



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:22 PM UTC

PDB ID : 3MO5 / pdb_00003mo5
Title : Human G9a-like (GLP, also known as EHMT1) in complex with inhibitor E72
Authors : Chang, Y.; Horton, J.R.; Cheng, X.
Deposited on : 2010-04-22
Resolution : 2.14 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (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

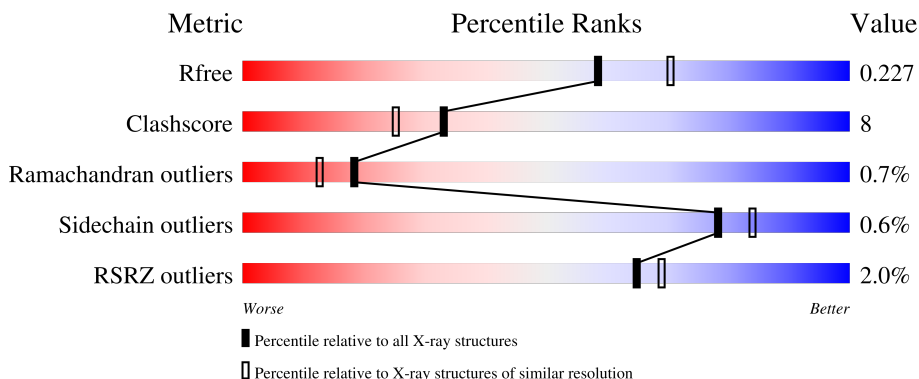
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	285	 3% 76% 12% • 9%
1	B	285	 2% 72% 17% • 9%
1	C	285	 % 77% 13% • 9%
1	D	285	 2% 73% 16% • 10%

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
4	SAH	C	103	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9067 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.

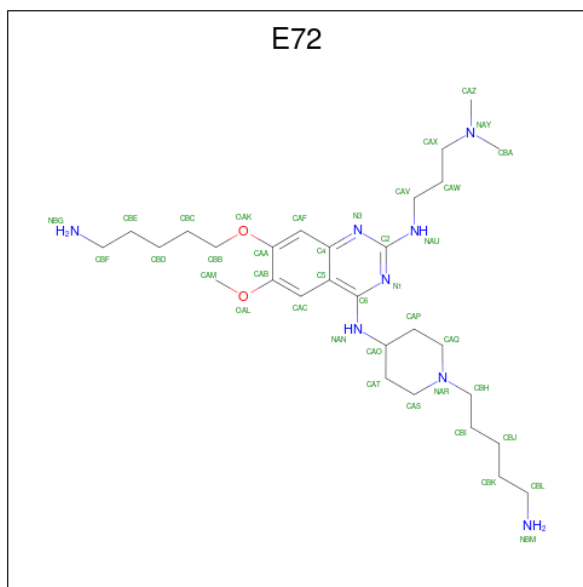
- Molecule 1 is a protein called Histone-lysine N-methyltransferase, H3 lysine-9 specific 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	255	2022	1262	363	373	24	0	0	0
1	B	258	2050	1282	366	377	25	0	0	0
1	C	258	2053	1282	368	378	25	0	0	0
1	D	256	2019	1263	359	372	25	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

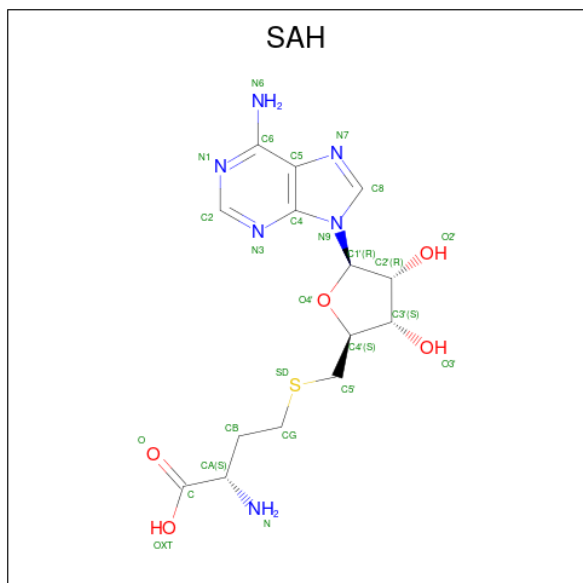
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Zn	0	0
			4	4		
2	B	4	Total	Zn	0	0
			4	4		
2	C	4	Total	Zn	0	0
			4	4		
2	D	4	Total	Zn	0	0
			4	4		

- Molecule 3 is 7-[(5-aminopentyl)oxy]-N 4 -[1-(5-aminopentyl)piperidin-4-yl]-N 2 -[3-(dimethylamino)propyl]-6-methoxyquinazoline-2,4-diamine (CCD ID: E72) (formula: C₂₉H₅₂N₈O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			39	29	8	2		
3	B	1	Total	C	N	O	0	0
			39	29	8	2		
3	C	1	Total	C	N	O	0	0
			39	29	8	2		
3	D	1	Total	C	N	O	0	0
			39	29	8	2		

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
4	D	1	Total	C	N	O	S	0	0
			26	14	6	5	1		


- Molecule 5 is water.

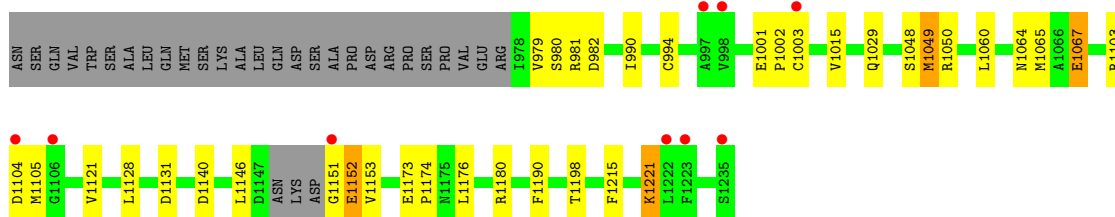
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	193	Total	O	0	0
			193	193		
5	B	201	Total	O	0	0
			201	201		
5	C	182	Total	O	0	0
			182	182		
5	D	123	Total	O	0	0
			123	123		

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.

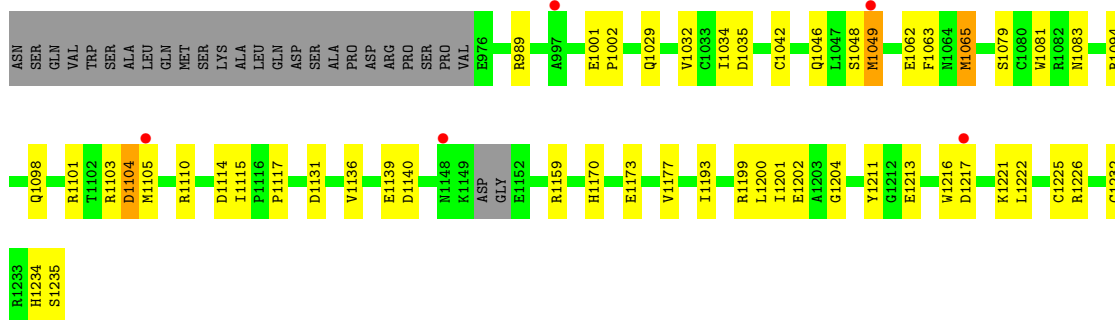
- Molecule 1: Histone-lysine N-methyltransferase, H3 lysine-9 specific 5

Chain A: 




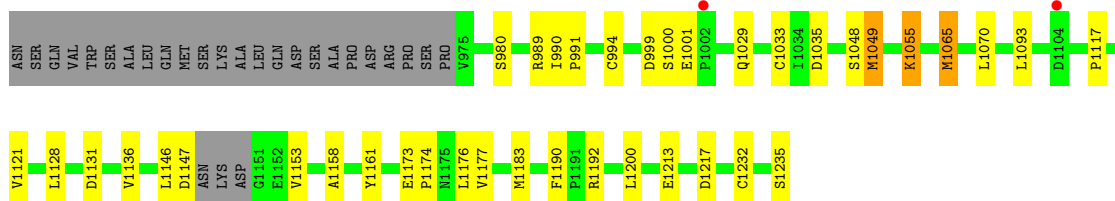
- Molecule 1: Histone-lysine N-methyltransferase, H3 lysine-9 specific 5

Chain B: 




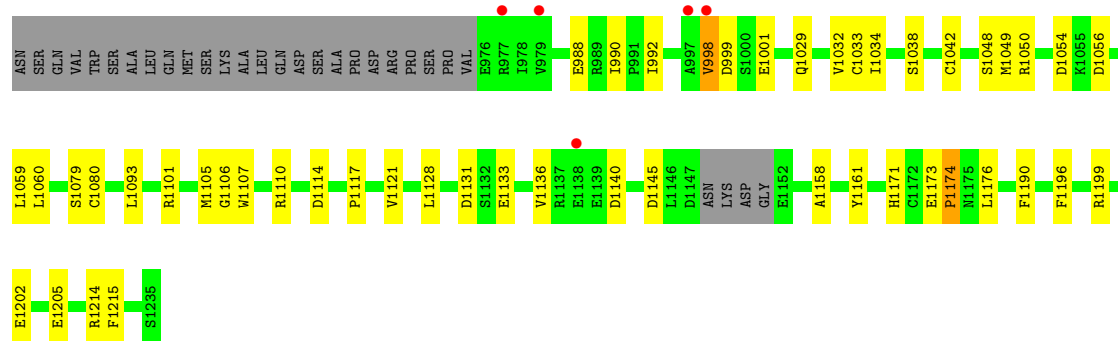
- Molecule 1: Histone-lysine N-methyltransferase, H3 lysine-9 specific 5

Chain C: 



- Molecule 1: Histone-lysine N-methyltransferase, H3 lysine-9 specific 5

Chain D:  2% 73% 16% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.90Å 162.90Å 69.10Å 90.00° 99.00° 90.00°	Depositor
Resolution (Å)	34.14 – 2.14 34.14 – 2.14	Depositor EDS
% Data completeness (in resolution range)	93.3 (34.14-2.14) 93.4 (34.14-2.14)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 2.12Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.196 , 0.233 0.193 , 0.227	Depositor DCC
R_{free} test set	3646 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtrriage
Anisotropy	0.309	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	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	0.95	EDS
Total number of atoms	9067	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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: ZN, E72, SAH

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	0.37	0/2072	0.88	6/2807 (0.2%)
1	B	0.36	0/2100	0.87	5/2844 (0.2%)
1	C	0.35	0/2103	0.88	7/2848 (0.2%)
1	D	0.34	0/2069	0.85	5/2807 (0.2%)
All	All	0.36	0/8344	0.87	23/11306 (0.2%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1173	GLU	CA-C-N	7.74	127.73	119.76
1	C	1173	GLU	C-N-CA	7.74	127.73	119.76
1	D	1173	GLU	CA-C-N	7.65	127.64	119.76
1	D	1173	GLU	C-N-CA	7.65	127.64	119.76
1	A	1173	GLU	CA-C-N	7.48	127.53	119.90
1	A	1173	GLU	C-N-CA	7.48	127.53	119.90
1	B	1173	GLU	CA-C-N	7.42	127.47	119.90
1	B	1173	GLU	C-N-CA	7.42	127.47	119.90
1	B	1213	GLU	N-CA-C	6.92	118.47	111.07
1	C	1213	GLU	N-CA-C	6.37	118.30	111.36
1	C	1174	PRO	N-CA-C	6.28	120.94	111.14
1	D	1029	GLN	N-CA-C	-6.24	99.11	109.46
1	C	1029	GLN	N-CA-C	-5.84	100.15	109.96
1	D	1038	SER	N-CA-C	-5.71	106.67	113.97
1	A	1029	GLN	N-CA-C	-5.46	100.80	109.96
1	A	1174	PRO	N-CA-C	5.42	119.72	111.15
1	B	1029	GLN	N-CA-C	-5.39	100.51	109.46
1	A	1067	GLU	CA-C-N	5.36	125.90	120.38
1	A	1067	GLU	C-N-CA	5.36	125.90	120.38
1	B	1193	ILE	N-CA-C	5.33	115.45	107.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1174	PRO	N-CA-C	5.31	119.42	111.14
1	C	1217	ASP	N-CA-C	-5.11	105.89	111.82
1	C	1070	LEU	N-CA-C	-5.07	102.97	110.48

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	2022	0	1879	32	0
1	B	2050	0	1916	36	0
1	C	2053	0	1916	24	0
1	D	2019	0	1868	36	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
3	A	39	0	52	3	0
3	B	39	0	52	4	0
3	C	39	0	52	1	0
3	D	39	0	52	3	0
4	C	26	0	18	0	0
4	D	26	0	20	2	0
5	A	193	0	0	0	0
5	B	201	0	0	0	0
5	C	182	0	0	1	0
5	D	123	0	0	1	0
All	All	9067	0	7825	126	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 8.

All (126) 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:1050:ARG:HH22	1:D:1060:LEU:HD12	1.30	0.95
1:C:1065:MET:HE2	1:C:1177:VAL:HG11	1.49	0.92
1:B:989:ARG:NH1	1:B:1094:ARG:HE	1.71	0.87
1:D:1101:ARG:NH1	1:D:1106:GLY:HA2	1.93	0.83
1:A:1131:ASP:HB2	1:A:1153:VAL:HG23	1.62	0.82
1:C:1065:MET:HE2	1:C:1177:VAL:CG1	2.13	0.78
1:D:1080:CYS:SG	5:D:548:HOH:O	2.40	0.78
1:A:1151:GLY:O	1:A:1152:GLU:HG2	1.85	0.76
1:A:1050:ARG:HH12	1:A:1060:LEU:HD12	1.50	0.74
1:D:1050:ARG:NH2	1:D:1060:LEU:HD12	2.05	0.70
1:B:1083:ASN:O	1:C:1055:LYS:HE3	1.94	0.68
1:A:990:ILE:HD12	1:A:990:ILE:O	1.94	0.67
1:B:1065:MET:HE2	1:B:1177:VAL:HG11	1.75	0.67
1:A:1050:ARG:NH1	1:A:1060:LEU:HD12	2.09	0.66
1:D:1117:PRO:HB3	1:D:1199:ARG:HA	1.78	0.65
1:B:1034:ILE:HD12	1:B:1035:ASP:N	2.12	0.65
1:D:1101:ARG:HH12	1:D:1106:GLY:HA2	1.62	0.65
1:D:1131:ASP:OD1	3:D:4:E72:HAZA	1.96	0.64
1:A:1065:MET:HE3	1:A:1198:THR:HA	1.80	0.64
1:D:1048:SER:O	1:D:1049:MET:HB2	1.98	0.63
1:B:1048:SER:O	1:B:1049:MET:HB2	2.00	0.60
1:B:1062:GLU:OE1	1:B:1062:GLU:N	2.31	0.60
1:B:1139:GLU:HG2	1:B:1159:ARG:HD3	1.84	0.58
1:A:1048:SER:O	1:A:1049:MET:HB2	2.02	0.57
1:B:1001:GLU:HG3	1:B:1101:ARG:NH2	2.20	0.57
1:A:1221:LYS:HB2	1:A:1221:LYS:NZ	2.19	0.57
1:D:1133:GLU:O	1:D:1136:VAL:HG22	2.04	0.56
1:B:1103:ARG:C	1:B:1105:MET:H	2.13	0.56
1:C:1128:LEU:HD21	1:C:1190:PHE:CD1	2.41	0.56
1:B:1131:ASP:OD2	3:B:2:E72:HAZA	2.05	0.56
1:C:1121:VAL:HG21	1:C:1176:LEU:HD21	1.88	0.55
1:C:1232:CYS:SG	1:C:1235:SER:HB3	2.47	0.54
1:D:1101:ARG:HH11	1:D:1106:GLY:HA2	1.73	0.54
1:D:1110:ARG:HB2	1:D:1205:GLU:O	2.07	0.54
1:A:1152:GLU:O	1:A:1152:GLU:HG3	2.08	0.54
1:D:990:ILE:HD11	1:D:1093:LEU:HD13	1.90	0.54
1:A:1103:ARG:C	1:A:1105:MET:H	2.16	0.54
1:B:1140:ASP:O	3:B:2:E72:HAMA	2.07	0.54
1:B:1221:LYS:C	1:B:1222:LEU:HD12	2.33	0.54
1:D:988:GLU:HB3	1:D:1093:LEU:HD12	1.90	0.53
1:B:1232:CYS:SG	1:B:1235:SER:HB3	2.49	0.53
1:B:1042:CYS:O	1:B:1046:GLN:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1048:SER:O	1:C:1049:MET:HB2	2.08	0.53
1:C:989:ARG:HD3	1:C:1093:LEU:O	2.08	0.52
1:B:1217:ASP:O	1:B:1221:LYS:HE2	2.08	0.52
1:D:990:ILE:HD12	1:D:990:ILE:O	2.10	0.52
1:A:979:VAL:HG23	1:A:1003:CYS:HB2	1.91	0.52
1:D:1048:SER:C	1:D:1050:ARG:H	2.18	0.52
1:D:1215:PHE:HB2	3:D:4:E72:HBC	1.92	0.52
1:D:992:ILE:HD11	1:D:1093:LEU:HD11	1.92	0.51
1:A:990:ILE:HD12	1:A:990:ILE:C	2.34	0.51
1:A:1140:ASP:OD2	3:A:1236:E72:HAC	2.11	0.51
1:B:1104:ASP:OD2	1:B:1226:ARG:NE	2.41	0.51
1:C:1131:ASP:HB2	1:C:1153:VAL:HG23	1.92	0.51
1:C:980:SER:HB3	1:C:994:CYS:HB3	1.93	0.51
1:B:989:ARG:HH12	1:B:1094:ARG:HH21	1.57	0.50
1:A:1048:SER:O	1:A:1049:MET:CB	2.60	0.49
1:C:1033:CYS:HB3	1:C:1035:ASP:OD1	2.12	0.49
1:D:999:ASP:OD1	1:D:1001:GLU:HB2	2.12	0.49
1:D:1121:VAL:HG21	1:D:1176:LEU:HD21	1.94	0.49
1:A:1065:MET:CE	1:A:1198:THR:HA	2.43	0.49
1:A:1221:LYS:HB2	1:A:1221:LYS:HZ2	1.77	0.49
1:C:990:ILE:HG23	1:C:991:PRO:HD2	1.93	0.49
1:B:1065:MET:HE2	1:B:1177:VAL:CG1	2.41	0.48
1:A:1152:GLU:O	1:A:1152:GLU:CG	2.60	0.48
1:B:1131:ASP:OD2	3:B:2:E72:HAVA	2.14	0.48
1:D:1033:CYS:SG	1:D:1042:CYS:HA	2.53	0.48
1:B:1034:ILE:HD12	1:B:1034:ILE:C	2.39	0.48
1:D:1128:LEU:HD21	1:D:1190:PHE:CD1	2.48	0.48
1:B:1170:HIS:CE1	1:B:1216:TRP:HE1	2.32	0.48
1:B:1063:PHE:CD2	1:B:1065:MET:HE3	2.49	0.47
1:D:1171:HIS:O	1:D:1174:PRO:HD3	2.14	0.47
1:B:1032:VAL:HA	1:B:1079:SER:OG	2.15	0.47
1:D:1034:ILE:HD12	1:D:1034:ILE:C	2.40	0.47
1:B:1225:CYS:HB2	1:B:1234:HIS:HB2	1.97	0.46
1:D:1054:ASP:OD1	1:D:1056:ASP:N	2.49	0.46
1:C:1065:MET:CE	1:C:1177:VAL:HG11	2.33	0.46
1:A:982:ASP:HB3	1:B:1081:TRP:CH2	2.52	0.45
1:B:1110:ARG:HD3	1:B:1204:GLY:HA2	1.99	0.45
1:A:1140:ASP:O	3:A:1236:E72:HAMA	2.17	0.44
1:D:1054:ASP:OD1	1:D:1054:ASP:C	2.60	0.44
1:B:1063:PHE:HD2	1:B:1065:MET:HE3	1.83	0.44
1:A:981:ARG:HD2	1:C:1117:PRO:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1114:ASP:OD1	1:B:1202:GLU:HA	2.18	0.43
1:A:1064:ASN:ND2	1:A:1067:GLU:HB3	2.32	0.43
1:D:1117:PRO:HB3	1:D:1199:ARG:CA	2.46	0.43
1:D:1158:ALA:HA	1:D:1161:TYR:O	2.19	0.43
1:C:1048:SER:O	1:C:1049:MET:CB	2.66	0.43
1:D:1114:ASP:OD1	1:D:1202:GLU:HA	2.18	0.43
1:C:1065:MET:HG3	1:C:1177:VAL:HG11	2.01	0.43
1:A:1001:GLU:HA	1:A:1002:PRO:HD3	1.91	0.43
1:B:1170:HIS:HB2	1:B:1211:TYR:CG	2.54	0.42
1:D:1001:GLU:HG3	1:D:1101:ARG:HH21	1.83	0.42
1:D:1140:ASP:O	3:D:4:E72:HAMA	2.19	0.42
1:A:1146:LEU:C	1:A:1180:ARG:HH22	2.28	0.42
1:B:1117:PRO:HG3	1:B:1199:ARG:C	2.44	0.42
1:A:1064:ASN:HD21	1:A:1067:GLU:HB3	1.84	0.42
1:A:1221:LYS:NZ	1:A:1221:LYS:CB	2.83	0.42
1:A:1128:LEU:HD21	1:A:1190:PHE:CD1	2.55	0.42
1:C:999:ASP:HB2	1:C:1000:SER:H	1.71	0.42
1:C:1001:GLU:OE1	1:C:1001:GLU:HA	2.20	0.42
1:C:1183:MET:HE3	1:C:1192:ARG:HD3	2.02	0.42
1:B:1115:ILE:HB	1:B:1201:ILE:HB	2.02	0.42
1:C:1093:LEU:HD12	5:C:33:HOH:O	2.20	0.41
1:C:1146:LEU:O	1:C:1147:ASP:C	2.62	0.41
1:D:998:VAL:HG12	1:D:999:ASP:N	2.35	0.41
1:D:1145:ASP:OD2	1:D:1214:ARG:HD2	2.20	0.41
4:D:104:SAH:HG2	4:D:104:SAH:O4'	2.21	0.41
1:B:1117:PRO:HG3	1:B:1200:LEU:N	2.34	0.41
1:D:1032:VAL:HA	1:D:1079:SER:OG	2.20	0.41
1:A:980:SER:HB3	1:A:994:CYS:HB3	2.02	0.41
1:A:979:VAL:CG2	1:A:1003:CYS:HB2	2.49	0.41
1:A:1015:VAL:HG12	1:A:1128:LEU:HB3	2.03	0.41
1:A:1121:VAL:HG21	1:A:1176:LEU:HD21	2.03	0.41
1:C:1117:PRO:HG3	1:C:1200:LEU:N	2.36	0.41
1:C:1136:VAL:HA	3:C:1236:E72:HBJ	2.03	0.41
1:C:1158:ALA:HA	1:C:1161:TYR:O	2.20	0.41
1:B:1048:SER:O	1:B:1049:MET:CB	2.65	0.41
1:D:1049:MET:O	1:D:1050:ARG:HB2	2.20	0.41
1:D:1059:LEU:HD11	1:D:1196:PHE:CG	2.55	0.41
1:D:1107:TRP:O	4:D:104:SAH:N	2.54	0.41
1:B:1001:GLU:HA	1:B:1002:PRO:HD3	1.80	0.40
1:B:1136:VAL:HA	3:B:2:E72:HBJ	2.03	0.40
1:A:1146:LEU:C	1:A:1180:ARG:NH2	2.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1215:PHE:HB2	3:A:1236:E72:HBC	2.04	0.40
1:B:1098:GLN:OE1	1:B:1110:ARG:NH1	2.52	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	251/285 (88%)	235 (94%)	13 (5%)	3 (1%)	10	5
1	B	254/285 (89%)	239 (94%)	14 (6%)	1 (0%)	30	26
1	C	254/285 (89%)	237 (93%)	16 (6%)	1 (0%)	30	26
1	D	252/285 (88%)	231 (92%)	19 (8%)	2 (1%)	16	9
All	All	1011/1140 (89%)	942 (93%)	62 (6%)	7 (1%)	18	13

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1105	MET
1	A	1049	MET
1	C	1049	MET
1	A	1104	ASP
1	A	1152	GLU
1	B	1049	MET
1	D	998	VAL

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	221/257 (86%)	220 (100%)	1 (0%)	81	86
1	B	225/257 (88%)	223 (99%)	2 (1%)	70	77
1	C	225/257 (88%)	223 (99%)	2 (1%)	70	77
1	D	220/257 (86%)	220 (100%)	0	100	100
All	All	891/1028 (87%)	886 (99%)	5 (1%)	78	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1221	LYS
1	B	1065	MET
1	B	1104	ASP
1	C	1055	LYS
1	C	1065	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1046	GLN
1	A	1064	ASN
1	A	1086	ASN
1	B	1234	HIS
1	C	1113	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 22 ligands modelled in this entry, 16 are monoatomic - leaving 6 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
3	E72	D	4	-	40,41,41	1.26	4 (10%)	51,52,52	1.75	13 (25%)
4	SAH	D	104	-	27,28,28	1.24	4 (14%)	36,40,40	2.28	9 (25%)
3	E72	C	1236	-	40,41,41	1.19	4 (10%)	51,52,52	1.76	10 (19%)
3	E72	B	2	-	40,41,41	1.24	4 (10%)	51,52,52	1.66	11 (21%)
3	E72	A	1236	-	40,41,41	1.22	4 (10%)	51,52,52	1.70	10 (19%)
4	SAH	C	103	-	27,28,28	3.97	21 (77%)	36,40,40	2.77	20 (55%)

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	E72	D	4	-	-	10/26/36/36	0/3/3/3
4	SAH	D	104	-	-	2/15/31/31	0/3/3/3
3	E72	C	1236	-	-	8/26/36/36	0/3/3/3
3	E72	B	2	-	-	13/26/36/36	0/3/3/3
3	E72	A	1236	-	-	8/26/36/36	0/3/3/3
4	SAH	C	103	-	-	2/15/31/31	0/3/3/3

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	103	SAH	C4-N9	-7.20	1.22	1.37
4	C	103	SAH	C8-N9	-6.71	1.26	1.37
4	C	103	SAH	O3'-C3'	-6.70	1.26	1.43
4	C	103	SAH	C5-N7	-6.03	1.28	1.39
4	C	103	SAH	C3'-C4'	-5.16	1.39	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	103	SAH	C2'-C3'	-5.15	1.39	1.53
4	C	103	SAH	CG-SD	-4.74	1.63	1.81
4	C	103	SAH	C1'-N9	-4.50	1.33	1.46
4	C	103	SAH	O4'-C1'	-4.40	1.31	1.42
4	C	103	SAH	C8-N7	-4.32	1.23	1.31
4	C	103	SAH	C2-N1	-4.04	1.26	1.33
3	B	2	E72	CAF-CAA	3.91	1.43	1.36
3	C	1236	E72	CAF-CAA	3.74	1.43	1.36
3	A	1236	E72	CAF-CAA	3.69	1.43	1.36
3	D	4	E72	CAC-CAB	3.66	1.43	1.36
4	C	103	SAH	C2-N3	-3.61	1.27	1.33
4	C	103	SAH	O4'-C4'	-3.59	1.37	1.45
3	D	4	E72	CAF-CAA	3.48	1.42	1.36
3	B	2	E72	CAC-CAB	3.47	1.42	1.36
3	A	1236	E72	CAC-CAB	3.37	1.42	1.36
4	D	104	SAH	OXT-C	3.35	1.41	1.30
4	C	103	SAH	C6-N6	-3.34	1.25	1.34
4	C	103	SAH	C4-N3	-3.27	1.28	1.34
4	C	103	SAH	C5-C4	-3.27	1.33	1.39
4	D	104	SAH	C5-N7	-3.23	1.33	1.39
3	C	1236	E72	C6-C5	-3.16	1.40	1.44
4	C	103	SAH	C5'-SD	-3.14	1.68	1.81
3	B	2	E72	C6-N1	3.11	1.37	1.33
3	A	1236	E72	C6-N1	3.11	1.37	1.33
3	D	4	E72	C6-N1	3.08	1.37	1.33
3	A	1236	E72	C6-C5	-3.07	1.41	1.44
3	C	1236	E72	CAC-CAB	3.05	1.42	1.36
3	B	2	E72	C6-C5	-2.86	1.41	1.44
3	D	4	E72	C6-C5	-2.82	1.41	1.44
4	C	103	SAH	C6-N1	-2.69	1.28	1.35
3	C	1236	E72	C6-N1	2.64	1.36	1.33
4	D	104	SAH	C8-N9	-2.59	1.33	1.37
4	C	103	SAH	C5'-C4'	2.46	1.62	1.52
4	D	104	SAH	C4-N9	-2.45	1.32	1.37
4	C	103	SAH	O2'-C2'	-2.06	1.37	1.43
4	C	103	SAH	O-C	-2.05	1.16	1.22

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	104	SAH	OXT-C-O	-7.69	106.64	124.08
4	C	103	SAH	C5-C4-N3	-5.37	119.32	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	104	SAH	C5-C4-N3	-5.16	119.62	126.72
4	C	103	SAH	C4-C5-N7	-5.02	104.84	110.58
4	D	104	SAH	N3-C2-N1	-4.69	121.48	128.58
4	C	103	SAH	C2-N3-C4	4.40	122.59	111.83
4	C	103	SAH	O3'-C3'-C2'	-4.29	98.06	111.82
3	C	1236	E72	CAC-C5-C6	-4.26	121.38	124.84
4	C	103	SAH	N3-C2-N1	-4.23	122.18	128.58
3	A	1236	E72	CAC-C5-C6	-4.08	121.52	124.84
3	C	1236	E72	OAL-CAB-CAC	-4.00	120.09	125.16
3	D	4	E72	CAC-C5-C6	-3.99	121.59	124.84
3	C	1236	E72	C6-C5-C4	3.98	118.21	115.86
4	C	103	SAH	O4'-C1'-N9	-3.98	100.45	108.09
3	B	2	E72	CAC-C5-C6	-3.96	121.62	124.84
3	D	4	E72	C6-C5-C4	3.87	118.14	115.86
4	C	103	SAH	C6-C5-N7	3.87	139.55	132.09
4	C	103	SAH	CB-CG-SD	3.85	122.05	113.45
3	B	2	E72	N3-C2-N1	-3.84	119.96	126.25
3	D	4	E72	N3-C2-N1	-3.80	120.03	126.25
3	A	1236	E72	C6-C5-C4	3.75	118.08	115.86
4	D	104	SAH	N3-C4-N9	3.74	133.53	127.17
3	A	1236	E72	N3-C2-N1	-3.74	120.13	126.25
3	B	2	E72	C6-C5-C4	3.73	118.06	115.86
3	C	1236	E72	N3-C2-N1	-3.71	120.18	126.25
3	A	1236	E72	CAM-OAL-CAB	-3.65	112.16	117.51
3	D	4	E72	C2-N3-C4	3.63	121.29	115.54
3	B	2	E72	C2-N3-C4	3.62	121.28	115.54
3	A	1236	E72	OAL-CAB-CAC	-3.55	120.66	125.16
4	D	104	SAH	N9-C8-N7	-3.51	108.95	113.94
3	D	4	E72	OAL-CAB-CAC	-3.51	120.71	125.16
3	A	1236	E72	C2-N3-C4	3.51	121.10	115.54
4	D	104	SAH	C2-N3-C4	3.51	120.40	111.83
4	C	103	SAH	C5-N7-C8	3.48	108.91	103.45
3	D	4	E72	OAK-CAA-CAF	-3.46	119.52	125.20
4	C	103	SAH	OXT-C-O	-3.39	116.38	124.08
3	C	1236	E72	C2-N3-C4	3.39	120.92	115.54
3	C	1236	E72	CAM-OAL-CAB	-3.32	112.64	117.51
4	C	103	SAH	N3-C4-N9	3.32	132.81	127.17
3	C	1236	E72	OAL-CAB-CAA	3.32	119.90	115.40
3	B	2	E72	CAM-OAL-CAB	-3.31	112.66	117.51
3	D	4	E72	OAL-CAB-CAA	3.25	119.82	115.40
4	C	103	SAH	N6-C6-N1	-3.18	111.30	118.38
4	C	103	SAH	N9-C8-N7	-3.17	109.44	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	103	SAH	C4-N9-C8	3.11	109.00	105.74
3	C	1236	E72	OAK-CAA-CAF	-3.10	120.11	125.20
3	C	1236	E72	C5-C4-N3	-3.07	119.55	122.80
3	D	4	E72	CAM-OAL-CAB	-3.04	113.06	117.51
4	D	104	SAH	C5-N7-C8	3.02	108.19	103.45
3	B	2	E72	OAL-CAB-CAC	-3.01	121.34	125.16
3	B	2	E72	C5-C4-N3	-2.99	119.64	122.80
3	A	1236	E72	OAL-CAB-CAA	2.94	119.39	115.40
3	A	1236	E72	OAK-CAA-CAF	-2.90	120.43	125.20
4	C	103	SAH	O3'-C3'-C4'	-2.88	102.82	111.08
3	D	4	E72	C5-C4-N3	-2.81	119.82	122.80
4	D	104	SAH	C4-C5-N7	-2.80	107.38	110.58
3	A	1236	E72	C5-C4-N3	-2.79	119.85	122.80
4	D	104	SAH	C4-N9-C8	2.74	108.62	105.74
4	C	103	SAH	C5'-C4'-C3'	-2.71	108.28	115.06
3	B	2	E72	OAL-CAB-CAA	2.56	118.87	115.40
3	D	4	E72	CBB-OAK-CAA	-2.47	111.73	117.69
4	C	103	SAH	C4'-C5'-SD	2.38	122.29	113.78
4	C	103	SAH	O4'-C4'-C5'	2.33	114.84	108.83
4	C	103	SAH	O2'-C2'-C3'	-2.33	104.36	111.82
3	D	4	E72	NAU-C2-N1	2.31	121.15	117.16
3	B	2	E72	NAU-C2-N1	2.28	121.09	117.16
3	B	2	E72	OAK-CAA-CAF	-2.23	121.55	125.20
3	D	4	E72	OAK-CAA-CAB	2.20	120.30	115.75
3	A	1236	E72	C2-N1-C6	2.17	121.69	116.36
3	C	1236	E72	C2-N1-C6	2.12	121.57	116.36
4	C	103	SAH	C2'-C1'-N9	2.09	118.49	113.30
3	D	4	E72	C2-N1-C6	2.07	121.45	116.36
3	B	2	E72	C2-N1-C6	2.05	121.39	116.36

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1236	E72	CAA-CAB-OAL-CAM
3	B	2	E72	CAA-CAB-OAL-CAM
3	C	1236	E72	CAA-CAB-OAL-CAM
3	A	1236	E72	CAC-CAB-OAL-CAM
3	C	1236	E72	CAC-CAB-OAL-CAM
3	B	2	E72	CAW-CAX-NAY-CAZ
3	B	2	E72	CAC-CAB-OAL-CAM
3	D	4	E72	CAA-CAB-OAL-CAM

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Mol	Chain	Res	Type	Atoms
3	D	4	E72	CAC-CAB-OAL-CAM
3	C	1236	E72	NAR-CBH-CBI-CBJ
3	D	4	E72	CAV-CAW-CAX-NAY
3	B	2	E72	CBB-CBC-CBD-CBE
3	B	2	E72	NAR-CBH-CBI-CBJ
3	B	2	E72	CBC-CBD-CBE-CBF
3	B	2	E72	CAW-CAX-NAY-CBA
3	D	4	E72	CAW-CAX-NAY-CAZ
3	D	4	E72	CAB-CAA-OAK-CBB
3	D	4	E72	CBI-CBJ-CBK-CBL
3	B	2	E72	CAV-CAW-CAX-NAY
3	C	1236	E72	CAB-CAA-OAK-CBB
3	A	1236	E72	CAB-CAA-OAK-CBB
3	D	4	E72	CAF-CAA-OAK-CBB
3	B	2	E72	CAB-CAA-OAK-CBB
4	C	103	SAH	CA-CB-CG-SD
4	D	104	SAH	CA-CB-CG-SD
3	C	1236	E72	CAV-CAW-CAX-NAY
3	B	2	E72	CBI-CBH-NAR-CAQ
3	A	1236	E72	CAF-CAA-OAK-CBB
3	C	1236	E72	CAF-CAA-OAK-CBB
3	A	1236	E72	CBI-CBH-NAR-CAQ
3	B	2	E72	CAF-CAA-OAK-CBB
3	A	1236	E72	OAK-CBB-CBC-CBD
3	C	1236	E72	OAK-CBB-CBC-CBD
4	C	103	SAH	CB-CG-SD-C5'
3	B	2	E72	CBI-CBH-NAR-CAS
3	C	1236	E72	CBI-CBH-NAR-CAQ
3	A	1236	E72	CAV-CAW-CAX-NAY
3	A	1236	E72	CBI-CBH-NAR-CAS
3	D	4	E72	CBB-CBC-CBD-CBE
3	D	4	E72	CBJ-CBK-CBL-NBM
4	D	104	SAH	CB-CG-SD-C5'
3	B	2	E72	CBC-CBB-OAK-CAA
3	D	4	E72	CBI-CBH-NAR-CAQ

There are no ring outliers.

5 monomers are involved in 13 short contacts:

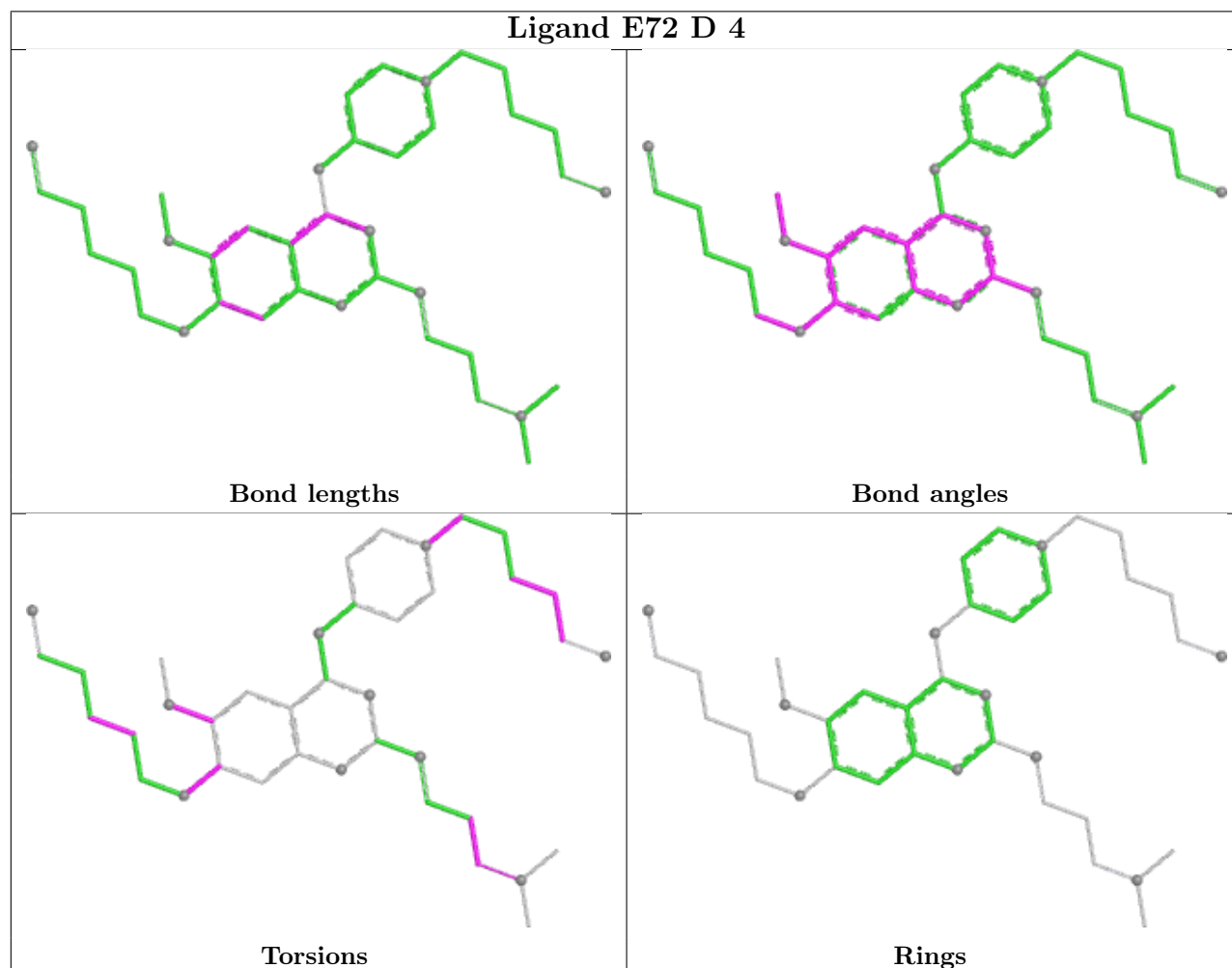
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	4	E72	3	0
4	D	104	SAH	2	0

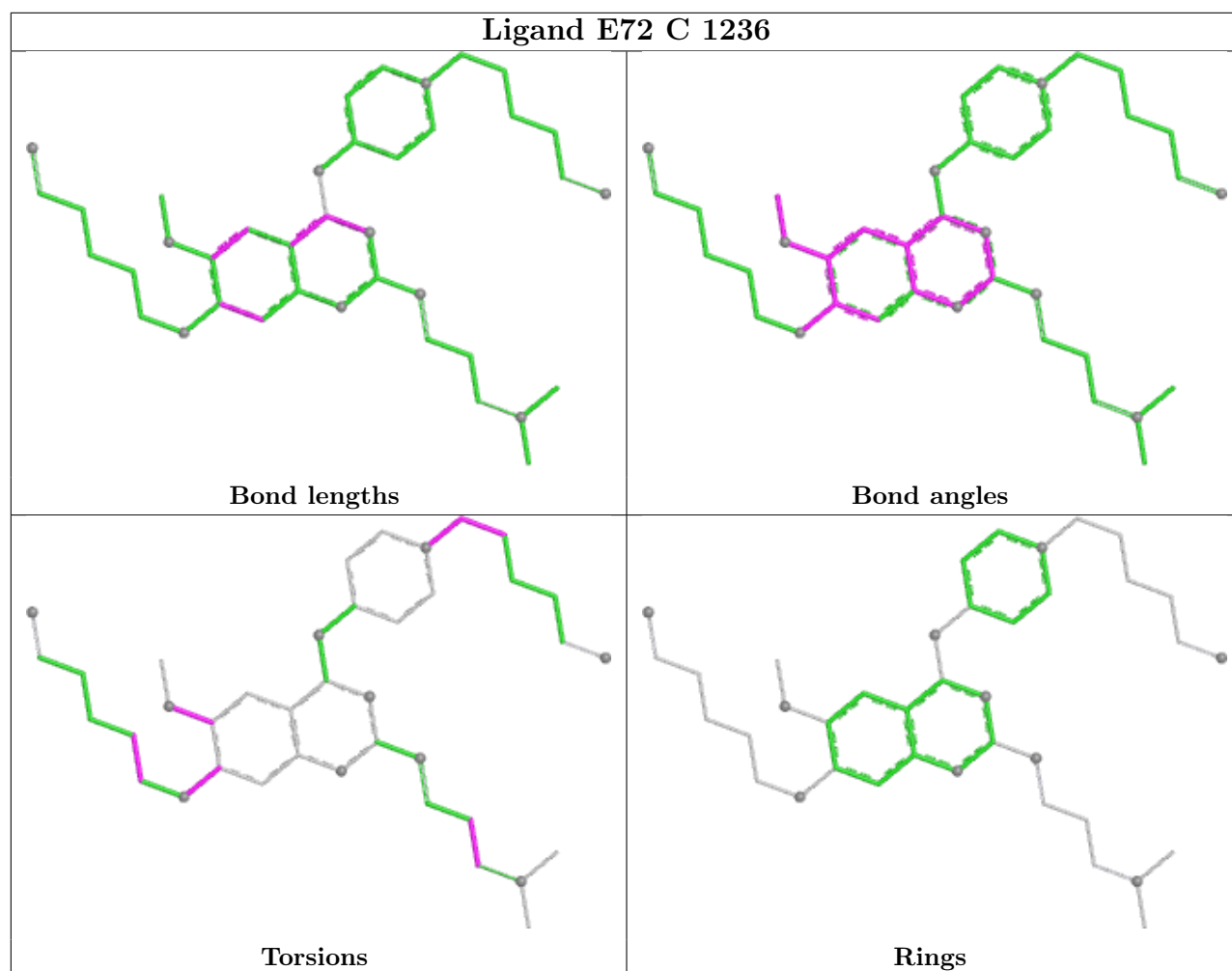
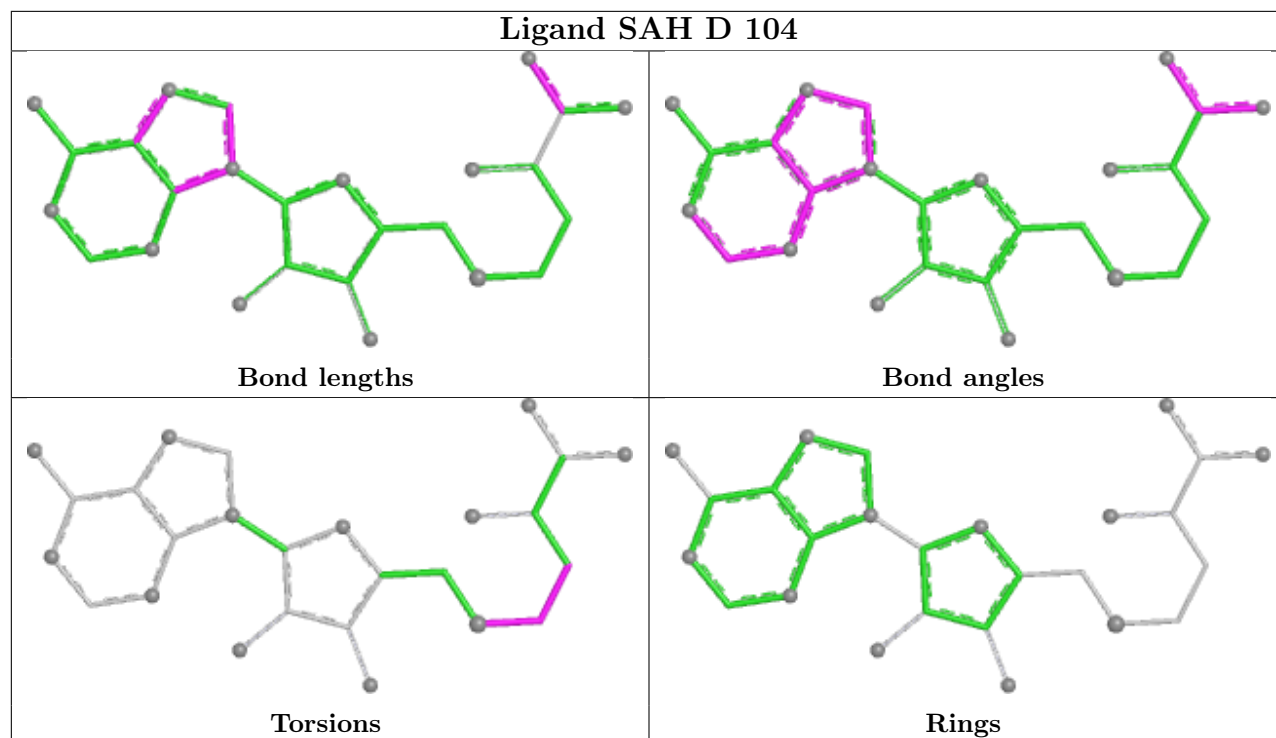
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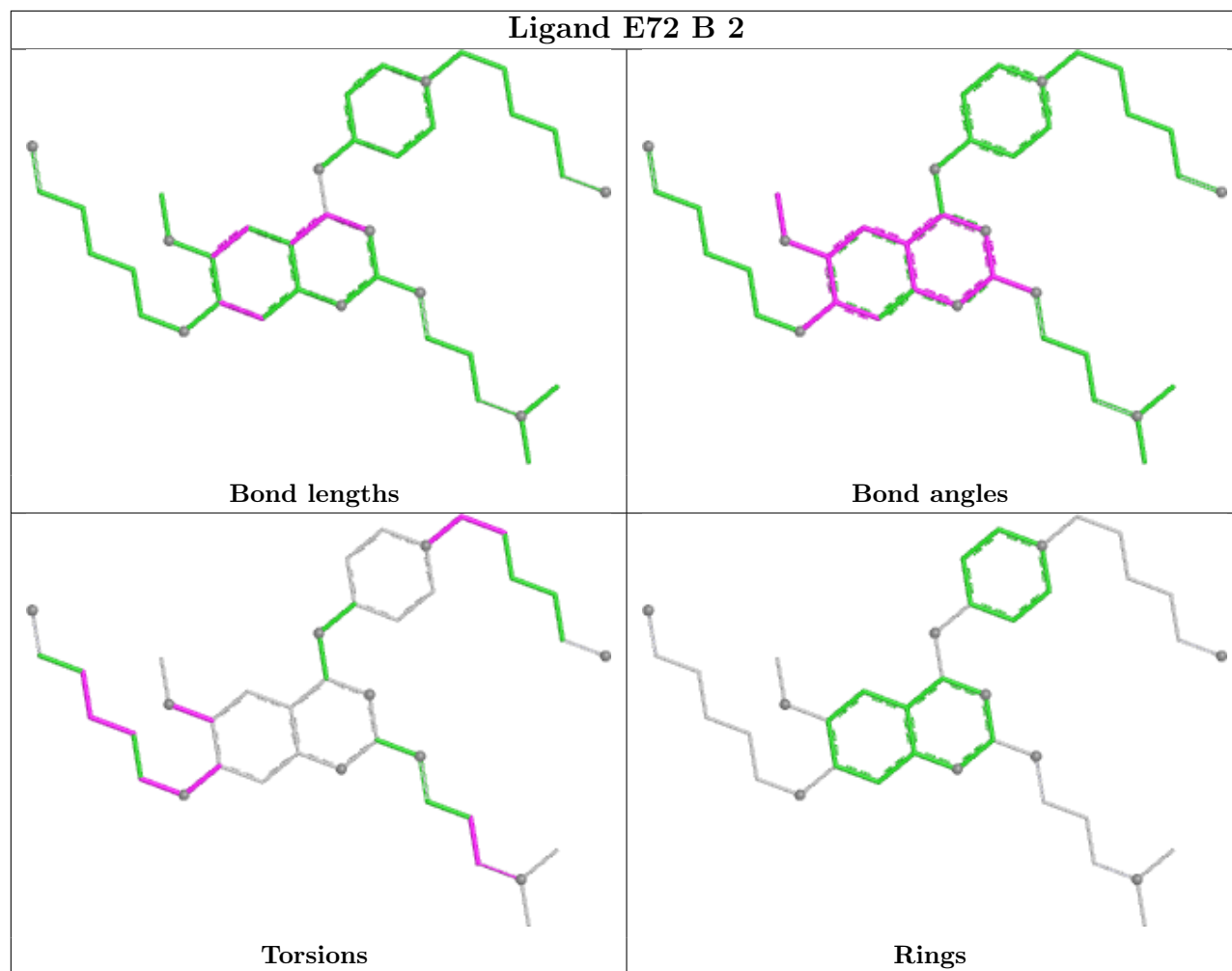
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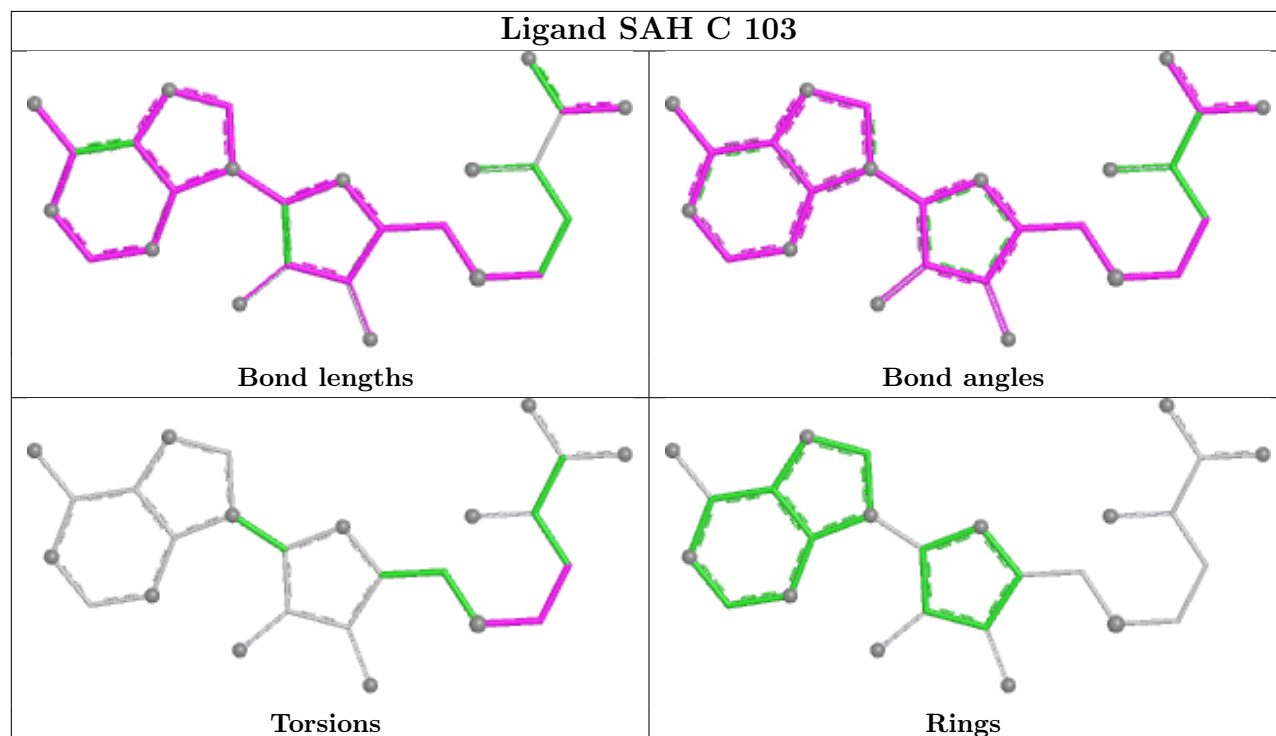
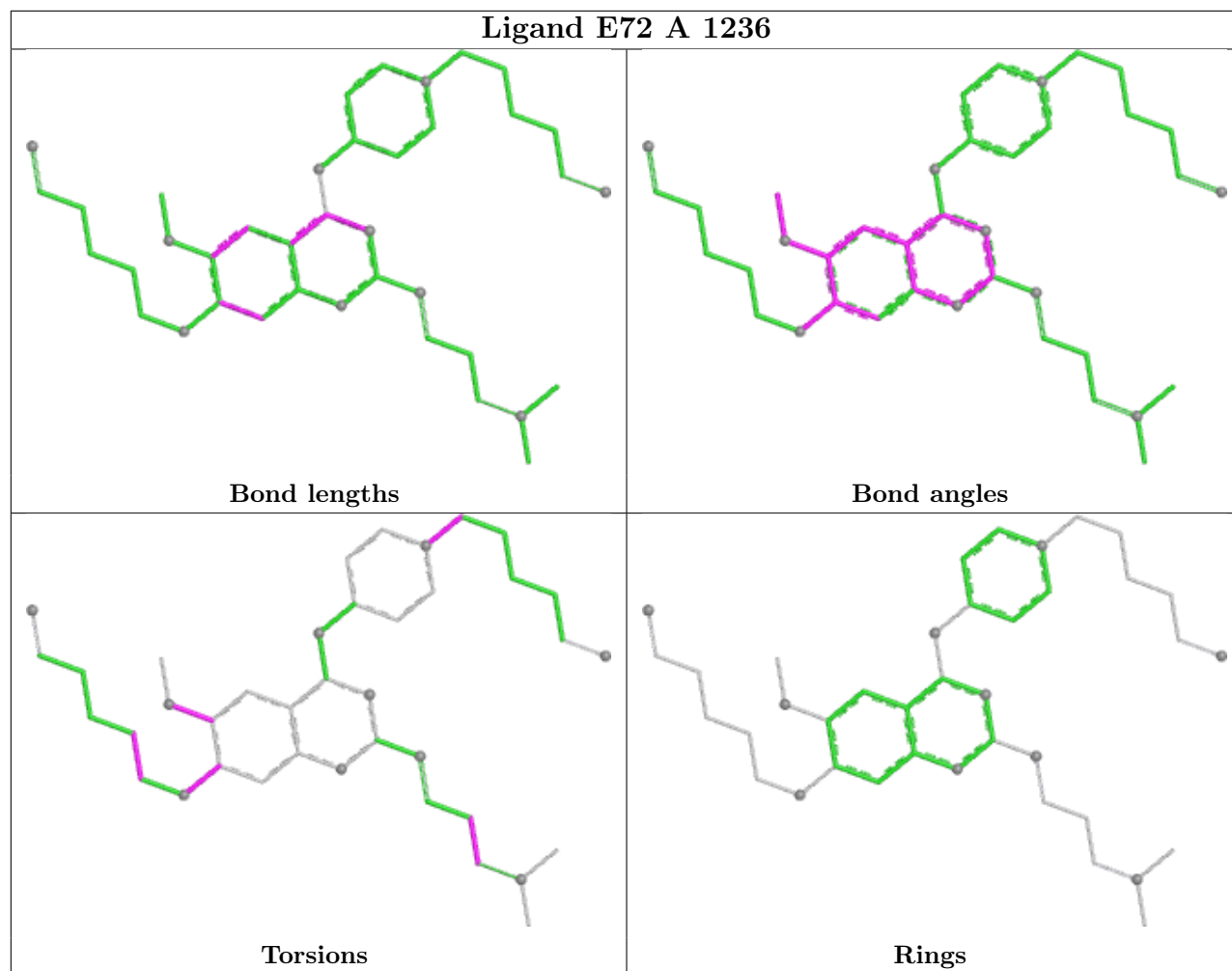
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1236	E72	1	0
3	B	2	E72	4	0
3	A	1236	E72	3	0

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	255/285 (89%)	0.03	9 (3%) 47 51	17, 32, 54, 59	0
1	B	258/285 (90%)	-0.03	5 (1%) 66 70	18, 31, 53, 69	0
1	C	258/285 (90%)	-0.07	2 (0%) 82 85	21, 32, 53, 58	0
1	D	256/285 (89%)	0.38	5 (1%) 65 69	26, 41, 61, 71	0
All	All	1027/1140 (90%)	0.07	21 (2%) 65 69	17, 34, 56, 71	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1104	ASP	3.4
1	A	1151	GLY	3.3
1	B	1148	ASN	2.9
1	D	977	ARG	2.9
1	C	1002	PRO	2.8
1	D	997	ALA	2.8
1	D	979	VAL	2.7
1	A	997	ALA	2.6
1	A	998	VAL	2.4
1	A	1235	SER	2.4
1	B	1105	MET	2.4
1	A	1003	CYS	2.3
1	A	1223	PHE	2.2
1	D	1138	GLU	2.2
1	C	1104	ASP	2.2
1	D	998	VAL	2.1
1	A	1106	GLY	2.1
1	B	1217	ASP	2.1
1	A	1222	LEU	2.1
1	B	997	ALA	2.1
1	B	1049	MET	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

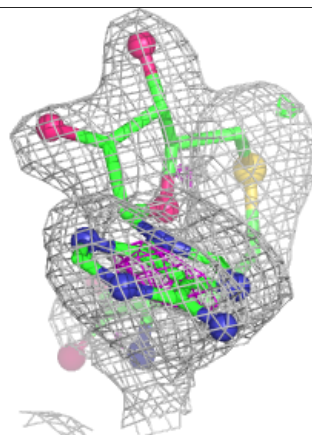
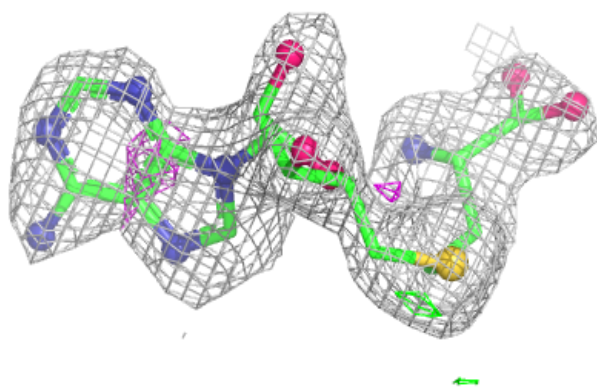
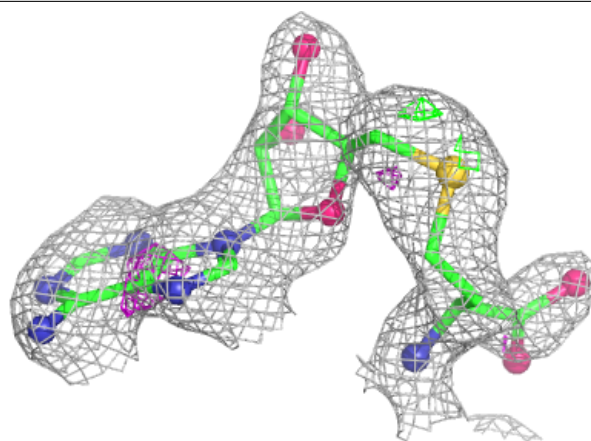
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SAH	D	104	26/26	0.83	0.15	62,68,69,70	0
4	SAH	C	103	26/26	0.87	0.12	50,56,58,59	0
3	E72	A	1236	39/39	0.90	0.11	38,43,51,52	0
3	E72	D	4	39/39	0.90	0.11	44,48,59,61	0
3	E72	C	1236	39/39	0.91	0.10	30,34,45,45	0
3	E72	B	2	39/39	0.92	0.10	31,36,45,47	0
2	ZN	A	4	1/1	0.96	0.04	41,41,41,41	0
2	ZN	D	7	1/1	0.97	0.03	39,39,39,39	0
2	ZN	D	8	1/1	0.97	0.04	49,49,49,49	0
2	ZN	B	8	1/1	0.98	0.03	41,41,41,41	0
2	ZN	D	6	1/1	0.98	0.04	34,34,34,34	0
2	ZN	A	1	1/1	0.99	0.02	22,22,22,22	0
2	ZN	B	5	1/1	0.99	0.01	28,28,28,28	0
2	ZN	B	7	1/1	0.99	0.02	28,28,28,28	0
2	ZN	A	2	1/1	0.99	0.02	18,18,18,18	0
2	ZN	C	1	1/1	0.99	0.02	27,27,27,27	0
2	ZN	C	2	1/1	0.99	0.03	28,28,28,28	0
2	ZN	C	3	1/1	0.99	0.03	28,28,28,28	0
2	ZN	C	4	1/1	0.99	0.03	39,39,39,39	0
2	ZN	D	5	1/1	0.99	0.02	35,35,35,35	0
2	ZN	A	3	1/1	1.00	0.01	20,20,20,20	0
2	ZN	B	6	1/1	1.00	0.03	27,27,27,27	0

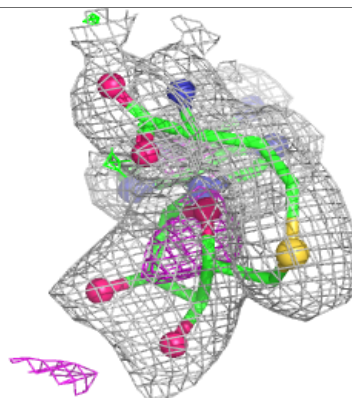
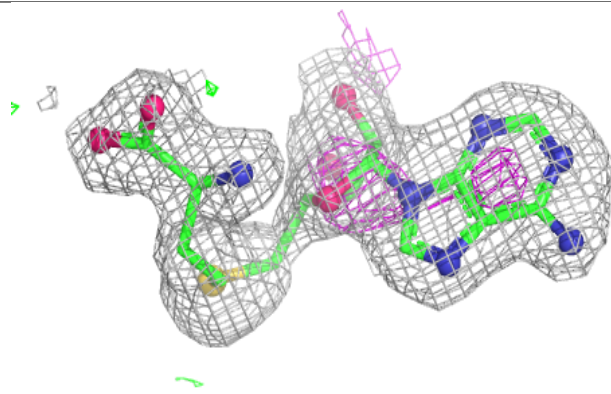
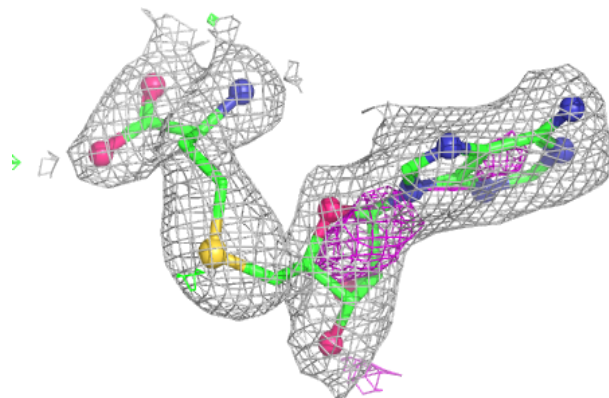
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

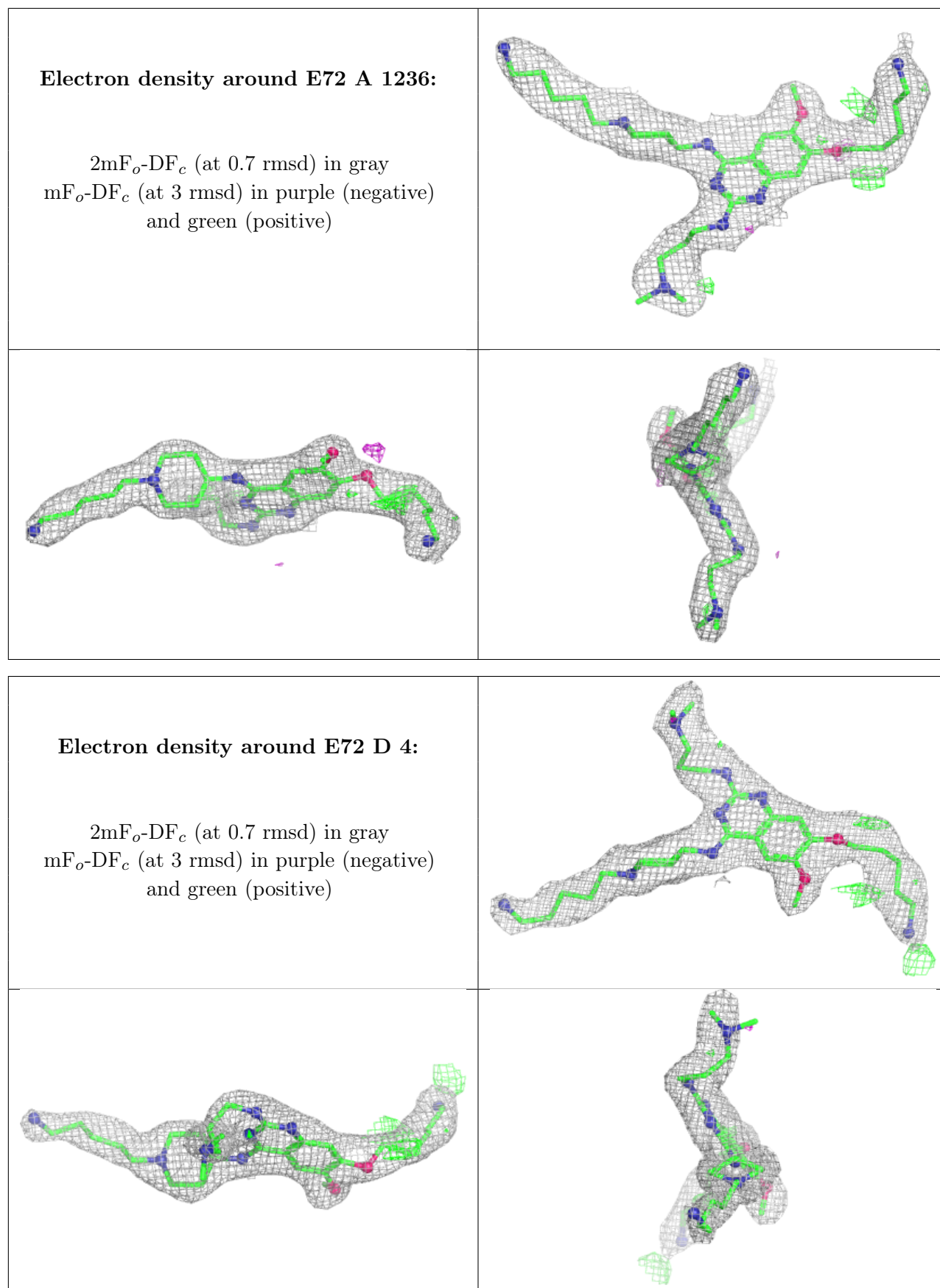
Electron density around SAH D 104:

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

**Electron density around SAH C 103:**

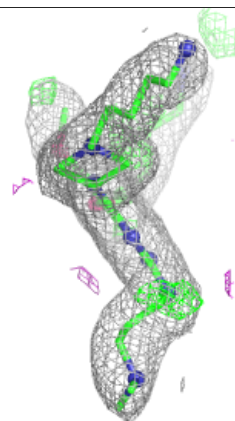
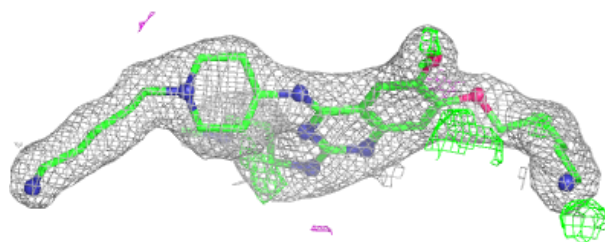
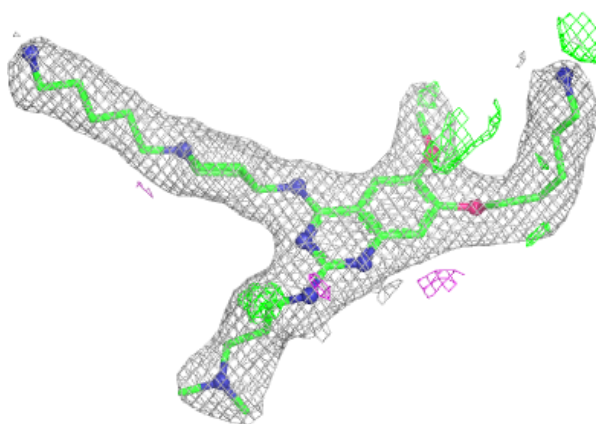
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



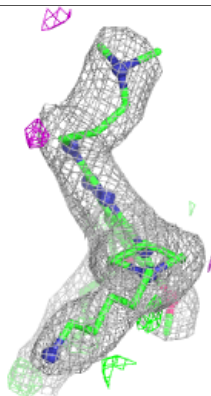
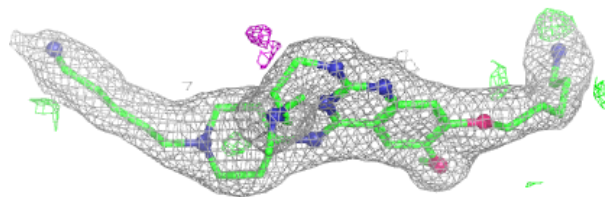
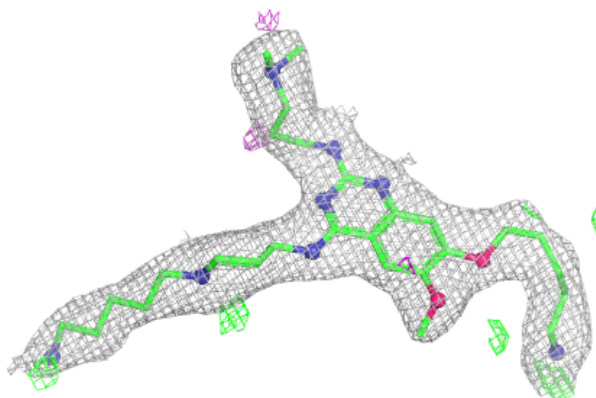


Electron density around E72 C 1236:

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

**Electron density around E72 B 2:**

$2mF_o-DF_c$ (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.