



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:10 PM UTC

PDB ID : 8W07 / pdb_00008w07
Title : Crystal Structure of the ER-alpha Ligand-binding Domain (L372S, L536S) in complex with k-402
Authors : Min, C.K.; Nwachukwu, J.C.; Hou, Y.; Russo, R.J.; Papa, A.; Min, J.; Peng, R.; Kim, S.H.; Ziegler, Y.; Rangarajan, E.S.; Izard, T.; Katzenellenbogen, B.S.; Katzenellenbogen, J.K.; Nettles, K.W.
Deposited on : 2024-02-13
Resolution : 1.83 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

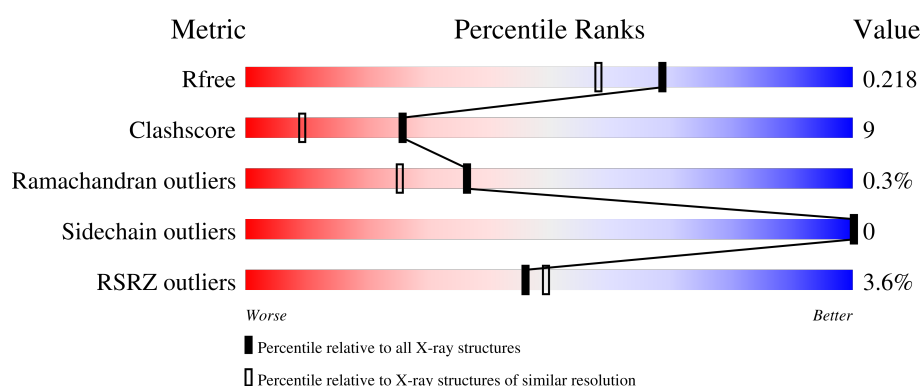
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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

Mol	Chain	Length	Quality of chain
1	A	242	5% 79% 16% • •
1	B	242	2% 81% 13% • 5%
1	C	242	2% 83% 13% •
1	D	242	5% 73% 17% • 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15119 atoms, of which 7425 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.

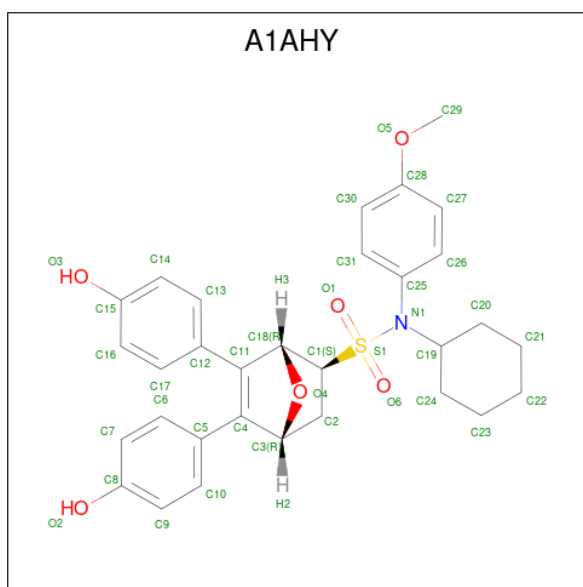
- Molecule 1 is a protein called Estrogen receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	233	Total	C	H	N	O	S	0	2	0
			3691	1177	1853	314	330	17			
1	B	229	Total	C	H	N	O	S	0	0	0
			3622	1150	1826	306	323	17			
1	C	232	Total	C	H	N	O	S	0	2	0
			3690	1174	1855	315	329	17			
1	D	221	Total	C	H	N	O	S	0	0	0
			3498	1115	1759	297	310	17			

There are 8 discrepancies between the modelled and reference sequences:

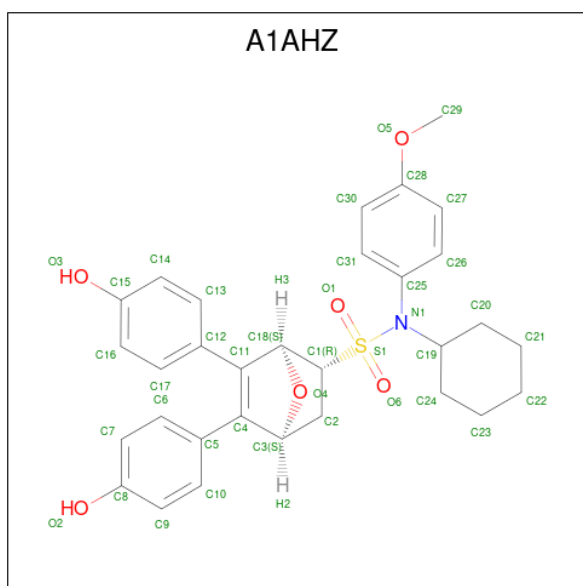
Chain	Residue	Modelled	Actual	Comment	Reference
A	372	SER	LEU	engineered mutation	UNP P03372
A	536	SER	LEU	engineered mutation	UNP P03372
B	372	SER	LEU	engineered mutation	UNP P03372
B	536	SER	LEU	engineered mutation	UNP P03372
C	372	SER	LEU	engineered mutation	UNP P03372
C	536	SER	LEU	engineered mutation	UNP P03372
D	372	SER	LEU	engineered mutation	UNP P03372
D	536	SER	LEU	engineered mutation	UNP P03372

- Molecule 2 is (1R,2S,4R)-N-cyclohexyl-5,6-bis(4-hydroxyphenyl)-N-(4-methoxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonamide (CCD ID: A1AHY) (formula: C₃₁H₃₃NO₆S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

- Molecule 3 is (1S,2R,4S)-N-cyclohexyl-5,6-bis(4-hydroxyphenyl)-N-(4-methoxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonamide (CCD ID: A1AHZ) (formula: C₃₁H₃₃NO₆S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		
3	C	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	D	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

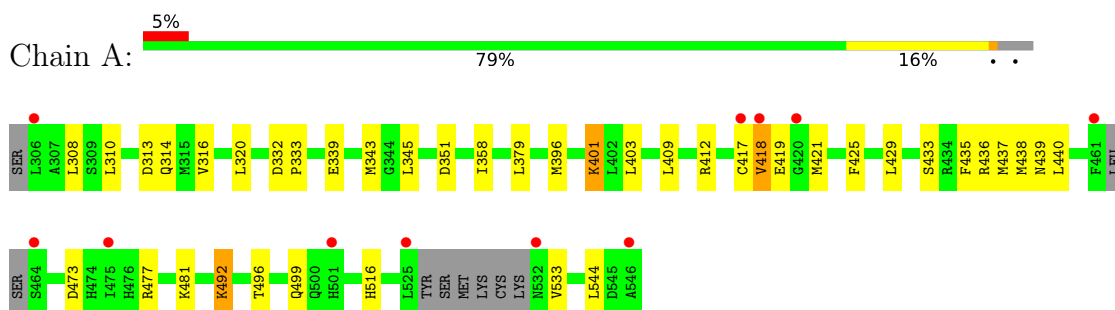
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total	O	0	0
			88	88		
4	B	87	Total	O	0	0
			87	87		
4	C	77	Total	O	0	0
			77	77		
4	D	78	Total	O	0	0
			78	78		

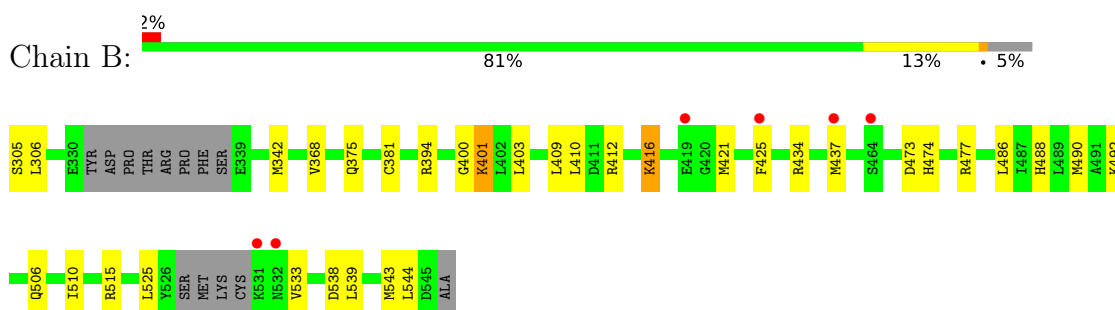
3 Residue-property plots [i](#)

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

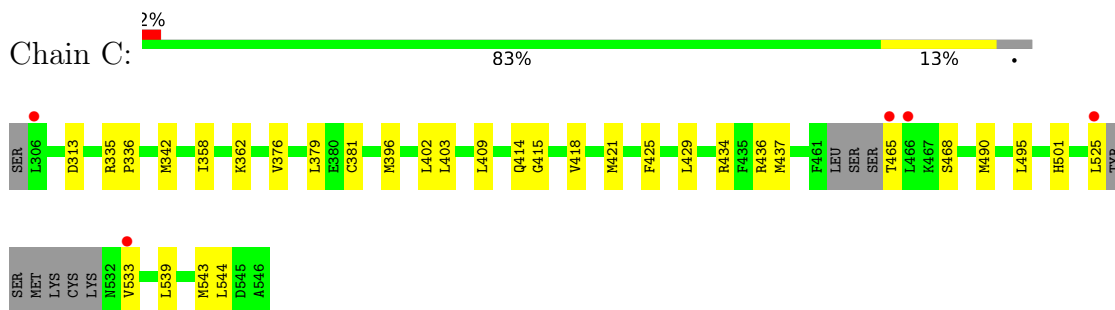
- Molecule 1: Estrogen receptor



- Molecule 1: Estrogen receptor

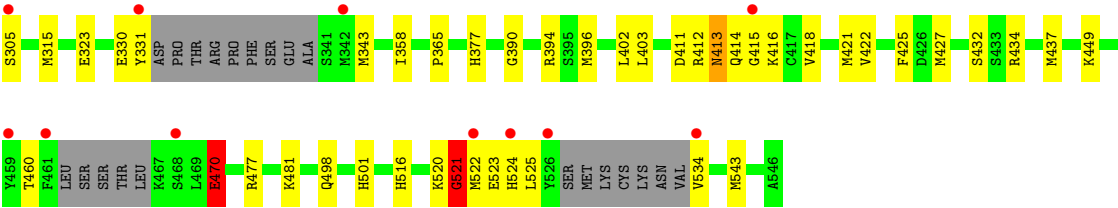


- Molecule 1: Estrogen receptor



- Molecule 1: Estrogen receptor





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.58Å 59.03Å 93.75Å 86.59° 75.01° 63.14°	Depositor
Resolution (Å)	37.54 – 1.83 37.54 – 1.83	Depositor EDS
% Data completeness (in resolution range)	71.4 (37.54-1.83) 71.4 (37.54-1.83)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.179 , 0.218 0.180 , 0.218	Depositor DCC
R_{free} test set	3117 reflections (3.59%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.110 for h,h-k,h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15119	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: A1AHZ, A1AHY

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	0.39	2/1883 (0.1%)	0.65	2/2549 (0.1%)
1	B	0.51	5/1826 (0.3%)	0.72	5/2467 (0.2%)
1	C	0.36	0/1880	0.61	0/2545
1	D	0.54	4/1768 (0.2%)	0.81	13/2387 (0.5%)
All	All	0.45	11/7357 (0.1%)	0.70	20/9948 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	4
All	All	0	5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	416	LYS	CE-NZ	10.56	1.81	1.49
1	D	521	GLY	C-N	-8.08	1.21	1.33
1	D	522	MET	CG-SD	7.69	2.00	1.80
1	B	401	LYS	CB-CG	-7.07	1.31	1.52
1	A	401	LYS	CE-NZ	-6.84	1.28	1.49
1	D	522	MET	CA-C	-6.55	1.43	1.52
1	B	401	LYS	CE-NZ	6.47	1.68	1.49
1	D	522	MET	SD-CE	6.17	1.95	1.79
1	A	401	LYS	CB-CG	-5.27	1.36	1.52
1	B	416	LYS	CD-CE	5.22	1.68	1.52
1	B	416	LYS	CA-C	-5.06	1.45	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	416	LYS	CD-CE-NZ	-10.38	78.67	111.90
1	D	522	MET	CG-SD-CE	-10.29	78.26	100.90
1	D	522	MET	CA-CB-CG	8.93	131.96	114.10
1	B	416	LYS	CA-CB-CG	-7.68	98.73	114.10
1	D	522	MET	N-CA-CB	-6.91	99.14	110.40
1	A	492	LYS	CG-CD-CE	-6.89	95.46	111.30
1	D	413	ASN	N-CA-CB	6.52	120.34	110.30
1	D	522	MET	O-C-N	6.10	130.88	122.46
1	D	470	GLU	OE1-CD-OE2	-5.77	109.05	122.90
1	D	413	ASN	N-CA-C	-5.67	105.09	112.23
1	D	413	ASN	OD1-CG-ND2	-5.65	116.95	122.60
1	D	524	HIS	N-CA-CB	-5.56	101.09	110.49
1	D	522	MET	CB-CG-SD	-5.54	96.08	112.70
1	B	400	GLY	CA-C-N	-5.46	114.03	122.59
1	B	400	GLY	C-N-CA	-5.46	114.03	122.59
1	A	439	ASN	CB-CA-C	5.40	119.10	111.86
1	B	401	LYS	N-CA-C	5.08	117.39	109.52
1	D	522	MET	N-CA-C	5.08	119.18	112.89
1	D	521	GLY	CA-C-N	-5.01	112.37	121.14
1	D	521	GLY	C-N-CA	-5.01	112.37	121.14

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	313	ASP	Sidechain
1	D	412	ARG	Peptide
1	D	413	ASN	Sidechain
1	D	470	GLU	Sidechain
1	D	521	GLY	Mainchain

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	1838	1853	1843	47	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1796	1826	1826	36	1
1	C	1835	1855	1845	26	0
1	D	1739	1759	1767	29	0
2	A	39	33	0	6	0
3	B	39	33	0	2	0
3	C	39	33	0	3	0
3	D	39	33	0	3	0
4	A	88	0	0	5	0
4	B	87	0	0	4	0
4	C	77	0	0	4	0
4	D	78	0	0	1	0
All	All	7694	7425	7281	139	1

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 9.

All (139) 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:401:LYS:CE	1:B:401:LYS:NZ	1.68	1.52
1:B:416:LYS:CE	1:B:416:LYS:NZ	1.81	1.40
1:B:416:LYS:NZ	1:B:416:LYS:CD	2.21	1.03
1:B:473:ASP:OD1	1:B:477:ARG:NH1	1.95	0.99
1:C:381:CYS:SG	4:C:773:HOH:O	2.23	0.94
1:B:381:CYS:SG	4:B:777:HOH:O	2.26	0.93
1:A:396:MET:O	1:A:436:ARG:NH1	2.04	0.91
1:D:520:LYS:NZ	1:D:523:GLU:OE1	2.05	0.90
1:B:401:LYS:NZ	1:B:401:LYS:CD	2.36	0.87
1:C:533:VAL:HG11	3:C:601:A1AHZ:O3	1.77	0.84
1:A:421:MET:HE2	2:A:601:A1AHY:C26	2.12	0.79
1:D:305:SER:O	4:D:701:HOH:O	1.99	0.79
1:A:477:ARG:NH1	4:A:704:HOH:O	2.15	0.78
1:D:411:ASP:OD1	1:D:414:GLN:NE2	2.16	0.78
1:C:434:ARG:HH11	1:C:437:MET:HE3	1.52	0.75
1:B:305:SER:N	4:B:701:HOH:O	2.20	0.74
1:B:421:MET:HE2	1:B:425:PHE:CE1	2.23	0.73
1:C:362:LYS:NZ	4:C:701:HOH:O	2.21	0.73
1:A:351:ASP:OD2	4:A:701:HOH:O	2.06	0.73
1:A:417:CYS:SG	4:A:773:HOH:O	2.48	0.72
1:A:403:LEU:HD13	1:A:409:LEU:HD13	1.70	0.71
1:C:539:LEU:HD11	1:C:543:MET:HE2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:525:LEU:C	1:B:525:LEU:HD23	2.17	0.70
1:D:377:HIS:CE1	1:D:460:THR:HG23	2.27	0.70
1:D:415:GLY:O	1:D:421:MET:HG2	1.92	0.69
1:D:427:MET:HE1	1:D:516:HIS:CD2	2.28	0.69
1:A:437:MET:HA	1:A:437:MET:HE2	1.75	0.68
1:A:418:VAL:HG12	1:A:418:VAL:O	1.93	0.68
1:C:501[A]:HIS:NE2	4:C:703:HOH:O	2.26	0.67
1:A:313:ASP:O	4:A:703:HOH:O	2.13	0.66
1:A:339:GLU:HG2	1:A:418:VAL:HA	1.77	0.65
1:C:415:GLY:O	1:C:421:MET:HG2	1.96	0.65
1:A:436:ARG:NH2	4:A:705:HOH:O	2.27	0.64
1:D:534:VAL:HG22	3:D:601:A1AHZ:C29	2.29	0.63
1:A:496:THR:HG23	1:A:499:GLN:H	1.64	0.63
1:C:376:VAL:HG22	1:C:544:LEU:HD12	1.80	0.63
1:C:418:VAL:HB	1:C:421:MET:SD	2.39	0.63
1:D:315:MET:SD	1:D:365:PRO:HG2	2.39	0.62
1:B:416:LYS:NZ	1:B:416:LYS:HD3	2.14	0.61
1:D:343:MET:HA	1:D:343:MET:HE2	1.81	0.61
1:C:533:VAL:CG1	3:C:601:A1AHZ:O3	2.49	0.59
1:B:421:MET:HE2	1:B:425:PHE:CZ	2.38	0.59
1:A:533:VAL:CG1	2:A:601:A1AHY:O2	2.51	0.58
1:B:412:ARG:HH11	1:B:412:ARG:HG2	1.68	0.58
1:A:339:GLU:HG2	1:A:418:VAL:H	1.68	0.57
1:C:425:PHE:O	1:C:429:LEU:HD23	2.05	0.56
1:B:434:ARG:NH1	1:B:437:MET:SD	2.74	0.55
1:A:421:MET:HA	2:A:601:A1AHY:C24	2.36	0.55
1:B:416:LYS:CD	1:B:416:LYS:HZ3	2.19	0.54
1:B:525:LEU:HD23	1:B:525:LEU:O	2.08	0.54
2:A:601:A1AHY:C26	2:A:601:A1AHY:O4	2.55	0.54
1:A:403:LEU:CD1	1:A:409:LEU:HD13	2.36	0.54
1:B:409:LEU:C	1:B:410:LEU:HD12	2.33	0.53
1:B:525:LEU:HD13	3:B:601:A1AHZ:C28	2.39	0.53
1:A:339:GLU:HG2	1:A:418:VAL:CA	2.39	0.53
1:A:316:VAL:HG12	1:A:320:LEU:CD1	2.38	0.53
1:B:486:LEU:O	1:B:490:MET:HG3	2.09	0.52
1:A:308:LEU:HD11	1:A:477:ARG:HE	1.75	0.52
1:C:402:LEU:HD21	1:C:429:LEU:HD22	1.92	0.51
1:B:403:LEU:O	1:B:403:LEU:HD23	2.10	0.51
1:A:333:PRO:HB3	1:A:345:LEU:HD21	1.91	0.51
1:C:358:ILE:HD12	1:C:379:LEU:HD13	1.93	0.51
1:C:403:LEU:HD13	1:C:409:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:MET:SD	1:A:418:VAL:HG11	2.51	0.50
1:A:310:LEU:HD22	1:A:314:GLN:HB3	1.93	0.50
1:A:339:GLU:HG2	1:A:418:VAL:N	2.27	0.50
1:B:416:LYS:HD3	1:B:416:LYS:HZ3	1.73	0.50
1:B:306:LEU:H	1:B:306:LEU:HD23	1.77	0.49
1:D:434:ARG:NH1	1:D:437:MET:SD	2.84	0.49
1:C:335:ARG:NH2	4:C:707:HOH:O	2.45	0.49
1:B:412:ARG:HG2	1:B:412:ARG:NH1	2.27	0.49
1:B:474:HIS:ND1	4:B:702:HOH:O	2.35	0.49
1:D:427:MET:HE1	1:D:516:HIS:HD2	1.75	0.48
1:C:376:VAL:CG2	1:C:544:LEU:HD12	2.43	0.48
1:C:421:MET:HE2	1:C:425:PHE:CE2	2.48	0.48
1:C:490:MET:HB3	1:C:495:LEU:HD12	1.96	0.48
1:A:435:PHE:CD1	1:A:440:LEU:HD22	2.49	0.48
1:A:316:VAL:HG12	1:A:320:LEU:HD12	1.96	0.47
1:D:498:GLN:HA	1:D:501:HIS:CE1	2.49	0.47
3:D:601:A1AHZ:C26	3:D:601:A1AHZ:C24	2.92	0.47
1:A:473:ASP:O	1:A:477:ARG:HG3	2.15	0.47
1:C:539:LEU:CD1	1:C:543:MET:HE2	2.44	0.47
1:D:411:ASP:H	1:D:414:GLN:NE2	2.12	0.47
1:D:396:MET:HA	1:D:432:SER:OG	2.16	0.46
1:A:412:ARG:HA	1:A:425:PHE:CZ	2.51	0.46
1:D:525:LEU:HD22	3:D:601:A1AHZ:C28	2.45	0.46
1:B:342:MET:HE1	1:B:410:LEU:HD21	1.98	0.46
1:A:496:THR:HG22	1:A:499:GLN:CG	2.46	0.46
1:C:465:THR:HG23	1:C:468:SER:OG	2.16	0.46
1:D:520:LYS:O	1:D:521:GLY:C	2.58	0.46
1:D:390:GLY:O	1:D:394:ARG:HG3	2.16	0.46
1:A:358:ILE:HD12	1:A:379:LEU:HD13	1.97	0.46
1:A:533:VAL:HG12	2:A:601:A1AHY:O2	2.16	0.46
1:A:401:LYS:NZ	1:A:409:LEU:HD21	2.31	0.45
1:D:377:HIS:NE2	1:D:460:THR:HG23	2.31	0.45
1:A:516:HIS:CG	1:B:515:ARG:NH1	2.85	0.45
1:D:470:GLU:H	1:D:470:GLU:CD	2.25	0.44
1:A:358:ILE:HG23	1:A:544:LEU:HD23	1.99	0.44
1:A:425:PHE:HD2	2:A:601:A1AHY:O5	2.00	0.44
1:A:308:LEU:HD11	1:A:477:ARG:NE	2.33	0.44
1:B:394:ARG:HB3	1:B:403:LEU:HD22	2.00	0.44
1:A:433:SER:O	1:A:437:MET:HG2	2.19	0.43
1:D:411:ASP:H	1:D:414:GLN:HE21	1.65	0.43
1:A:492:LYS:HE2	1:A:492:LYS:CA	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:488:HIS:CD2	1:B:492:LYS:HD3	2.54	0.43
1:C:335:ARG:HA	1:C:336:PRO:C	2.44	0.43
1:A:308:LEU:HD11	1:A:477:ARG:HH21	1.84	0.43
1:A:492:LYS:HE2	1:A:492:LYS:HA	2.00	0.43
1:A:418:VAL:HB	1:A:421:MET:SD	2.59	0.43
1:B:539:LEU:O	1:B:543:MET:HG3	2.19	0.42
1:D:418:VAL:O	1:D:421:MET:HB3	2.19	0.42
1:B:525:LEU:CD1	3:B:601:A1AHZ:C28	2.98	0.42
1:C:525:LEU:HD22	3:C:601:A1AHZ:O5	2.20	0.42
1:A:308:LEU:CD1	1:A:477:ARG:HE	2.32	0.42
1:A:418:VAL:O	1:A:418:VAL:CG1	2.63	0.42
1:D:402:LEU:HD12	1:D:425:PHE:CE2	2.55	0.41
1:D:403:LEU:HD23	1:D:403:LEU:O	2.19	0.41
1:A:316:VAL:HG12	1:A:320:LEU:HD11	2.01	0.41
1:B:434:ARG:O	1:B:437:MET:HB3	2.21	0.41
1:A:438:MET:HE2	1:A:438:MET:HB3	1.92	0.41
1:B:375:GLN:HB3	1:B:544:LEU:HD21	2.02	0.41
1:D:330:GLU:O	1:D:331:TYR:CB	2.68	0.41
1:B:473:ASP:OD1	1:B:477:ARG:CZ	2.64	0.41
1:D:358:ILE:HG13	1:D:543:MET:HE2	2.02	0.41
1:B:306:LEU:HD23	1:B:306:LEU:N	2.35	0.41
1:C:396:MET:O	1:C:436:ARG:HD3	2.20	0.41
1:A:425:PHE:CD1	1:A:429:LEU:HD13	2.56	0.41
1:C:342:MET:HE1	1:C:414:GLN:O	2.21	0.41
1:D:477:ARG:O	1:D:481:LYS:HG2	2.21	0.41
1:A:425:PHE:CE1	1:A:429:LEU:CD1	3.04	0.40
1:B:506:GLN:O	1:B:510:ILE:HG13	2.21	0.40
1:C:415:GLY:O	1:C:421:MET:CG	2.65	0.40
1:C:335:ARG:HH12	1:C:414:GLN:HE22	1.69	0.40
1:D:520:LYS:HD2	1:D:520:LYS:HA	1.94	0.40
1:D:323:GLU:OE2	1:D:449:LYS:NZ	2.51	0.40
1:A:332:ASP:O	1:A:332:ASP:CG	2.65	0.40
1:B:416:LYS:NZ	1:B:416:LYS:HD2	2.27	0.40
1:B:368:VAL:HG22	4:B:713:HOH:O	2.20	0.40
1:D:416:LYS:HG3	1:D:422:VAL:HB	2.03	0.40

All (1) 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:481:LYS:NZ	1:B:538:ASP:OD2[1_655]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	229/242 (95%)	226 (99%)	1 (0%)	2 (1%)	14	4
1	B	223/242 (92%)	219 (98%)	3 (1%)	1 (0%)	30	18
1	C	228/242 (94%)	227 (100%)	1 (0%)	0	100	100
1	D	213/242 (88%)	208 (98%)	5 (2%)	0	100	100
All	All	893/968 (92%)	880 (98%)	10 (1%)	3 (0%)	36	25

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	419	GLU
1	B	533	VAL
1	A	418	VAL

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	203/218 (93%)	203 (100%)	0	100	100
1	B	199/218 (91%)	199 (100%)	0	100	100
1	C	204/218 (94%)	204 (100%)	0	100	100
1	D	192/218 (88%)	192 (100%)	0	100	100
All	All	798/872 (92%)	798 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	375	GLN
1	A	441	GLN
1	A	506	GLN
1	A	513	HIS
1	B	455	ASN
1	B	476	HIS
1	B	513	HIS
1	C	414	GLN
1	C	455	ASN
1	C	474	HIS
1	C	519	ASN
1	C	532	ASN
1	D	413	ASN
1	D	474	HIS
1	D	501	HIS
1	D	519	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	A1AHZ	C	601	-	42,44,44	1.67	6 (14%)	54,65,65	1.34	6 (11%)
3	A1AHZ	D	601	-	42,44,44	1.91	5 (11%)	54,65,65	1.26	5 (9%)
2	A1AHY	A	601	-	42,44,44	1.75	6 (14%)	54,65,65	1.78	11 (20%)
3	A1AHZ	B	601	-	42,44,44	1.83	5 (11%)	54,65,65	1.28	5 (9%)

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
3	A1AHZ	C	601	-	-	4/28/62/62	0/7/6/6
3	A1AHZ	D	601	-	-	7/28/62/62	0/7/6/6
2	A1AHY	A	601	-	-	2/28/62/62	0/7/6/6
3	A1AHZ	B	601	-	-	4/28/62/62	0/7/6/6

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	A1AHY	O6-S1	6.43	1.48	1.43
3	D	601	A1AHZ	S1-N1	5.99	1.80	1.67
3	D	601	A1AHZ	O6-S1	5.73	1.48	1.43
3	B	601	A1AHZ	S1-N1	5.47	1.79	1.67
3	B	601	A1AHZ	O6-S1	5.41	1.48	1.43
3	B	601	A1AHZ	C1-S1	5.40	1.89	1.77
3	D	601	A1AHZ	C1-S1	5.36	1.88	1.77
3	D	601	A1AHZ	O1-S1	5.19	1.47	1.43
3	C	601	A1AHZ	C1-S1	5.05	1.88	1.77
3	B	601	A1AHZ	O1-S1	4.95	1.47	1.43
3	C	601	A1AHZ	S1-N1	4.61	1.77	1.67
2	A	601	A1AHY	S1-N1	4.59	1.77	1.67
3	C	601	A1AHZ	O1-S1	4.53	1.47	1.43
3	C	601	A1AHZ	O6-S1	4.48	1.47	1.43
2	A	601	A1AHY	C1-S1	4.43	1.87	1.77
2	A	601	A1AHY	O4-C18	-3.54	1.38	1.43
2	A	601	A1AHY	O1-S1	3.09	1.46	1.43
3	D	601	A1AHZ	C25-N1	-2.88	1.40	1.44
3	C	601	A1AHZ	O4-C18	-2.68	1.40	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	A1AHZ	C25-N1	-2.65	1.41	1.44
2	A	601	A1AHY	O4-C3	-2.27	1.39	1.44
3	C	601	A1AHZ	C25-N1	-2.10	1.41	1.44

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	A1AHY	C20-C19-N1	7.14	123.38	112.02
3	B	601	A1AHZ	O6-S1-O1	4.65	122.67	119.17
3	D	601	A1AHZ	C3-C2-C1	-4.37	96.75	100.61
3	C	601	A1AHZ	O6-S1-O1	4.25	122.38	119.17
3	B	601	A1AHZ	C3-C2-C1	-3.86	97.20	100.61
3	B	601	A1AHZ	O4-C3-C2	-3.50	97.89	104.73
2	A	601	A1AHY	C21-C20-C19	3.41	117.29	110.81
2	A	601	A1AHY	C24-C19-C20	-3.31	103.68	111.17
2	A	601	A1AHY	C22-C21-C20	3.23	118.06	111.42
2	A	601	A1AHY	C3-C2-C1	-3.19	97.79	100.61
3	C	601	A1AHZ	C3-C2-C1	-3.18	97.80	100.61
3	D	601	A1AHZ	C23-C24-C19	3.03	116.57	110.81
3	C	601	A1AHZ	C23-C24-C19	2.91	116.33	110.81
3	D	601	A1AHZ	O6-S1-O1	2.87	121.33	119.17
3	D	601	A1AHZ	O4-C3-C2	-2.80	99.26	104.73
2	A	601	A1AHY	O6-S1-C1	-2.70	104.50	107.79
2	A	601	A1AHY	C24-C19-N1	2.70	116.31	112.02
2	A	601	A1AHY	C12-C11-C4	2.46	135.17	128.81
3	C	601	A1AHZ	O4-C3-C2	-2.42	100.01	104.73
3	C	601	A1AHZ	C16-C15-C14	2.40	123.58	119.77
3	B	601	A1AHZ	O1-S1-C1	2.35	110.65	107.79
2	A	601	A1AHY	O6-S1-N1	2.32	111.82	107.02
3	D	601	A1AHZ	C6-C5-C4	-2.30	117.93	120.91
2	A	601	A1AHY	C27-C26-C25	2.28	123.19	120.30
2	A	601	A1AHY	C26-C25-N1	2.21	123.56	120.06
3	C	601	A1AHZ	C17-C16-C15	-2.11	117.64	119.88
3	B	601	A1AHZ	C17-C12-C11	-2.03	118.27	120.91

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	601	A1AHZ	C25-N1-S1-O1
2	A	601	A1AHY	C30-C28-O5-C29
2	A	601	A1AHY	C27-C28-O5-C29

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Mol	Chain	Res	Type	Atoms
3	C	601	A1AHZ	C19-N1-S1-O1
3	D	601	A1AHZ	C25-N1-S1-O1
3	D	601	A1AHZ	C24-C19-N1-S1
3	B	601	A1AHZ	C30-C28-O5-C29
3	C	601	A1AHZ	C27-C28-O5-C29
3	C	601	A1AHZ	C30-C28-O5-C29
3	B	601	A1AHZ	C18-C11-C12-C13
3	B	601	A1AHZ	C18-C11-C12-C17
3	D	601	A1AHZ	C18-C11-C12-C17
3	D	601	A1AHZ	C19-N1-S1-O1
3	B	601	A1AHZ	C25-N1-S1-O1
3	D	601	A1AHZ	C27-C28-O5-C29
3	D	601	A1AHZ	C20-C19-N1-S1
3	D	601	A1AHZ	C18-C11-C12-C13

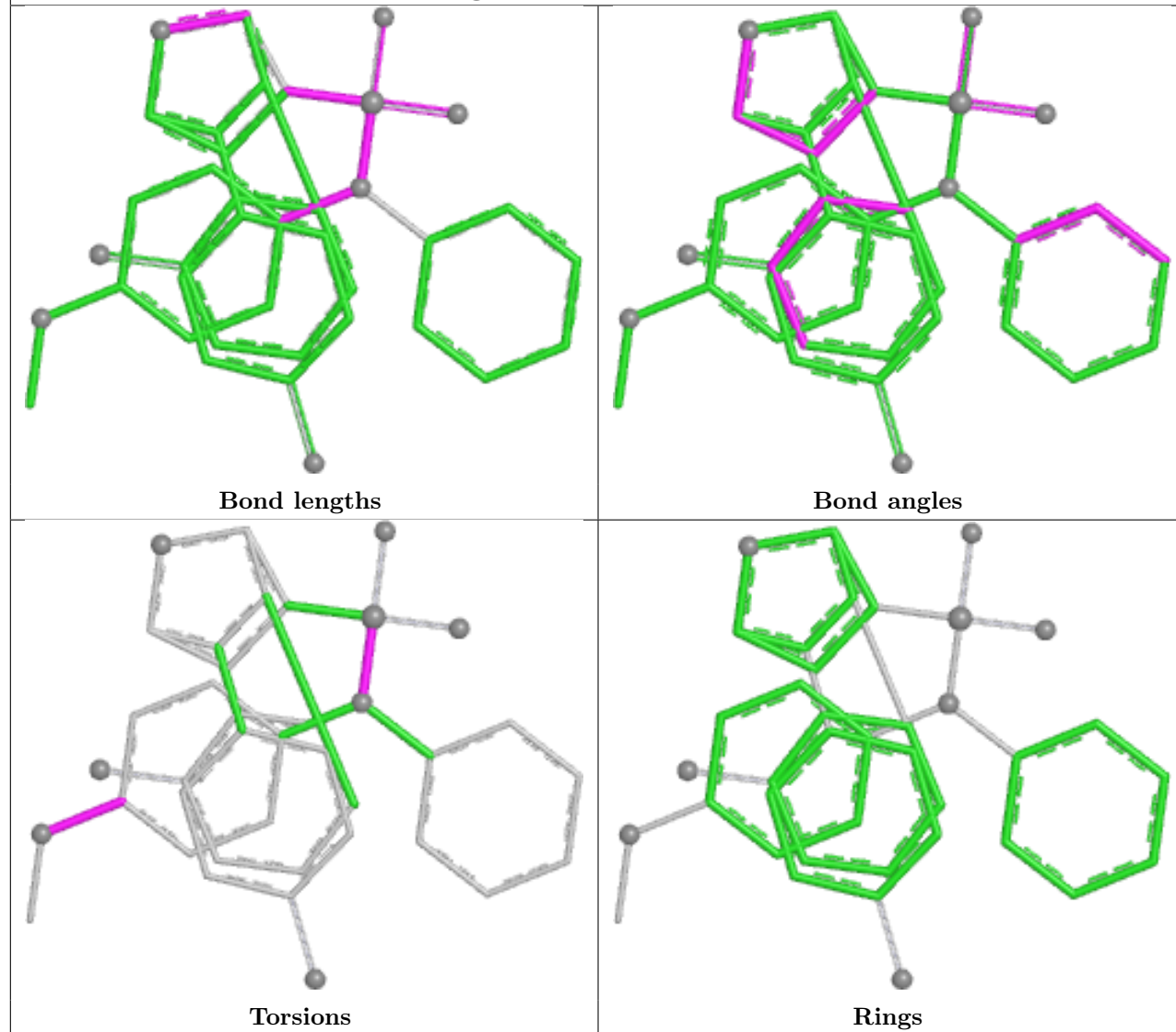
There are no ring outliers.

4 monomers are involved in 14 short contacts:

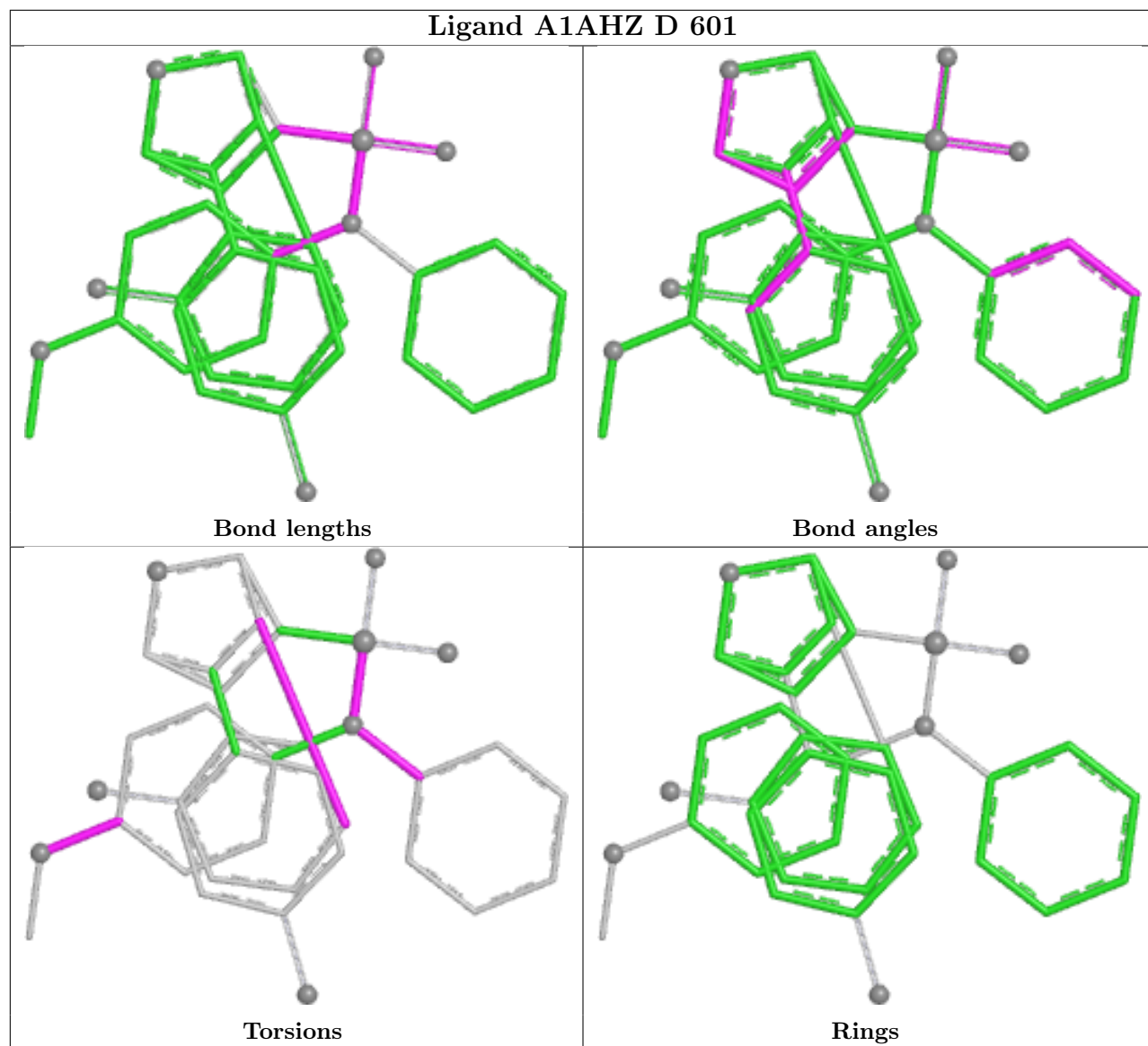
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	601	A1AHZ	3	0
3	D	601	A1AHZ	3	0
2	A	601	A1AHY	6	0
3	B	601	A1AHZ	2	0

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.

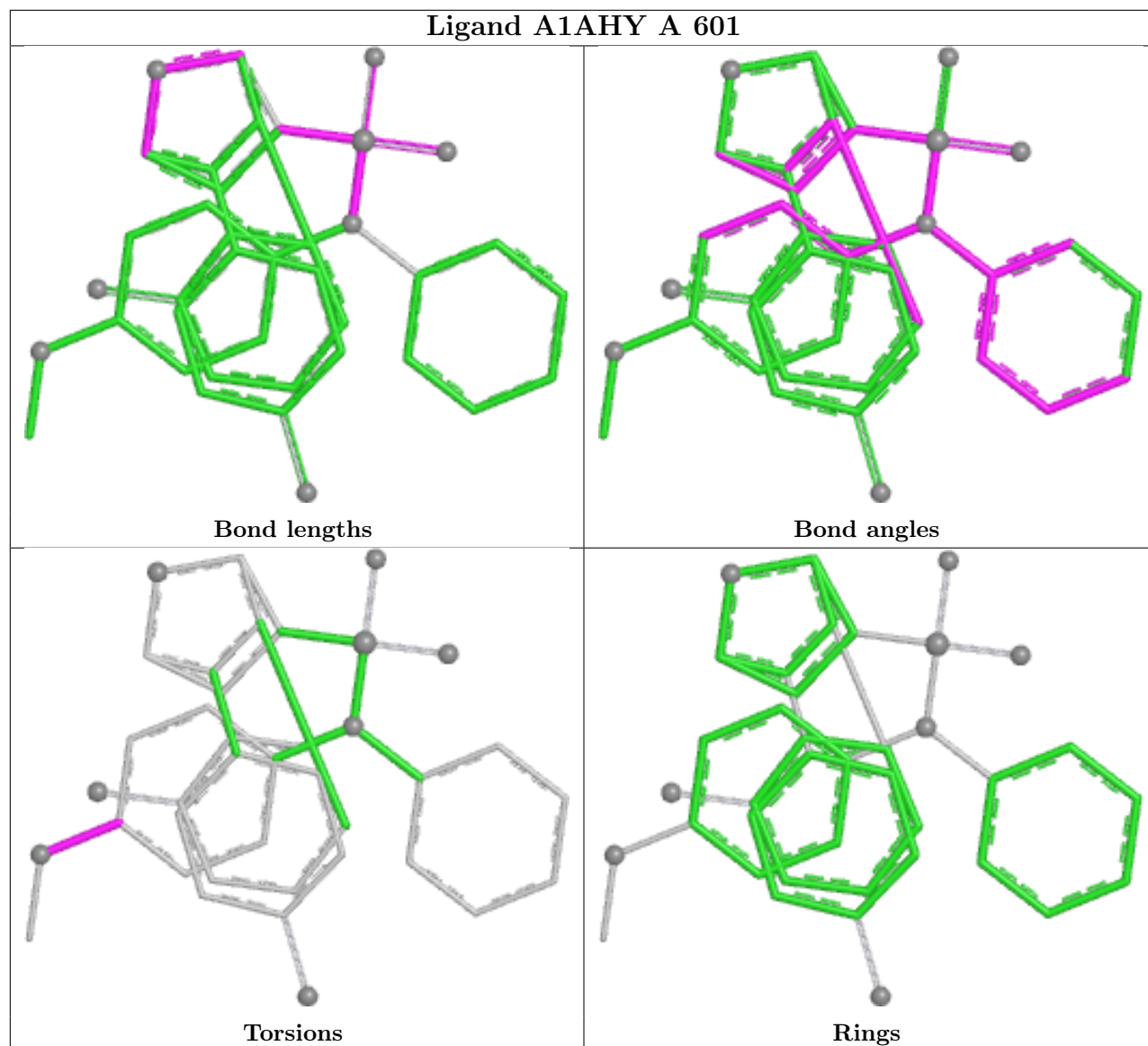
Ligand A1AHZ C 601

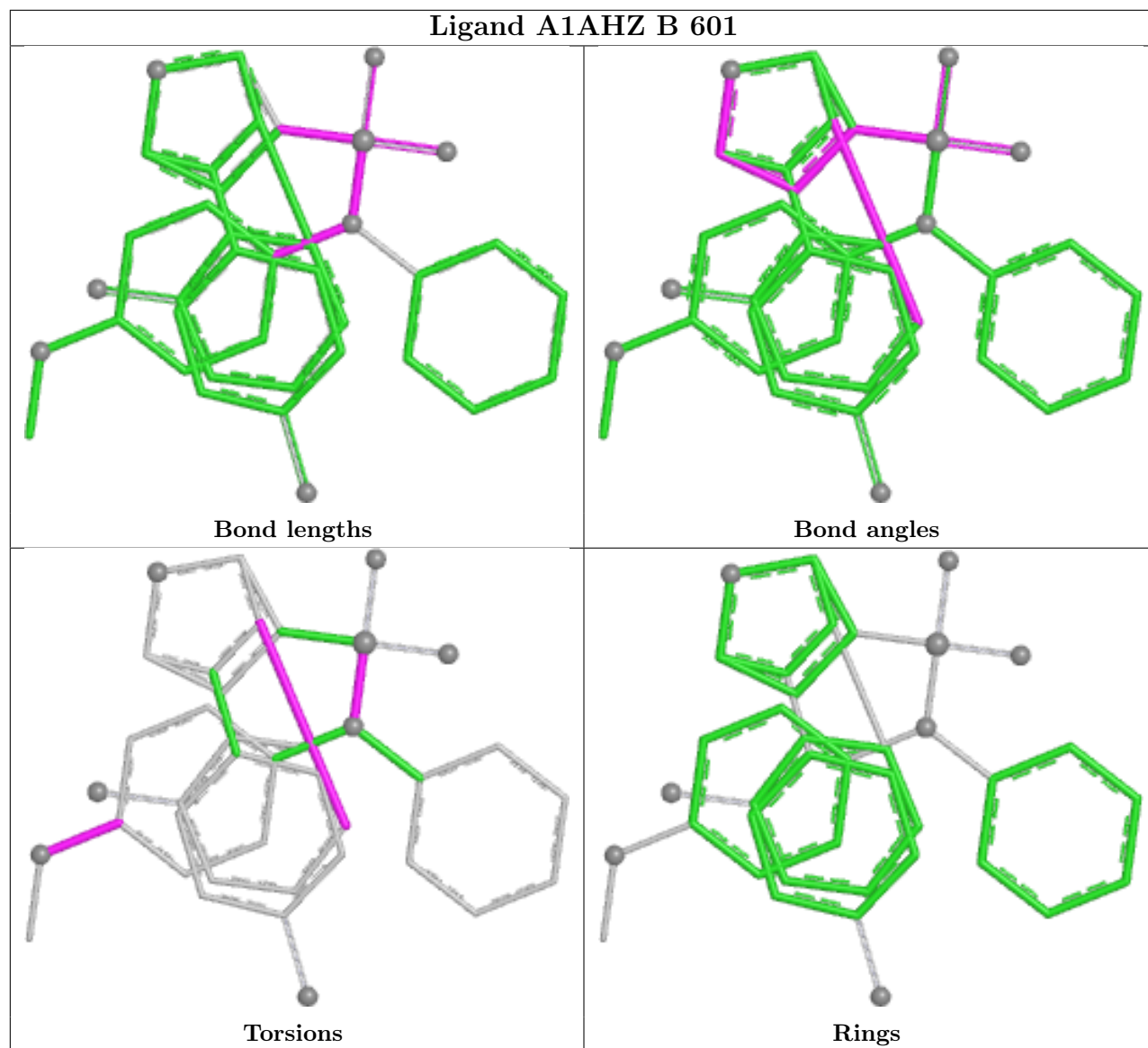


Ligand A1AHZ D 601



Ligand A1AHY A 601





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	233/242 (96%)	0.05	11 (4%) 36 38	19, 46, 76, 96	1 (0%)
1	B	229/242 (94%)	-0.08	6 (2%) 57 62	26, 42, 81, 103	0
1	C	232/242 (95%)	-0.11	5 (2%) 62 69	17, 41, 75, 100	1 (0%)
1	D	221/242 (91%)	0.01	11 (4%) 34 36	25, 43, 86, 116	0
All	All	915/968 (94%)	-0.03	33 (3%) 46 49	17, 43, 79, 116	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	331	TYR	5.0
1	A	418	VAL	4.0
1	A	464	SER	3.9
1	C	306	LEU	3.4
1	A	306	LEU	3.3
1	A	525	LEU	3.2
1	C	465	THR	3.2
1	C	533	VAL	3.0
1	A	532	ASN	2.8
1	C	525	LEU	2.6
1	D	522	MET	2.6
1	D	468	SER	2.5
1	A	461	PHE	2.5
1	C	466	LEU	2.5
1	D	526	TYR	2.4
1	D	461	PHE	2.4
1	D	524	HIS	2.3
1	B	437	MET	2.3
1	A	420	GLY	2.3
1	B	419	GLU	2.3
1	A	501[A]	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	415	GLY	2.2
1	A	546	ALA	2.2
1	D	305	SER	2.2
1	B	464	SER	2.1
1	B	531	LYS	2.1
1	B	532	ASN	2.1
1	D	459	TYR	2.1
1	D	534	VAL	2.1
1	A	417	CYS	2.1
1	A	475	ILE	2.0
1	D	342	MET	2.0
1	B	425	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

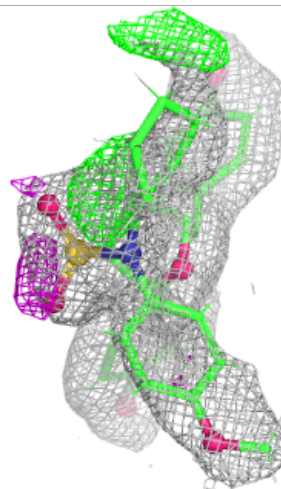
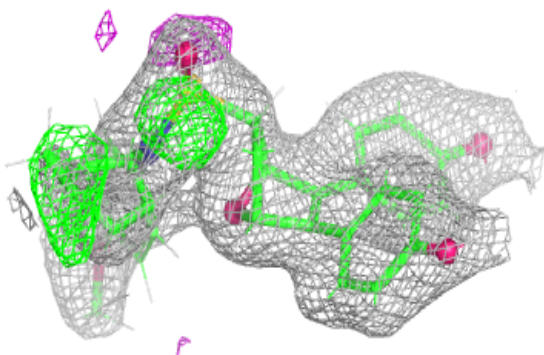
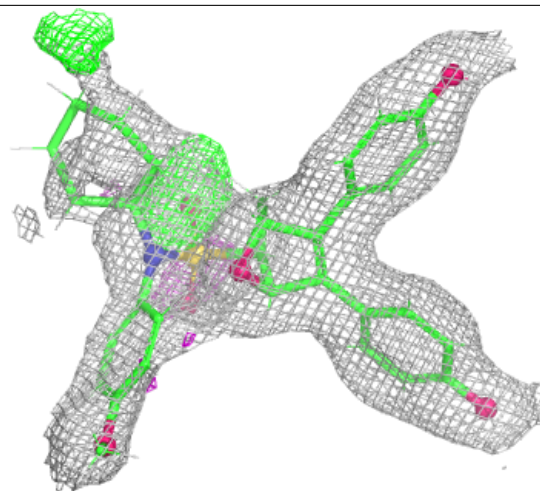
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	A1AHY	A	601	39/39	0.91	0.11	29,55,79,87	0
3	A1AHZ	B	601	39/39	0.91	0.11	29,53,83,93	0
3	A1AHZ	D	601	39/39	0.92	0.11	28,55,84,99	0
3	A1AHZ	C	601	39/39	0.94	0.10	24,50,80,96	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.

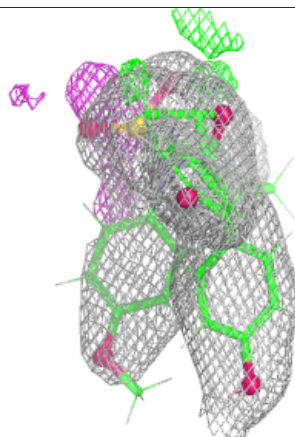
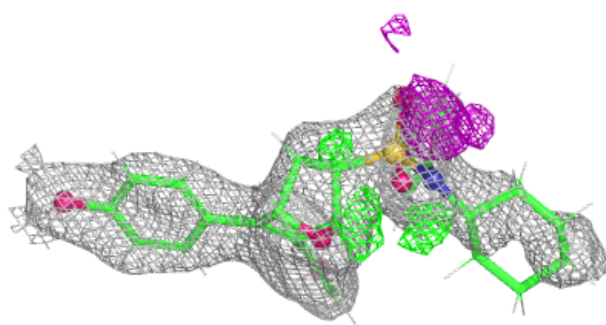
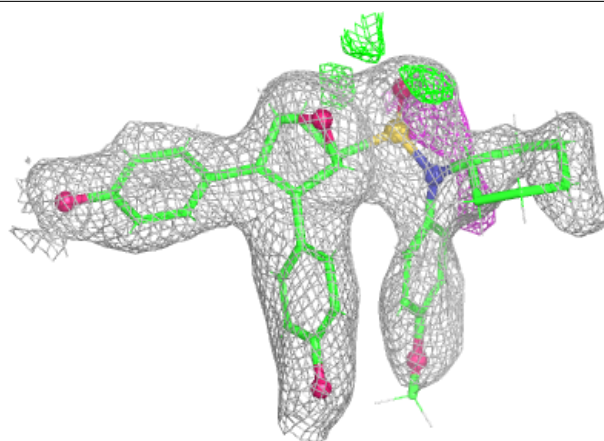
Electron density around A1AHY A 601:

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



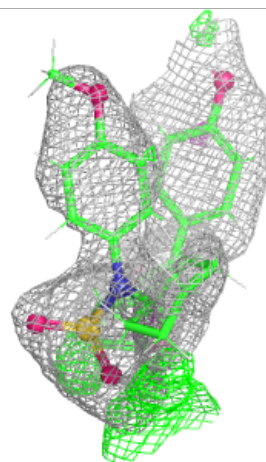
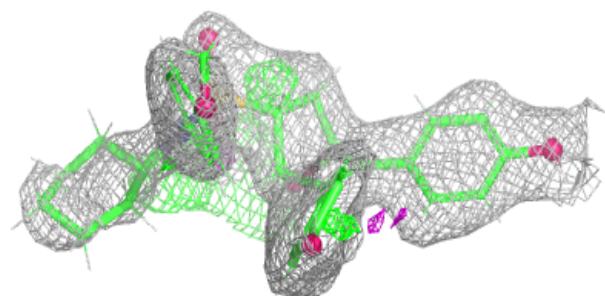
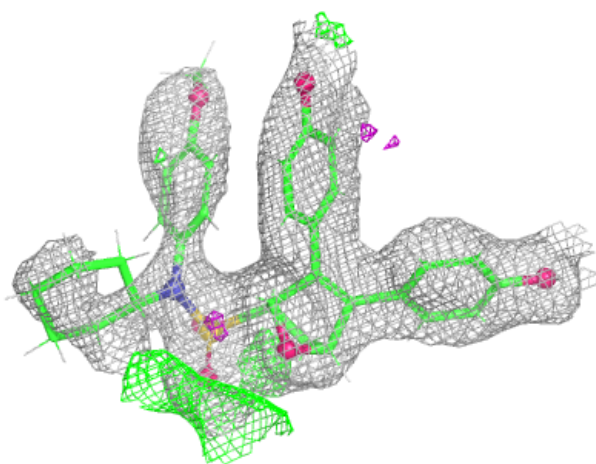
Electron density around A1AHZ B 601:

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



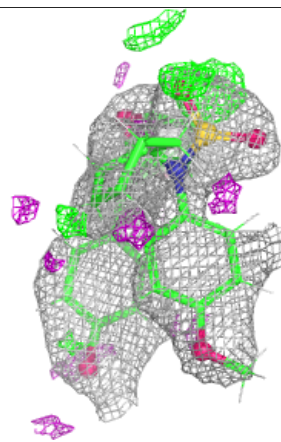
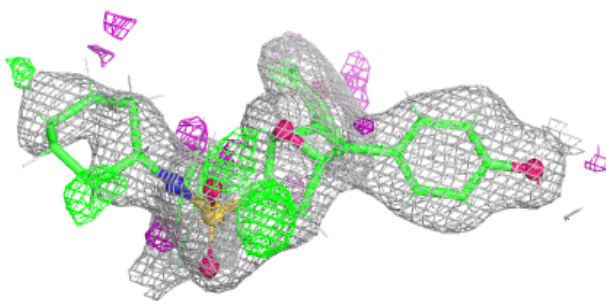
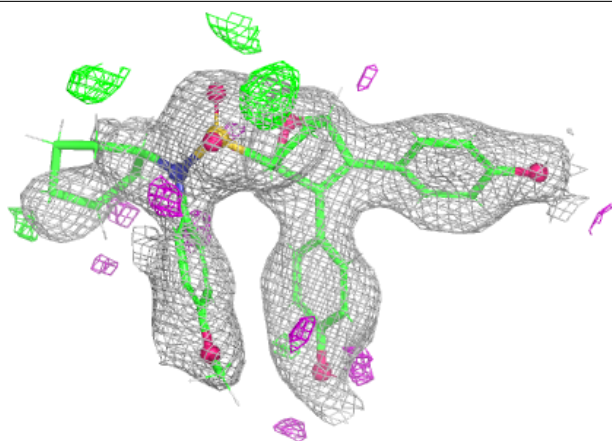
Electron density around A1AHZ D 601:

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



Electron density around A1AHZ C 601:

$2mF_o-DF_c$ (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.