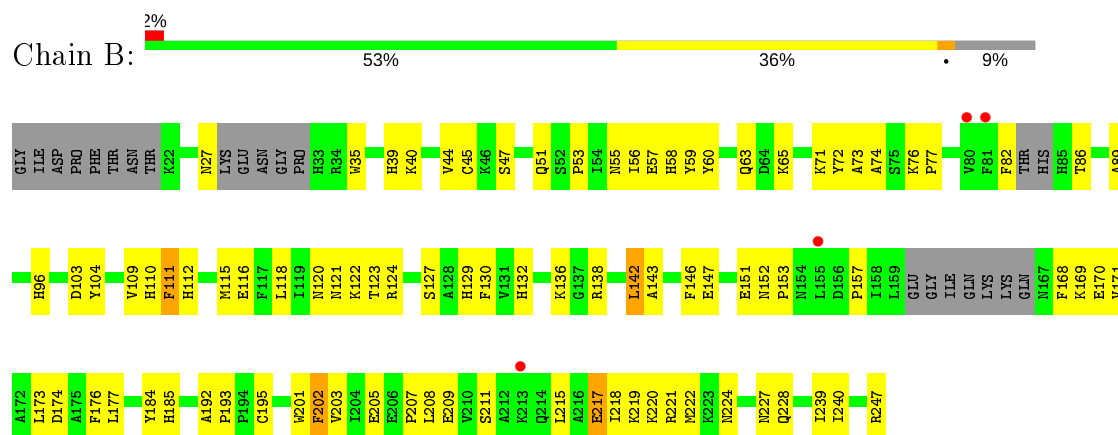
### 3 Residue-property plots [i](#)

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

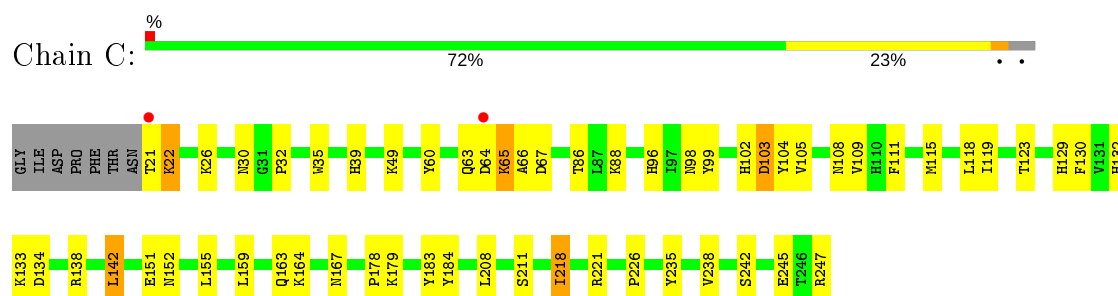
#### • Molecule 1: Alpha-carbonic anhydrase



#### • Molecule 1: Alpha-carbonic anhydrase

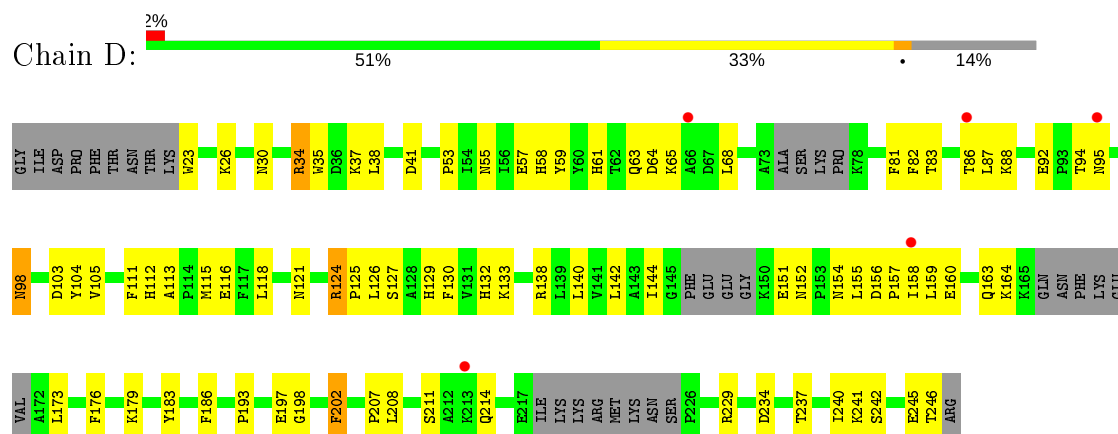


#### • Molecule 1: Alpha-carbonic anhydrase

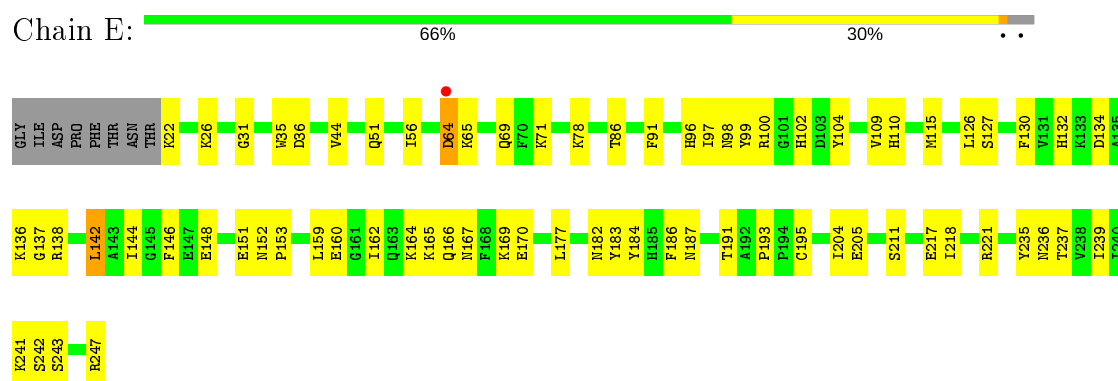




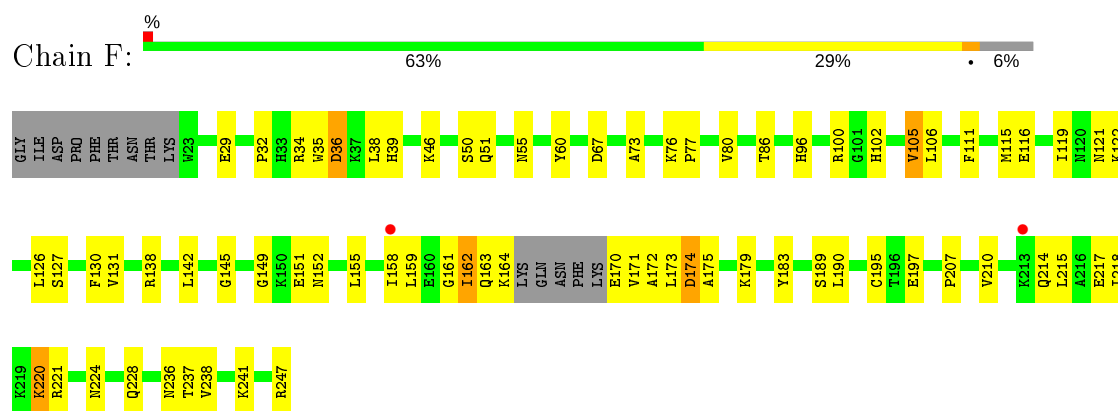
- Molecule 1: Alpha-carbonic anhydrase



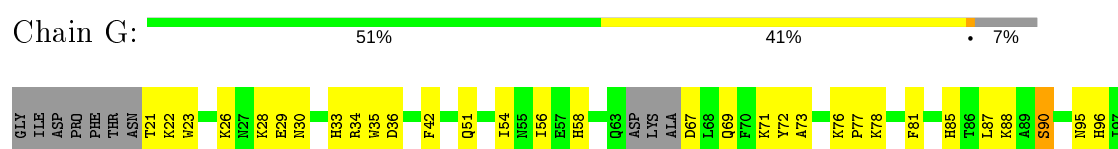
- Molecule 1: Alpha-carbonic anhydrase

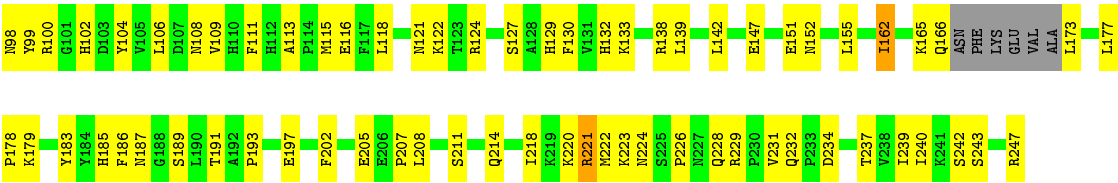


- Molecule 1: Alpha-carbonic anhydrase

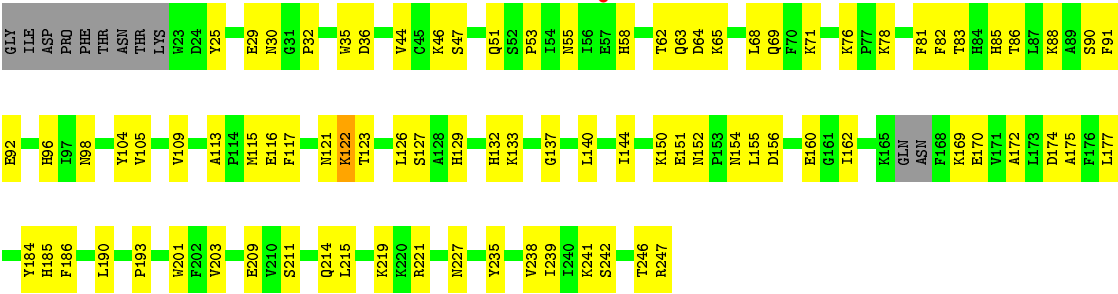


- Molecule 1: Alpha-carbonic anhydrase





● Molecule 1: Alpha-carbonic anhydrase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.98 Å   138.86 Å   168.18 Å 90.00°   90.04°   90.00°	Depositor
Resolution (Å)	39.89 – 2.20 39.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (39.89-2.20) 96.7 (39.89-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 2.20 Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.202   ,   0.240 0.198   ,   0.234	Depositor DCC
$R_{free}$ test set	4846 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.9	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34   ,   48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
Reported twinning fraction	0.500 for h,-k,-l	Depositor
Outliers	1 of 96754 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15076	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: EZL, GOL, ZN, CL

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	0.50	0/1898	0.66	0/2568
1	B	0.48	0/1802	0.67	1/2435 (0.0%)
1	C	0.54	0/1925	0.72	1/2604 (0.0%)
1	D	0.48	0/1710	0.69	0/2316
1	E	0.54	0/1918	0.71	1/2594 (0.0%)
1	F	0.46	0/1862	0.66	0/2521
1	G	0.49	0/1851	0.66	0/2502
1	H	0.47	0/1885	0.67	0/2549
All	All	0.50	0/14851	0.68	3/20089 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	142	LEU	CB-CG-CD1	-6.15	100.55	111.00
1	C	142	LEU	CB-CG-CD1	-5.71	101.28	111.00
1	B	142	LEU	CA-CB-CG	5.67	128.34	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	1835	0	1801	56	2
1	B	1746	0	1711	82	2
1	C	1864	0	1832	50	0
1	D	1656	0	1612	88	0
1	E	1857	0	1825	66	0
1	F	1803	0	1766	60	0
1	G	1793	0	1760	76	0
1	H	1831	0	1789	80	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	3	0
3	C	1	0	0	1	0
3	E	1	0	0	0	0
3	G	1	0	0	1	0
3	H	1	0	0	1	0
4	A	16	0	9	3	0
4	B	16	0	9	1	0
4	C	16	0	9	0	0
4	E	16	0	9	2	0
4	F	16	0	9	1	0
4	G	16	0	9	0	0
4	H	16	0	9	1	0
5	A	6	0	8	2	0
5	B	6	0	8	0	0
5	C	6	0	8	0	0
5	E	6	0	8	2	0
5	H	6	0	8	1	0
6	A	56	0	0	7	0
6	B	46	0	0	15	1
6	C	110	0	0	5	1
6	D	38	0	0	5	0
6	E	125	0	0	13	0
6	F	41	0	0	5	0
6	G	65	0	0	9	0
6	H	54	0	0	6	0
All	All	15076	0	14199	526	3

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 18.

All (526) 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:D:95:ASN:ND2	1:D:173:LEU:HD12	1.57	1.16
1:D:95:ASN:ND2	1:D:173:LEU:CD1	2.15	1.08
1:H:81:PHE:CE2	1:H:83[A]:THR:CG2	2.39	1.06
1:C:21:THR:HG22	1:C:22:LYS:H	0.96	1.05
1:B:76:LYS:HB2	1:B:170:GLU:HG2	1.43	0.99
1:D:95:ASN:HD21	1:D:173:LEU:HD12	1.16	0.99
1:C:21:THR:HG22	1:C:22:LYS:N	1.76	0.98
1:B:142:LEU:HA	6:B:401:HOH:O	1.63	0.98
1:D:95:ASN:HD22	1:D:173:LEU:CD1	1.74	0.97
1:H:81:PHE:CE2	1:H:83[A]:THR:HG21	1.99	0.96
1:B:45:CYS:SG	6:B:442:HOH:O	2.26	0.93
1:H:81:PHE:HE2	1:H:83[A]:THR:HG21	1.34	0.91
1:C:21:THR:CG2	1:C:22:LYS:H	1.82	0.90
1:B:202:PHE:O	6:B:401:HOH:O	1.89	0.89
1:D:64:ASP:OD1	1:D:65:LYS:N	2.06	0.87
3:B:302:CL:CL	6:B:422:HOH:O	2.30	0.87
1:H:81:PHE:CD2	1:H:83[A]:THR:HG23	2.09	0.86
1:B:129:HIS:NE2	3:B:302:CL:CL	2.44	0.85
1:G:69:GLN:HB2	1:G:98:ASN:HB3	1.56	0.85
1:H:174:ASP:O	1:H:247:ARG:NE	2.10	0.84
1:D:95:ASN:HD22	1:D:173:LEU:HD13	1.43	0.83
1:H:81:PHE:HE2	1:H:83[A]:THR:CG2	1.86	0.82
1:A:136:LYS:HE3	1:A:138:ARG:HD2	1.61	0.81
1:A:76:LYS:NZ	1:A:170:GLU:OE2	2.13	0.81
1:G:71:LYS:HD2	1:G:96:HIS:HB2	1.63	0.80
1:A:124:ARG:NH1	1:A:147:GLU:OE1	2.14	0.80
1:B:65:LYS:CA	1:E:64:ASP:O	2.29	0.79
1:F:152:ASN:HB3	1:F:155:LEU:HD13	1.62	0.79
1:D:159:LEU:HD11	1:D:214:GLN:HE21	1.45	0.79
1:C:138:ARG:NH1	1:D:234:ASP:O	2.16	0.79
1:B:65:LYS:N	1:E:64:ASP:O	2.15	0.79
1:D:144:ILE:HD11	1:D:208:LEU:HD13	1.64	0.79
1:H:81:PHE:CE2	1:H:83[A]:THR:HG23	2.15	0.78
1:B:157:PRO:HA	1:B:169:LYS:HE2	1.66	0.78
1:C:179:LYS:HG3	1:C:247:ARG:HB3	1.63	0.78
1:H:78:LYS:NZ	1:H:92:GLU:OE2	2.17	0.77
1:E:110:HIS:CE1	5:E:304:GOL:H32	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:TYR:HA	1:D:138:ARG:HH12	1.52	0.75
1:A:29:GLU:O	1:A:34:ARG:NH1	2.21	0.74
1:H:151:GLU:HA	1:H:211:SER:HB3	1.68	0.73
1:G:130:PHE:HB2	1:G:142:LEU:HB3	1.71	0.72
1:C:21:THR:HG22	1:C:22:LYS:HG3	1.69	0.72
1:D:98:ASN:ND2	1:D:103:ASP:OD1	2.22	0.72
1:D:34:ARG:NH2	6:D:401:HOH:O	2.23	0.72
1:C:96:HIS:CE1	1:C:105:VAL:HG22	2.24	0.72
1:D:55:ASN:OD1	1:D:55:ASN:O	2.07	0.72
1:D:159:LEU:HD11	1:D:214:GLN:NE2	2.04	0.72
1:D:87:LEU:HD23	1:D:87:LEU:H	1.55	0.71
1:B:130:PHE:HB2	1:B:142:LEU:HB3	1.73	0.71
1:D:130:PHE:HB2	1:D:142:LEU:HB3	1.72	0.71
1:A:160:GLU:O	1:A:163:GLN:HG2	1.90	0.70
1:F:161:GLY:HA2	1:F:164:LYS:HD2	1.73	0.70
1:H:122:LYS:HD2	1:H:123:THR:H	1.57	0.70
1:F:29:GLU:O	1:F:34:ARG:NH1	2.25	0.70
1:A:115:MET:SD	6:A:438:HOH:O	2.50	0.69
1:C:64:ASP:OD1	1:C:65:LYS:N	2.25	0.69
1:F:224:ASN:O	6:F:401:HOH:O	2.10	0.69
1:B:147:GLU:N	1:B:208:LEU:O	2.24	0.69
1:C:238:VAL:HG21	1:D:186:PHE:HA	1.74	0.69
1:H:81:PHE:CD2	1:H:83[A]:THR:CG2	2.73	0.69
1:G:243:SER:O	6:G:401:HOH:O	2.10	0.69
1:D:95:ASN:ND2	1:D:173:LEU:HD13	2.03	0.69
1:H:132:HIS:HB2	1:H:140:LEU:HB3	1.73	0.68
1:B:55:ASN:HA	1:B:118:LEU:HB2	1.75	0.68
1:H:64:ASP:OD1	1:H:65:LYS:N	2.26	0.68
1:C:179:LYS:NZ	1:C:245:GLU:OE1	2.27	0.68
1:E:36:ASP:OD2	6:E:401:HOH:O	2.12	0.67
1:E:134:ASP:OD2	6:E:402:HOH:O	2.12	0.67
1:H:133:LYS:CE	1:H:137:GLY:HA2	2.24	0.67
1:H:76:LYS:HA	1:H:170:GLU:HA	1.77	0.67
1:A:233:PRO:O	6:A:401:HOH:O	2.13	0.67
1:D:115:MET:HB3	1:D:124:ARG:H	1.61	0.66
1:F:179:LYS:NZ	1:F:247:ARG:O	2.27	0.66
1:B:110:HIS:HD2	6:B:415:HOH:O	1.78	0.65
1:E:71:LYS:HD3	1:E:96:HIS:HB2	1.78	0.65
1:B:205:GLU:OE2	6:B:403:HOH:O	2.13	0.65
1:D:65:LYS:NZ	1:D:245:GLU:HB3	2.12	0.65
1:F:238:VAL:O	6:F:402:HOH:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:130:PHE:HB2	1:F:142:LEU:HB3	1.79	0.64
1:A:187:ASN:OD1	6:A:402:HOH:O	2.14	0.64
1:E:187:ASN:ND2	6:E:411:HOH:O	2.30	0.64
1:E:86:THR:HG21	5:E:304:GOL:H2	1.80	0.63
1:B:121:ASN:ND2	6:B:404:HOH:O	2.29	0.63
1:A:122:LYS:HD3	1:A:124:ARG:CZ	2.28	0.63
1:G:151:GLU:HG2	1:G:211:SER:HB3	1.81	0.63
1:G:72:TYR:OH	1:G:132:HIS:NE2	2.31	0.63
1:G:87:LEU:HD13	1:G:221:ARG:HD2	1.80	0.63
1:D:112:HIS:O	1:D:127:SER:N	2.29	0.63
1:A:26:LYS:NZ	1:A:225:SER:OG	2.30	0.63
1:B:104:TYR:HB3	1:B:132:HIS:HB3	1.81	0.63
1:H:247:ARG:NH2	6:H:403:HOH:O	2.22	0.63
1:B:142:LEU:HD12	6:B:401:HOH:O	1.97	0.62
1:C:167:ASN:ND2	6:C:407:HOH:O	2.31	0.62
1:D:124:ARG:NH2	1:D:207:PRO:HB2	2.14	0.62
1:A:130:PHE:HB3	1:A:132:HIS:CE1	2.34	0.62
1:B:202:PHE:HB2	6:B:401:HOH:O	1.99	0.62
1:H:129:HIS:NE2	3:H:302:CL:CL	2.67	0.62
1:B:217:GLU:HA	1:B:220:LYS:HE3	1.81	0.62
1:F:55:ASN:ND2	1:F:121:ASN:OD1	2.33	0.62
1:E:97:ILE:CG2	1:E:104:TYR:HB2	2.29	0.61
1:A:76:LYS:HA	1:A:170:GLU:HA	1.82	0.61
1:H:64:ASP:O	1:H:242:SER:OG	2.16	0.61
1:B:143:ALA:HB2	1:B:201:TRP:HZ3	1.65	0.61
1:C:226:PRO:O	6:C:401:HOH:O	2.16	0.61
1:G:35:TRP:CZ3	1:G:193:PRO:HD3	2.35	0.61
1:B:53:PRO:HG3	1:B:116:GLU:HB3	1.83	0.61
1:B:65:LYS:HA	1:E:64:ASP:O	2.00	0.61
1:A:116:GLU:OE2	1:A:229:ARG:N	2.22	0.61
1:H:96:HIS:CE1	1:H:105:VAL:HG22	2.36	0.61
1:E:151:GLU:HA	1:E:211:SER:HB3	1.83	0.60
1:G:33:HIS:CE1	1:G:34:ARG:HG3	2.36	0.60
1:E:136:LYS:NZ	6:E:416:HOH:O	2.33	0.60
1:H:113:ALA:N	6:H:409:HOH:O	2.35	0.60
1:B:57:GLU:OE1	6:B:404:HOH:O	2.16	0.60
1:G:178:PRO:HD3	1:G:208:LEU:HD21	1.84	0.60
1:G:23:TRP:O	6:G:402:HOH:O	2.16	0.60
1:D:81:PHE:O	1:D:88:LYS:N	2.23	0.60
1:E:205:GLU:OE2	6:E:403:HOH:O	2.16	0.59
1:G:78:LYS:HB3	1:G:90:SER:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:174:ASP:OD1	1:F:174:ASP:N	2.27	0.59
1:H:88:LYS:NZ	1:H:90:SER:HB3	2.18	0.59
1:D:124:ARG:CZ	1:D:207:PRO:HB2	2.33	0.59
1:A:104:TYR:HB3	1:A:132:HIS:HB3	1.84	0.59
1:G:22:LYS:O	1:G:30:ASN:ND2	2.35	0.59
1:A:126:LEU:HB3	1:A:146:PHE:HB2	1.84	0.59
1:C:164:LYS:NZ	6:C:403:HOH:O	2.24	0.59
1:G:104:TYR:HB3	1:G:132:HIS:HB3	1.84	0.59
1:H:71:LYS:HB2	1:H:96:HIS:HB2	1.84	0.59
1:F:116:GLU:HA	1:F:228:GLN:HG3	1.84	0.58
1:G:87:LEU:HD13	1:G:221:ARG:HH11	1.68	0.58
1:A:115:MET:HG3	1:A:127:SER:HB3	1.84	0.58
1:A:191:THR:OG1	4:A:303:EZL:N1	2.35	0.58
1:F:76:LYS:HA	1:F:170:GLU:HA	1.85	0.58
1:H:156:ASP:OD1	1:H:214:GLN:NE2	2.37	0.58
1:H:186:PHE:HB3	1:H:239:ILE:HG12	1.86	0.58
1:H:88:LYS:HZ1	1:H:90:SER:HB3	1.68	0.58
1:H:241:LYS:NZ	6:H:412:HOH:O	2.36	0.58
1:H:246:THR:O	6:H:401:HOH:O	2.17	0.58
1:H:113:ALA:HB2	1:H:126:LEU:HD12	1.84	0.58
1:D:151:GLU:HA	1:D:211:SER:HB3	1.86	0.57
1:A:64:ASP:OD2	1:A:243:SER:OG	2.21	0.57
1:B:57:GLU:N	6:B:407:HOH:O	2.37	0.57
1:H:82:PHE:CZ	1:H:85:HIS:HA	2.39	0.57
1:A:160:GLU:HG3	1:A:163:GLN:HE21	1.69	0.57
1:H:69:GLN:HB3	1:H:98:ASN:HB3	1.86	0.57
1:D:124:ARG:HD3	1:D:125:PRO:HD2	1.86	0.57
1:D:156:ASP:HA	1:D:159:LEU:HD12	1.85	0.57
1:H:91:PHE:HE2	1:H:109:VAL:HG23	1.70	0.57
4:A:303:EZL:C3	5:A:304:GOL:H31	2.35	0.57
1:G:220:LYS:HA	1:G:224:ASN:OD1	2.04	0.57
1:D:26:LYS:NZ	6:D:403:HOH:O	2.36	0.57
1:E:164:LYS:NZ	1:E:167:ASN:O	2.35	0.57
1:F:237:THR:OG1	6:F:403:HOH:O	2.17	0.56
1:C:163:GLN:HE21	1:C:221:ARG:HH21	1.53	0.56
1:C:235:TYR:HA	1:D:138:ARG:NH1	2.19	0.56
1:G:54:ILE:HA	1:G:231:VAL:HG13	1.88	0.56
1:E:191:THR:OG1	4:E:303:EZL:N1	2.37	0.56
1:H:172:ALA:HB1	1:H:175:ALA:HB3	1.86	0.56
1:D:35:TRP:CH2	1:D:193:PRO:HD3	2.41	0.56
1:D:37:LYS:NZ	6:D:405:HOH:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:MET:SD	1:D:127:SER:OG	2.63	0.56
1:F:241:LYS:NZ	6:F:409:HOH:O	2.38	0.56
1:D:65:LYS:HZ1	1:D:245:GLU:HB3	1.69	0.56
1:C:21:THR:CG2	1:C:22:LYS:N	2.50	0.55
1:E:177:LEU:O	1:E:247:ARG:NH1	2.35	0.55
1:F:111:PHE:HD2	1:F:126:LEU:HD21	1.70	0.55
1:G:162:ILE:HG12	1:G:221:ARG:HG3	1.89	0.55
1:B:58:HIS:N	6:B:407:HOH:O	2.39	0.55
1:D:133:LYS:HA	1:D:138:ARG:O	2.06	0.55
1:B:220:LYS:HG2	1:B:224:ASN:HD21	1.71	0.54
1:G:152:ASN:HB3	1:G:155:LEU:HB2	1.89	0.54
1:B:27:ASN:ND2	6:B:410:HOH:O	2.40	0.54
1:D:82:PHE:HA	1:D:87:LEU:HA	1.89	0.54
1:F:32:PRO:HA	1:F:35:TRP:CD2	2.43	0.54
1:B:136:LYS:HB2	1:B:138:ARG:HD3	1.88	0.54
1:H:133:LYS:HE3	1:H:137:GLY:CA	2.38	0.54
1:F:190:LEU:HD22	4:F:302:EZL:C1	2.37	0.54
1:D:179:LYS:HD3	1:G:147:GLU:OE1	2.08	0.54
1:G:71:LYS:HD2	1:G:96:HIS:CB	2.35	0.54
1:B:173:LEU:HA	1:B:176:PHE:HB2	1.90	0.54
1:C:63:GLN:OE1	1:D:63:GLN:NE2	2.37	0.54
1:C:22:LYS:O	1:C:30:ASN:ND2	2.41	0.54
1:E:159:LEU:HD21	1:E:218:ILE:HG12	1.90	0.53
1:D:152:ASN:HB3	1:D:155:LEU:HD13	1.91	0.53
1:F:161:GLY:HA2	1:F:164:LYS:CD	2.38	0.53
1:E:35:TRP:CH2	1:E:193:PRO:HD3	2.43	0.53
1:B:82:PHE:HE2	1:B:222:MET:HA	1.74	0.53
1:C:86:THR:OG1	1:C:111:PHE:O	2.24	0.53
1:F:217:GLU:O	1:F:221:ARG:HG2	2.08	0.53
1:A:91:PHE:HE1	1:A:109[B]:VAL:HG12	1.73	0.53
1:G:102:HIS:HB2	6:G:449:HOH:O	2.08	0.53
1:A:116:GLU:HG2	1:A:228:GLN:HG3	1.89	0.53
1:B:35:TRP:CZ3	1:B:193:PRO:HD3	2.44	0.53
1:F:115:MET:HG3	1:F:127:SER:HB3	1.90	0.53
1:B:127:SER:HB3	3:B:302:CL:CL	2.46	0.53
1:E:134:ASP:OD1	1:E:138:ARG:N	2.42	0.53
1:C:115:MET:HG3	3:C:302:CL:CL	2.45	0.53
1:A:172:ALA:HB1	1:A:175:ALA:HB3	1.90	0.53
1:A:22:LYS:O	1:A:30:ASN:ND2	2.42	0.53
1:D:132:HIS:HB2	1:D:140:LEU:HB3	1.91	0.53
1:D:142:LEU:HD12	1:D:202:PHE:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:HIS:HB3	1:C:103:ASP:OD1	2.09	0.52
4:E:303:EZL:H4	6:E:439:HOH:O	2.08	0.52
1:E:51:GLN:HG3	6:E:488:HOH:O	2.09	0.52
1:H:83[A]:THR:O	1:H:86:THR:HG22	2.09	0.52
1:A:122:LYS:HG2	6:A:419:HOH:O	2.08	0.52
1:C:21:THR:HG21	1:C:39:HIS:NE2	2.24	0.52
1:H:105:VAL:O	1:H:132:HIS:HA	2.09	0.52
1:H:62:THR:HG22	1:H:241:LYS:O	2.10	0.52
1:G:67:ASP:OD1	1:G:67:ASP:N	2.43	0.52
1:H:83[B]:THR:O	1:H:86:THR:HG22	2.09	0.52
1:B:215:LEU:O	1:B:219:LYS:HG3	2.09	0.52
1:B:39:HIS:HA	1:D:41:ASP:OD2	2.10	0.52
1:F:152:ASN:CB	1:F:155:LEU:HD13	2.35	0.52
1:B:73:ALA:O	1:B:173:LEU:HB2	2.11	0.51
1:H:35:TRP:CZ3	1:H:193:PRO:HD3	2.44	0.51
1:B:217:GLU:O	1:B:221:ARG:HG2	2.10	0.51
1:B:218:ILE:HA	1:B:221:ARG:HB2	1.92	0.51
1:C:49:LYS:HG3	1:D:197:GLU:C	2.31	0.51
1:C:152:ASN:HB3	1:C:155:LEU:HG	1.92	0.51
1:B:115:MET:O	1:B:228:GLN:NE2	2.42	0.51
1:D:130:PHE:HB3	1:D:132:HIS:HE1	1.76	0.51
1:D:160:GLU:O	1:D:163:GLN:HG2	2.11	0.51
1:D:163:GLN:HG3	1:D:164:LYS:HG2	1.92	0.51
1:F:80:VAL:HG12	1:F:162:ILE:HG23	1.93	0.51
1:E:148:GLU:OE2	6:E:404:HOH:O	2.19	0.51
1:H:133:LYS:HE3	1:H:137:GLY:HA2	1.92	0.51
1:C:179:LYS:NZ	6:C:411:HOH:O	2.38	0.51
1:E:130:PHE:HB2	1:E:142:LEU:HB3	1.92	0.51
1:F:236:ASN:ND2	6:F:411:HOH:O	2.41	0.51
1:G:116:GLU:HA	1:G:228:GLN:HG3	1.92	0.51
1:G:205:GLU:OE2	6:G:403:HOH:O	2.18	0.51
1:D:179:LYS:NZ	1:D:245:GLU:OE2	2.39	0.51
1:A:178:PRO:O	1:A:246:THR:OG1	2.26	0.51
1:B:51:GLN:OE1	1:B:195:CYS:HB3	2.12	0.50
1:B:71:LYS:HB2	1:B:96:HIS:HB2	1.93	0.50
1:G:87:LEU:HD23	1:G:218:ILE:HG13	1.92	0.50
1:E:170:GLU:HB3	6:E:465:HOH:O	2.10	0.50
1:D:115:MET:HA	1:D:127:SER:OG	2.11	0.50
1:E:236:ASN:OD1	1:F:100:ARG:NH1	2.44	0.50
1:G:56:ILE:HG23	1:G:239:ILE:HD13	1.92	0.50
1:A:47:SER:O	1:A:49:LYS:NZ	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109[B]:VAL:HA	1:B:129:HIS:O	2.12	0.50
1:B:184:TYR:O	1:B:202:PHE:HA	2.11	0.50
1:H:32:PRO:HA	1:H:35:TRP:CD2	2.45	0.50
1:H:133:LYS:HE2	1:H:137:GLY:HA2	1.92	0.50
1:A:160:GLU:O	1:A:163:GLN:CG	2.58	0.50
1:B:65:LYS:HB3	1:E:64:ASP:O	2.11	0.50
1:G:187:ASN:ND2	6:G:414:HOH:O	2.42	0.50
1:G:22:LYS:O	6:G:404:HOH:O	2.20	0.50
1:C:98:ASN:ND2	1:C:103:ASP:OD1	2.44	0.50
1:A:76:LYS:HB3	1:A:170:GLU:HG2	1.92	0.50
1:B:143:ALA:HB2	1:B:201:TRP:CZ3	2.47	0.50
1:G:187:ASN:ND2	1:H:235:TYR:O	2.45	0.50
1:G:191:THR:O	1:G:229:ARG:HD2	2.12	0.49
1:B:185:HIS:HB3	1:B:240:ILE:HD11	1.94	0.49
1:C:183:TYR:CZ	1:C:242:SER:HB3	2.48	0.49
1:C:88:LYS:HE3	1:C:108:ASN:CB	2.42	0.49
1:G:95:ASN:HB2	1:G:106:LEU:HB3	1.94	0.49
1:H:88:LYS:HD2	5:H:304:GOL:H32	1.93	0.49
1:E:236:ASN:HA	1:F:100:ARG:HH12	1.77	0.49
1:A:35:TRP:CZ3	1:A:193:PRO:HD3	2.47	0.49
1:C:104:TYR:HB3	1:C:132:HIS:HB3	1.95	0.49
1:F:51:GLN:OE1	1:F:195:CYS:HB3	2.12	0.49
6:C:442:HOH:O	1:D:198:GLY:HA2	2.13	0.49
1:H:162:ILE:HD13	1:H:221:ARG:HD2	1.95	0.49
1:B:56:ILE:N	1:B:118:LEU:O	2.29	0.49
1:D:126:LEU:HG	1:D:127:SER:N	2.28	0.49
1:E:35:TRP:CZ3	1:E:193:PRO:HD3	2.47	0.49
1:E:99:TYR:OH	1:F:60:TYR:OH	2.11	0.49
1:H:53:PRO:HG3	1:H:116:GLU:HB3	1.95	0.49
1:B:112:HIS:CD2	6:B:415:HOH:O	2.66	0.48
1:E:236:ASN:HA	1:F:100:ARG:NH1	2.28	0.48
1:G:118:LEU:HD23	1:G:121:ASN:HA	1.94	0.48
1:D:92:GLU:HB2	1:D:94:THR:HG23	1.95	0.48
1:F:96:HIS:CD2	1:F:105[B]:VAL:HG22	2.48	0.48
1:A:100:ARG:HB2	6:A:417:HOH:O	2.14	0.48
1:C:130:PHE:HB2	1:C:142:LEU:HB3	1.94	0.48
1:F:32:PRO:HA	1:F:35:TRP:CE2	2.49	0.48
1:A:118:LEU:HD22	1:A:123:THR:HA	1.96	0.48
1:E:97:ILE:HG22	1:E:104:TYR:HB2	1.95	0.48
1:B:115:MET:HB3	1:B:123:THR:OG1	2.14	0.48
1:E:217:GLU:O	1:E:221:ARG:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:GLN:O	1:E:65:LYS:CB	2.62	0.48
1:G:124:ARG:NE	1:G:207:PRO:HB3	2.29	0.48
1:G:58:HIS:NE2	6:G:406:HOH:O	2.22	0.48
1:H:160:GLU:OE2	1:H:169:LYS:HE3	2.13	0.48
1:E:56:ILE:HG23	1:E:239:ILE:HD13	1.96	0.48
1:G:29:GLU:HA	1:G:34:ARG:HD3	1.96	0.48
1:D:159:LEU:CD1	1:D:214:GLN:HE21	2.21	0.48
1:F:172:ALA:HB1	1:F:175:ALA:HB3	1.95	0.48
1:B:151:GLU:HA	1:B:211:SER:HB3	1.95	0.47
1:E:26:LYS:HB2	6:E:454:HOH:O	2.14	0.47
1:A:130:PHE:HB3	1:A:132:HIS:HE1	1.77	0.47
1:A:136:LYS:HD2	1:A:138:ARG:HE	1.79	0.47
1:D:237:THR:HG23	6:D:426:HOH:O	2.14	0.47
1:G:185:HIS:HB3	1:G:240:ILE:HD11	1.97	0.47
1:D:155:LEU:O	1:D:158:ILE:HG12	2.14	0.47
1:E:26:LYS:O	1:E:31:GLY:HA3	2.15	0.47
1:E:104:TYR:HB3	1:E:132:HIS:HB3	1.95	0.47
1:D:35:TRP:CZ3	1:D:193:PRO:HD3	2.50	0.47
1:F:155:LEU:O	1:F:158:ILE:HG12	2.15	0.47
1:H:152:ASN:HB2	1:H:209:GLU:O	2.14	0.47
1:E:104:TYR:OH	1:F:236:ASN:OD1	2.31	0.47
1:G:179:LYS:NZ	1:G:247:ARG:HG3	2.30	0.47
1:D:118:LEU:HD23	1:D:121:ASN:HA	1.95	0.47
1:D:87:LEU:HD21	1:D:111:PHE:HB2	1.96	0.47
1:B:65:LYS:CB	1:E:64:ASP:O	2.63	0.47
1:F:151:GLU:HG3	1:F:214:GLN:CD	2.35	0.47
1:H:62:THR:OG1	1:H:63:GLN:N	2.47	0.47
1:A:174:ASP:OD1	1:A:174:ASP:O	2.33	0.47
1:B:72:TYR:O	1:B:174:ASP:HB3	2.15	0.47
1:C:164:LYS:HD2	1:C:167:ASN:O	2.15	0.47
4:A:303:EZL:C4	5:A:304:GOL:H31	2.45	0.46
1:G:186:PHE:HA	1:H:238:VAL:HG21	1.97	0.46
1:G:23:TRP:O	1:G:85:HIS:NE2	2.48	0.46
1:B:195:CYS:SG	6:B:442:HOH:O	2.60	0.46
1:D:59:TYR:HE2	1:D:61:HIS:CE1	2.33	0.46
1:G:177:LEU:O	1:G:247:ARG:NH2	2.44	0.46
1:G:183:TYR:CZ	1:G:242:SER:HB3	2.51	0.46
1:F:38:LEU:O	1:F:39:HIS:ND1	2.48	0.46
1:D:154:ASN:HD22	1:D:176:PHE:HA	1.79	0.46
1:H:117:PHE:HE2	1:H:201:TRP:CZ3	2.33	0.46
1:D:241:LYS:NZ	6:D:402:HOH:O	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:ASP:OD1	1:E:137:GLY:N	2.49	0.46
1:F:73:ALA:O	1:F:173:LEU:HB2	2.16	0.46
1:H:152:ASN:HB3	1:H:155:LEU:HG	1.97	0.46
1:D:115:MET:N	1:D:124:ARG:O	2.23	0.46
1:E:69:GLN:HB2	1:E:98:ASN:HB3	1.97	0.46
1:G:165:LYS:HB3	1:G:165:LYS:HE2	1.83	0.46
1:H:150:LYS:HE3	1:H:151:GLU:O	2.16	0.46
1:D:104:TYR:HB3	1:D:132:HIS:HB3	1.96	0.46
1:F:111:PHE:CD2	1:F:126:LEU:HD21	2.48	0.46
1:D:124:ARG:NH1	1:D:208:LEU:O	2.48	0.46
1:C:119:ILE:HD13	1:C:184:TYR:CE1	2.51	0.46
1:C:151:GLU:HG2	1:C:211:SER:HB3	1.98	0.46
1:G:232:GLN:NE2	6:G:408:HOH:O	2.33	0.46
1:H:144:ILE:HD11	6:H:413:HOH:O	2.15	0.46
1:D:83:THR:N	1:D:86:THR:O	2.38	0.46
1:E:44:VAL:HG13	1:E:195:CYS:HB2	1.98	0.46
1:G:111:PHE:HB2	1:G:222:MET:HE1	1.98	0.46
1:G:223:LYS:O	1:G:223:LYS:HG2	2.16	0.46
1:A:52:SER:HB3	1:A:117:PHE:CZ	2.51	0.45
1:H:55:ASN:ND2	1:H:121:ASN:OD1	2.44	0.45
1:B:112:HIS:CD2	1:B:129:HIS:CE1	3.04	0.45
1:C:21:THR:CG2	1:C:22:LYS:HG3	2.42	0.45
1:G:76:LYS:HA	1:G:77:PRO:HD3	1.78	0.45
1:A:139:LEU:HD13	1:A:190:LEU:HD21	1.99	0.45
1:B:136:LYS:HG3	1:B:138:ARG:HH11	1.80	0.45
1:E:138:ARG:NH2	6:E:402:HOH:O	2.24	0.45
1:A:130:PHE:HB2	1:A:142:LEU:HB3	1.99	0.45
1:B:63:GLN:O	1:E:65:LYS:HB3	2.15	0.45
1:G:88:LYS:HE3	1:G:108:ASN:CG	2.36	0.45
1:A:37:LYS:HE2	1:A:37:LYS:HB3	1.90	0.45
1:E:64:ASP:OD2	1:E:243:SER:OG	2.33	0.45
1:G:133:LYS:HG2	1:G:139:LEU:CD2	2.45	0.45
1:A:115:MET:HB3	6:A:406:HOH:O	2.17	0.45
1:D:92:GLU:O	1:D:94:THR:N	2.46	0.45
1:F:106:LEU:HD12	1:F:131:VAL:O	2.17	0.45
1:C:32:PRO:HA	1:C:35:TRP:CD2	2.52	0.45
1:D:111:PHE:CD1	1:D:111:PHE:N	2.85	0.45
1:D:179:LYS:HA	1:D:246:THR:OG1	2.16	0.45
1:H:122:LYS:HD2	1:H:123:THR:N	2.29	0.45
1:A:177:LEU:O	1:A:247:ARG:NH2	2.50	0.45
1:D:116:GLU:OE1	1:D:129:HIS:CE1	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LYS:HB2	1:B:138:ARG:CD	2.47	0.45
1:D:30:ASN:HA	1:D:38:LEU:HD11	1.99	0.45
1:E:184:TYR:CE1	1:E:241:LYS:HD2	2.52	0.45
1:F:189:SER:HB3	1:F:197:GLU:HG2	1.99	0.45
1:H:44:VAL:HA	1:H:47:SER:OG	2.17	0.45
1:E:126:LEU:HB3	1:E:146:PHE:HB2	1.98	0.45
1:G:115:MET:HG3	1:G:127:SER:HB3	1.99	0.45
1:G:214:GLN:O	1:G:218:ILE:HG22	2.17	0.45
1:C:133:LYS:HG2	1:C:134:ASP:O	2.17	0.44
1:F:149:GLY:N	1:F:210:VAL:O	2.37	0.44
1:F:67:ASP:OD1	1:F:183:TYR:OH	2.34	0.44
1:E:115:MET:HG3	1:E:127:SER:HB3	1.98	0.44
1:F:159:LEU:HD13	1:F:217:GLU:CD	2.37	0.44
1:G:162:ILE:HD11	1:G:221:ARG:HD2	1.99	0.44
1:G:71:LYS:HB2	1:G:96:HIS:HB2	1.99	0.44
1:H:177:LEU:O	1:H:247:ARG:NH2	2.48	0.44
1:H:51:GLN:HB2	6:H:415:HOH:O	2.17	0.44
1:C:159:LEU:HD21	1:C:218:ILE:HG13	2.00	0.44
1:B:65:LYS:HB3	1:E:64:ASP:N	2.33	0.44
1:F:116:GLU:HG2	1:F:228:GLN:HG3	2.00	0.44
1:H:82:PHE:HA	1:H:86:THR:O	2.18	0.44
1:H:115:MET:HG3	1:H:127:SER:HB3	1.99	0.44
1:E:235:TYR:HD1	1:F:138:ARG:NH1	2.16	0.44
1:A:150:LYS:HB3	1:A:150:LYS:HE2	1.81	0.43
1:B:221:ARG:NH1	1:B:221:ARG:HB3	2.33	0.43
1:D:124:ARG:NE	1:D:207:PRO:HB2	2.31	0.43
1:G:234:ASP:OD1	1:G:237:THR:OG1	2.29	0.43
1:H:186:PHE:HD1	1:H:239:ILE:HG23	1.83	0.43
1:D:23:TRP:HA	1:D:30:ASN:HB3	2.00	0.43
1:B:86:THR:OG1	1:B:227:ASN:ND2	2.51	0.43
1:E:91:PHE:HE2	1:E:109[B]:VAL:HG12	1.83	0.43
1:E:186:PHE:HA	1:F:238:VAL:HG21	1.99	0.43
1:E:237:THR:HG23	6:E:497:HOH:O	2.17	0.43
1:G:71:LYS:CD	1:G:96:HIS:HB2	2.40	0.43
1:H:133:LYS:CE	1:H:137:GLY:CA	2.95	0.43
1:B:59:TYR:HB3	1:B:239:ILE:HB	1.99	0.43
1:F:36:ASP:CG	1:F:46:LYS:HB2	2.39	0.43
1:G:165:LYS:O	1:G:165:LYS:HG2	2.18	0.43
1:D:105[A]:VAL:HG12	1:D:133:LYS:O	2.18	0.43
1:H:104:TYR:HB3	1:H:132:HIS:HB3	2.01	0.43
1:G:100:ARG:HD2	1:H:58:HIS:ND1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:THR:OG1	1:A:110:HIS:HB2	2.18	0.43
1:A:56:ILE:HG23	1:A:239:ILE:HD13	1.99	0.43
1:B:177:LEU:O	1:B:247:ARG:NH1	2.52	0.43
1:B:192:ALA:HB3	4:B:303:EZL:H7	2.00	0.43
1:G:100:ARG:HB3	1:G:100:ARG:HE	1.52	0.43
1:E:142:LEU:HD21	1:E:204:ILE:HD11	2.00	0.43
1:B:111:PHE:N	1:B:111:PHE:CD1	2.87	0.43
1:F:86:THR:OG1	1:F:111:PHE:O	2.34	0.43
1:G:162:ILE:HD12	1:G:162:ILE:HA	1.77	0.43
1:E:144:ILE:HD12	1:E:204:ILE:HG21	2.00	0.43
1:F:119:ILE:O	1:F:122:LYS:HB2	2.19	0.43
1:G:166:GLN:O	6:G:405:HOH:O	2.22	0.43
1:B:109[A]:VAL:HA	1:B:129:HIS:O	2.18	0.43
1:E:78:LYS:NZ	6:E:434:HOH:O	2.51	0.43
1:H:68:LEU:HA	1:H:68:LEU:HD12	1.75	0.43
1:B:124:ARG:HB3	1:B:146:PHE:O	2.19	0.42
1:D:113:ALA:HB2	1:D:126:LEU:HD12	2.00	0.42
1:F:158:ILE:HG13	1:F:159:LEU:N	2.34	0.42
1:H:152:ASN:OD1	1:H:154:ASN:HB2	2.19	0.42
1:B:152:ASN:HA	1:B:153:PRO:HD2	1.89	0.42
1:G:26:LYS:NZ	1:G:223:LYS:HE2	2.33	0.42
1:H:25:TYR:CZ	1:H:227:ASN:HB2	2.54	0.42
1:H:36:ASP:OD2	1:H:46:LYS:HD2	2.19	0.42
1:C:26:LYS:HD2	1:C:26:LYS:HA	1.80	0.42
1:D:154:ASN:O	1:D:157:PRO:HD2	2.19	0.42
1:G:189:SER:HB3	1:G:197:GLU:HG2	2.00	0.42
1:B:115:MET:HB2	1:B:124:ARG:O	2.20	0.42
1:B:184:TYR:O	1:B:203:VAL:N	2.45	0.42
1:C:109[B]:VAL:HA	1:C:129:HIS:O	2.20	0.42
1:D:23:TRP:CZ2	1:D:193:PRO:HD2	2.54	0.42
1:G:51:GLN:HB3	1:G:232:GLN:HG3	2.00	0.42
1:D:105[B]:VAL:HG23	1:D:133:LYS:O	2.20	0.42
1:E:100:ARG:HH21	1:E:102:HIS:CE1	2.38	0.42
1:H:133:LYS:CG	1:H:137:GLY:HA2	2.49	0.42
1:H:29:GLU:HG2	1:H:30:ASN:N	2.34	0.42
1:B:129:HIS:HA	1:B:142:LEU:O	2.20	0.42
1:B:74:ALA:HA	1:B:171:VAL:O	2.19	0.42
1:C:118:LEU:HG	1:C:123:THR:HB	2.02	0.42
1:C:66:ALA:O	1:C:67:ASP:C	2.58	0.42
1:B:40:LYS:N	1:D:41:ASP:OD1	2.48	0.42
1:E:152:ASN:HA	1:E:153:PRO:HD3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:160:GLU:OE1	1:E:169:LYS:HE2	2.20	0.42
1:E:235:TYR:HD1	1:F:138:ARG:HH12	1.67	0.42
1:G:113:ALA:O	1:G:226:PRO:HA	2.20	0.42
1:G:36:ASP:HA	1:G:42:PHE:O	2.20	0.42
1:A:110:HIS:HE1	1:A:131:VAL:CG2	2.32	0.42
1:A:76:LYS:HA	1:A:77:PRO:HD3	1.88	0.42
1:B:118:LEU:CD2	1:B:123:THR:HB	2.50	0.42
1:B:89:ALA:HB3	1:B:109[B]:VAL:HG13	2.02	0.42
1:C:60:TYR:CE2	1:D:240:ILE:HG12	2.55	0.42
1:D:183:TYR:CE1	1:D:242:SER:HB3	2.55	0.42
1:A:215:LEU:HD12	1:A:215:LEU:HA	1.85	0.42
1:G:142:LEU:HD12	1:G:202:PHE:HB2	2.02	0.42
1:G:28:LYS:HB3	1:G:29:GLU:H	1.58	0.42
1:H:83[B]:THR:HG21	1:H:88:LYS:HD3	2.02	0.42
1:D:124:ARG:CG	1:D:125:PRO:HD2	2.50	0.42
1:E:159:LEU:O	1:E:162:ILE:HG22	2.19	0.42
1:F:220:LYS:HG2	1:F:220:LYS:H	1.61	0.42
1:G:138:ARG:NH2	1:H:235:TYR:HA	2.35	0.42
1:H:151:GLU:CA	1:H:211:SER:HB3	2.43	0.42
1:C:60:TYR:CD2	1:D:240:ILE:HG21	2.55	0.41
1:E:183:TYR:CE1	1:E:242:SER:HB3	2.55	0.41
1:G:67:ASP:O	1:G:99:TYR:HA	2.20	0.41
1:B:129:HIS:CE1	1:B:201:TRP:HH2	2.38	0.41
1:C:49:LYS:HG3	1:D:197:GLU:O	2.20	0.41
1:H:29:GLU:HG2	1:H:30:ASN:OD1	2.20	0.41
1:A:179:LYS:O	1:A:245:GLU:HA	2.19	0.41
1:A:23:TRP:HZ3	1:A:25:TYR:CE1	2.38	0.41
1:C:178:PRO:HD3	1:C:208:LEU:HD21	2.02	0.41
1:F:77:PRO:HD3	1:F:171:VAL:HG23	2.03	0.41
1:G:81:PHE:HA	1:G:221:ARG:HH12	1.85	0.41
1:B:152:ASN:HB2	1:B:209:GLU:O	2.20	0.41
1:B:44:VAL:HA	1:B:47:SER:OG	2.20	0.41
1:D:53:PRO:HD3	1:D:229:ARG:HB3	2.02	0.41
1:E:236:ASN:OD1	1:F:100:ARG:HD2	2.20	0.41
1:F:145:GLY:O	1:F:207:PRO:HA	2.20	0.41
1:A:34:ARG:HH21	1:A:37:LYS:HD3	1.85	0.41
1:A:63:GLN:NE2	1:A:63:GLN:O	2.53	0.41
1:A:118:LEU:CD2	1:A:123:THR:HG22	2.50	0.41
1:D:154:ASN:ND2	1:D:176:PHE:HA	2.34	0.41
1:A:100:ARG:HH21	1:B:60:TYR:HE1	1.68	0.41
1:A:197:GLU:OE1	6:A:404:HOH:O	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LEU:O	1:A:110:HIS:HA	2.21	0.41
1:B:130:PHE:HB2	1:B:142:LEU:CB	2.45	0.41
1:D:124:ARG:NH2	1:D:208:LEU:O	2.54	0.41
1:E:165:LYS:HE3	1:E:166:GLN:HG3	2.02	0.41
1:F:215:LEU:HD12	1:F:215:LEU:HA	1.78	0.41
1:A:87:LEU:HD21	1:A:158:ILE:CG2	2.51	0.41
1:B:174:ASP:OD1	1:B:174:ASP:N	2.53	0.41
1:B:147:GLU:HB2	1:B:207:PRO:HB2	2.02	0.41
1:B:76:LYS:HA	1:B:77:PRO:HD3	1.69	0.41
1:C:67:ASP:O	1:C:99:TYR:HA	2.21	0.41
1:F:130:PHE:CD1	1:F:130:PHE:N	2.88	0.41
1:G:109[B]:VAL:HA	1:G:129:HIS:O	2.21	0.41
1:G:73:ALA:O	1:G:173:LEU:HB2	2.20	0.41
1:F:115:MET:CG	1:F:127:SER:HB3	2.50	0.41
1:F:32:PRO:HA	1:F:35:TRP:CG	2.56	0.41
1:H:185:HIS:O	1:H:239:ILE:HA	2.20	0.41
1:C:221:ARG:HA	1:C:221:ARG:HD3	1.82	0.41
1:E:165:LYS:HE2	1:E:165:LYS:HB3	1.82	0.41
1:A:105:VAL:HG12	1:A:133:LYS:O	2.20	0.40
1:G:115:MET:HG3	3:G:302:CL:CL	2.58	0.40
1:F:159:LEU:HD13	1:F:217:GLU:OE2	2.21	0.40
1:D:179:LYS:HD3	1:G:147:GLU:CD	2.41	0.40
1:G:78:LYS:N	1:G:90:SER:O	2.50	0.40
1:H:215:LEU:HG	1:H:219:LYS:HE2	2.01	0.40
1:H:190:LEU:HD22	4:H:303:EZL:C1	2.50	0.40
1:C:151:GLU:HG2	1:C:211:SER:CB	2.52	0.40
1:C:98:ASN:HA	1:C:102:HIS:O	2.21	0.40
1:D:142:LEU:CD1	1:D:202:PHE:HB2	2.51	0.40
1:E:182:ASN:OD1	1:E:243:SER:HB3	2.21	0.40
1:H:184:TYR:O	1:H:203:VAL:N	2.38	0.40
1:B:63:GLN:O	1:E:65:LYS:HB2	2.21	0.40
1:F:218:ILE:O	1:F:221:ARG:HB2	2.21	0.40
1:H:150:LYS:HG2	1:H:151:GLU:N	2.36	0.40
1:F:126:LEU:HD21	1:F:218:ILE:HD13	2.02	0.40
1:G:129:HIS:HA	1:G:142:LEU:O	2.21	0.40
1:H:35:TRP:CH2	1:H:193:PRO:HD3	2.57	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ASN:ND2	1:B:122:LYS:CE[1_455]	2.06	0.14
6:B:446:HOH:O	6:C:505:HOH:O[2_846]	2.15	0.05
1:A:121:ASN:ND2	1:B:122:LYS:CG[1_455]	2.18	0.02

## 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	222/234 (95%)	213 (96%)	9 (4%)	0	100	100
1	B	206/234 (88%)	196 (95%)	10 (5%)	0	100	100
1	C	227/234 (97%)	219 (96%)	8 (4%)	0	100	100
1	D	194/234 (83%)	188 (97%)	6 (3%)	0	100	100
1	E	226/234 (97%)	217 (96%)	9 (4%)	0	100	100
1	F	218/234 (93%)	211 (97%)	7 (3%)	0	100	100
1	G	214/234 (92%)	208 (97%)	6 (3%)	0	100	100
1	H	220/234 (94%)	212 (96%)	8 (4%)	0	100	100
All	All	1727/1872 (92%)	1664 (96%)	63 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	201/208 (97%)	196 (98%)	5 (2%)	47	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	191/208 (92%)	185 (97%)	6 (3%)	40	51
1	C	204/208 (98%)	200 (98%)	4 (2%)	55	69
1	D	181/208 (87%)	174 (96%)	7 (4%)	32	41
1	E	203/208 (98%)	201 (99%)	2 (1%)	76	86
1	F	197/208 (95%)	188 (95%)	9 (5%)	27	34
1	G	197/208 (95%)	192 (98%)	5 (2%)	47	60
1	H	199/208 (96%)	198 (100%)	1 (0%)	88	94
All	All	1573/1664 (94%)	1534 (98%)	39 (2%)	49	60

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50[A]	SER
1	A	50[B]	SER
1	A	63	GLN
1	A	122	LYS
1	A	176	PHE
1	B	103	ASP
1	B	111	PHE
1	B	120	ASN
1	B	168	PHE
1	B	202	PHE
1	B	217	GLU
1	C	22	LYS
1	C	65	LYS
1	C	103	ASP
1	C	218	ILE
1	D	34	ARG
1	D	57	GLU
1	D	58	HIS
1	D	68	LEU
1	D	98	ASN
1	D	124	ARG
1	D	202	PHE
1	E	22	LYS
1	E	64	ASP
1	F	36	ASP
1	F	50	SER
1	F	102	HIS
1	F	105[A]	VAL

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Mol	Chain	Res	Type
1	F	105[B]	VAL
1	F	162	ILE
1	F	163	GLN
1	F	174	ASP
1	F	220	LYS
1	G	21	THR
1	G	90	SER
1	G	122	LYS
1	G	162	ILE
1	G	221	ARG
1	H	122	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	GLN
1	C	96	HIS
1	C	163	GLN
1	D	55	ASN
1	D	95	ASN
1	D	96	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 14 are monoatomic - leaving 12 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	GOL	A	304	-	5,5,5	0.61	0	5,5,5	0.83	0
5	GOL	E	304	-	5,5,5	0.44	0	5,5,5	0.81	0
4	EZL	G	303	2	13,17,17	2.08	2 (15%)	19,25,25	3.45	9 (47%)
4	EZL	E	303	2	13,17,17	2.08	2 (15%)	19,25,25	3.44	9 (47%)
4	EZL	A	303	2	13,17,17	2.07	2 (15%)	19,25,25	3.44	9 (47%)
4	EZL	H	303	2	13,17,17	2.07	2 (15%)	19,25,25	3.44	9 (47%)
5	GOL	C	304	-	5,5,5	0.71	0	5,5,5	0.81	0
4	EZL	B	303	2	13,17,17	2.07	2 (15%)	19,25,25	3.45	9 (47%)
5	GOL	B	304	-	5,5,5	0.39	0	5,5,5	0.25	0
4	EZL	F	302	2	13,17,17	2.08	2 (15%)	19,25,25	3.44	9 (47%)
5	GOL	H	304	-	5,5,5	0.38	0	5,5,5	0.35	0
4	EZL	C	303	2	13,17,17	2.06	2 (15%)	19,25,25	3.44	9 (47%)

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	GOL	A	304	-	-	2/4/4/4	-
5	GOL	E	304	-	-	2/4/4/4	-
4	EZL	G	303	2	-	0/3/9/9	0/2/2/2
4	EZL	E	303	2	-	1/3/9/9	0/2/2/2
4	EZL	A	303	2	-	1/3/9/9	0/2/2/2
4	EZL	H	303	2	-	0/3/9/9	0/2/2/2
5	GOL	C	304	-	-	2/4/4/4	-
4	EZL	B	303	2	-	0/3/9/9	0/2/2/2
5	GOL	B	304	-	-	0/4/4/4	-
4	EZL	F	302	2	-	0/3/9/9	0/2/2/2
5	GOL	H	304	-	-	2/4/4/4	-
4	EZL	C	303	2	-	0/3/9/9	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	303	EZL	C2-N2	6.15	1.59	1.38
4	F	302	EZL	C2-N2	6.14	1.59	1.38
4	G	303	EZL	C2-N2	6.14	1.59	1.38
4	A	303	EZL	C2-N2	6.13	1.59	1.38
4	B	303	EZL	C2-N2	6.12	1.58	1.38
4	H	303	EZL	C2-N2	6.12	1.58	1.38
4	C	303	EZL	C2-N2	6.11	1.58	1.38
4	F	302	EZL	S1-N1	2.15	1.64	1.60
4	H	303	EZL	S1-N1	2.14	1.64	1.60
4	G	303	EZL	S1-N1	2.14	1.64	1.60
4	B	303	EZL	S1-N1	2.13	1.64	1.60
4	E	303	EZL	S1-N1	2.13	1.64	1.60
4	C	303	EZL	S1-N1	2.12	1.64	1.60
4	A	303	EZL	S1-N1	2.10	1.64	1.60

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	303	EZL	O2-S1-O1	-10.72	101.14	118.76
4	G	303	EZL	O2-S1-O1	-10.68	101.20	118.76
4	F	302	EZL	O2-S1-O1	-10.68	101.21	118.76
4	H	303	EZL	O2-S1-O1	-10.68	101.21	118.76
4	A	303	EZL	O2-S1-O1	-10.68	101.21	118.76
4	E	303	EZL	O2-S1-O1	-10.67	101.22	118.76
4	C	303	EZL	O2-S1-O1	-10.67	101.22	118.76
4	G	303	EZL	O3-C5-C4	-6.76	101.11	123.96
4	F	302	EZL	O3-C5-C4	-6.75	101.16	123.96
4	E	303	EZL	O3-C5-C4	-6.74	101.17	123.96
4	H	303	EZL	O3-C5-C4	-6.74	101.17	123.96
4	B	303	EZL	O3-C5-C4	-6.73	101.21	123.96
4	A	303	EZL	O3-C5-C4	-6.73	101.23	123.96
4	C	303	EZL	O3-C5-C4	-6.72	101.25	123.96
4	E	303	EZL	O3-C5-C6	3.80	138.65	119.94
4	G	303	EZL	O3-C5-C6	3.80	138.64	119.94
4	A	303	EZL	O3-C5-C6	3.80	138.60	119.94
4	H	303	EZL	O3-C5-C6	3.79	138.58	119.94
4	C	303	EZL	O3-C5-C6	3.79	138.58	119.94
4	B	303	EZL	O3-C5-C6	3.79	138.56	119.94
4	F	302	EZL	O3-C5-C6	3.78	138.55	119.94
4	F	302	EZL	C4-C3-S2	3.57	132.25	125.10
4	C	303	EZL	C4-C3-S2	3.57	132.25	125.10
4	G	303	EZL	C4-C3-S2	3.57	132.24	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	303	EZL	C4-C3-S2	3.56	132.22	125.10
4	H	303	EZL	C4-C3-S2	3.55	132.20	125.10
4	B	303	EZL	C4-C3-S2	3.55	132.20	125.10
4	E	303	EZL	C4-C3-S2	3.55	132.19	125.10
4	F	302	EZL	C2-C3-S2	-3.06	107.79	111.85
4	C	303	EZL	C2-C3-S2	-3.04	107.82	111.85
4	B	303	EZL	C2-C3-S2	-3.03	107.83	111.85
4	H	303	EZL	C2-C3-S2	-3.02	107.85	111.85
4	G	303	EZL	C2-C3-S2	-3.01	107.86	111.85
4	A	303	EZL	C2-C3-S2	-2.99	107.88	111.85
4	E	303	EZL	C2-C3-S2	-2.98	107.90	111.85
4	F	302	EZL	O2-S1-N1	2.67	111.32	107.36
4	A	303	EZL	O2-S1-N1	2.67	111.32	107.36
4	H	303	EZL	O1-S1-N1	2.66	111.31	107.36
4	B	303	EZL	O1-S1-N1	2.66	111.30	107.36
4	E	303	EZL	O1-S1-N1	2.65	111.30	107.36
4	E	303	EZL	O2-S1-N1	2.65	111.29	107.36
4	C	303	EZL	O1-S1-N1	2.65	111.28	107.36
4	H	303	EZL	O2-S1-N1	2.64	111.27	107.36
4	B	303	EZL	O2-S1-N1	2.63	111.27	107.36
4	G	303	EZL	O1-S1-N1	2.63	111.26	107.36
4	A	303	EZL	O1-S1-N1	2.63	111.26	107.36
4	G	303	EZL	O2-S1-N1	2.63	111.26	107.36
4	C	303	EZL	O2-S1-N1	2.62	111.25	107.36
4	F	302	EZL	O1-S1-N1	2.62	111.24	107.36
4	E	303	EZL	O1-S1-C1	2.31	111.31	108.59
4	G	303	EZL	O1-S1-C1	2.31	111.31	108.59
4	G	303	EZL	O2-S1-C1	2.30	111.29	108.59
4	H	303	EZL	O1-S1-C1	2.30	111.29	108.59
4	F	302	EZL	O2-S1-C1	2.29	111.28	108.59
4	B	303	EZL	O2-S1-C1	2.29	111.28	108.59
4	C	303	EZL	O1-S1-C1	2.29	111.28	108.59
4	F	302	EZL	O1-S1-C1	2.28	111.27	108.59
4	A	303	EZL	O1-S1-C1	2.28	111.27	108.59
4	A	303	EZL	O2-S1-C1	2.28	111.27	108.59
4	B	303	EZL	O1-S1-C1	2.27	111.26	108.59
4	C	303	EZL	O2-S1-C1	2.27	111.26	108.59
4	H	303	EZL	O2-S1-C1	2.26	111.25	108.59
4	E	303	EZL	O2-S1-C1	2.26	111.24	108.59

There are no chirality outliers.

All (10) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	C	304	GOL	C1-C2-C3-O3
5	C	304	GOL	O2-C2-C3-O3
5	A	304	GOL	O1-C1-C2-C3
5	E	304	GOL	O1-C1-C2-C3
5	H	304	GOL	O1-C1-C2-C3
4	E	303	EZL	C9-C8-O3-C5
4	A	303	EZL	C9-C8-O3-C5
5	E	304	GOL	O1-C1-C2-O2
5	H	304	GOL	O1-C1-C2-O2
5	A	304	GOL	O1-C1-C2-O2

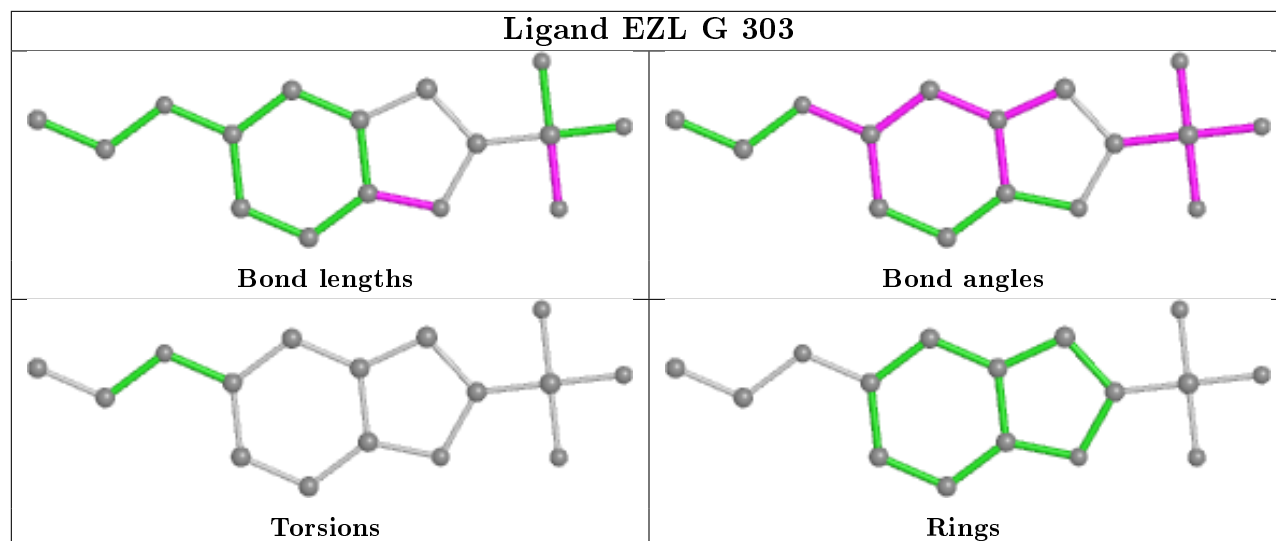
There are no ring outliers.

8 monomers are involved in 11 short contacts:

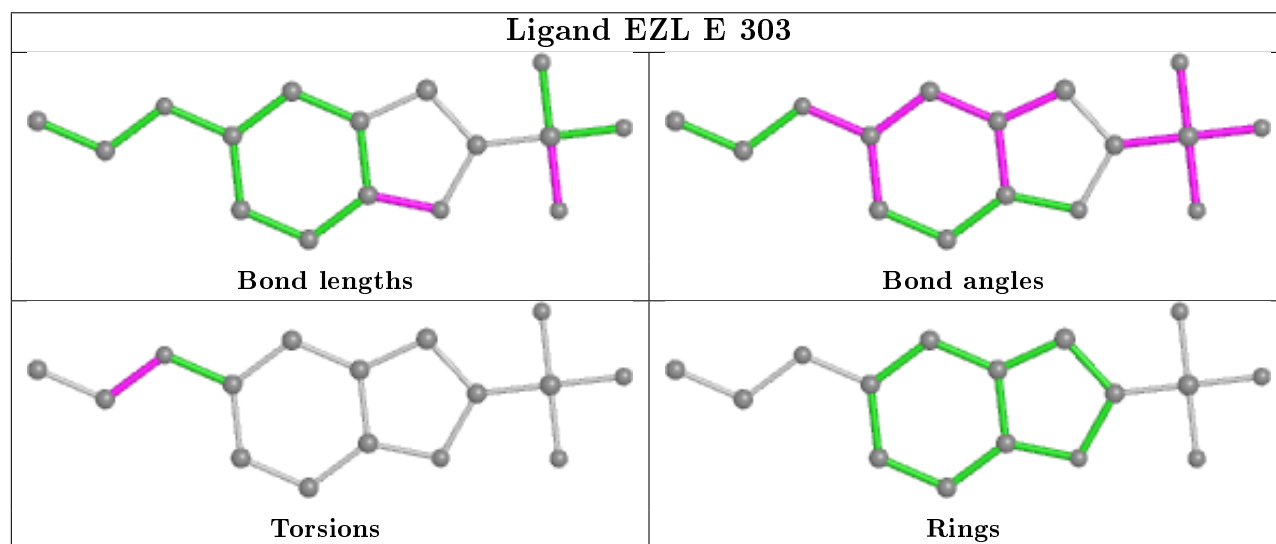
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	304	GOL	2	0
5	E	304	GOL	2	0
4	E	303	EZL	2	0
4	A	303	EZL	3	0
4	H	303	EZL	1	0
4	B	303	EZL	1	0
4	F	302	EZL	1	0
5	H	304	GOL	1	0

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

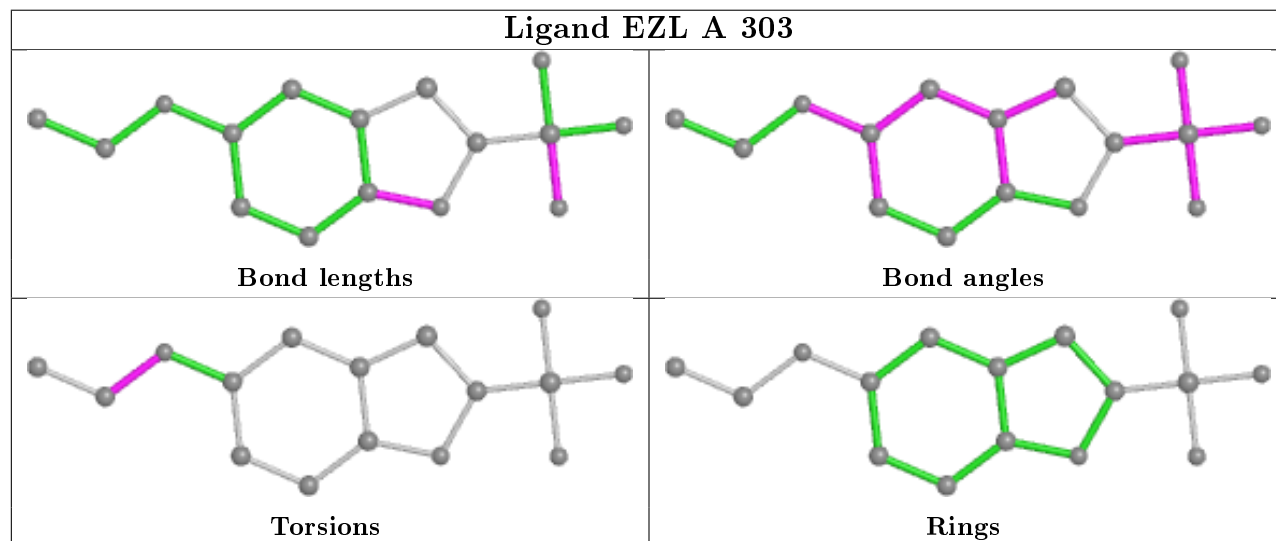
## Ligand EZL G 303



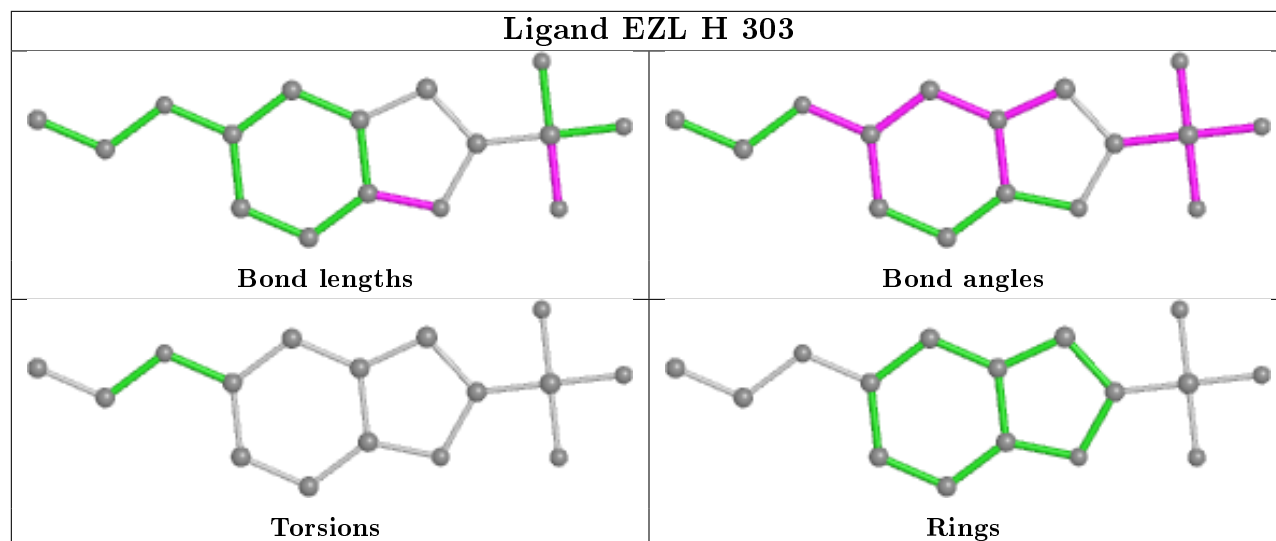
## Ligand EZL E 303



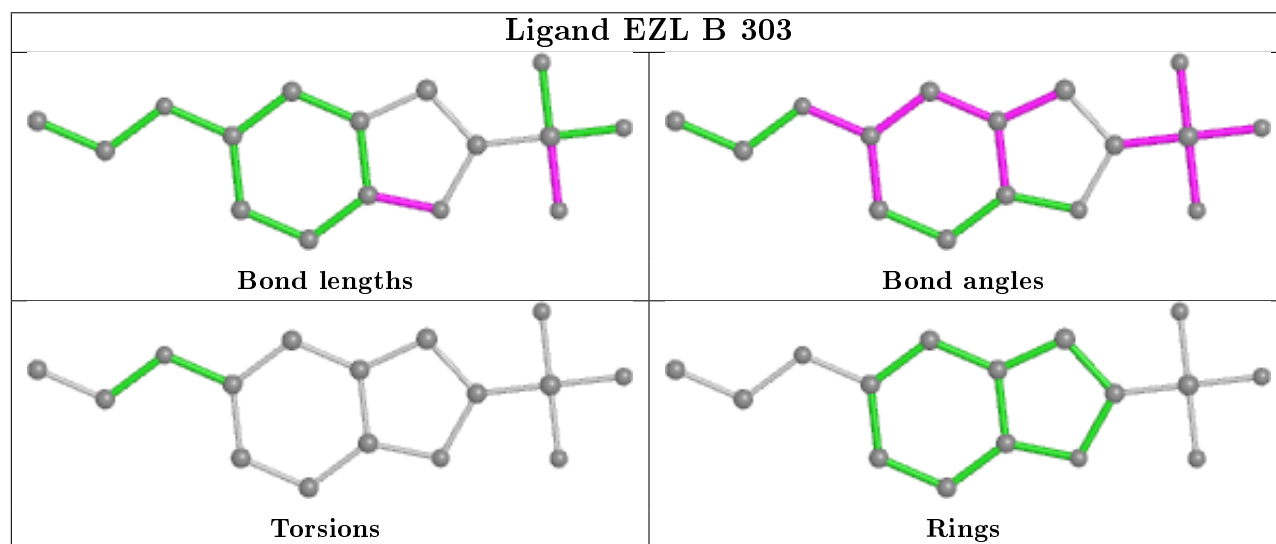
## Ligand EZL A 303



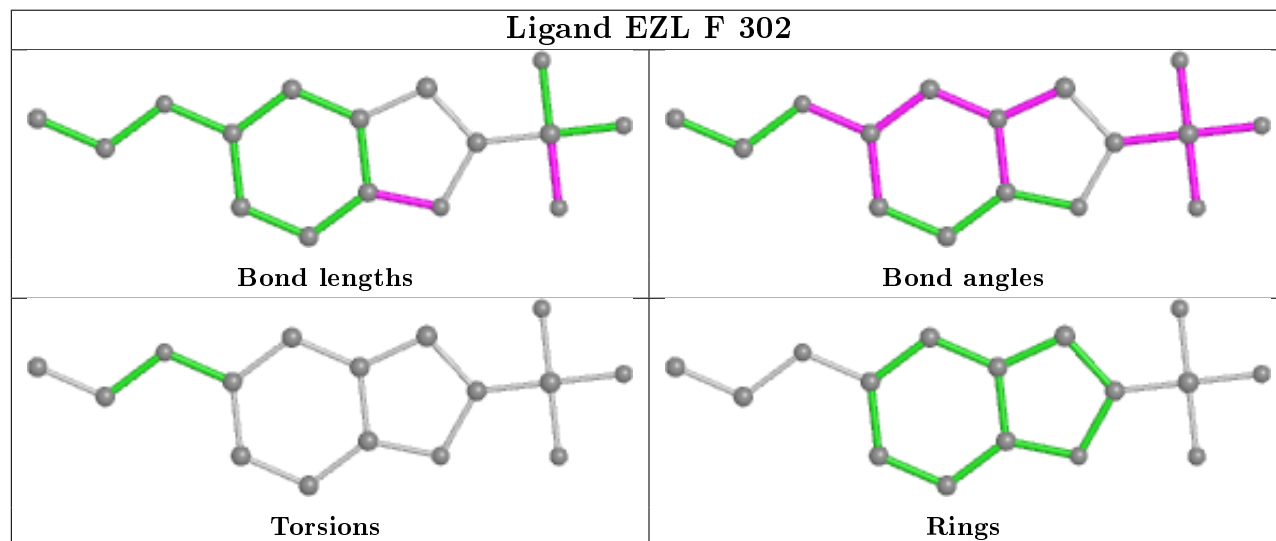
## Ligand EZL H 303

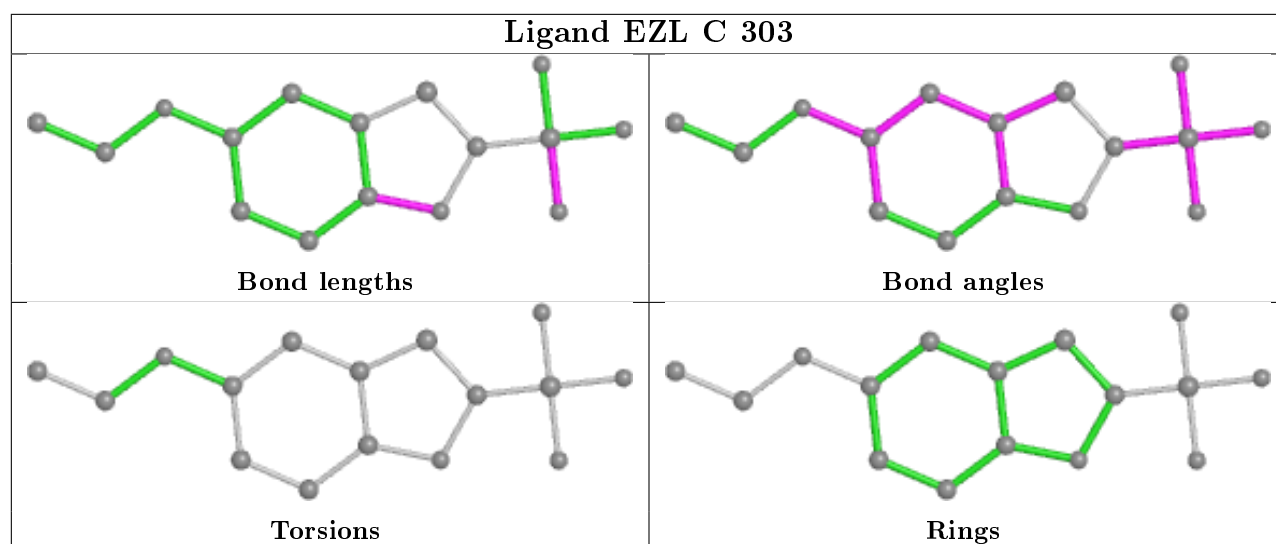


## Ligand EZL B 303



## Ligand EZL F 302





## 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	223/234 (95%)	-0.30	3 (1%) 77 75	22, 44, 71, 88	0
1	B	212/234 (90%)	-0.14	4 (1%) 66 65	26, 51, 71, 80	0
1	C	227/234 (97%)	-0.57	2 (0%) 84 83	16, 28, 47, 65	0
1	D	202/234 (86%)	0.24	5 (2%) 57 55	27, 65, 83, 94	0
1	E	226/234 (96%)	-0.57	1 (0%) 92 91	16, 28, 50, 70	0
1	F	220/234 (94%)	-0.20	2 (0%) 84 83	27, 50, 74, 83	0
1	G	218/234 (93%)	-0.41	0 100 100	22, 44, 63, 69	0
1	H	223/234 (95%)	-0.29	1 (0%) 92 91	26, 44, 62, 81	0
All	All	1751/1872 (93%)	-0.29	18 (1%) 82 81	16, 44, 73, 94	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	86	THR	4.6
1	A	101	GLY	4.3
1	D	158	ILE	4.0
1	F	213	LYS	3.3
1	B	81	PHE	3.2
1	B	80	VAL	2.9
1	A	158	ILE	2.8
1	E	64	ASP	2.7
1	C	64	ASP	2.7
1	B	213	LYS	2.5
1	C	21	THR	2.4
1	H	57	GLU	2.3
1	B	155	LEU	2.3
1	D	95	ASN	2.3
1	F	158	ILE	2.3
1	D	213	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	163	GLN	2.1
1	D	66	ALA	2.1

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
5	GOL	E	304	6/6	0.90	0.30	34,37,48,52	0
2	ZN	D	301	1/1	0.91	0.08	65,65,65,65	1
5	GOL	B	304	6/6	0.93	0.12	42,46,48,49	0
5	GOL	A	304	6/6	0.94	0.13	33,36,40,42	0
4	EZL	B	303	16/16	0.94	0.14	36,48,64,69	0
4	EZL	F	302	16/16	0.96	0.14	36,44,66,74	0
4	EZL	A	303	16/16	0.97	0.13	27,38,63,64	0
5	GOL	C	304	6/6	0.97	0.12	15,23,24,25	0
3	CL	B	302	1/1	0.97	0.05	46,46,46,46	0
4	EZL	E	303	16/16	0.97	0.12	16,27,44,49	0
4	EZL	H	303	16/16	0.97	0.12	26,36,51,66	0
5	GOL	H	304	6/6	0.97	0.08	32,34,38,44	0
4	EZL	C	303	16/16	0.97	0.15	17,28,55,57	0
4	EZL	G	303	16/16	0.98	0.13	24,30,43,49	0
3	CL	A	302	1/1	0.98	0.09	38,38,38,38	0
2	ZN	H	301	1/1	0.99	0.12	31,31,31,31	0
2	ZN	G	301	1/1	0.99	0.15	33,33,33,33	0
2	ZN	B	301	1/1	0.99	0.11	50,50,50,50	0
3	CL	H	302	1/1	0.99	0.09	33,33,33,33	0
3	CL	G	302	1/1	0.99	0.09	30,30,30,30	0
3	CL	E	302	1/1	0.99	0.13	22,22,22,22	0

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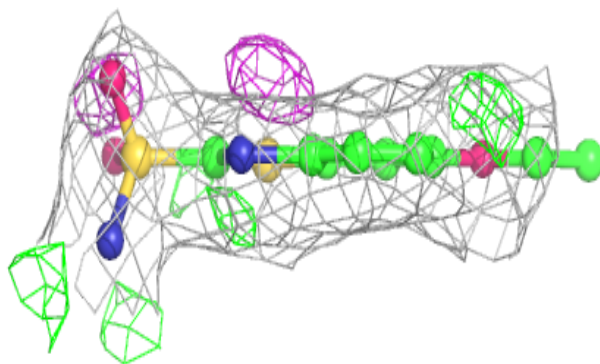
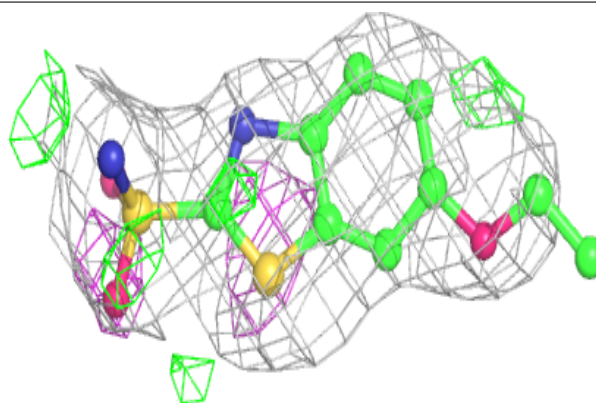
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	301	1/1	0.99	0.13	36,36,36,36	0
2	ZN	E	301	1/1	1.00	0.14	19,19,19,19	0
2	ZN	F	301	1/1	1.00	0.10	46,46,46,46	0
3	CL	C	302	1/1	1.00	0.10	23,23,23,23	0
2	ZN	C	301	1/1	1.00	0.15	21,21,21,21	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.

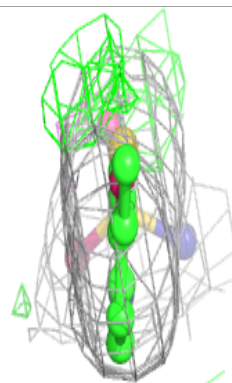
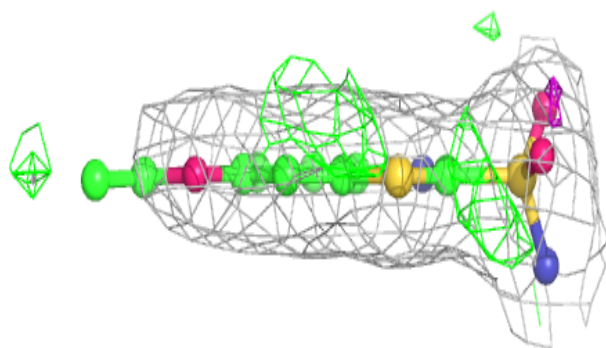
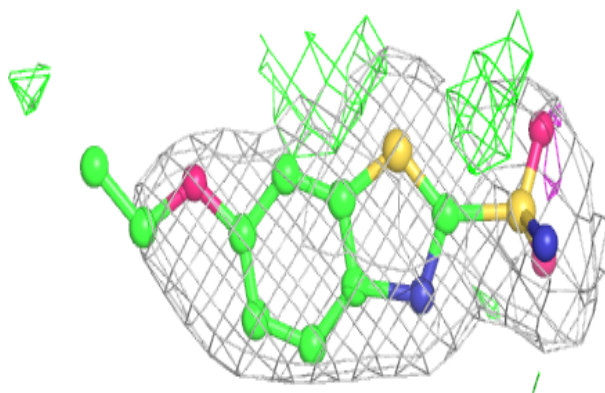
**Electron density around EZL B 303:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

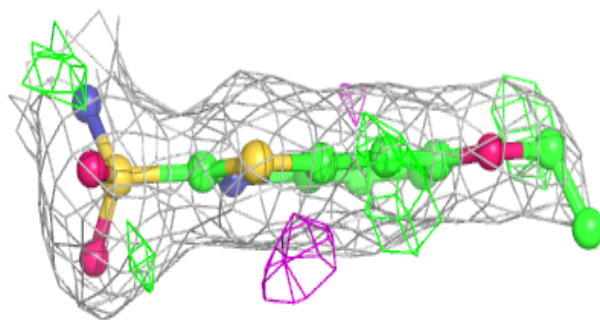
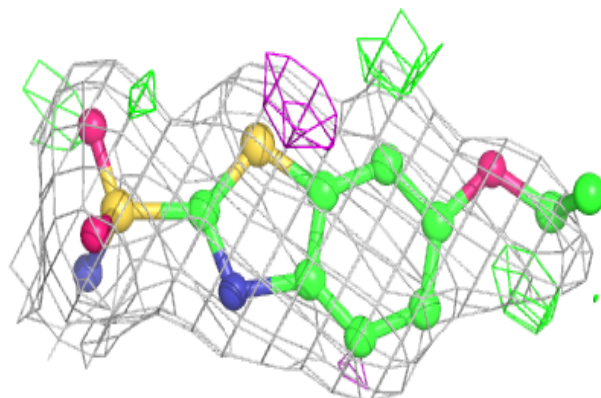


**Electron density around EZL F 302:**

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

**Electron density around EZL A 303:**

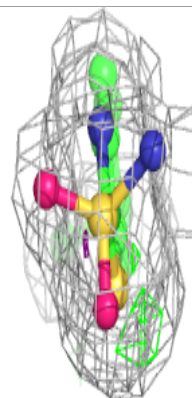
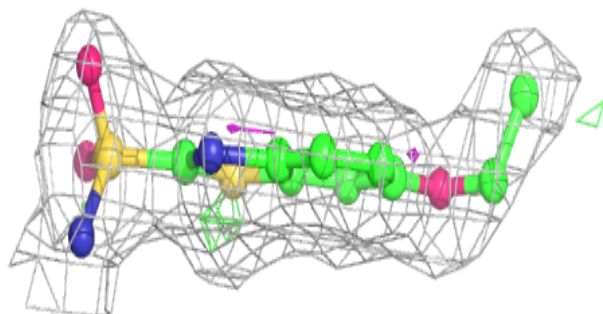
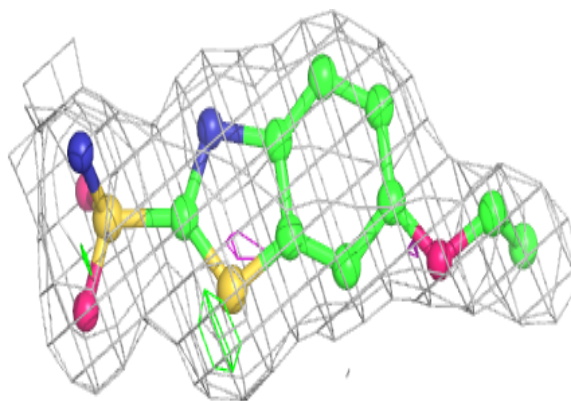
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



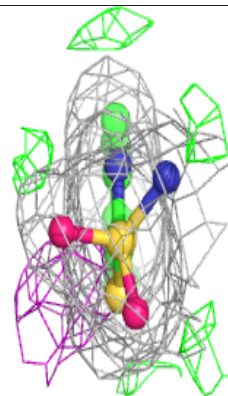
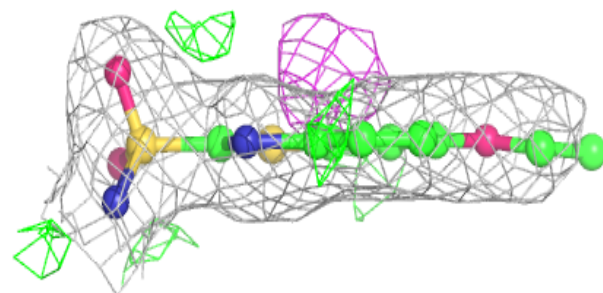
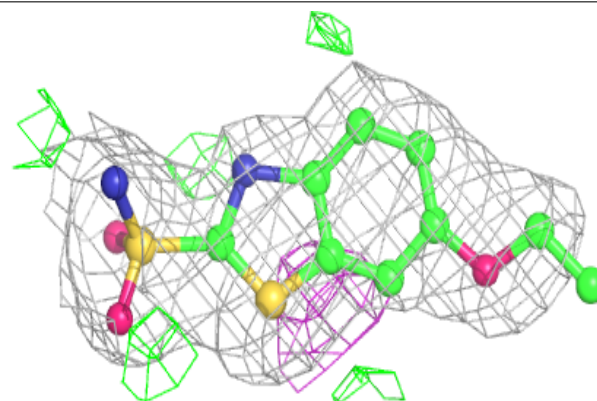


**Electron density around EZL E 303:**

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

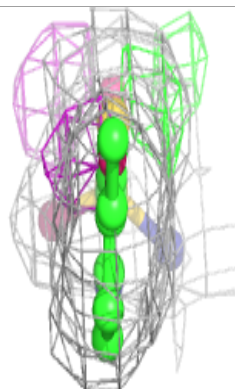
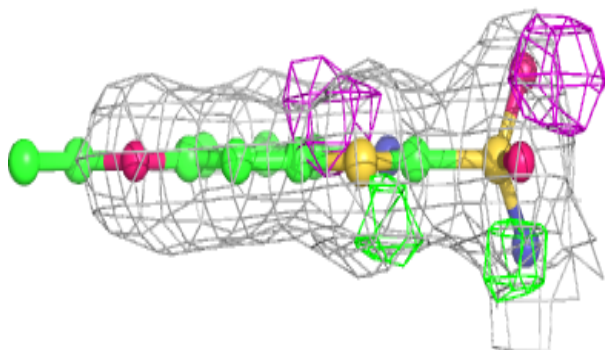
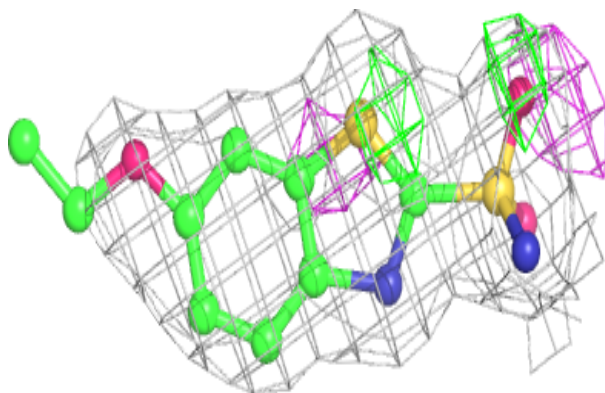
**Electron density around EZL H 303:**

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

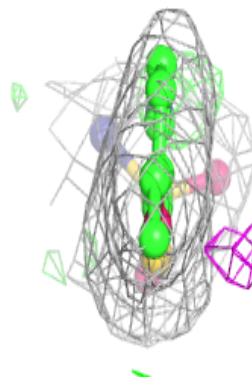
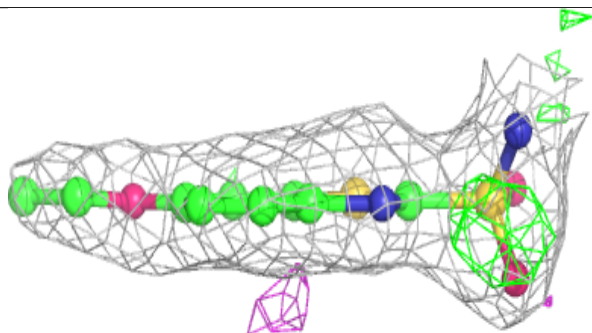
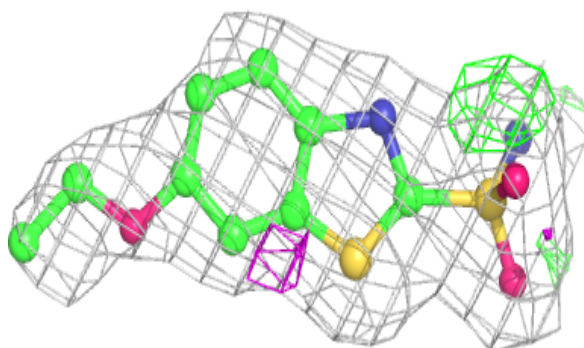


**Electron density around EZL C 303:**

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

**Electron density around EZL G 303:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.