



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 11, 2023 – 09:48 am GMT

PDB ID : 5NXA
Title : Crystal structure of Neanderthal Adenylosuccinate Lyase (ADSL)in complex with its products AICAR and fumarate
Authors : Van Laer, B.; Kapp, U.; Soler-Lopez, M.; Leonard, G.; Mueller-Dieckmann, C.
Deposited on : 2017-05-09
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

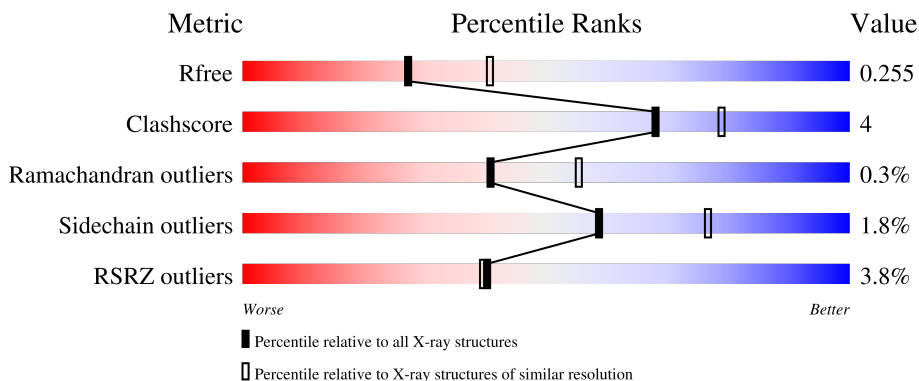
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



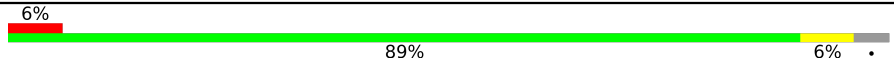

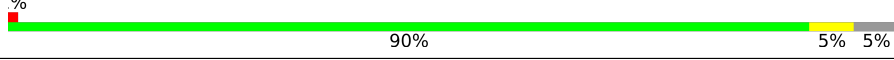
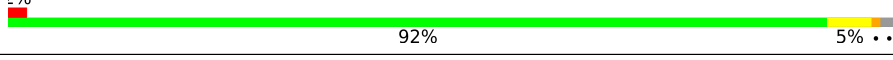
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	487	 4% 89% 7% 5%
1	B	487	 5% 78% 6% 15%
1	C	487	 5% 78% 7% 14%
1	D	487	 4% 83% 7% 10%

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Mol	Chain	Length	Quality of chain
1	E	487	 <p>6% 89% 6% •</p>
1	F	487	 <p>2% 88% 6% ••</p>
1	G	487	 <p>% 90% 5% 5% ••</p>
1	H	487	 <p>2% 92% 5% ••</p>

2 Entry composition

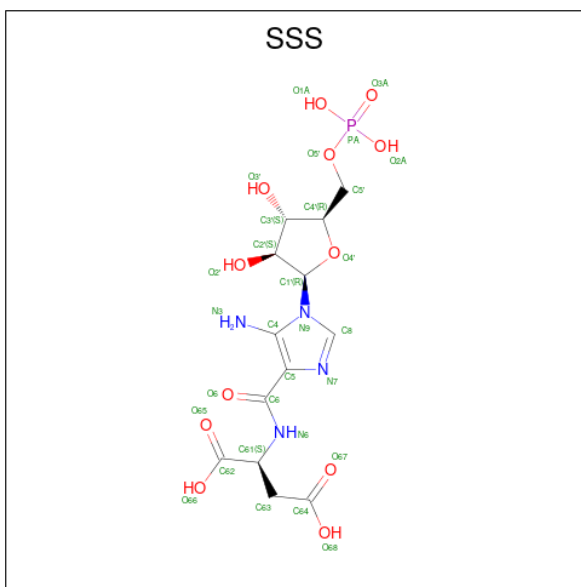
There are 6 unique types of molecules in this entry. The entry contains 29423 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Adenylosuccinate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	464	Total 3696	C 2328	N 657	O 684	S 27	0	0	0
1	B	415	Total 3312	C 2092	N 586	O 611	S 23	0	0	0
1	C	418	Total 3355	C 2123	N 592	O 615	S 25	0	0	0
1	D	440	Total 3521	C 2218	N 625	O 653	S 25	0	0	0
1	E	466	Total 3723	C 2350	N 657	O 689	S 27	0	0	0
1	F	466	Total 3716	C 2342	N 659	O 688	S 27	0	0	0
1	G	463	Total 3692	C 2326	N 656	O 683	S 27	0	0	0
1	H	477	Total 3799	C 2394	N 673	O 704	S 28	0	0	0

- Molecule 2 is N- $\{[5\text{-AMINO-1-(5-O-PHOSPHONO-BETA-D-ARABINOFURANOSYL)-1H-IMIDAZOL-4-YL]CARBONYL}\}$ -L-ASPARTIC ACID (three-letter code: SSS) (formula: $\text{C}_{13}\text{H}_{19}\text{N}_4\text{O}_{12}\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			30	13	4	12	1		
2	B	1	Total	C	N	O	P	0	0
			30	13	4	12	1		
2	D	1	Total	C	N	O	P	0	0
			30	13	4	12	1		
2	F	1	Total	C	N	O	P	0	0
			30	13	4	12	1		
2	G	1	Total	C	N	O	P	0	0
			30	13	4	12	1		
2	H	1	Total	C	N	O	P	0	0
			30	13	4	12	1		

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

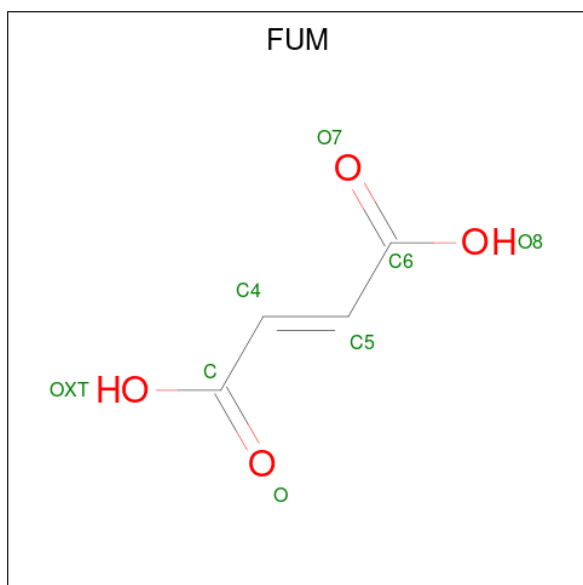
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		
3	E	1	Total	Cl	0	0
			1	1		
3	F	1	Total	Cl	0	0
			1	1		

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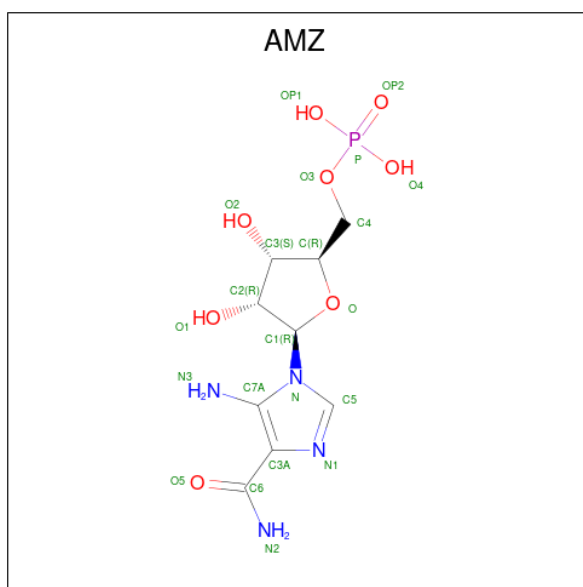
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0
3	H	1	Total Cl 1 1	0	0

- Molecule 4 is FUMARIC ACID (three-letter code: FUM) (formula: C₄H₄O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 8 4 4	0	0
4	E	1	Total C O 8 4 4	0	0

- Molecule 5 is AMINOIMIDAZOLE 4-CARBOXAMIDE RIBONUCLEOTIDE (three-letter code: AMZ) (formula: C₉H₁₅N₄O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	C	1	22	9	4	8	1	0	0
5	H	1	22	9	4	8	1	0	0

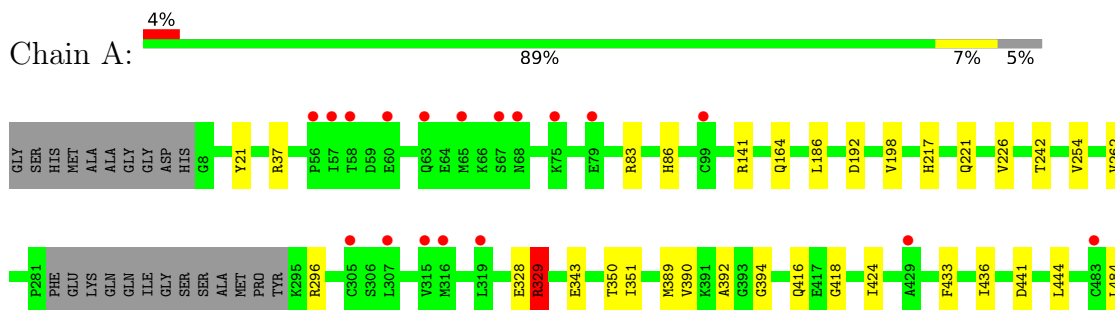
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	35	Total	O	0	0
			35	35		
6	B	39	Total	O	0	0
			39	39		
6	C	27	Total	O	0	0
			27	27		
6	D	33	Total	O	0	0
			33	33		
6	E	62	Total	O	0	0
			62	62		
6	F	41	Total	O	0	0
			41	41		
6	G	53	Total	O	0	0
			53	53		
6	H	71	Total	O	0	0
			71	71		

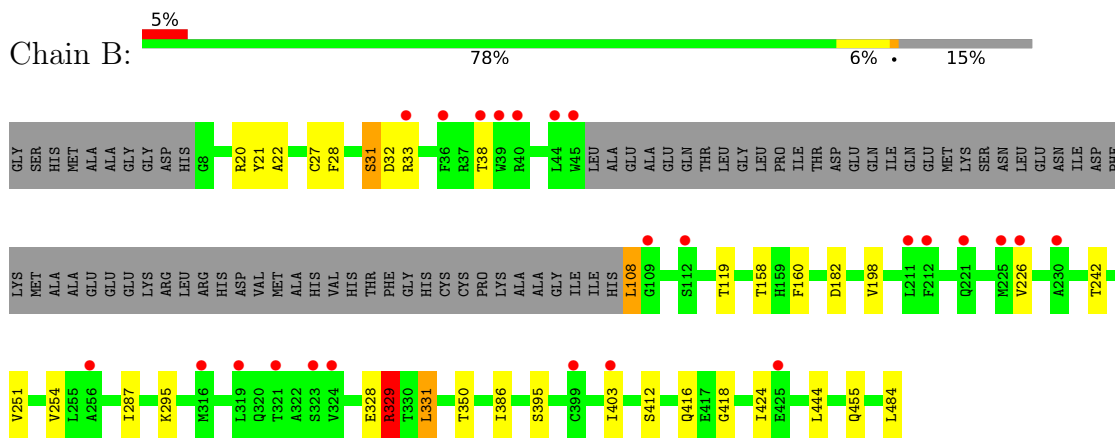
3 Residue-property plots [i](#)

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.

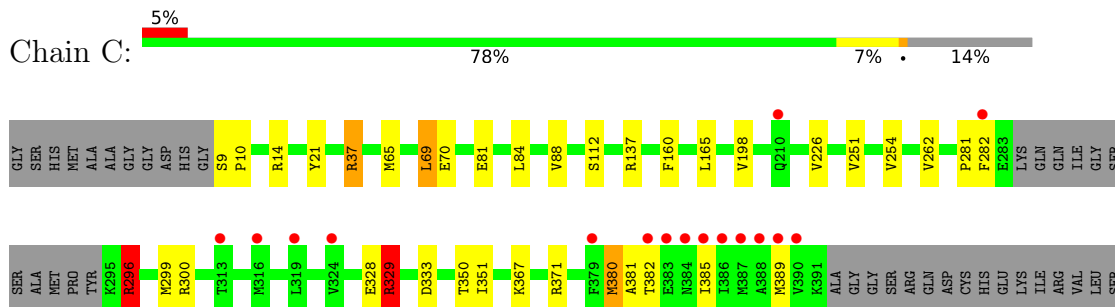
- Molecule 1: Adenylosuccinate lyase

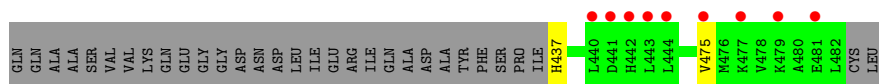


- Molecule 1: Adenylosuccinate lyase

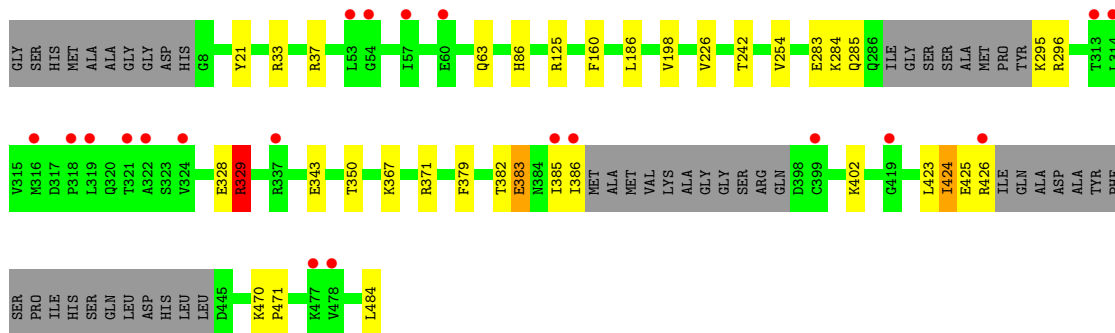
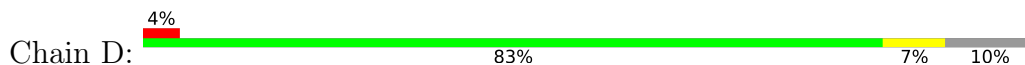


- Molecule 1: Adenylosuccinate lyase

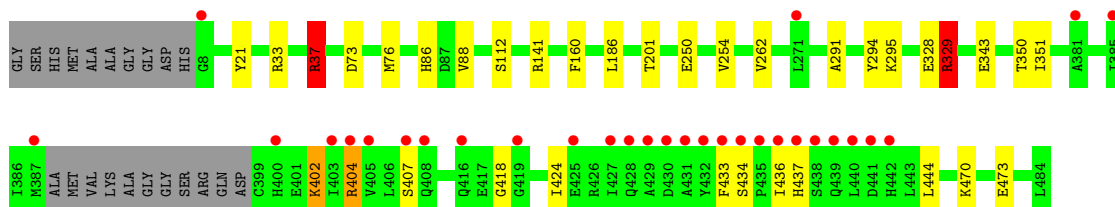
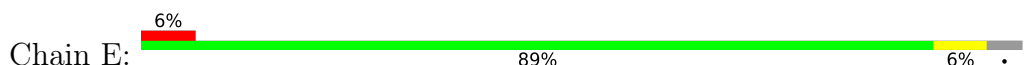




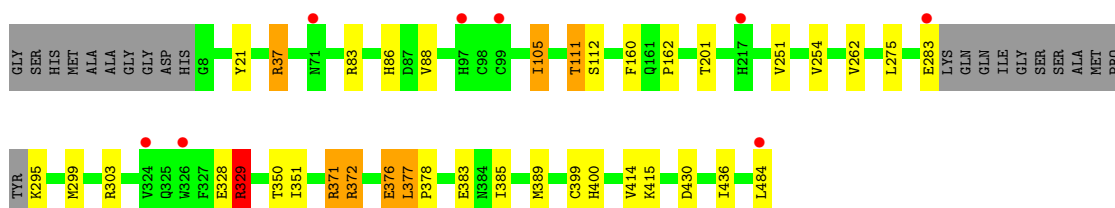
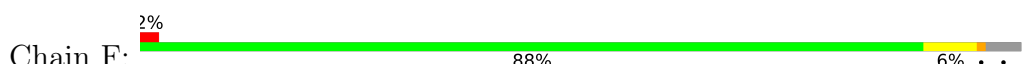
• Molecule 1: Adenylosuccinate lyase



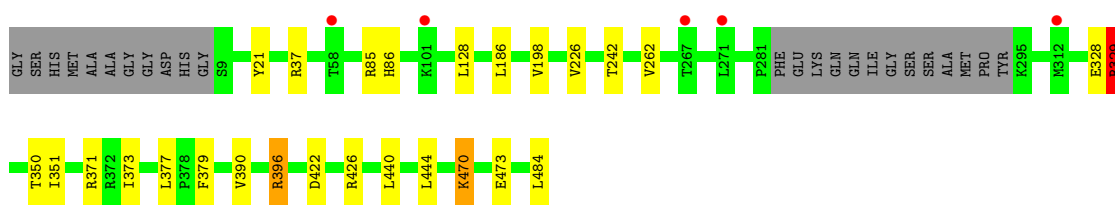
• Molecule 1: Adenylosuccinate lyase



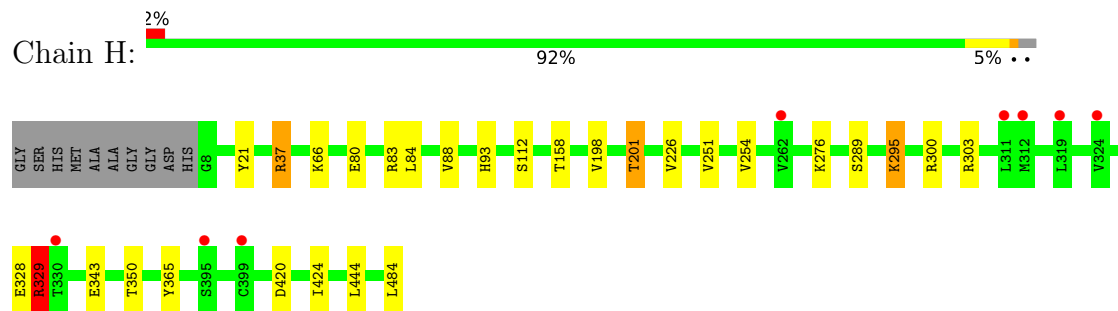
• Molecule 1: Adenylosuccinate lyase



• Molecule 1: Adenylosuccinate lyase



- Molecule 1: Adenylosuccinate lyase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	356.53Å 74.21Å 160.31Å 90.00° 108.99° 90.00°	Depositor
Resolution (Å)	47.85 – 2.40 47.85 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.85-2.40) 98.9 (47.85-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.220 , 0.254 0.224 , 0.255	Depositor DCC
R_{free} test set	7694 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.5	Xtrriage
Anisotropy	0.276	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	29423	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: CL, AMZ, FUM, SSS

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	0.55	0/3761	0.65	3/5076 (0.1%)
1	B	0.65	0/3371	0.72	2/4550 (0.0%)
1	C	0.55	0/3416	0.69	6/4610 (0.1%)
1	D	0.58	1/3580 (0.0%)	0.68	2/4827 (0.0%)
1	E	0.56	0/3791	0.67	6/5118 (0.1%)
1	F	0.60	1/3782 (0.0%)	0.69	2/5104 (0.0%)
1	G	0.58	0/3757	0.67	0/5071
1	H	0.58	0/3868	0.67	4/5221 (0.1%)
All	All	0.58	2/29326 (0.0%)	0.68	25/39577 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	383	GLU	CD-OE2	5.96	1.32	1.25
1	F	383	GLU	CG-CD	-5.07	1.44	1.51

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	424	ILE	N-CA-C	-8.73	87.42	111.00
1	A	141	ARG	NE-CZ-NH1	7.37	123.98	120.30
1	C	296	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	A	141	ARG	NE-CZ-NH2	-6.89	116.85	120.30
1	H	329	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	H	295	LYS	CD-CE-NZ	6.64	126.97	111.70
1	B	108	LEU	CB-CG-CD2	6.49	122.03	111.00
1	C	69	LEU	CB-CG-CD1	6.44	121.94	111.00
1	E	37	ARG	CB-CG-CD	6.44	128.33	111.60
1	D	296	ARG	NE-CZ-NH2	-6.25	117.17	120.30
1	E	37	ARG	CA-CB-CG	6.25	127.15	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	329	ARG	CG-CD-NE	5.88	124.14	111.80
1	E	141	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	B	33	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	E	329	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	F	329	ARG	NE-CZ-NH1	5.77	123.19	120.30
1	F	329	ARG	CG-CD-NE	5.73	123.83	111.80
1	E	329	ARG	CG-CD-NE	5.54	123.44	111.80
1	H	300	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	C	329	ARG	NE-CZ-NH2	5.21	122.91	120.30
1	C	69	LEU	CB-CG-CD2	-5.21	102.14	111.00
1	E	141	ARG	NE-CZ-NH2	-5.17	117.71	120.30
1	C	329	ARG	CG-CD-NE	-5.07	101.16	111.80
1	A	441	ASP	CB-CG-OD2	5.04	122.83	118.30
1	C	37	ARG	CG-CD-NE	5.00	122.30	111.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3696	0	3730	29	0
1	B	3312	0	3352	22	0
1	C	3355	0	3393	39	0
1	D	3521	0	3552	39	0
1	E	3723	0	3751	25	0
1	F	3716	0	3745	45	0
1	G	3692	0	3727	24	0
1	H	3799	0	3829	19	0
2	A	30	0	15	1	0
2	B	30	0	15	0	0
2	D	30	0	15	2	0
2	F	30	0	15	2	0
2	G	30	0	15	2	0
2	H	30	0	15	2	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	B	8	0	1	0	0
4	E	8	0	1	0	0
5	C	22	0	13	1	0
5	H	22	0	13	0	0
6	A	35	0	0	1	0
6	B	39	0	0	2	0
6	C	27	0	0	0	0
6	D	33	0	0	0	0
6	E	62	0	0	0	0
6	F	41	0	0	2	0
6	G	53	0	0	0	0
6	H	71	0	0	0	0
All	All	29423	0	29197	220	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (220) 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:F:283:GLU:OE1	1:G:85:ARG:NH1	1.80	1.15
1:C:10:PRO:HA	1:C:14:ARG:HH21	1.12	1.09
1:C:10:PRO:CA	1:C:14:ARG:HH21	1.72	1.02
1:D:385:ILE:HD12	1:D:426:ARG:NH1	1.76	1.01
1:C:10:PRO:CA	1:C:14:ARG:NH2	2.25	0.99
1:C:10:PRO:HA	1:C:14:ARG:NH2	1.80	0.97
1:A:217:HIS:NE2	1:A:221:GLN:NE2	2.22	0.88
1:E:402:LYS:N	1:E:402:LYS:HD2	1.89	0.87
1:D:37:ARG:HG3	1:D:37:ARG:HH11	1.38	0.87
1:E:402:LYS:HD2	1:E:402:LYS:H	1.41	0.85
1:F:111:THR:HG21	1:F:201:THR:HA	1.58	0.83
1:A:389:MET:HE3	1:A:433:PHE:HA	1.61	0.82
1:D:385:ILE:HD12	1:D:426:ARG:HH12	1.46	0.81
1:H:328:GLU:O	1:H:329:ARG:HB3	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:303:ARG:HH12	1:F:484:LEU:CD2	1.96	0.79
1:C:475:VAL:HG12	1:C:475:VAL:O	1.82	0.79
1:F:328:GLU:O	1:F:329:ARG:HB3	1.82	0.79
1:B:418:GLY:O	1:D:371:ARG:HD2	1.83	0.78
1:F:303:ARG:HH12	1:F:484:LEU:HD23	1.47	0.78
1:E:328:GLU:O	1:E:329:ARG:HB3	1.83	0.78
1:D:385:ILE:CD1	1:D:426:ARG:NH1	2.46	0.77
1:C:328:GLU:O	1:C:329:ARG:HB3	1.84	0.77
1:D:423:LEU:HB3	1:D:426:ARG:HG2	1.65	0.77
1:A:217:HIS:CD2	1:A:221:GLN:NE2	2.53	0.77
1:A:389:MET:N	1:A:436:ILE:HD11	2.01	0.76
1:D:283:GLU:O	1:D:285:GLN:N	2.19	0.75
1:A:389:MET:HG2	1:A:436:ILE:HD12	1.70	0.73
1:H:37:ARG:HD3	1:H:37:ARG:C	2.09	0.72
1:F:83:ARG:HG2	1:F:83:ARG:HH21	1.53	0.72
1:G:328:GLU:O	1:G:329:ARG:HB2	1.89	0.72
1:C:137:ARG:NH2	1:C:475:VAL:HG12	2.04	0.72
1:D:328:GLU:O	1:D:329:ARG:HB2	1.90	0.71
1:A:328:GLU:O	1:A:329:ARG:HB2	1.90	0.71
1:E:86:HIS:HA	2:H:501:SSS:H2'	1.72	0.71
1:A:389:MET:CE	1:A:433:PHE:HA	2.20	0.71
1:A:192:ASP:OD2	6:A:601:HOH:O	2.09	0.70
1:B:328:GLU:O	1:B:329:ARG:HB2	1.89	0.70
1:C:381:ALA:O	1:C:382:THR:OG1	2.06	0.70
1:C:10:PRO:CB	1:C:14:ARG:NH2	2.56	0.69
1:F:86:HIS:HA	2:F:502:SSS:H2'	1.74	0.68
1:F:299:MET:CE	1:F:484:LEU:HD13	2.23	0.67
1:B:455:GLN:HG3	6:B:631:HOH:O	1.94	0.67
1:A:186:LEU:HD12	1:A:254:VAL:CG1	2.25	0.67
1:A:390:VAL:HA	1:A:394:GLY:HA2	1.75	0.67
1:C:10:PRO:CB	1:C:14:ARG:HH22	2.08	0.67
1:F:299:MET:HE1	1:F:484:LEU:HD13	1.77	0.67
1:E:186:LEU:HD12	1:E:254:VAL:CG1	2.26	0.65
1:D:186:LEU:HD12	1:D:254:VAL:CG1	2.25	0.65
1:C:37:ARG:HG3	1:C:70:GLU:HG3	1.78	0.64
1:C:10:PRO:HB3	1:C:14:ARG:HH22	1.61	0.64
1:F:303:ARG:NH1	1:F:484:LEU:HD23	2.13	0.64
1:G:422:ASP:OD2	1:G:426:ARG:NH1	2.31	0.64
1:F:484:LEU:HB2	1:G:85:ARG:HD2	1.80	0.64
1:C:385:ILE:O	1:C:389:MET:HG2	1.98	0.64
1:D:423:LEU:HD13	1:D:426:ARG:NH2	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:423:LEU:HD13	1:D:426:ARG:HH21	1.62	0.63
1:A:389:MET:CA	1:A:436:ILE:HD11	2.28	0.63
1:F:275:LEU:O	1:F:372:ARG:NH2	2.31	0.63
1:G:262:VAL:HG11	1:G:351:ILE:HG23	1.81	0.62
1:A:86:HIS:HA	2:A:501:SSS:H2'	1.80	0.62
1:F:262:VAL:HG11	1:F:351:ILE:HG23	1.82	0.62
1:A:262:VAL:HG11	1:A:351:ILE:HG23	1.82	0.61
1:F:484:LEU:HD12	1:G:85:ARG:CG	2.31	0.61
1:G:86:HIS:HA	2:G:502:SSS:H2'	1.83	0.61
1:C:475:VAL:O	1:C:475:VAL:CG1	2.49	0.61
1:E:262:VAL:HG11	1:E:351:ILE:HG23	1.83	0.60
1:D:423:LEU:HB3	1:D:426:ARG:CG	2.30	0.60
1:B:182:ASP:OD1	6:B:601:HOH:O	2.16	0.60
1:C:10:PRO:N	1:C:14:ARG:NH2	2.49	0.60
1:F:303:ARG:NH1	1:F:484:LEU:CD2	2.64	0.60
1:C:10:PRO:HB3	1:C:14:ARG:NH2	2.15	0.60
1:D:423:LEU:HD22	1:D:426:ARG:HE	1.67	0.60
1:B:416:GLN:O	1:D:367:LYS:HG3	2.00	0.59
1:D:37:ARG:HG3	1:D:37:ARG:NH1	2.09	0.59
1:E:404:ARG:CG	1:E:404:ARG:HH11	2.15	0.59
1:E:418:GLY:O	1:G:371:ARG:HD2	2.03	0.58
1:C:262:VAL:HG11	1:C:351:ILE:HG23	1.84	0.58
1:A:262:VAL:HG11	1:A:351:ILE:CG2	2.33	0.58
1:G:262:VAL:HG11	1:G:351:ILE:CG2	2.34	0.58
1:H:21:TYR:CE1	1:H:303:ARG:HD2	2.39	0.58
1:C:9:SER:O	1:C:14:ARG:HD2	2.03	0.58
1:F:262:VAL:HG11	1:F:351:ILE:CG2	2.34	0.57
1:B:21:TYR:HB3	1:B:350:THR:HG21	1.86	0.57
1:B:424:ILE:HD12	1:B:444:LEU:HD11	1.86	0.57
1:C:65:MET:O	1:C:69:LEU:CD1	2.52	0.57
1:E:434:SER:HA	1:E:437:HIS:ND1	2.20	0.57
1:A:217:HIS:CE1	1:A:221:GLN:HE21	2.21	0.56
1:D:86:HIS:HA	2:D:502:SSS:H2'	1.86	0.56
1:C:137:ARG:HH21	1:C:475:VAL:HG12	1.70	0.56
1:E:262:VAL:HG11	1:E:351:ILE:CG2	2.35	0.56
1:F:83:ARG:HG2	1:F:83:ARG:NH2	2.20	0.56
1:C:262:VAL:HG11	1:C:351:ILE:CG2	2.35	0.56
1:B:386:ILE:CG1	1:B:403:ILE:HD12	2.36	0.56
1:C:10:PRO:N	1:C:14:ARG:HH21	2.03	0.56
1:E:424:ILE:HD12	1:E:444:LEU:HD11	1.88	0.56
1:D:425:GLU:O	1:D:426:ARG:C	2.43	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:382:THR:HG23	1:D:426:ARG:NH2	2.21	0.56
1:F:37:ARG:HG3	1:F:37:ARG:HH11	1.72	0.55
1:F:389:MET:HB3	1:F:399:CYS:SG	2.46	0.55
1:C:282:PHE:HB3	1:C:296:ARG:NH1	2.21	0.55
1:D:383:GLU:O	1:D:386:ILE:HG13	2.07	0.54
1:D:423:LEU:HD22	1:D:426:ARG:NE	2.22	0.54
1:A:424:ILE:HD12	1:A:444:LEU:HD11	1.88	0.54
1:H:289:SER:OG	2:H:501:SSS:H631	2.07	0.54
1:H:424:ILE:HD12	1:H:444:LEU:HD11	1.89	0.54
1:B:20:ARG:NH2	1:C:81:GLU:OE2	2.40	0.54
1:E:470:LYS:NZ	1:E:473:GLU:OE1	2.38	0.54
1:E:33:ARG:O	1:E:37:ARG:HB3	2.07	0.54
1:G:470:LYS:NZ	1:G:473:GLU:OE1	2.40	0.54
1:F:111:THR:CG2	1:F:201:THR:HA	2.34	0.53
1:D:33:ARG:O	1:D:37:ARG:HB3	2.08	0.53
1:E:436:ILE:O	1:E:436:ILE:HG22	2.08	0.53
1:F:414:VAL:HG11	1:H:276:LYS:HE3	1.90	0.52
1:D:383:GLU:HA	1:D:386:ILE:HG12	1.92	0.52
1:A:436:ILE:HG22	1:A:436:ILE:O	2.10	0.52
1:D:382:THR:CG2	1:D:426:ARG:NH2	2.73	0.52
1:A:389:MET:HA	1:A:436:ILE:HD11	1.89	0.52
1:E:294:TYR:HB2	1:G:379:PHE:CD1	2.45	0.52
1:F:484:LEU:CD1	1:G:85:ARG:HB3	2.40	0.51
1:G:242:THR:HG23	1:G:329:ARG:HG3	1.92	0.51
1:D:242:THR:HG23	1:D:329:ARG:HG3	1.92	0.51
1:E:433:PHE:O	1:E:437:HIS:ND1	2.44	0.51
1:A:242:THR:HG23	1:A:329:ARG:HG3	1.92	0.51
1:D:379:PHE:O	1:D:382:THR:OG1	2.24	0.51
1:F:371:ARG:NH2	1:H:420:ASP:OD1	2.42	0.51
1:F:37:ARG:HH11	1:F:37:ARG:CG	2.24	0.51
1:F:385:ILE:HG23	1:F:436:ILE:HD13	1.91	0.51
1:H:198:VAL:HG23	1:H:226:VAL:HG21	1.93	0.51
1:B:329:ARG:CZ	1:B:331:LEU:HD23	2.40	0.50
2:F:502:SSS:O2'	2:F:502:SSS:H8	2.11	0.50
1:H:80:GLU:OE1	1:H:83:ARG:NH1	2.44	0.50
1:A:418:GLY:O	1:C:371:ARG:HD2	2.11	0.50
1:E:404:ARG:HH11	1:E:404:ARG:HG3	1.76	0.50
1:B:386:ILE:HG13	1:B:403:ILE:HD12	1.92	0.50
1:B:28:PHE:HA	1:B:31:SER:HB3	1.93	0.49
2:D:502:SSS:H8	2:D:502:SSS:O2'	2.12	0.49
1:F:484:LEU:HD12	1:G:85:ARG:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:THR:HG23	1:B:329:ARG:HG3	1.93	0.48
1:B:386:ILE:HG13	1:B:403:ILE:CD1	2.43	0.48
1:D:37:ARG:NH1	1:D:37:ARG:CG	2.73	0.48
1:C:65:MET:O	1:C:69:LEU:HD13	2.13	0.48
1:F:484:LEU:HD12	1:G:85:ARG:CD	2.44	0.48
1:A:198:VAL:HG23	1:A:226:VAL:HG21	1.96	0.47
1:G:390:VAL:CG2	1:G:396:ARG:HB3	2.44	0.47
1:C:198:VAL:HG23	1:C:226:VAL:HG21	1.96	0.47
1:C:251:VAL:O	1:C:254:VAL:HG22	2.15	0.47
1:B:21:TYR:HB3	1:B:350:THR:CG2	2.45	0.47
1:F:251:VAL:O	1:F:254:VAL:HG22	2.15	0.47
1:A:186:LEU:HD12	1:A:254:VAL:HG11	1.96	0.46
1:B:20:ARG:NH1	5:C:502:AMZ:O4	2.47	0.46
1:F:83:ARG:HB2	1:F:83:ARG:CZ	2.45	0.46
1:G:390:VAL:HG21	1:G:396:ARG:HB3	1.97	0.46
1:A:21:TYR:HB3	1:A:350:THR:HG21	1.97	0.46
1:D:424:ILE:O	1:D:425:GLU:C	2.52	0.46
1:D:385:ILE:CD1	1:D:426:ARG:HH11	2.25	0.46
1:F:415:LYS:HB3	1:H:365:TYR:CG	2.51	0.46
1:B:251:VAL:O	1:B:254:VAL:HG22	2.16	0.46
1:E:294:TYR:CB	1:G:379:PHE:CD1	2.99	0.46
1:D:21:TYR:HB3	1:D:350:THR:HG21	1.98	0.46
1:F:430:ASP:OD2	6:F:601:HOH:O	2.21	0.46
1:F:303:ARG:HH12	1:F:484:LEU:HD22	1.79	0.45
1:B:287:ILE:CD1	1:C:84:LEU:HD22	2.47	0.45
1:H:251:VAL:O	1:H:254:VAL:HG22	2.15	0.45
1:A:389:MET:HG2	1:A:436:ILE:CD1	2.44	0.45
1:G:198:VAL:HG23	1:G:226:VAL:HG21	1.97	0.45
1:C:21:TYR:HB3	1:C:350:THR:HG21	1.99	0.45
1:D:198:VAL:HG23	1:D:226:VAL:HG21	1.99	0.45
1:D:385:ILE:CD1	1:D:426:ARG:HH12	2.20	0.45
1:E:21:TYR:HB3	1:E:350:THR:HG21	1.97	0.45
1:G:21:TYR:HB3	1:G:350:THR:HG21	1.99	0.45
1:F:295:LYS:NZ	1:H:158:THR:OG1	2.48	0.44
1:F:83:ARG:NH2	1:F:83:ARG:CG	2.73	0.44
1:F:303:ARG:NH1	1:F:484:LEU:HD22	2.32	0.44
1:F:37:ARG:CG	1:F:37:ARG:NH1	2.79	0.44
1:H:21:TYR:HB3	1:H:350:THR:HG21	1.98	0.44
1:A:436:ILE:O	1:A:436:ILE:CG2	2.66	0.44
1:F:21:TYR:HB3	1:F:350:THR:HG21	1.99	0.44
1:G:128:LEU:CD2	1:G:186:LEU:HD22	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:LEU:CD2	1:C:380:MET:HE1	2.48	0.43
1:F:377:LEU:HB3	1:F:378:PRO:HD3	2.00	0.43
1:D:186:LEU:HD12	1:D:254:VAL:HG11	1.97	0.43
1:G:373:ILE:HG22	1:G:377:LEU:HD13	1.99	0.43
1:H:21:TYR:HE1	1:H:303:ARG:HD2	1.82	0.43
1:A:389:MET:HE2	1:A:436:ILE:HD12	1.99	0.43
1:C:281:PRO:O	1:C:300:ARG:NH2	2.51	0.43
1:D:382:THR:HG23	1:D:426:ARG:HH22	1.83	0.43
1:E:291:ALA:HB3	1:H:201:THR:HG23	1.99	0.43
1:C:282:PHE:CB	1:C:296:ARG:NH1	2.81	0.43
1:B:22:ALA:HB3	1:B:27:CYS:SG	2.59	0.42
1:F:162:PRO:HG2	6:F:636:HOH:O	2.19	0.42
1:D:423:LEU:HD13	1:D:426:ARG:CZ	2.49	0.42
1:F:88:VAL:HG21	1:F:112:SER:HB3	2.01	0.42
1:H:88:VAL:HG21	1:H:112:SER:HB3	2.02	0.42
1:B:38:THR:HG21	1:B:119:THR:HG23	2.01	0.42
1:C:329:ARG:NH2	1:C:333:ASP:OD1	2.52	0.42
1:D:423:LEU:HD23	1:D:423:LEU:HA	1.85	0.42
1:F:385:ILE:HG23	1:F:436:ILE:CD1	2.49	0.42
1:A:416:GLN:O	1:C:367:LYS:HG3	2.20	0.42
1:B:158:THR:OG1	1:D:295:LYS:NZ	2.49	0.42
1:E:404:ARG:CG	1:E:404:ARG:NH1	2.78	0.42
1:C:65:MET:O	1:C:69:LEU:HD12	2.20	0.42
1:A:343:GLU:OE2	1:D:343:GLU:OE1	2.38	0.41
1:C:165:LEU:HD23	1:C:380:MET:HE1	2.02	0.41
1:E:186:LEU:HD12	1:E:254:VAL:HG11	2.01	0.41
1:F:105:ILE:HA	1:F:105:ILE:HD12	1.59	0.41
1:E:343:GLU:OE2	1:H:343:GLU:OE1	2.39	0.41
1:E:73:ASP:OD2	1:E:76:MET:HG2	2.21	0.41
1:B:198:VAL:HG23	1:B:226:VAL:HG21	2.02	0.41
1:G:440:LEU:O	1:G:444:LEU:HG	2.20	0.41
1:D:423:LEU:HD13	1:D:426:ARG:NE	2.35	0.41
1:C:88:VAL:HG21	1:C:112:SER:HB3	2.03	0.41
1:E:88:VAL:HG21	1:E:112:SER:HB3	2.03	0.41
1:F:376:GLU:OE2	1:H:276:LYS:NZ	2.50	0.41
1:F:389:MET:CB	1:F:399:CYS:SG	3.09	0.41
2:G:502:SSS:O2'	2:G:502:SSS:H8	2.20	0.41
1:A:217:HIS:O	1:A:221:GLN:HG3	2.21	0.41
1:C:137:ARG:NH2	1:C:475:VAL:CG1	2.78	0.40
1:H:84:LEU:HD11	1:H:93:HIS:HD2	1.86	0.40
1:F:484:LEU:HD12	1:G:85:ARG:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:470:LYS:HB3	1:D:471:PRO:HD3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	460/487 (94%)	449 (98%)	9 (2%)	2 (0%)	34	48
1	B	411/487 (84%)	403 (98%)	7 (2%)	1 (0%)	47	62
1	C	412/487 (85%)	401 (97%)	10 (2%)	1 (0%)	47	62
1	D	432/487 (89%)	420 (97%)	10 (2%)	2 (0%)	29	41
1	E	462/487 (95%)	454 (98%)	7 (2%)	1 (0%)	47	62
1	F	462/487 (95%)	453 (98%)	8 (2%)	1 (0%)	47	62
1	G	459/487 (94%)	451 (98%)	7 (2%)	1 (0%)	47	62
1	H	475/487 (98%)	467 (98%)	7 (2%)	1 (0%)	47	62
All	All	3573/3896 (92%)	3498 (98%)	65 (2%)	10 (0%)	41	55

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	ARG
1	B	329	ARG
1	C	329	ARG
1	D	284	LYS
1	D	329	ARG
1	E	329	ARG
1	F	329	ARG
1	G	329	ARG
1	H	329	ARG

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Mol	Chain	Res	Type
1	A	392	ALA

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	406/422 (96%)	400 (98%)	6 (2%)	65 80
1	B	365/422 (86%)	355 (97%)	10 (3%)	44 65
1	C	370/422 (88%)	364 (98%)	6 (2%)	62 79
1	D	388/422 (92%)	382 (98%)	6 (2%)	65 80
1	E	410/422 (97%)	401 (98%)	9 (2%)	52 71
1	F	408/422 (97%)	398 (98%)	10 (2%)	47 67
1	G	406/422 (96%)	401 (99%)	5 (1%)	71 85
1	H	417/422 (99%)	411 (99%)	6 (1%)	67 82
All	All	3170/3376 (94%)	3112 (98%)	58 (2%)	59 76

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	83	ARG
1	A	164	GLN
1	A	296	ARG
1	A	329	ARG
1	A	484	LEU
1	B	31	SER
1	B	32	ASP
1	B	108	LEU
1	B	160	PHE
1	B	295	LYS
1	B	329	ARG
1	B	331	LEU
1	B	395	SER

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Mol	Chain	Res	Type
1	B	412	SER
1	B	484	LEU
1	C	160	PHE
1	C	296	ARG
1	C	299	MET
1	C	329	ARG
1	C	380	MET
1	C	437	HIS
1	D	63	GLN
1	D	125	ARG
1	D	160	PHE
1	D	329	ARG
1	D	402	LYS
1	D	484	LEU
1	E	37	ARG
1	E	160	PHE
1	E	201	THR
1	E	250	GLU
1	E	295	LYS
1	E	329	ARG
1	E	402	LYS
1	E	404	ARG
1	E	407	SER
1	F	37	ARG
1	F	105	ILE
1	F	111	THR
1	F	160	PHE
1	F	329	ARG
1	F	371	ARG
1	F	372	ARG
1	F	376	GLU
1	F	377	LEU
1	F	400	HIS
1	G	37	ARG
1	G	329	ARG
1	G	396	ARG
1	G	470	LYS
1	G	484	LEU
1	H	37	ARG
1	H	66	LYS
1	H	201	THR
1	H	295	LYS

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Mol	Chain	Res	Type
1	H	329	ARG
1	H	484	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	397	GLN
1	B	458	GLN
1	D	221	GLN
1	G	93	HIS
1	G	221	GLN
1	H	93	HIS
1	H	221	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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
2	SSS	G	502	-	26,31,31	0.97	1 (3%)	32,46,46	1.52	6 (18%)
4	FUM	E	502	-	7,7,7	1.24	0	8,8,8	1.12	0
2	SSS	D	502	-	26,31,31	1.18	3 (11%)	32,46,46	1.67	8 (25%)
5	AMZ	C	502	-	18,23,23	0.99	0	22,35,35	1.76	3 (13%)
4	FUM	B	503	-	7,7,7	1.18	1 (14%)	8,8,8	1.26	1 (12%)
2	SSS	F	502	-	26,31,31	0.94	0	32,46,46	1.56	7 (21%)
5	AMZ	H	503	-	18,23,23	0.70	0	22,35,35	2.09	5 (22%)
2	SSS	B	502	-	26,31,31	1.27	2 (7%)	32,46,46	1.42	4 (12%)
2	SSS	A	501	-	26,31,31	1.19	2 (7%)	32,46,46	1.57	7 (21%)
2	SSS	H	501	-	26,31,31	0.98	0	32,46,46	1.83	10 (31%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SSS	G	502	-	-	6/18/42/42	0/2/2/2
4	FUM	E	502	-	-	1/5/5/5	-
2	SSS	D	502	-	-	1/18/42/42	0/2/2/2
5	AMZ	C	502	-	-	1/6/30/30	0/2/2/2
4	FUM	B	503	-	-	0/5/5/5	-
2	SSS	F	502	-	-	6/18/42/42	0/2/2/2
5	AMZ	H	503	-	-	2/6/30/30	0/2/2/2
2	SSS	B	502	-	-	8/18/42/42	0/2/2/2
2	SSS	A	501	-	-	7/18/42/42	0/2/2/2
2	SSS	H	501	-	-	4/18/42/42	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	SSS	C8-N7	3.47	1.40	1.35
2	A	501	SSS	C5-C6	-3.32	1.45	1.50
2	B	502	SSS	O4'-C1'	2.62	1.44	1.41
2	D	502	SSS	C5-C6	-2.57	1.46	1.50
2	G	502	SSS	C5-C6	-2.30	1.47	1.50
2	D	502	SSS	O4'-C4'	-2.28	1.39	1.45
2	D	502	SSS	C2'-C1'	-2.22	1.50	1.53
2	A	501	SSS	O68-C64	-2.19	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	FUM	OXT-C	-2.18	1.24	1.30

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	503	AMZ	C3A-C6-N2	6.82	126.52	115.75
5	C	502	AMZ	C3A-C6-N2	5.82	124.94	115.75
2	A	501	SSS	O6-C6-N6	4.00	129.81	122.45
2	D	502	SSS	O6-C6-N6	3.94	129.70	122.45
2	B	502	SSS	O6-C6-N6	-3.68	115.67	122.45
5	H	503	AMZ	O5-C6-C3A	-3.54	111.40	119.89
2	H	501	SSS	C61-N6-C6	3.52	130.21	121.60
2	B	502	SSS	C8-N7-C5	3.40	109.46	102.99
2	B	502	SSS	O5'-PA-O3A	-3.40	96.95	106.47
2	H	501	SSS	O3'-C3'-C2'	-3.32	101.09	111.82
5	C	502	AMZ	C5-N1-C3A	3.16	109.02	102.99
2	D	502	SSS	O1A-PA-O5'	-3.10	98.49	106.73
2	H	501	SSS	C63-C61-C62	-3.09	104.86	110.83
2	D	502	SSS	C8-N7-C5	3.09	108.88	102.99
2	H	501	SSS	C2'-C3'-C4'	2.99	108.46	102.64
2	G	502	SSS	O1A-PA-O5'	-2.99	98.78	106.73
2	H	501	SSS	O6-C6-C5	-2.98	116.13	120.59
5	H	503	AMZ	C5-N1-C3A	2.98	108.66	102.99
2	F	502	SSS	C8-N7-C5	2.97	108.66	102.99
2	D	502	SSS	C61-N6-C6	2.94	128.79	121.60
2	D	502	SSS	C3'-C2'-C1'	2.94	105.40	100.98
2	G	502	SSS	O2'-C2'-C1'	2.92	121.65	110.85
2	H	501	SSS	C8-N7-C5	2.73	108.19	102.99
2	G	502	SSS	O3'-C3'-C2'	-2.72	103.02	111.82
5	H	503	AMZ	O3-P-OP2	-2.67	98.99	106.47
2	H	501	SSS	C63-C61-N6	-2.66	105.39	110.60
2	G	502	SSS	C8-N7-C5	2.61	107.95	102.99
2	F	502	SSS	C3'-C2'-C1'	2.55	104.82	100.98
2	A	501	SSS	O1A-PA-O5'	-2.50	100.09	106.73
2	F	502	SSS	O2A-PA-O5'	-2.49	100.12	106.73
2	B	502	SSS	C61-N6-C6	2.44	127.58	121.60
2	H	501	SSS	O2'-C2'-C1'	2.40	119.73	110.85
2	F	502	SSS	O4'-C4'-C3'	2.38	109.83	105.11
2	G	502	SSS	O6-C6-N6	2.38	126.83	122.45
2	A	501	SSS	C61-N6-C6	2.38	127.42	121.60
2	A	501	SSS	O2'-C2'-C1'	2.35	119.55	110.85
2	H	501	SSS	O2A-PA-O1A	2.35	116.64	107.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	SSS	O4'-C4'-C3'	2.30	109.67	105.11
2	G	502	SSS	C3'-C2'-C1'	2.30	104.44	100.98
4	B	503	FUM	OXT-C-O	-2.25	118.00	122.67
2	D	502	SSS	O2A-PA-O1A	2.24	116.21	107.64
2	F	502	SSS	O1A-PA-O5'	-2.24	100.78	106.73
5	H	503	AMZ	O4-P-OP1	2.17	115.93	107.64
2	F	502	SSS	O6-C6-N6	2.14	126.39	122.45
2	F	502	SSS	O2A-PA-O1A	2.14	115.81	107.64
2	D	502	SSS	O4'-C4'-C5'	-2.10	102.47	109.37
5	C	502	AMZ	O5-C6-C3A	-2.09	114.87	119.89
2	A	501	SSS	C8-N7-C5	2.09	106.97	102.99
2	D	502	SSS	O66-C62-C61	2.07	120.29	113.40
2	A	501	SSS	C3'-C2'-C1'	2.05	104.06	100.98
2	H	501	SSS	C62-C61-N6	2.02	115.33	110.55

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	SSS	C5'-O5'-PA-O1A
2	A	501	SSS	C5'-O5'-PA-O2A
2	B	502	SSS	C5'-O5'-PA-O1A
2	B	502	SSS	C5'-O5'-PA-O2A
2	B	502	SSS	C5'-O5'-PA-O3A
2	B	502	SSS	C3'-C4'-C5'-O5'
2	B	502	SSS	O6-C6-N6-C61
2	B	502	SSS	C5-C6-N6-C61
2	F	502	SSS	O4'-C4'-C5'-O5'
2	H	501	SSS	O6-C6-N6-C61
2	H	501	SSS	C5-C6-N6-C61
2	A	501	SSS	O4'-C4'-C5'-O5'
2	B	502	SSS	O4'-C4'-C5'-O5'
2	F	502	SSS	C3'-C4'-C5'-O5'
2	H	501	SSS	O4'-C4'-C5'-O5'
5	H	503	AMZ	O-C-C4-O3
2	A	501	SSS	N6-C61-C63-C64
2	F	502	SSS	N6-C61-C63-C64
2	G	502	SSS	N6-C61-C63-C64
2	A	501	SSS	C3'-C4'-C5'-O5'
2	G	502	SSS	C5-C6-N6-C61
2	H	501	SSS	C3'-C4'-C5'-O5'
2	F	502	SSS	C61-C63-C64-O67

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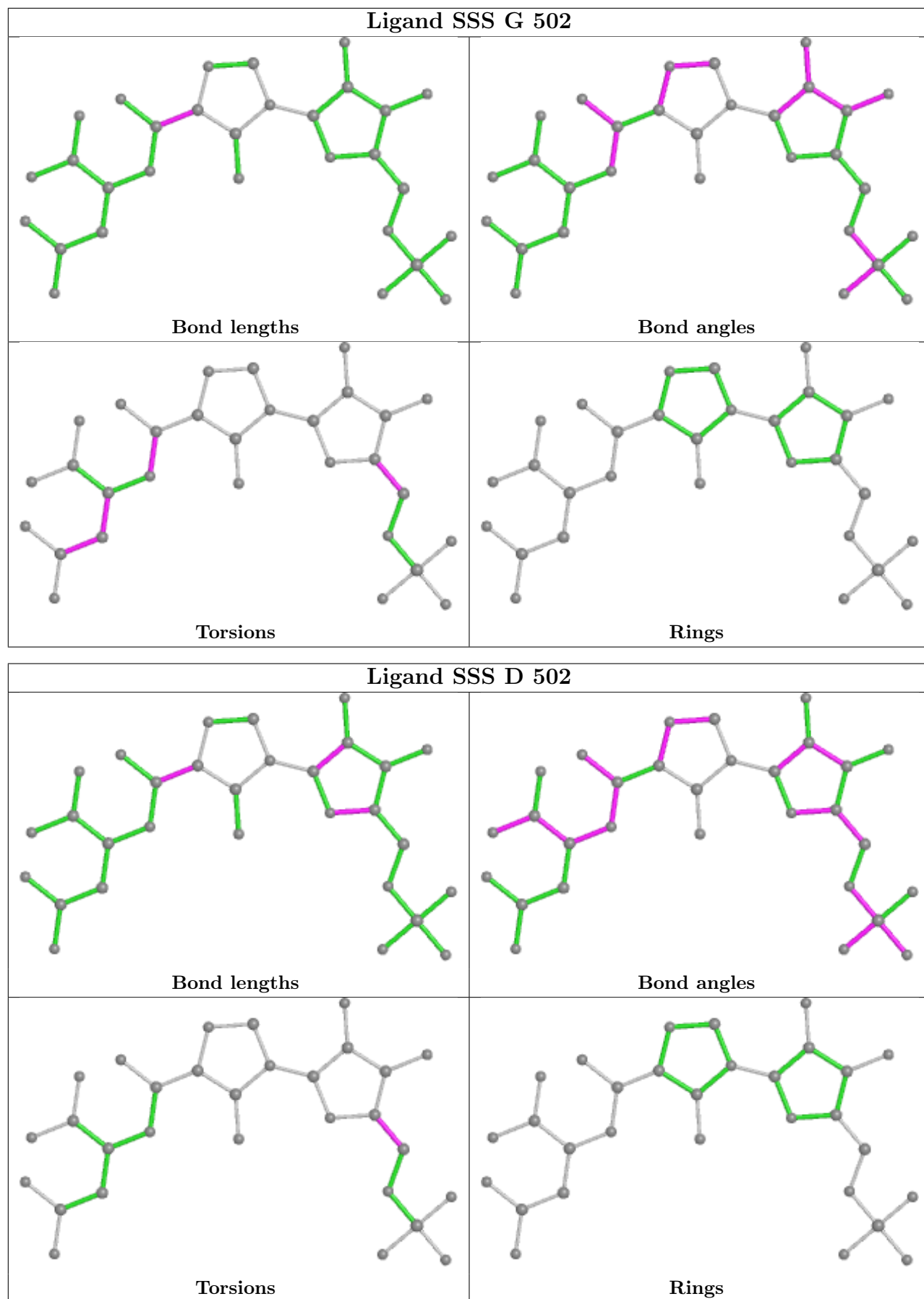
Mol	Chain	Res	Type	Atoms
2	F	502	SSS	C61-C63-C64-O68
2	G	502	SSS	C61-C63-C64-O67
2	G	502	SSS	C61-C63-C64-O68
2	A	501	SSS	N6-C61-C62-O66
5	C	502	AMZ	O-C-C4-O3
5	H	503	AMZ	C3-C-C4-O3
2	A	501	SSS	N6-C61-C62-O65
2	G	502	SSS	O4'-C4'-C5'-O5'
2	F	502	SSS	C5-C6-N6-C61
2	B	502	SSS	N6-C61-C63-C64
4	E	502	FUM	C4-C5-C6-O7
2	D	502	SSS	O4'-C4'-C5'-O5'
2	G	502	SSS	O6-C6-N6-C61

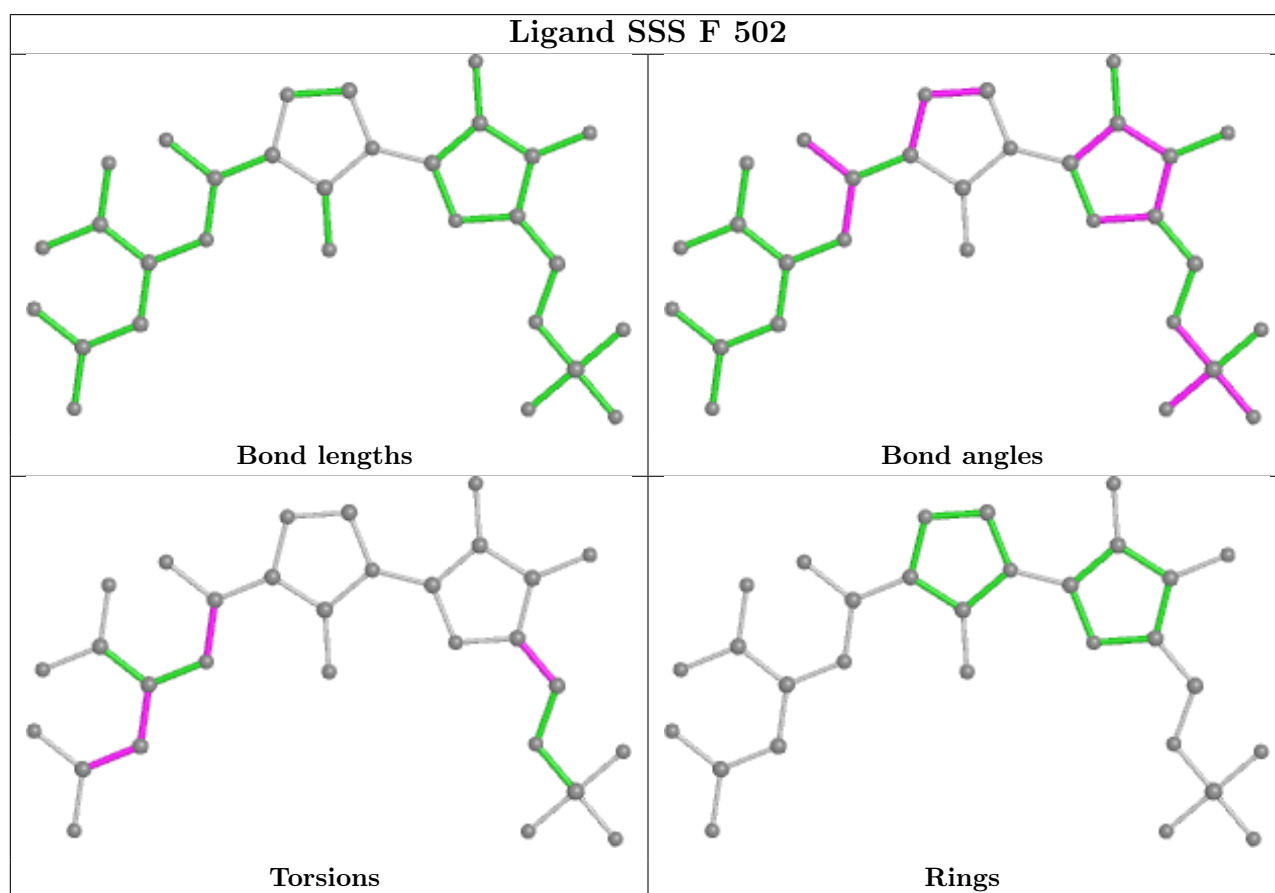
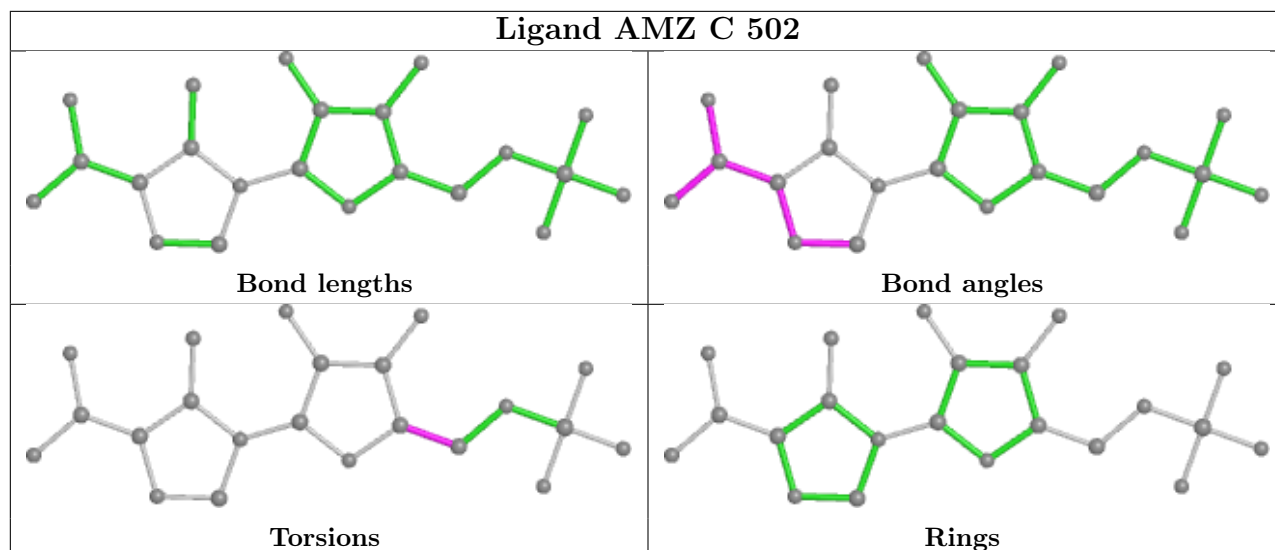
There are no ring outliers.

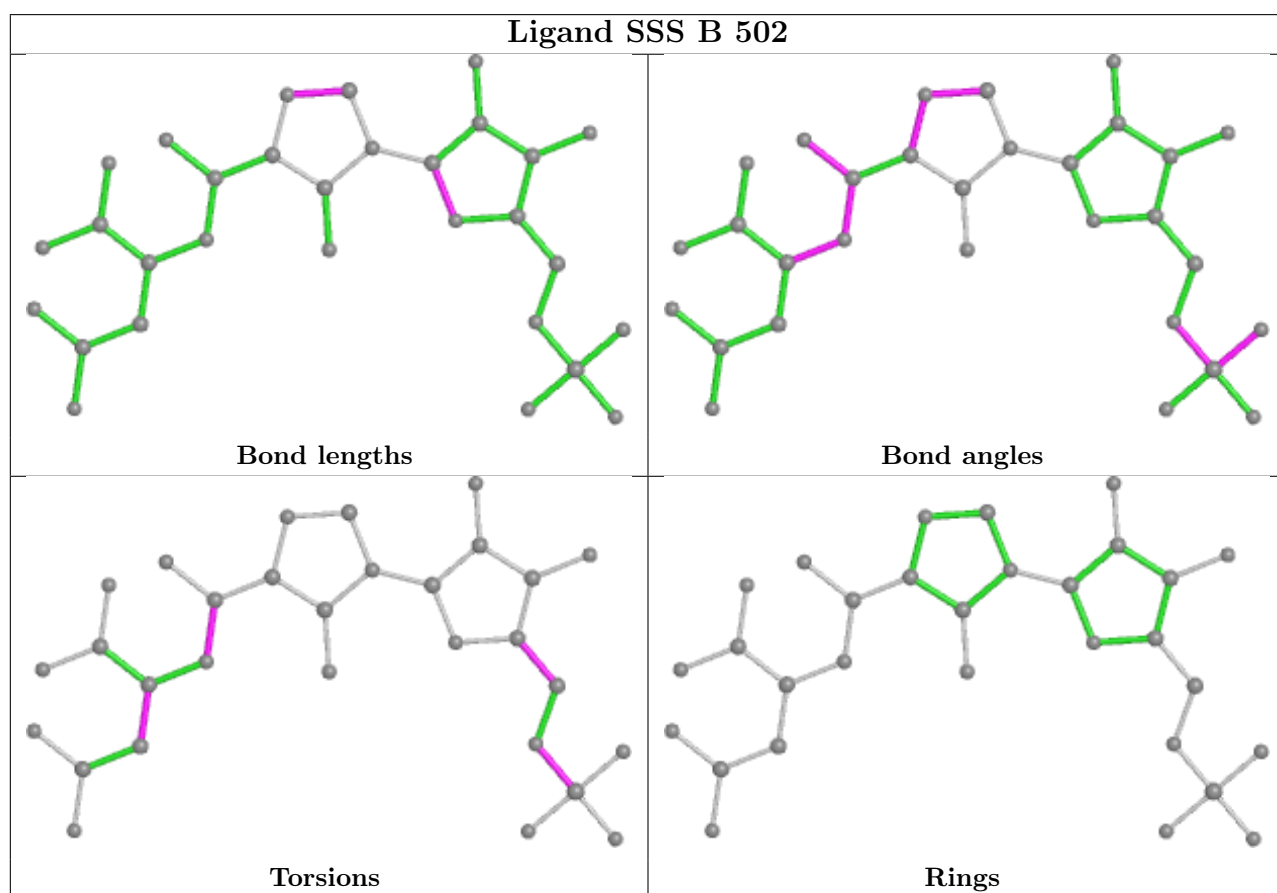
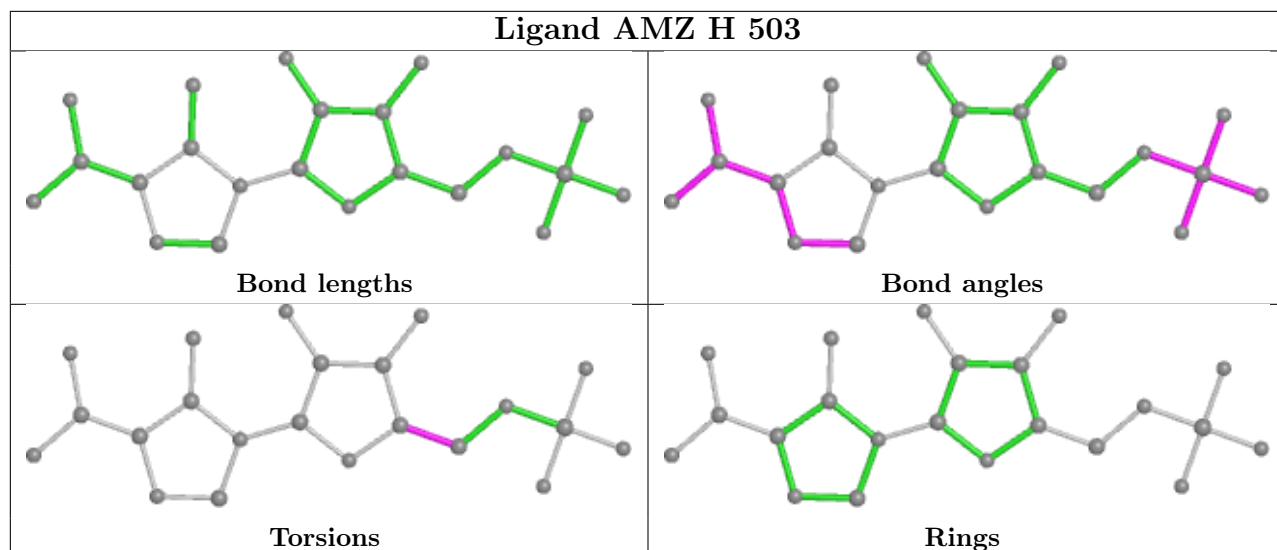
6 monomers are involved in 10 short contacts:

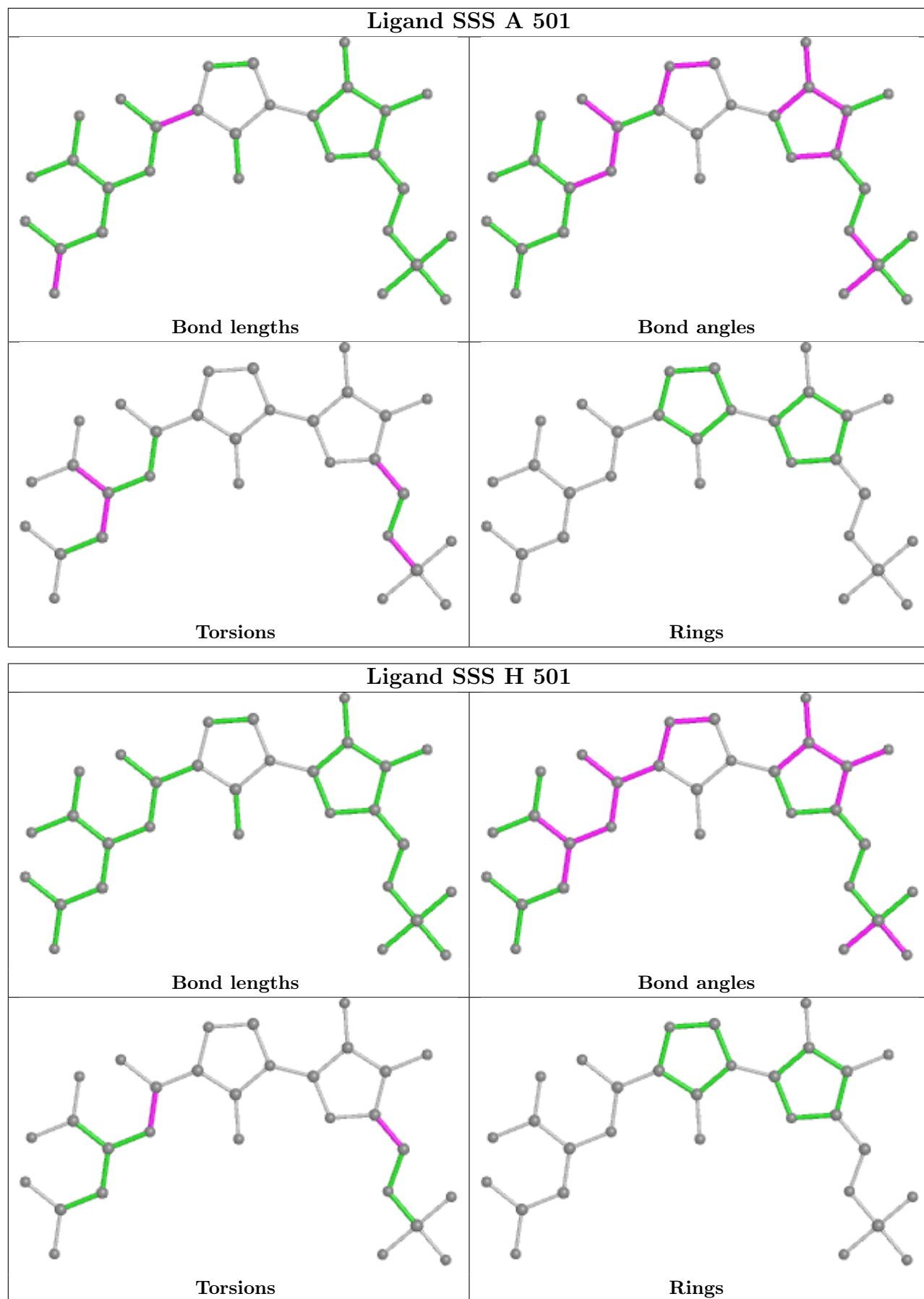
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	502	SSS	2	0
2	D	502	SSS	2	0
5	C	502	AMZ	1	0
2	F	502	SSS	2	0
2	A	501	SSS	1	0
2	H	501	SSS	2	0

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.









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	464/487 (95%)	0.16	18 (3%) 39 38	35, 53, 81, 112	0
1	B	415/487 (85%)	0.19	24 (5%) 23 22	33, 52, 86, 108	0
1	C	418/487 (85%)	0.26	25 (5%) 21 20	35, 53, 95, 132	0
1	D	440/487 (90%)	0.21	20 (4%) 33 31	33, 51, 81, 138	0
1	E	466/487 (95%)	0.15	30 (6%) 19 18	30, 45, 99, 131	0
1	F	466/487 (95%)	-0.02	8 (1%) 70 68	30, 48, 79, 110	0
1	G	463/487 (95%)	-0.03	5 (1%) 80 79	29, 47, 70, 92	0
1	H	477/487 (97%)	-0.04	8 (1%) 70 68	27, 41, 69, 100	0
All	All	3609/3896 (92%)	0.11	138 (3%) 40 39	27, 49, 81, 138	0

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	440	LEU	7.2
1	D	386	ILE	6.3
1	C	386	ILE	5.0
1	C	387	MET	4.8
1	C	390	VAL	4.8
1	B	44	LEU	4.7
1	D	426	ARG	4.7
1	E	438	SER	4.6
1	C	382	THR	4.6
1	C	441	ASP	4.6
1	C	282	PHE	4.3
1	E	433	PHE	4.3
1	E	431	ALA	4.3
1	E	419	GLY	4.1
1	C	444	LEU	3.8
1	E	385	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	481	GLU	3.8
1	E	437	HIS	3.7
1	C	385	ILE	3.7
1	A	65	MET	3.6
1	C	442	HIS	3.6
1	A	60	GLU	3.5
1	A	429	ALA	3.4
1	E	387	MET	3.4
1	E	428	GLN	3.2
1	A	99	CYS	3.2
1	C	389	MET	3.2
1	E	404	ARG	3.2
1	D	319	LEU	3.1
1	D	321	THR	3.1
1	C	479	LYS	3.1
1	E	434	SER	3.1
1	E	403	ILE	3.0
1	E	425	GLU	3.0
1	B	316	MET	3.0
1	A	483	CYS	3.0
1	F	283	GLU	3.0
1	E	429	ALA	3.0
1	B	403	ILE	2.9
1	B	225	MET	2.9
1	B	324	VAL	2.8
1	E	427	ILE	2.8
1	D	477	LYS	2.8
1	B	45	TRP	2.8
1	C	388	ALA	2.8
1	A	67	SER	2.8
1	F	484	LEU	2.7
1	E	430	ASP	2.7
1	E	440	LEU	2.7
1	E	400	HIS	2.7
1	A	316	MET	2.7
1	D	316	MET	2.7
1	E	405	VAL	2.7
1	B	211	LEU	2.7
1	H	319	LEU	2.7
1	H	395	SER	2.6
1	A	58	THR	2.6
1	D	314	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	226	VAL	2.6
1	E	8	GLY	2.6
1	A	56	PRO	2.6
1	E	439	GLN	2.6
1	H	262	VAL	2.6
1	B	319	LEU	2.6
1	E	416	GLN	2.5
1	B	109	GLY	2.5
1	E	271	LEU	2.5
1	D	385	ILE	2.5
1	C	324	VAL	2.5
1	H	312	MET	2.5
1	D	478	VAL	2.4
1	G	101	LYS	2.4
1	A	319	LEU	2.4
1	D	57	ILE	2.4
1	D	60	GLU	2.4
1	E	441	ASP	2.4
1	C	316	MET	2.4
1	D	318	PRO	2.4
1	C	313	THR	2.4
1	G	271	LEU	2.4
1	E	408	GLN	2.4
1	F	99	CYS	2.4
1	A	307	LEU	2.3
1	B	221	GLN	2.3
1	E	442	HIS	2.3
1	D	324	VAL	2.3
1	G	58	THR	2.3
1	E	432	TYR	2.3
1	B	212	PHE	2.3
1	B	256	ALA	2.3
1	B	38	THR	2.3
1	D	399	CYS	2.3
1	B	40	ARG	2.2
1	C	475	VAL	2.2
1	E	436	ILE	2.2
1	D	313	THR	2.2
1	A	305	CYS	2.2
1	H	399	CYS	2.2
1	H	324	VAL	2.2
1	E	381	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	425	GLU	2.2
1	F	97	HIS	2.2
1	G	312	MET	2.2
1	D	322	ALA	2.2
1	E	435	PRO	2.2
1	E	407	SER	2.2
1	B	33	ARG	2.1
1	B	321	THR	2.1
1	B	112	SER	2.1
1	B	230	ALA	2.1
1	D	54	GLY	2.1
1	G	267	THR	2.1
1	F	326	TRP	2.1
1	B	323	SER	2.1
1	F	71	ASN	2.1
1	A	315	VAL	2.1
1	D	337	ARG	2.1
1	A	75	LYS	2.1
1	C	477	LYS	2.1
1	C	384	ASN	2.1
1	H	330	THR	2.1
1	C	443	LEU	2.1
1	C	210	GLN	2.1
1	F	217	HIS	2.1
1	B	39	TRP	2.1
1	C	383	GLU	2.1
1	D	419	GLY	2.1
1	F	324	VAL	2.0
1	B	36	PHE	2.0
1	C	379	PHE	2.0
1	D	53	LEU	2.0
1	A	63	GLN	2.0
1	A	57	ILE	2.0
1	H	311	LEU	2.0
1	A	79	GLU	2.0
1	B	399	CYS	2.0
1	A	68	ASN	2.0
1	C	319	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

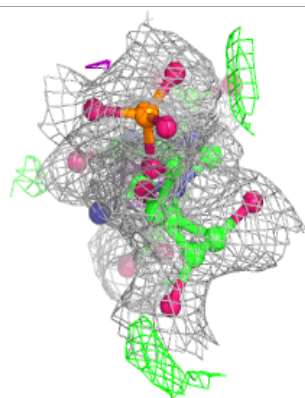
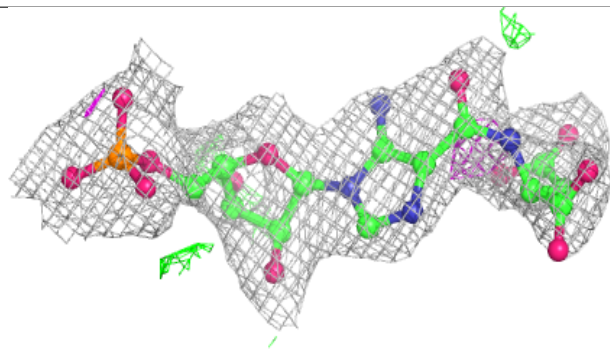
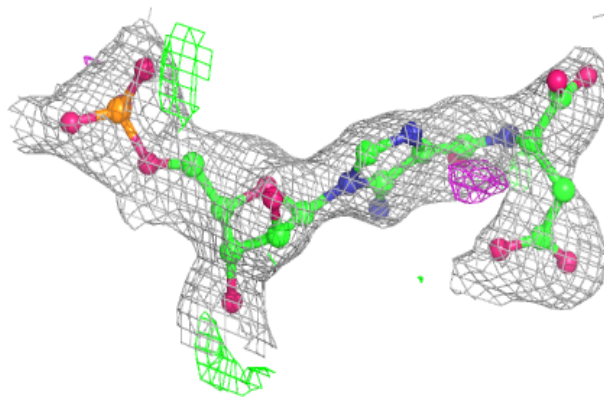
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SSS	B	502	30/30	0.90	0.16	49,68,75,76	0
2	SSS	A	501	30/30	0.94	0.14	47,57,70,76	0
3	CL	D	501	1/1	0.94	0.09	48,48,48,48	0
2	SSS	F	502	30/30	0.96	0.11	44,50,63,65	0
3	CL	B	501	1/1	0.96	0.10	61,61,61,61	0
2	SSS	D	502	30/30	0.96	0.14	34,54,67,70	0
4	FUM	B	503	8/8	0.96	0.13	48,52,53,54	0
2	SSS	H	501	30/30	0.97	0.15	35,39,42,44	0
3	CL	G	501	1/1	0.97	0.07	39,39,39,39	0
2	SSS	G	502	30/30	0.97	0.13	34,40,62,68	0
5	AMZ	C	502	22/22	0.97	0.11	34,43,46,50	0
5	AMZ	H	503	22/22	0.97	0.14	31,36,38,40	0
3	CL	C	501	1/1	0.98	0.09	51,51,51,51	0
3	CL	H	502	1/1	0.99	0.09	43,43,43,43	0
3	CL	E	501	1/1	0.99	0.11	37,37,37,37	0
4	FUM	E	502	8/8	0.99	0.12	29,32,34,34	0
3	CL	F	501	1/1	0.99	0.11	48,48,48,48	0
3	CL	A	502	1/1	0.99	0.07	43,43,43,43	0

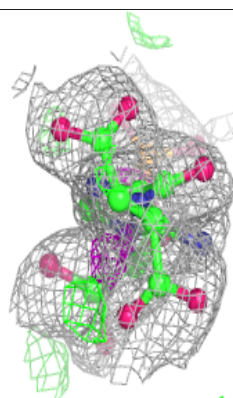
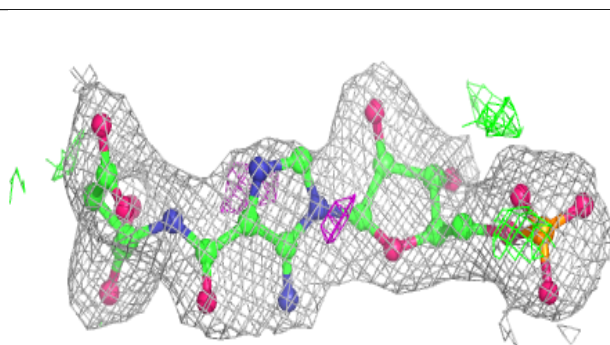
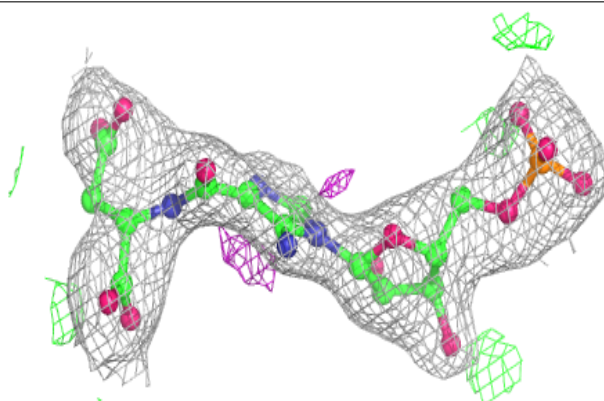
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SSS B 502:

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

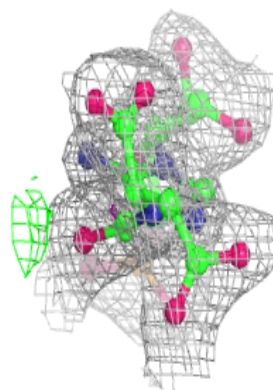
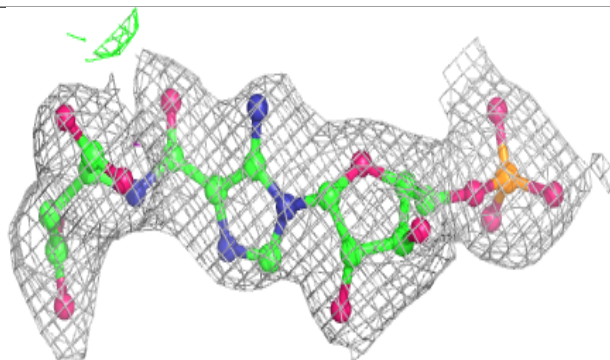
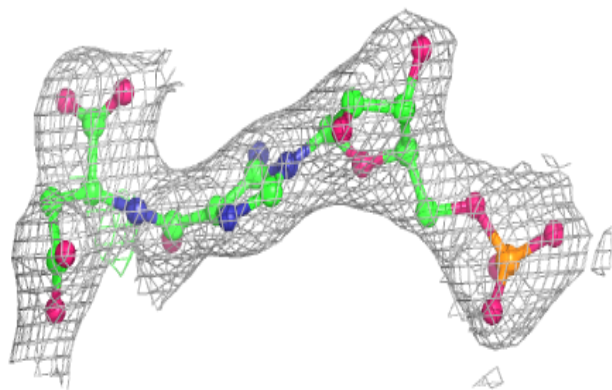
**Electron density around SSS A 501:**

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

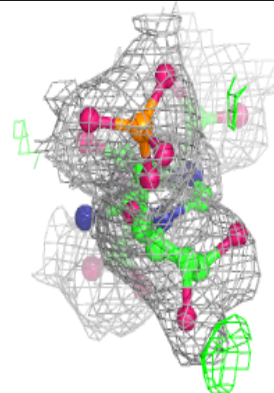
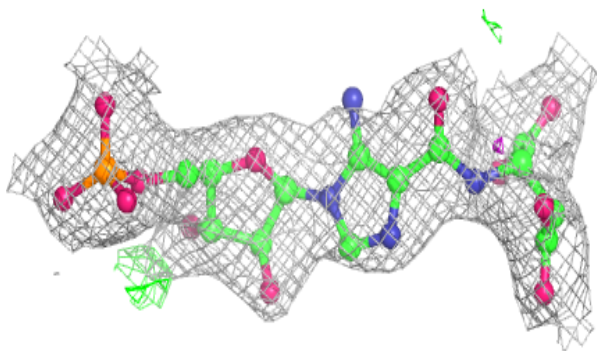
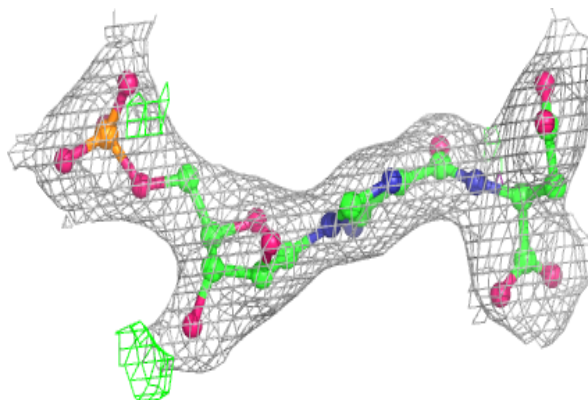


Electron density around SSS F 502:

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

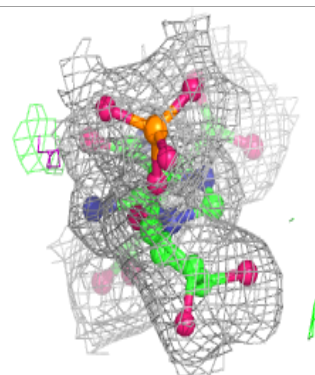
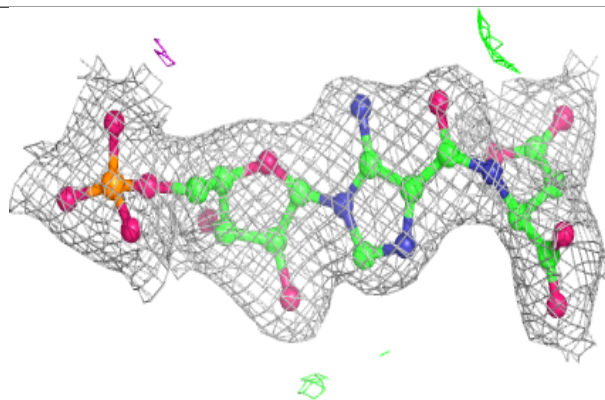
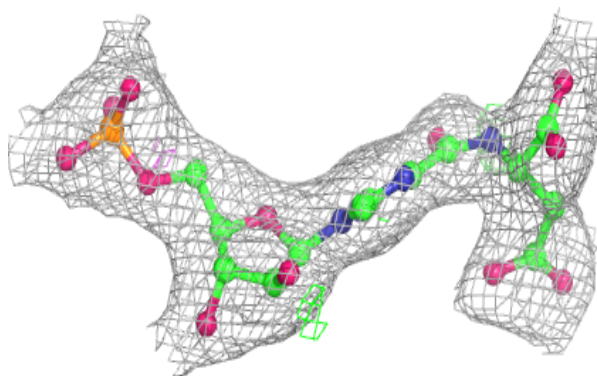
**Electron density around SSS D 502:**

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

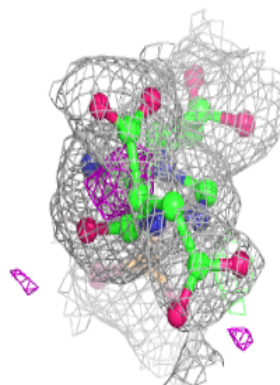
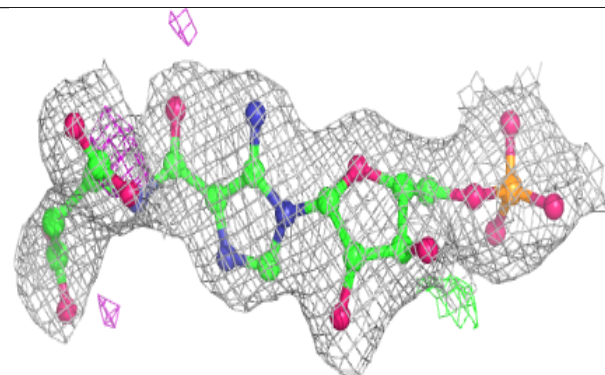
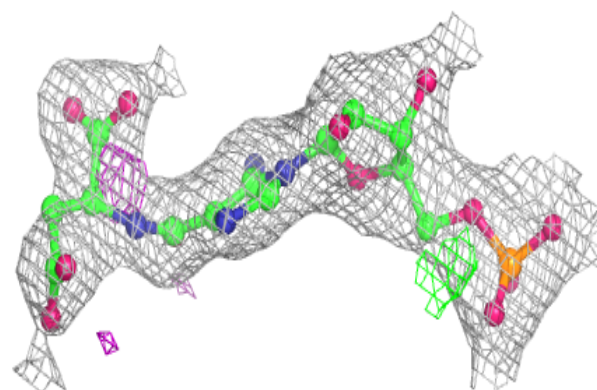


Electron density around SSS H 501:

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

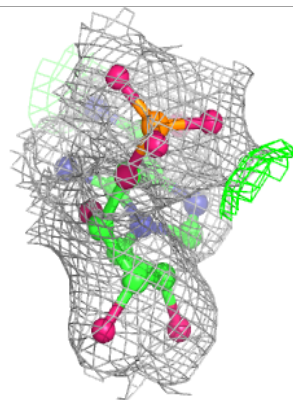
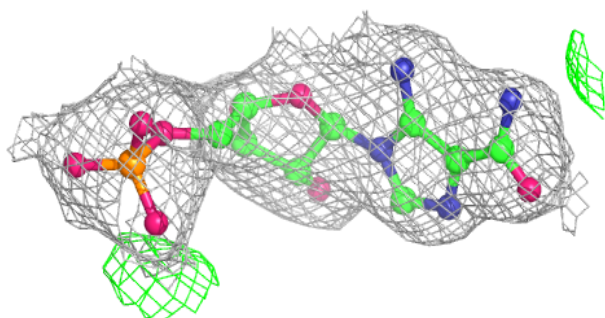
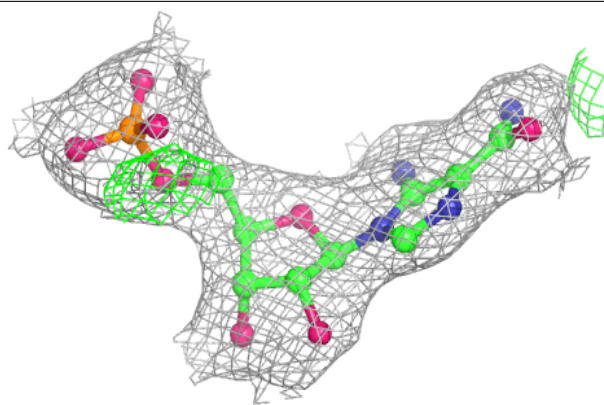
**Electron density around SSS G 502:**

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

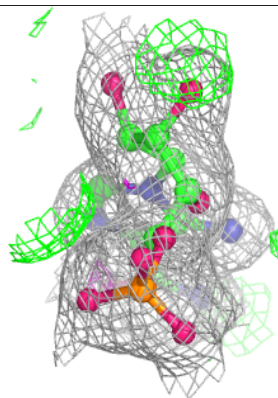
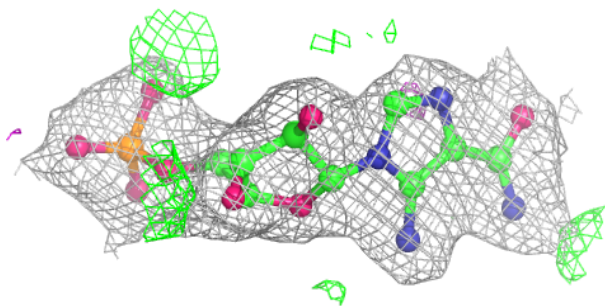
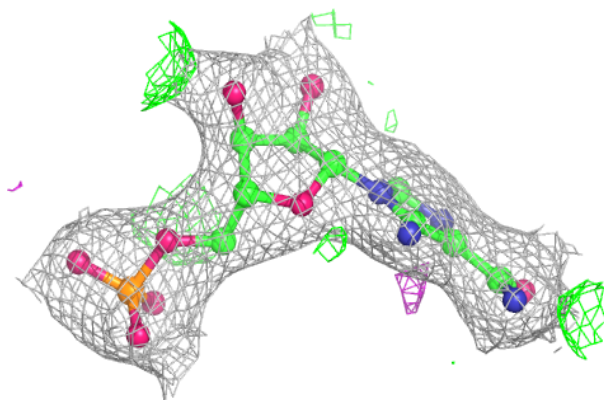


Electron density around AMZ C 502:

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

**Electron density around AMZ H 503:**

$2mF_o-DF_c$ (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.