



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2024 – 04:46 AM EST

PDB ID : 3GMD
Title : Structure-based design of 7-Azaindole-pyrrolidines as inhibitors of 11beta-Hydroxysteroid-Dehydrogenase type I
Authors : Valeur, E.; Lepifre, F.; Roche, D.; Christmann-Franck, S.; Hillertz, P.; Musil, D.
Deposited on : 2009-03-13
Resolution : 2.28 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 : 1.8.5 (274361), 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

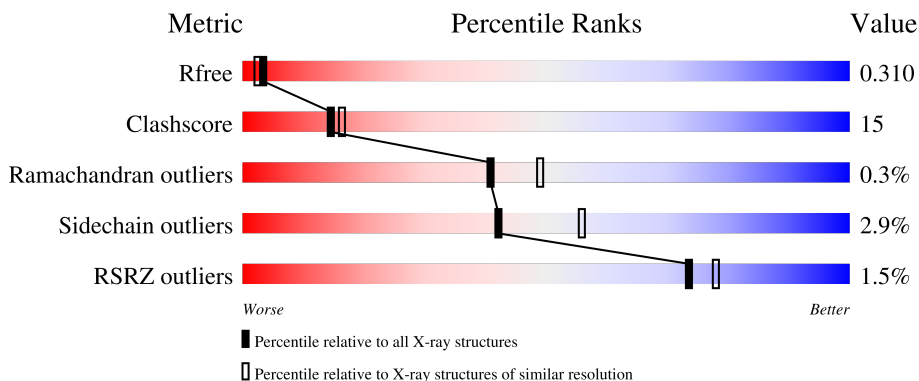
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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.



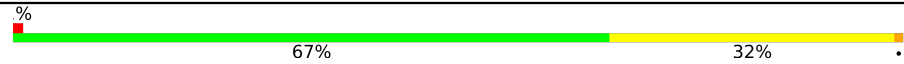


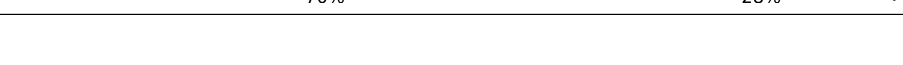
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	264	 2% 65% 34%
1	B	264	 3% 57% 41%
1	C	264	 0% 75% 23%
1	D	264	 2% 75% 23%

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Mol	Chain	Length	Quality of chain
1	E	264	 % 67% 32% .
1	F	264	 2% 69% 30% .
1	G	264	 66% 32% .
1	H	264	 2% 70% 28% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17364 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 Corticosteroid 11-beta-dehydrogenase isozyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	264	2025	1297	337	374	17	27	0	0
1	B	264	2025	1297	337	374	17	10	0	0
1	C	264	2025	1297	337	374	17	17	0	0
1	D	264	2025	1297	337	374	17	29	0	0
1	E	264	2025	1297	337	374	17	23	0	0
1	F	264	2025	1297	337	374	17	15	0	0
1	G	264	2025	1297	337	374	17	30	0	0
1	H	264	2025	1297	337	374	17	25	0	0

There are 48 discrepancies between the modelled and reference sequences:

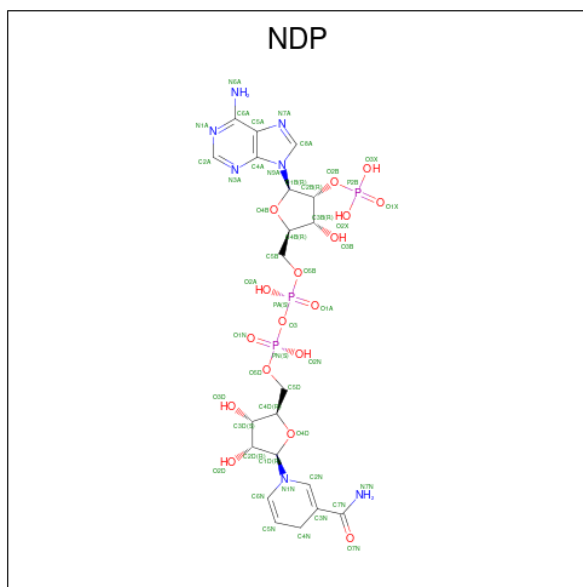
Chain	Residue	Modelled	Actual	Comment	Reference
A	175	VAL	MET	engineered mutation	UNP P50172
A	177	TYR	GLN	engineered mutation	UNP P50172
A	180	VAL	ILE	engineered mutation	UNP P50172
A	226	ALA	GLU	engineered mutation	UNP P50172
A	227	VAL	ILE	engineered mutation	UNP P50172
A	231	VAL	ILE	engineered mutation	UNP P50172
B	175	VAL	MET	engineered mutation	UNP P50172
B	177	TYR	GLN	engineered mutation	UNP P50172
B	180	VAL	ILE	engineered mutation	UNP P50172
B	226	ALA	GLU	engineered mutation	UNP P50172
B	227	VAL	ILE	engineered mutation	UNP P50172
B	231	VAL	ILE	engineered mutation	UNP P50172
C	175	VAL	MET	engineered mutation	UNP P50172

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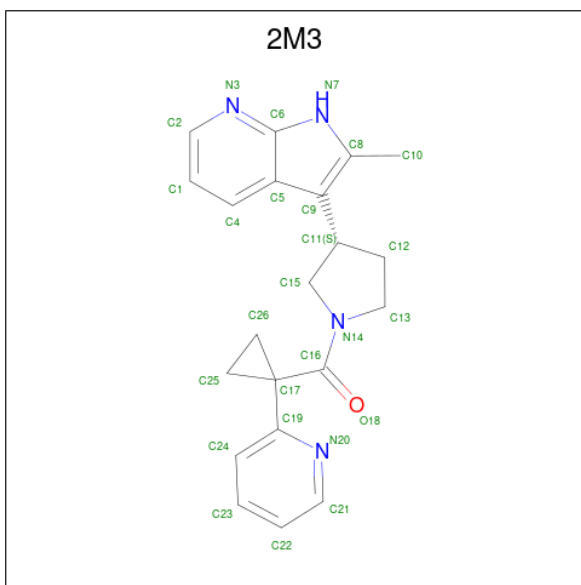
Chain	Residue	Modelled	Actual	Comment	Reference
C	177	TYR	GLN	engineered mutation	UNP P50172
C	180	VAL	ILE	engineered mutation	UNP P50172
C	226	ALA	GLU	engineered mutation	UNP P50172
C	227	VAL	ILE	engineered mutation	UNP P50172
C	231	VAL	ILE	engineered mutation	UNP P50172
D	175	VAL	MET	engineered mutation	UNP P50172
D	177	TYR	GLN	engineered mutation	UNP P50172
D	180	VAL	ILE	engineered mutation	UNP P50172
D	226	ALA	GLU	engineered mutation	UNP P50172
D	227	VAL	ILE	engineered mutation	UNP P50172
D	231	VAL	ILE	engineered mutation	UNP P50172
E	175	VAL	MET	engineered mutation	UNP P50172
E	177	TYR	GLN	engineered mutation	UNP P50172
E	180	VAL	ILE	engineered mutation	UNP P50172
E	226	ALA	GLU	engineered mutation	UNP P50172
E	227	VAL	ILE	engineered mutation	UNP P50172
E	231	VAL	ILE	engineered mutation	UNP P50172
F	175	VAL	MET	engineered mutation	UNP P50172
F	177	TYR	GLN	engineered mutation	UNP P50172
F	180	VAL	ILE	engineered mutation	UNP P50172
F	226	ALA	GLU	engineered mutation	UNP P50172
F	227	VAL	ILE	engineered mutation	UNP P50172
F	231	VAL	ILE	engineered mutation	UNP P50172
G	175	VAL	MET	engineered mutation	UNP P50172
G	177	TYR	GLN	engineered mutation	UNP P50172
G	180	VAL	ILE	engineered mutation	UNP P50172
G	226	ALA	GLU	engineered mutation	UNP P50172
G	227	VAL	ILE	engineered mutation	UNP P50172
G	231	VAL	ILE	engineered mutation	UNP P50172
H	175	VAL	MET	engineered mutation	UNP P50172
H	177	TYR	GLN	engineered mutation	UNP P50172
H	180	VAL	ILE	engineered mutation	UNP P50172
H	226	ALA	GLU	engineered mutation	UNP P50172
H	227	VAL	ILE	engineered mutation	UNP P50172
H	231	VAL	ILE	engineered mutation	UNP P50172

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	E	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	F	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	G	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	H	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is 2-methyl-3-[(3S)-1-[(1-pyridin-2-ylcyclopropyl)carbonyl]pyrrolidin-3-yl]-1H-pyrrolo[2,3-b]pyridine (three-letter code: 2M3) (formula: C₂₁H₂₂N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total	C	N	O	0	0
			26	21	4	1		
3	B	1	Total	C	N	O	0	0
			26	21	4	1		
3	C	1	Total	C	N	O	0	0
			26	21	4	1		
3	D	1	Total	C	N	O	0	0
			26	21	4	1		
3	E	1	Total	C	N	O	0	0
			26	21	4	1		
3	F	1	Total	C	N	O	0	0
			26	21	4	1		
3	G	1	Total	C	N	O	0	0
			26	21	4	1		
3	H	1	Total	C	N	O	0	0
			26	21	4	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	72	Total	O	0	0
			72	72		
5	B	56	Total	O	0	0
			56	56		
5	C	86	Total	O	0	0
			86	86		

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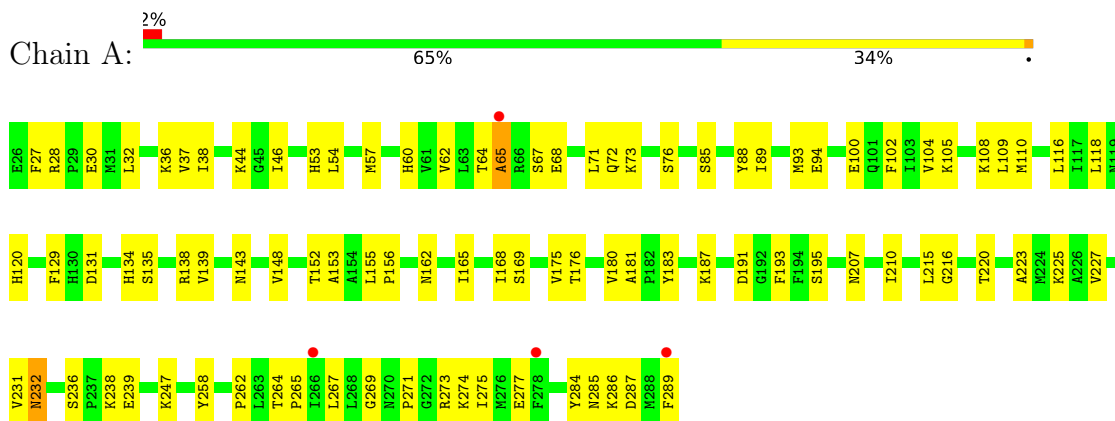
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	70	Total O 70 70	0	0
5	E	71	Total O 71 71	0	0
5	F	61	Total O 61 61	0	0
5	G	64	Total O 64 64	0	0
5	H	47	Total O 47 47	0	0

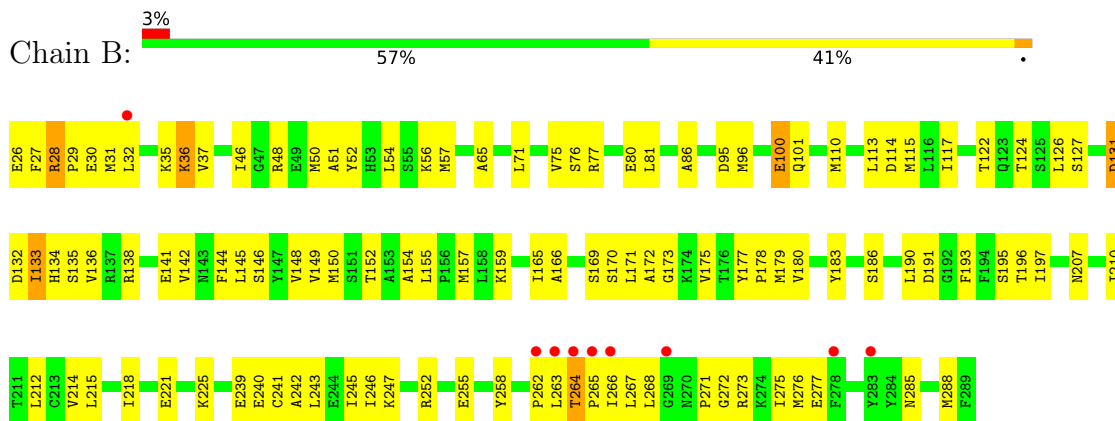
3 Residue-property plots [i](#)

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.

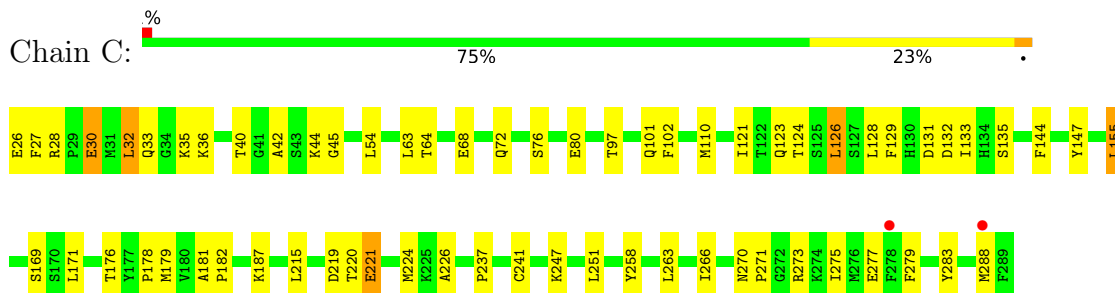
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



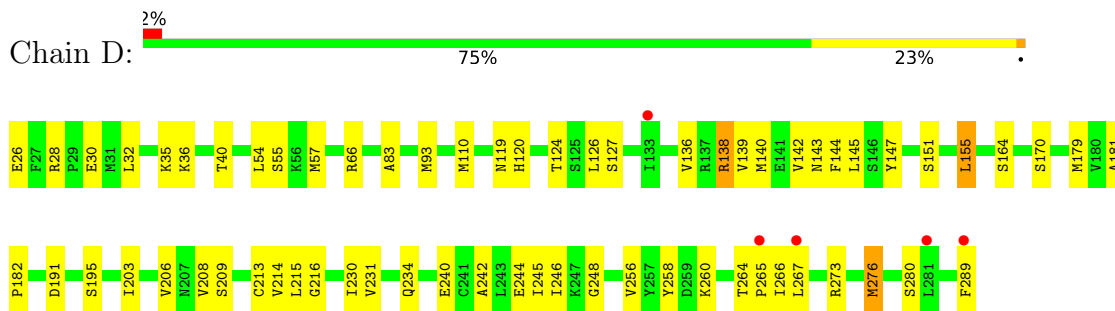
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



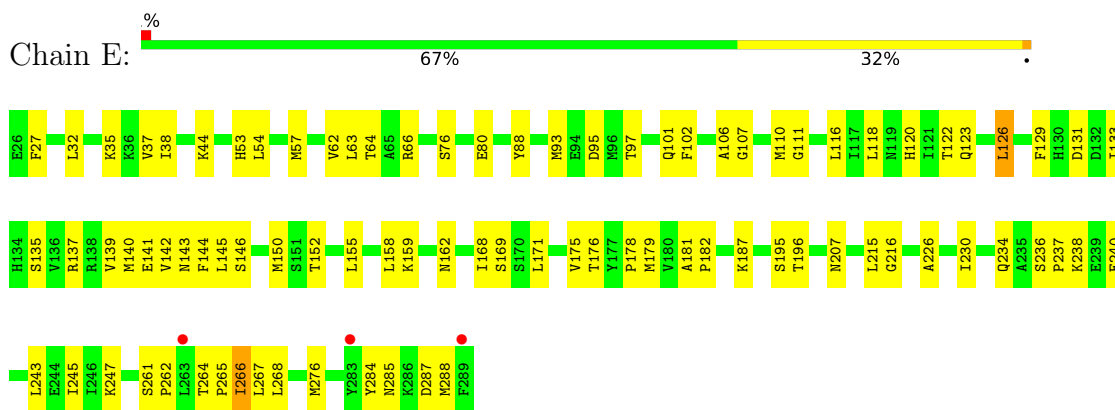
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



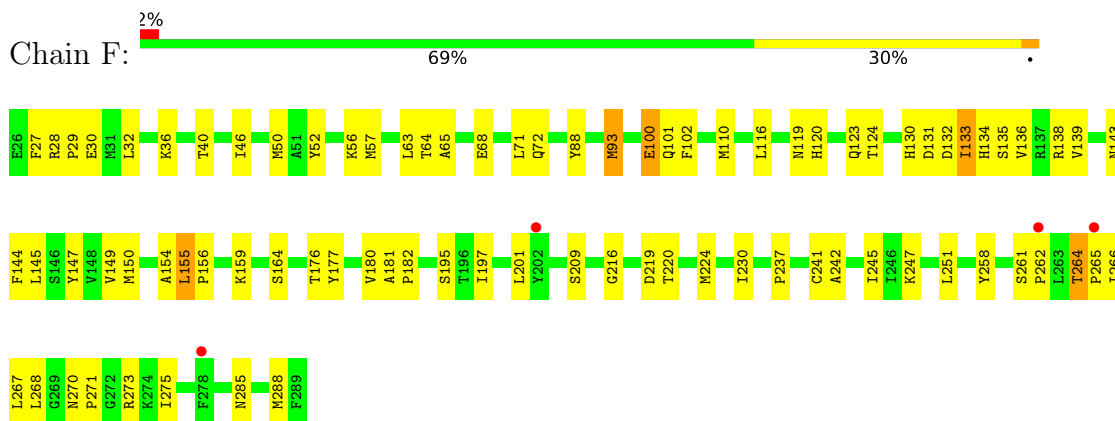
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



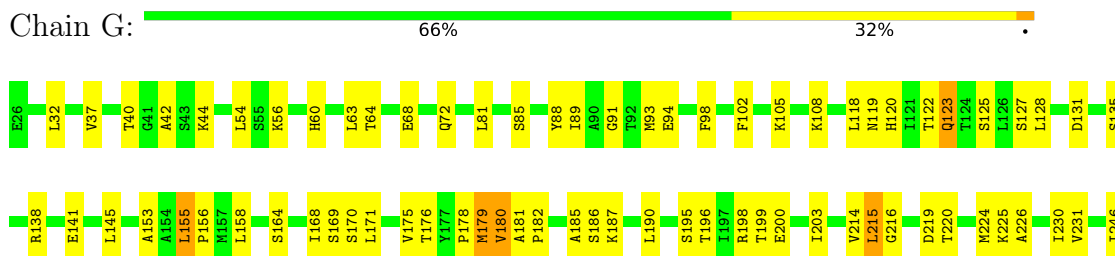
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1

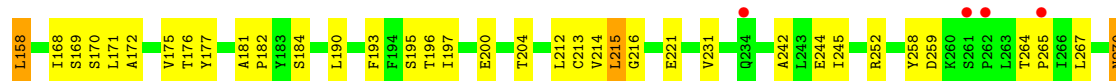
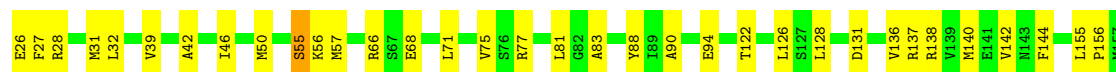


- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1





● Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	127.34Å 70.49Å 132.96Å 90.00° 91.78° 90.00°	Depositor
Resolution (Å)	70.00 – 2.28 48.35 – 2.28	Depositor EDS
% Data completeness (in resolution range)	95.4 (70.00-2.28) 95.9 (48.35-2.28)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.29Å)	Xtrriage
Refinement program	CNX	Depositor
R, R_{free}	0.252 , 0.306 0.261 , 0.310	Depositor DCC
R_{free} test set	1260 reflections (1.22%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtrriage
Anisotropy	1.260	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for l,k,-h 0.160 for h,-k,-l 0.006 for l,-k,h	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17364	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2618e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NDP, 2M3, SO4

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	0.33	0/2059	0.50	0/2775
1	B	0.32	0/2059	0.51	0/2775
1	C	0.37	0/2059	0.53	0/2775
1	D	0.36	0/2059	0.53	0/2775
1	E	0.39	0/2059	0.55	0/2775
1	F	0.35	0/2059	0.54	0/2775
1	G	0.33	0/2059	0.52	0/2775
1	H	0.33	0/2059	0.52	0/2775
All	All	0.35	0/16472	0.52	0/22200

There are no bond length outliers.

There are no bond angle outliers.

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	2025	0	2092	70	0
1	B	2025	0	2092	109	0
1	C	2025	0	2092	48	0
1	D	2025	0	2092	58	0
1	E	2025	0	2092	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2025	0	2092	64	0
1	G	2025	0	2092	79	0
1	H	2025	0	2092	66	0
2	A	48	0	26	2	0
2	B	48	0	26	2	0
2	C	48	0	26	0	0
2	D	48	0	26	3	0
2	E	48	0	26	4	0
2	F	48	0	26	3	0
2	G	48	0	26	4	0
2	H	48	0	26	2	0
3	A	26	0	22	0	0
3	B	26	0	22	5	0
3	C	26	0	22	5	0
3	D	26	0	22	3	0
3	E	26	0	22	3	0
3	F	26	0	22	4	0
3	G	26	0	22	2	0
3	H	26	0	22	1	0
4	B	5	0	0	1	0
4	C	10	0	0	1	0
4	D	5	0	0	0	0
4	E	5	0	0	1	0
4	F	5	0	0	0	0
4	G	5	0	0	0	0
4	H	10	0	0	0	0
5	A	72	0	0	2	0
5	B	56	0	0	2	0
5	C	86	0	0	2	0
5	D	70	0	0	2	0
5	E	71	0	0	5	0
5	F	61	0	0	0	0
5	G	64	0	0	2	0
5	H	47	0	0	0	0
All	All	17364	0	17120	516	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 15.

All (516) 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:E:133:ILE:HD11	1:F:145:LEU:HG	1.43	1.01
1:A:273:ARG:HG3	1:B:175:VAL:HG12	1.46	0.98
1:C:133:ILE:HD11	1:D:145:LEU:HG	1.52	0.91
1:B:36:LYS:HG3	1:B:110:MET:HB3	1.54	0.90
1:D:138:ARG:HH11	1:D:138:ARG:HG3	1.39	0.87
1:B:132:ASP:HB3	1:B:135:SER:HB2	1.56	0.85
1:D:26:GLU:HB3	1:H:252:ARG:HD3	1.58	0.85
1:C:181:ALA:HB3	1:C:182:PRO:HD3	1.59	0.84
1:E:238:LYS:HE3	5:E:396:HOH:O	1.78	0.82
1:H:32:LEU:HD12	1:H:57:MET:SD	2.19	0.82
1:G:273:ARG:HG3	1:H:175:VAL:HG12	1.61	0.81
1:A:162:ASN:HB3	1:A:207:ASN:HD22	1.44	0.80
1:A:271:PRO:HA	1:A:274:LYS:HD2	1.63	0.78
1:C:128:LEU:HD21	1:D:289:PHE:HE1	1.48	0.78
1:E:181:ALA:HB3	1:E:182:PRO:HD3	1.66	0.78
1:D:138:ARG:HH11	1:D:138:ARG:CG	1.96	0.78
1:C:283:TYR:HB3	1:D:231:VAL:HG13	1.65	0.77
1:A:162:ASN:HB3	1:A:207:ASN:ND2	2.00	0.77
1:A:175:VAL:HG12	1:B:273:ARG:HG3	1.65	0.77
1:B:264:THR:H	1:B:265:PRO:HD2	1.51	0.75
1:F:28:ARG:HB2	1:F:30:GLU:OE1	1.85	0.75
1:A:262:PRO:O	1:A:265:PRO:HD2	1.87	0.75
1:D:181:ALA:HB3	1:D:182:PRO:HD3	1.70	0.74
1:B:134:HIS:O	1:B:138:ARG:HG2	1.87	0.74
1:B:243:LEU:HG	1:B:247:LYS:HD2	1.68	0.74
1:G:181:ALA:HB3	1:G:182:PRO:HD3	1.68	0.74
1:B:273:ARG:O	1:B:277:GLU:HG3	1.87	0.74
1:C:30:GLU:HB3	1:C:33:GLN:HE21	1.54	0.73
1:D:266:ILE:HG13	1:D:267:LEU:N	2.03	0.73
1:B:148:VAL:O	1:B:152:THR:HG22	1.89	0.72
1:B:28:ARG:HB2	1:B:30:GLU:OE1	1.88	0.72
1:D:144:PHE:O	1:D:147:TYR:HB2	1.88	0.72
1:H:50:MET:HG2	1:H:242:ALA:HB1	1.73	0.71
1:C:169:SER:HA	1:C:187:LYS:HD2	1.73	0.70
1:D:36:LYS:HE3	1:D:110:MET:O	1.90	0.70
1:B:141:GLU:HA	1:B:145:LEU:HD13	1.71	0.70
1:D:213:CYS:SG	1:D:245:ILE:HG23	2.32	0.70
1:H:94:GLU:OE2	1:H:138:ARG:HG3	1.91	0.70
1:A:152:THR:HG21	1:B:131:ASP:HA	1.74	0.69
1:B:28:ARG:HG3	1:B:31:MET:HG3	1.73	0.69
1:E:97:THR:O	1:E:101:GLN:HG2	1.92	0.69
1:A:273:ARG:O	1:A:277:GLU:HG3	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:GLU:HA	1:B:145:LEU:HB2	1.75	0.68
1:F:134:HIS:O	1:F:138:ARG:HG3	1.94	0.67
1:A:232:ASN:C	1:A:232:ASN:HD22	1.97	0.67
1:C:263:LEU:HA	1:C:266:ILE:HD11	1.77	0.67
1:H:273:ARG:O	1:H:277:GLU:HG3	1.94	0.67
1:C:128:LEU:HD21	1:D:289:PHE:CE1	2.30	0.67
1:B:35:LYS:HD3	1:B:114:ASP:OD2	1.93	0.67
1:B:132:ASP:O	1:B:136:VAL:HG23	1.95	0.66
1:E:176:THR:HA	5:E:298:HOH:O	1.94	0.66
1:D:127:SER:O	1:D:179:MET:HA	1.96	0.66
1:G:93:MET:HG3	1:G:120:HIS:CE1	2.30	0.65
1:E:178:PRO:HD3	5:E:320:HOH:O	1.97	0.65
1:B:221:GLU:O	1:B:225:LYS:HG3	1.97	0.65
1:G:180:VAL:HG13	1:G:180:VAL:O	1.97	0.65
1:A:36:LYS:HG2	1:A:110:MET:HB3	1.78	0.64
1:F:124:THR:HG22	3:F:290:2M3:H10A	1.79	0.64
1:D:191:ASP:O	1:D:195:SER:HB3	1.97	0.64
1:G:153:ALA:O	1:G:156:PRO:HD2	1.98	0.64
1:F:30:GLU:CD	1:F:30:GLU:H	2.00	0.63
1:G:91:GLY:HA3	1:G:98:PHE:CZ	2.33	0.63
1:B:100:GLU:HG3	1:B:101:GLN:N	2.12	0.63
1:E:175:VAL:HG12	1:F:273:ARG:HG3	1.80	0.63
1:D:240:GLU:O	1:D:244:GLU:HG2	1.99	0.63
1:H:171:LEU:HD23	1:H:214:VAL:HG12	1.81	0.63
1:B:180:VAL:O	1:B:180:VAL:HG22	1.97	0.63
1:G:264:THR:H	1:G:265:PRO:HD2	1.64	0.63
1:H:144:PHE:HD1	1:H:190:LEU:HD23	1.64	0.62
1:B:155:LEU:HG	1:B:159:LYS:HE3	1.81	0.62
1:D:124:THR:HG22	3:D:3:2M3:H10A	1.81	0.62
1:C:219:ASP:OD2	1:C:237:PRO:HA	1.98	0.62
1:E:32:LEU:HD22	1:E:57:MET:SD	2.40	0.62
1:C:129:PHE:HA	5:C:325:HOH:O	1.98	0.62
1:B:36:LYS:CG	1:B:110:MET:HB3	2.28	0.62
1:A:273:ARG:HG3	1:B:175:VAL:CG1	2.28	0.61
1:B:243:LEU:O	1:B:247:LYS:HG3	1.99	0.61
1:G:187:LYS:HA	1:G:190:LEU:HD12	1.82	0.61
1:A:129:PHE:CE1	1:A:131:ASP:HB2	2.35	0.61
1:D:242:ALA:O	1:D:246:ILE:HG13	2.01	0.61
1:E:27:PHE:CD2	1:E:247:LYS:HG2	2.35	0.60
1:F:100:GLU:HG3	1:F:101:GLN:N	2.15	0.60
1:A:227:VAL:HB	1:A:231:VAL:HB	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:VAL:HG22	1:A:183:TYR:HB3	1.84	0.60
1:E:196:THR:HG23	1:F:177:TYR:O	2.01	0.60
1:F:132:ASP:O	1:F:136:VAL:HG23	2.02	0.60
1:B:124:THR:HG22	3:B:1:2M3:H10A	1.84	0.59
1:E:141:GLU:HA	1:E:145:LEU:HB2	1.84	0.59
1:F:266:ILE:HG13	1:F:267:LEU:N	2.17	0.59
1:H:169:SER:HB2	1:H:212:LEU:HD11	1.85	0.59
1:A:207:ASN:ND2	1:A:207:ASN:O	2.36	0.59
1:H:181:ALA:HB3	1:H:182:PRO:HD3	1.84	0.58
1:A:269:GLY:O	1:A:274:LYS:HE2	2.03	0.58
1:A:273:ARG:CG	1:B:175:VAL:HG12	2.28	0.58
1:B:32:LEU:HD11	1:B:246:ILE:HG23	1.83	0.58
1:B:36:LYS:N	1:B:36:LYS:HD3	2.17	0.58
1:B:141:GLU:CD	1:B:145:LEU:HD22	2.24	0.58
1:E:133:ILE:HD13	1:F:149:VAL:HG23	1.85	0.58
1:F:155:LEU:HD12	1:F:159:LYS:HE2	1.85	0.58
1:E:76:SER:O	1:E:80:GLU:HG3	2.03	0.58
1:G:56:LYS:HE2	1:G:81:LEU:HD22	1.85	0.58
1:G:176:THR:HG21	1:H:195:SER:HB2	1.86	0.58
1:B:37:VAL:HG11	1:B:54:LEU:HD13	1.85	0.58
1:F:52:TYR:O	1:F:56:LYS:HG3	2.04	0.58
1:F:181:ALA:HB3	1:F:182:PRO:HD3	1.84	0.57
1:B:77:ARG:O	1:B:81:LEU:HG	2.04	0.57
1:G:164:SER:HB3	5:G:434:HOH:O	2.05	0.57
1:G:266:ILE:HG13	1:G:267:LEU:H	1.70	0.57
1:G:185:ALA:HB2	1:H:193:PHE:HB2	1.86	0.57
1:G:195:SER:HA	1:G:198:ARG:NH1	2.20	0.56
1:A:94:GLU:CD	1:A:138:ARG:HH11	2.09	0.56
1:A:169:SER:HA	1:A:187:LYS:HE3	1.87	0.56
1:H:71:LEU:O	1:H:75:VAL:HG23	2.04	0.56
1:C:27:PHE:CD2	1:C:247:LYS:HG2	2.41	0.56
1:C:288:MET:HG3	1:D:230:ILE:HG23	1.86	0.56
1:E:155:LEU:CD1	1:E:159:LYS:HD2	2.35	0.56
1:F:130:HIS:O	1:F:131:ASP:HB2	2.06	0.56
1:H:56:LYS:HE2	1:H:81:LEU:HD22	1.87	0.56
1:D:266:ILE:HG13	1:D:267:LEU:H	1.68	0.56
1:E:53:HIS:CE1	1:E:243:LEU:HD13	2.39	0.56
1:F:241:CYS:HB2	1:F:258:TYR:CE2	2.40	0.56
1:H:213:CYS:SG	1:H:245:ILE:HG23	2.46	0.56
1:A:139:VAL:O	1:A:143:ASN:HB2	2.06	0.56
1:A:175:VAL:HG12	1:B:273:ARG:CG	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:94:GLU:OE1	1:G:138:ARG:NH1	2.36	0.56
1:F:155:LEU:HB3	1:F:156:PRO:HD3	1.87	0.56
1:H:285:ASN:ND2	1:H:287:ASP:H	2.04	0.56
1:C:132:ASP:OD1	1:C:135:SER:HB2	2.05	0.56
1:D:216:GLY:O	2:D:300:NDP:H42N	2.06	0.55
1:G:231:VAL:HG13	1:H:283:TYR:HB3	1.88	0.55
1:G:264:THR:N	1:G:265:PRO:HD2	2.20	0.55
1:E:195:SER:HB2	1:F:176:THR:HG21	1.89	0.55
1:F:27:PHE:CD2	1:F:247:LYS:HE2	2.41	0.55
1:G:42:ALA:HB3	1:G:63:LEU:HB3	1.88	0.55
1:C:271:PRO:O	1:C:275:ILE:HG13	2.06	0.55
1:B:32:LEU:HD13	1:B:54:LEU:CD2	2.37	0.55
1:B:117:ILE:HG12	1:B:166:ALA:HB3	1.88	0.55
1:B:285:ASN:HB3	1:B:288:MET:HG2	1.88	0.55
1:E:95:ASP:OD1	1:E:97:THR:HB	2.07	0.55
1:B:146:SER:O	1:B:150:MET:HE2	2.06	0.55
1:G:64:THR:HB	1:G:102:PHE:CE1	2.41	0.55
1:B:124:THR:HB	3:B:1:2M3:N7	2.22	0.55
1:A:216:GLY:O	2:A:300:NDP:H42N	2.06	0.55
1:B:165:ILE:HD12	1:B:210:ILE:CD1	2.35	0.55
1:H:39:VAL:HG12	1:H:42:ALA:HB2	1.89	0.55
1:A:176:THR:HG21	1:B:195:SER:CB	2.36	0.54
1:A:238:LYS:HE3	1:A:239:GLU:OE2	2.06	0.54
1:C:275:ILE:HG23	1:C:279:PHE:HE2	1.71	0.54
2:F:300:NDP:O1A	3:F:290:2M3:H2	2.06	0.54
1:G:178:PRO:O	1:G:179:MET:HB2	2.06	0.54
1:E:144:PHE:HD2	1:E:145:LEU:HD12	1.73	0.54
1:G:230:ILE:HD12	1:H:288:MET:SD	2.48	0.54
1:A:152:THR:CG2	1:B:131:ASP:HA	2.37	0.54
1:G:60:HIS:ND1	1:G:85:SER:HB3	2.22	0.54
1:E:169:SER:HA	1:E:187:LYS:HD2	1.88	0.54
2:F:300:NDP:O2N	3:F:290:2M3:H1	2.08	0.54
1:G:200:GLU:OE2	1:H:128:LEU:HA	2.08	0.54
1:G:284:TYR:OH	1:H:177:TYR:HB3	2.08	0.54
1:H:46:ILE:O	1:H:50:MET:HG3	2.07	0.54
1:B:266:ILE:HG13	1:B:267:LEU:N	2.23	0.54
1:E:182:PRO:HD2	5:E:314:HOH:O	2.07	0.54
1:B:144:PHE:HD1	1:B:190:LEU:HD23	1.72	0.54
1:B:193:PHE:O	1:B:197:ILE:HG12	2.07	0.54
1:E:267:LEU:O	1:E:268:LEU:HD23	2.08	0.54
1:B:148:VAL:HG22	1:B:193:PHE:CE2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:THR:CG2	3:B:1:2M3:H10A	2.38	0.53
1:F:100:GLU:HG3	1:F:101:GLN:H	1.73	0.53
1:G:127:SER:HA	1:G:179:MET:CE	2.38	0.53
1:E:116:LEU:HD11	1:E:118:LEU:HD21	1.91	0.53
1:A:118:LEU:O	1:A:168:ILE:HG12	2.09	0.53
1:G:267:LEU:O	1:H:272:GLY:HA3	2.09	0.53
1:A:176:THR:HG21	1:B:195:SER:HB2	1.90	0.53
2:D:300:NDP:O2N	3:D:3:2M3:H1	2.09	0.53
1:C:76:SER:O	1:C:80:GLU:HG3	2.10	0.52
1:C:121:ILE:HD12	1:C:121:ILE:O	2.09	0.52
1:E:155:LEU:HD13	1:E:159:LYS:HD2	1.90	0.52
1:B:271:PRO:O	1:B:275:ILE:HG13	2.09	0.52
1:H:196:THR:O	1:H:200:GLU:HG3	2.09	0.52
1:B:180:VAL:CG2	1:B:183:TYR:HB3	2.39	0.52
1:D:234:GLN:NE2	1:D:260:LYS:HD3	2.25	0.52
1:F:132:ASP:HB2	1:F:135:SER:HB3	1.92	0.52
1:B:32:LEU:HD12	1:B:57:MET:SD	2.50	0.52
1:B:264:THR:N	1:B:265:PRO:HD2	2.24	0.52
1:A:68:GLU:OE1	1:A:88:TYR:HE1	1.93	0.52
1:F:64:THR:HB	1:F:102:PHE:CE1	2.45	0.52
1:E:168:ILE:HD12	1:E:245:ILE:HD13	1.92	0.52
1:A:191:ASP:O	1:A:195:SER:HB2	2.10	0.52
1:H:285:ASN:HD22	1:H:286:LYS:N	2.08	0.52
1:A:28:ARG:HB3	1:A:30:GLU:HG2	1.91	0.52
1:B:221:GLU:CG	1:B:225:LYS:HE3	2.40	0.52
1:D:139:VAL:O	1:D:143:ASN:HB2	2.10	0.52
1:A:62:VAL:HG23	1:A:110:MET:SD	2.51	0.51
1:D:40:THR:O	1:D:119:ASN:HB3	2.10	0.51
1:F:133:ILE:HG23	1:F:134:HIS:H	1.75	0.51
1:G:220:THR:O	1:G:224:MET:HG2	2.10	0.51
1:G:44:LYS:NZ	2:G:300:NDP:H3B	2.26	0.51
1:F:139:VAL:HG13	1:F:143:ASN:ND2	2.25	0.51
1:A:64:THR:O	1:A:65:ALA:HB2	2.11	0.51
1:B:170:SER:O	1:B:173:GLY:N	2.38	0.51
1:B:171:LEU:HD22	1:B:268:LEU:HD11	1.93	0.51
1:E:126:LEU:HB3	1:E:179:MET:CE	2.40	0.51
1:F:155:LEU:CD1	1:F:159:LYS:HE2	2.40	0.51
1:G:135:SER:O	1:G:138:ARG:HB2	2.11	0.51
1:A:232:ASN:C	1:A:232:ASN:ND2	2.64	0.51
1:H:168:ILE:HD11	1:H:245:ILE:HG21	1.93	0.51
1:C:221:GLU:HG2	4:C:8:SO4:O3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:271:PRO:O	1:F:275:ILE:HG13	2.10	0.51
1:G:145:LEU:HD22	5:G:319:HOH:O	2.10	0.51
1:G:266:ILE:HG13	1:G:267:LEU:N	2.26	0.50
2:G:300:NDP:O2N	3:G:8:2M3:H1	2.11	0.50
1:G:283:TYR:HB3	1:H:231:VAL:HG13	1.93	0.50
1:E:146:SER:O	1:E:150:MET:HG3	2.12	0.50
1:A:236:SER:HB3	1:A:258:TYR:CE2	2.46	0.50
1:D:138:ARG:CG	1:D:138:ARG:NH1	2.67	0.50
1:D:244:GLU:HG3	1:D:258:TYR:CD1	2.47	0.50
1:F:220:THR:O	1:F:224:MET:HG2	2.11	0.50
1:A:64:THR:HB	1:A:102:PHE:CE1	2.46	0.50
1:A:165:ILE:HB	1:A:210:ILE:HD13	1.94	0.50
1:D:273:ARG:NH1	5:D:359:HOH:O	2.44	0.50
1:H:172:ALA:HA	1:H:175:VAL:O	2.11	0.50
1:F:180:VAL:O	1:F:180:VAL:HG23	2.12	0.50
1:G:226:ALA:HB1	3:G:8:2M3:H10B	1.92	0.50
1:E:236:SER:HB3	1:E:237:PRO:HD2	1.94	0.50
1:G:91:GLY:HA3	1:G:98:PHE:CE1	2.47	0.50
1:A:264:THR:N	1:A:265:PRO:HD2	2.27	0.49
1:C:40:THR:HA	1:C:64:THR:HG22	1.92	0.49
1:D:127:SER:HA	1:D:179:MET:HE2	1.94	0.49
1:E:133:ILE:HD13	1:F:149:VAL:CG2	2.42	0.49
1:G:268:LEU:HD21	1:H:276:MET:SD	2.52	0.49
1:G:272:GLY:HA2	1:H:267:LEU:HD22	1.94	0.49
1:A:72:GLN:NE2	1:A:76:SER:OG	2.42	0.49
1:G:270:ASN:N	1:G:271:PRO:CD	2.74	0.49
1:A:105:LYS:O	1:A:109:LEU:HG	2.13	0.49
1:A:93:MET:HG3	1:A:120:HIS:NE2	2.27	0.49
1:B:32:LEU:HD13	1:B:54:LEU:HD23	1.94	0.49
1:D:93:MET:HG3	1:D:120:HIS:CE1	2.48	0.49
1:H:244:GLU:HG3	1:H:258:TYR:CD1	2.48	0.49
1:A:284:TYR:OH	1:B:177:TYR:HB3	2.13	0.49
1:A:60:HIS:ND1	1:A:85:SER:HB2	2.27	0.49
1:A:148:VAL:HG22	1:A:193:PHE:CE2	2.48	0.49
1:C:241:CYS:HB2	1:C:258:TYR:CE2	2.48	0.49
1:G:216:GLY:O	2:G:300:NDP:H42N	2.12	0.49
1:A:37:VAL:HG21	1:A:54:LEU:HD22	1.95	0.49
1:C:178:PRO:O	1:C:179:MET:HB2	2.12	0.49
1:C:220:THR:O	1:C:224:MET:HG2	2.12	0.49
1:B:264:THR:H	1:B:265:PRO:CD	2.24	0.49
1:B:52:TYR:O	1:B:56:LYS:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:PRO:O	1:B:179:MET:HB2	2.12	0.48
1:B:186:SER:O	1:B:190:LEU:HG	2.13	0.48
1:G:175:VAL:HG12	1:H:273:ARG:HG3	1.95	0.48
1:F:120:HIS:HE1	1:F:150:MET:HE1	1.79	0.48
1:F:133:ILE:HG23	1:F:134:HIS:N	2.28	0.48
2:A:300:NDP:H2A	5:A:290:HOH:O	2.12	0.48
1:B:207:ASN:O	1:B:252:ARG:NH2	2.46	0.48
1:D:32:LEU:HD13	1:D:54:LEU:HD23	1.96	0.48
1:G:187:LYS:HD3	1:G:190:LEU:HD12	1.96	0.48
1:D:151:SER:O	1:D:155:LEU:HD22	2.13	0.48
1:E:123:GLN:HB2	4:E:4:SO4:S	2.53	0.48
1:H:216:GLY:HA3	1:H:259:ASP:OD1	2.13	0.48
1:B:272:GLY:O	1:B:276:MET:HG3	2.12	0.48
1:D:138:ARG:NH1	1:D:138:ARG:HB2	2.28	0.48
1:E:276:MET:HG2	1:F:267:LEU:HD13	1.95	0.48
1:D:126:LEU:HB3	1:D:179:MET:HE1	1.95	0.48
1:D:138:ARG:HH11	1:D:138:ARG:HB2	1.79	0.48
1:E:122:THR:HG23	1:E:142:VAL:HB	1.95	0.48
1:H:122:THR:HB	1:H:142:VAL:HG11	1.96	0.48
1:B:28:ARG:HD2	1:B:30:GLU:HB2	1.96	0.48
1:D:136:VAL:O	1:D:140:MET:HG2	2.13	0.48
1:G:89:ILE:HB	1:G:102:PHE:CE1	2.49	0.48
1:A:181:ALA:HB2	1:B:196:THR:CG2	2.44	0.48
1:B:171:LEU:HD23	1:B:214:VAL:HG12	1.95	0.48
1:G:215:LEU:HD12	1:G:258:TYR:HB3	1.96	0.48
1:G:263:LEU:HG	1:G:266:ILE:HD11	1.96	0.48
1:E:264:THR:N	1:E:265:PRO:HD2	2.29	0.47
1:A:285:ASN:ND2	1:A:287:ASP:HB2	2.29	0.47
1:F:120:HIS:CE1	1:F:150:MET:HE1	2.49	0.47
1:C:237:PRO:HD3	1:E:240:GLU:OE2	2.14	0.47
1:G:72:GLN:OE1	1:G:88:TYR:HE2	1.96	0.47
1:B:96:MET:SD	1:B:149:VAL:HG21	2.54	0.47
1:D:191:ASP:HB2	5:D:485:HOH:O	2.15	0.47
1:E:171:LEU:HD21	1:E:264:THR:HG21	1.97	0.47
1:A:67:SER:O	1:A:71:LEU:HG	2.14	0.47
1:B:155:LEU:O	1:B:159:LYS:HG3	2.15	0.47
1:B:218:ILE:HB	2:B:300:NDP:N7N	2.30	0.47
1:D:138:ARG:HH11	1:D:138:ARG:CB	2.26	0.47
1:C:176:THR:HG21	1:D:195:SER:OG	2.15	0.47
1:E:64:THR:HB	1:E:102:PHE:CE1	2.49	0.47
1:D:138:ARG:HG3	1:D:138:ARG:NH1	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:28:ARG:O	1:H:31:MET:HB2	2.15	0.47
1:H:171:LEU:HG	1:H:215:LEU:O	2.14	0.47
1:A:155:LEU:HB3	1:A:156:PRO:HD3	1.97	0.46
1:G:64:THR:HB	1:G:102:PHE:CZ	2.50	0.46
1:A:65:ALA:HA	5:A:297:HOH:O	2.15	0.46
1:E:137:ARG:O	1:E:141:GLU:HG3	2.14	0.46
1:B:28:ARG:CG	1:B:31:MET:HG3	2.44	0.46
1:E:126:LEU:HB3	1:E:179:MET:HE1	1.97	0.46
1:D:138:ARG:O	1:D:142:VAL:HG23	2.15	0.46
1:B:239:GLU:CD	1:B:239:GLU:H	2.18	0.46
1:C:28:ARG:HB3	1:C:30:GLU:OE1	2.16	0.46
1:C:30:GLU:HB3	1:C:33:GLN:NE2	2.26	0.46
1:B:264:THR:O	1:B:268:LEU:HB2	2.15	0.46
1:G:231:VAL:HA	1:H:283:TYR:O	2.16	0.46
1:G:257:TYR:CE2	1:G:268:LEU:HD13	2.50	0.46
1:A:46:ILE:HG13	1:A:220:THR:HG21	1.98	0.46
1:C:126:LEU:HD13	3:C:4:2M3:H10	1.97	0.46
1:G:155:LEU:HD23	1:G:155:LEU:HA	1.78	0.46
1:G:186:SER:O	1:G:190:LEU:HG	2.16	0.46
1:D:126:LEU:N	1:D:126:LEU:HD12	2.30	0.45
1:D:164:SER:OG	1:D:209:SER:OG	2.33	0.45
1:H:126:LEU:HD12	1:H:126:LEU:N	2.31	0.45
1:B:138:ARG:HD2	5:B:517:HOH:O	2.16	0.45
1:D:248:GLY:HA3	1:D:256:VAL:HG21	1.98	0.45
1:E:66:ARG:HB2	2:E:300:NDP:O2X	2.16	0.45
1:H:200:GLU:O	1:H:204:THR:HG23	2.15	0.45
1:E:162:ASN:ND2	1:E:207:ASN:HD22	2.14	0.45
1:G:257:TYR:HE2	1:G:268:LEU:HD13	1.81	0.45
1:H:77:ARG:HD2	1:H:77:ARG:O	2.15	0.45
1:F:40:THR:O	1:F:119:ASN:HB3	2.17	0.45
1:F:242:ALA:HA	1:F:245:ILE:HD12	1.98	0.45
1:H:155:LEU:HA	1:H:158:LEU:HB2	1.98	0.45
1:B:144:PHE:CD1	1:B:190:LEU:HD23	2.51	0.45
1:E:53:HIS:ND1	1:E:243:LEU:HD13	2.32	0.45
1:F:29:PRO:HB3	1:F:57:MET:HG2	1.99	0.45
1:F:267:LEU:O	1:F:268:LEU:HD23	2.17	0.45
1:C:171:LEU:HB2	3:C:4:2M3:H25A	1.98	0.45
1:D:28:ARG:HB2	1:D:30:GLU:OE1	2.17	0.45
1:F:216:GLY:O	2:F:300:NDP:H42N	2.17	0.45
1:B:75:VAL:HG13	1:B:86:ALA:CB	2.47	0.45
1:H:68:GLU:HG2	1:H:90:ALA:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:VAL:HG13	1:A:180:VAL:O	2.17	0.45
1:F:197:ILE:O	1:F:201:LEU:HG	2.16	0.45
1:A:93:MET:HG3	1:A:120:HIS:CD2	2.51	0.44
1:B:76:SER:O	1:B:80:GLU:HG3	2.17	0.44
1:C:181:ALA:HB3	1:C:182:PRO:CD	2.39	0.44
1:C:226:ALA:HB1	3:C:4:2M3:H10B	1.99	0.44
1:B:133:ILE:HG23	1:B:134:HIS:N	2.32	0.44
1:B:241:CYS:HB2	1:B:258:TYR:CE2	2.51	0.44
1:C:26:GLU:HB2	5:C:463:HOH:O	2.15	0.44
1:C:36:LYS:NZ	1:C:110:MET:O	2.47	0.44
1:G:40:THR:O	1:G:119:ASN:HB3	2.17	0.44
1:B:262:PRO:HG2	1:B:263:LEU:CD1	2.47	0.44
1:C:27:PHE:HB2	1:C:251:LEU:HD11	1.99	0.44
1:E:133:ILE:CD1	1:F:149:VAL:HG23	2.46	0.44
1:G:169:SER:OG	1:G:170:SER:N	2.51	0.44
1:G:262:PRO:O	1:G:265:PRO:HD2	2.18	0.44
1:H:169:SER:O	2:H:300:NDP:H6N	2.18	0.44
1:C:64:THR:HB	1:C:102:PHE:CZ	2.52	0.44
1:E:140:MET:O	1:E:144:PHE:HB3	2.17	0.44
1:G:128:LEU:HD21	1:H:289:PHE:CE1	2.52	0.44
1:G:283:TYR:CB	1:H:231:VAL:HG13	2.47	0.44
1:B:37:VAL:HG11	1:B:54:LEU:CD1	2.47	0.44
1:E:63:LEU:O	1:E:88:TYR:HA	2.17	0.44
1:E:234:GLN:HA	5:E:502:HOH:O	2.17	0.44
1:F:144:PHE:O	1:F:147:TYR:HB2	2.17	0.44
1:F:264:THR:H	1:F:265:PRO:HD2	1.82	0.44
1:E:38:ILE:HD11	1:E:106:ALA:CB	2.48	0.44
1:E:178:PRO:O	1:E:179:MET:HB2	2.17	0.44
1:G:267:LEU:HD22	1:H:272:GLY:HA2	2.00	0.44
1:B:50:MET:HG2	1:B:242:ALA:HB1	1.99	0.44
1:D:127:SER:N	1:D:179:MET:HB3	2.31	0.44
1:G:37:VAL:HG11	1:G:54:LEU:HD11	2.00	0.44
1:C:273:ARG:O	1:C:277:GLU:HG3	2.17	0.44
1:D:66:ARG:HB2	2:D:300:NDP:O2X	2.17	0.44
1:D:140:MET:O	1:D:144:PHE:HB3	2.18	0.44
1:D:266:ILE:CG1	1:D:267:LEU:N	2.78	0.44
1:E:129:PHE:HE1	1:E:131:ASP:HB2	1.83	0.44
1:G:127:SER:HA	1:G:179:MET:HE3	1.99	0.44
1:B:113:LEU:CD2	1:B:154:ALA:HB1	2.48	0.43
1:B:122:THR:HB	1:B:142:VAL:HG11	1.99	0.43
1:D:264:THR:HB	1:D:265:PRO:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:107:GLY:O	1:E:111:GLY:N	2.51	0.43
1:G:89:ILE:HB	1:G:102:PHE:HE1	1.83	0.43
1:A:175:VAL:CG1	1:B:273:ARG:HG3	2.42	0.43
1:G:178:PRO:O	1:G:179:MET:CB	2.66	0.43
1:H:71:LEU:HB3	1:H:88:TYR:HB2	2.01	0.43
1:H:144:PHE:CD1	1:H:190:LEU:HD23	2.48	0.43
1:B:145:LEU:O	1:B:149:VAL:HG23	2.17	0.43
1:E:284:TYR:OH	1:F:177:TYR:HB3	2.18	0.43
1:F:124:THR:CG2	3:F:290:2M3:H10A	2.48	0.43
1:H:136:VAL:O	1:H:140:MET:HG2	2.18	0.43
1:B:172:ALA:HA	1:B:175:VAL:O	2.17	0.43
1:C:126:LEU:HD13	3:C:4:2M3:C10	2.48	0.43
1:G:122:THR:O	1:G:123:GLN:C	2.57	0.43
1:A:176:THR:HG21	1:B:195:SER:HB3	2.00	0.43
1:A:271:PRO:O	1:A:275:ILE:HG13	2.18	0.43
1:C:124:THR:HB	3:C:4:2M3:N7	2.33	0.43
1:E:162:ASN:CG	1:E:207:ASN:HD22	2.20	0.43
1:F:93:MET:HG2	1:F:120:HIS:CE1	2.54	0.43
1:A:38:ILE:HB	1:A:116:LEU:HD12	2.00	0.43
1:A:53:HIS:O	1:A:57:MET:HG3	2.19	0.43
1:C:97:THR:O	1:C:101:GLN:HG3	2.17	0.43
1:E:37:VAL:HG11	1:E:54:LEU:HD13	2.01	0.43
1:E:139:VAL:O	1:E:143:ASN:HB2	2.18	0.43
1:E:261:SER:HA	1:E:262:PRO:HD3	1.86	0.43
1:E:266:ILE:H	1:E:266:ILE:HG12	1.62	0.43
1:F:36:LYS:HE3	1:F:110:MET:O	2.19	0.43
1:F:63:LEU:O	1:F:88:TYR:HA	2.18	0.43
1:B:29:PRO:CB	1:B:57:MET:HG2	2.49	0.43
1:G:108:LYS:HB2	1:G:108:LYS:HE3	1.82	0.43
1:A:135:SER:O	1:A:138:ARG:HB2	2.19	0.43
1:B:65:ALA:N	1:B:71:LEU:HD11	2.34	0.43
1:B:135:SER:O	1:B:138:ARG:HG3	2.19	0.43
1:E:176:THR:HG21	1:F:195:SER:HB2	1.99	0.43
3:H:290:2M3:H10	3:H:290:2M3:H11	1.90	0.43
1:B:37:VAL:HG22	1:B:115:MET:HB3	2.01	0.43
1:C:40:THR:HA	1:C:64:THR:CG2	2.49	0.43
1:E:285:ASN:OD1	1:E:287:ASP:HB2	2.19	0.43
1:G:199:THR:O	1:G:203:ILE:HG23	2.19	0.43
1:A:89:ILE:HB	1:A:102:PHE:CD1	2.54	0.42
1:B:221:GLU:HB3	4:B:2:SO4:O2	2.18	0.42
1:D:55:SER:OG	1:D:83:ALA:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:105:LYS:O	1:G:108:LYS:N	2.51	0.42
1:G:195:SER:HA	1:G:198:ARG:HH12	1.82	0.42
1:A:27:PHE:CD2	1:A:247:LYS:HG2	2.54	0.42
1:F:46:ILE:HG22	1:F:50:MET:CE	2.49	0.42
1:G:141:GLU:OE1	1:H:137:ARG:NH2	2.51	0.42
1:H:169:SER:OG	1:H:170:SER:N	2.52	0.42
1:E:35:LYS:N	1:E:35:LYS:HD3	2.33	0.42
1:E:135:SER:O	1:E:139:VAL:HG23	2.19	0.42
1:G:267:LEU:HD13	1:H:276:MET:HG3	2.01	0.42
2:E:300:NDP:O2N	3:E:7:2M3:H1	2.20	0.42
1:G:196:THR:HG21	1:H:181:ALA:CA	2.50	0.42
1:A:129:PHE:HE1	1:A:131:ASP:HB2	1.83	0.42
1:B:157:MET:HG3	5:B:417:HOH:O	2.18	0.42
2:B:300:NDP:O2N	3:B:1:2M3:H1	2.20	0.42
1:F:164:SER:HB3	1:F:209:SER:OG	2.19	0.42
1:H:270:ASN:C	1:H:270:ASN:HD22	2.22	0.42
1:B:171:LEU:HD23	1:B:214:VAL:CG1	2.50	0.42
1:D:206:VAL:HG12	1:D:208:VAL:HG23	2.01	0.42
1:A:223:ALA:O	1:A:227:VAL:HG13	2.19	0.42
1:B:48:ARG:O	1:B:51:ALA:HB3	2.19	0.42
1:B:180:VAL:HG22	1:B:183:TYR:HB3	2.01	0.42
1:C:35:LYS:HD3	1:C:35:LYS:HA	1.65	0.42
1:C:68:GLU:O	1:C:72:GLN:HG3	2.19	0.42
1:D:191:ASP:O	1:D:195:SER:CB	2.67	0.42
1:D:234:GLN:CD	1:D:260:LYS:HZ3	2.23	0.42
1:G:123:GLN:HE21	1:G:123:GLN:HB3	1.66	0.42
1:G:285:ASN:HB3	1:G:288:MET:HG2	2.02	0.42
1:H:155:LEU:N	1:H:156:PRO:CD	2.83	0.42
3:B:1:2M3:H4	3:B:1:2M3:H15	2.02	0.42
1:D:32:LEU:HD12	1:D:57:MET:SD	2.59	0.42
1:D:234:GLN:CB	1:D:260:LYS:HD3	2.50	0.42
1:F:68:GLU:O	1:F:72:GLN:HG3	2.19	0.42
1:A:286:LYS:O	1:A:289:PHE:HB2	2.20	0.42
1:E:27:PHE:CG	1:E:247:LYS:HG2	2.55	0.42
1:F:219:ASP:OD2	1:F:237:PRO:HA	2.19	0.42
1:G:176:THR:HG21	1:H:195:SER:CB	2.48	0.42
1:A:104:VAL:HG12	1:A:108:LYS:HE2	2.02	0.41
1:B:95:ASP:C	1:B:95:ASP:OD1	2.58	0.41
1:E:44:LYS:HE2	2:E:300:NDP:H3B	2.01	0.41
1:F:65:ALA:N	1:F:71:LEU:HD11	2.36	0.41
1:F:135:SER:O	1:F:139:VAL:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:168:ILE:HG21	2:G:300:NDP:H4D	2.02	0.41
1:H:55:SER:OG	1:H:83:ALA:HB2	2.20	0.41
1:H:169:SER:CB	1:H:212:LEU:HD11	2.50	0.41
1:F:285:ASN:O	1:F:288:MET:HG2	2.20	0.41
1:H:94:GLU:OE1	1:H:138:ARG:NE	2.54	0.41
1:H:193:PHE:O	1:H:197:ILE:HG12	2.21	0.41
1:B:126:LEU:O	1:B:127:SER:HB3	2.21	0.41
1:B:169:SER:HB2	1:B:212:LEU:HD11	2.02	0.41
1:G:68:GLU:HG3	1:G:88:TYR:CE1	2.55	0.41
1:D:93:MET:HG3	1:D:120:HIS:NE2	2.35	0.41
3:D:3:2M3:H10	3:D:3:2M3:H11	1.92	0.41
1:A:60:HIS:ND1	1:A:85:SER:CB	2.84	0.41
1:B:241:CYS:O	1:B:245:ILE:HG13	2.21	0.41
1:E:62:VAL:HG23	1:E:110:MET:SD	2.60	0.41
1:H:26:GLU:HG3	1:H:27:PHE:N	2.35	0.41
1:H:66:ARG:HE	1:H:66:ARG:HB2	1.73	0.41
1:C:155:LEU:HA	1:C:155:LEU:HD23	1.77	0.41
1:E:175:VAL:HG12	1:F:273:ARG:CG	2.50	0.41
1:F:261:SER:HA	1:F:262:PRO:HD2	1.97	0.41
1:G:131:ASP:HB3	1:G:135:SER:HB3	2.03	0.41
1:A:153:ALA:O	1:A:156:PRO:HD2	2.20	0.41
1:A:267:LEU:HD22	1:B:272:GLY:HA2	2.03	0.41
1:B:240:GLU:O	1:B:243:LEU:HB3	2.20	0.41
1:B:263:LEU:N	1:B:263:LEU:HD12	2.35	0.41
1:B:264:THR:N	1:B:265:PRO:CD	2.83	0.41
1:E:288:MET:SD	1:F:230:ILE:HG23	2.61	0.41
1:B:131:ASP:OD1	1:B:131:ASP:O	2.39	0.41
1:B:214:VAL:O	1:B:215:LEU:HD12	2.21	0.41
1:C:144:PHE:O	1:C:147:TYR:HB2	2.20	0.41
1:D:170:SER:O	1:D:214:VAL:HG13	2.21	0.41
1:E:230:ILE:HG23	1:F:288:MET:HG3	2.02	0.41
3:E:7:2M3:H4	3:E:7:2M3:H15	2.03	0.41
1:G:171:LEU:HD23	1:G:214:VAL:HG12	2.03	0.41
1:A:32:LEU:HD12	1:A:32:LEU:N	2.36	0.41
1:A:215:LEU:N	1:A:215:LEU:CD1	2.84	0.41
1:C:275:ILE:HG23	1:C:279:PHE:CE2	2.54	0.41
1:D:276:MET:HE2	1:D:276:MET:HB3	1.93	0.41
1:F:46:ILE:HG22	1:F:50:MET:HE2	2.03	0.41
1:G:32:LEU:HD11	1:G:246:ILE:CG2	2.51	0.41
1:B:100:GLU:HG3	1:B:101:GLN:H	1.84	0.40
1:B:113:LEU:HD21	1:B:154:ALA:HB1	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:93:MET:HG3	1:E:120:HIS:CE1	2.56	0.40
1:G:118:LEU:O	1:G:168:ILE:HG12	2.21	0.40
1:G:171:LEU:HD22	1:G:268:LEU:HD11	2.03	0.40
1:H:168:ILE:HG21	2:H:300:NDP:H4D	2.03	0.40
1:D:234:GLN:HB2	1:D:260:LYS:HD3	2.03	0.40
1:E:216:GLY:O	2:E:300:NDP:H42N	2.21	0.40
1:E:226:ALA:HB1	3:E:7:2M3:H10B	2.02	0.40
1:F:116:LEU:HD22	1:F:154:ALA:CB	2.50	0.40
1:H:264:THR:N	1:H:265:PRO:HD2	2.36	0.40
1:A:27:PHE:CG	1:A:247:LYS:HG2	2.57	0.40
1:B:46:ILE:O	1:B:50:MET:HG3	2.21	0.40
1:B:191:ASP:CG	1:B:273:ARG:HH22	2.23	0.40
1:B:212:LEU:O	1:B:255:GLU:HA	2.21	0.40
1:C:32:LEU:HD22	1:C:54:LEU:CD2	2.50	0.40
1:C:42:ALA:HB3	1:C:63:LEU:HB3	2.04	0.40
1:C:44:LYS:HG3	1:C:45:GLY:N	2.37	0.40
1:F:133:ILE:HG23	1:F:134:HIS:CD2	2.55	0.40
1:F:251:LEU:HD23	1:F:251:LEU:HA	1.74	0.40
1:G:195:SER:HB2	1:H:176:THR:HG21	2.02	0.40
1:H:287:ASP:C	1:H:289:PHE:H	2.24	0.40
1:B:26:GLU:HG3	1:B:27:PHE:N	2.37	0.40
1:C:42:ALA:CB	1:C:63:LEU:HB3	2.51	0.40
1:E:152:THR:HG21	1:F:131:ASP:HA	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	262/264 (99%)	245 (94%)	16 (6%)	1 (0%)	34 40
1	B	262/264 (99%)	247 (94%)	13 (5%)	2 (1%)	19 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	262/264 (99%)	248 (95%)	14 (5%)	0	100	100
1	D	262/264 (99%)	251 (96%)	11 (4%)	0	100	100
1	E	262/264 (99%)	255 (97%)	7 (3%)	0	100	100
1	F	262/264 (99%)	249 (95%)	12 (5%)	1 (0%)	34	40
1	G	262/264 (99%)	246 (94%)	14 (5%)	2 (1%)	19	22
1	H	262/264 (99%)	249 (95%)	12 (5%)	1 (0%)	34	40
All	All	2096/2112 (99%)	1990 (95%)	99 (5%)	7 (0%)	41	49

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	ALA
1	G	179	MET
1	G	219	ASP
1	H	131	ASP
1	B	131	ASP
1	B	264	THR
1	F	264	THR

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	222/222 (100%)	216 (97%)	6 (3%)	44	59
1	B	222/222 (100%)	218 (98%)	4 (2%)	59	72
1	C	222/222 (100%)	213 (96%)	9 (4%)	30	41
1	D	222/222 (100%)	215 (97%)	7 (3%)	39	52
1	E	222/222 (100%)	218 (98%)	4 (2%)	59	72
1	F	222/222 (100%)	215 (97%)	7 (3%)	39	52
1	G	222/222 (100%)	215 (97%)	7 (3%)	39	52
1	H	222/222 (100%)	214 (96%)	8 (4%)	35	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1776/1776 (100%)	1724 (97%)	52 (3%)	42 56

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LYS
1	A	73	LYS
1	A	100	GLU
1	A	134	HIS
1	A	225	LYS
1	A	232	ASN
1	B	28	ARG
1	B	36	LYS
1	B	100	GLU
1	B	133	ILE
1	C	30	GLU
1	C	32	LEU
1	C	123	GLN
1	C	126	LEU
1	C	131	ASP
1	C	155	LEU
1	C	215	LEU
1	C	221	GLU
1	C	270	ASN
1	D	35	LYS
1	D	138	ARG
1	D	155	LEU
1	D	203	ILE
1	D	215	LEU
1	D	276	MET
1	D	280	SER
1	E	126	LEU
1	E	158	LEU
1	E	215	LEU
1	E	266	ILE
1	F	32	LEU
1	F	93	MET
1	F	100	GLU
1	F	123	GLN
1	F	133	ILE
1	F	155	LEU
1	F	270	ASN

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Mol	Chain	Res	Type
1	G	123	GLN
1	G	125	SER
1	G	155	LEU
1	G	158	LEU
1	G	180	VAL
1	G	215	LEU
1	G	225	LYS
1	H	55	SER
1	H	158	LEU
1	H	184	SER
1	H	215	LEU
1	H	221	GLU
1	H	270	ASN
1	H	285	ASN
1	H	288	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	87	HIS
1	A	162	ASN
1	A	207	ASN
1	A	232	ASN
1	B	101	GLN
1	C	33	GLN
1	C	72	GLN
1	C	101	GLN
1	C	232	ASN
1	C	270	ASN
1	D	33	GLN
1	D	162	ASN
1	E	120	HIS
1	E	207	ASN
1	F	101	GLN
1	F	134	HIS
1	F	162	ASN
1	F	232	ASN
1	F	270	ASN
1	G	33	GLN
1	G	101	GLN
1	G	123	GLN

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Mol	Chain	Res	Type
1	H	101	GLN
1	H	162	ASN
1	H	232	ASN
1	H	270	ASN
1	H	285	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

25 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	$\# Z > 2$
2	NDP	B	300	-	45,52,52	1.59	9 (20%)	53,80,80	1.31	4 (7%)
3	2M3	B	1	-	26,30,30	2.27	5 (19%)	32,45,45	2.22	14 (43%)
4	SO4	H	3	-	4,4,4	0.29	0	6,6,6	0.16	0
3	2M3	A	2	-	26,30,30	2.28	5 (19%)	32,45,45	2.18	12 (37%)
2	NDP	F	300	-	45,52,52	1.63	9 (20%)	53,80,80	1.25	4 (7%)
3	2M3	F	290	-	26,30,30	2.15	7 (26%)	32,45,45	2.23	12 (37%)
2	NDP	G	300	-	45,52,52	1.61	7 (15%)	53,80,80	1.26	4 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	2M3	G	8	-	26,30,30	2.25	5 (19%)	32,45,45	2.31	15 (46%)
2	NDP	D	300	-	45,52,52	1.46	7 (15%)	53,80,80	1.32	6 (11%)
2	NDP	C	300	-	45,52,52	1.63	10 (22%)	53,80,80	1.24	4 (7%)
4	SO4	G	9	-	4,4,4	0.28	0	6,6,6	0.10	0
3	2M3	C	4	-	26,30,30	2.26	6 (23%)	32,45,45	2.19	12 (37%)
4	SO4	E	4	-	4,4,4	0.27	0	6,6,6	0.10	0
4	SO4	H	6	-	4,4,4	0.27	0	6,6,6	0.09	0
3	2M3	D	3	-	26,30,30	2.22	5 (19%)	32,45,45	2.19	13 (40%)
4	SO4	C	8	-	4,4,4	0.28	0	6,6,6	0.15	0
4	SO4	C	7	-	4,4,4	0.27	0	6,6,6	0.09	0
4	SO4	F	5	-	4,4,4	0.27	0	6,6,6	0.11	0
2	NDP	E	300	-	45,52,52	1.61	7 (15%)	53,80,80	1.24	3 (5%)
2	NDP	A	300	-	45,52,52	1.61	8 (17%)	53,80,80	1.17	5 (9%)
4	SO4	D	1	-	4,4,4	0.24	0	6,6,6	0.06	0
2	NDP	H	300	-	45,52,52	1.64	8 (17%)	53,80,80	1.24	3 (5%)
4	SO4	B	2	-	4,4,4	0.26	0	6,6,6	0.11	0
3	2M3	E	7	-	26,30,30	2.28	5 (19%)	32,45,45	2.21	14 (43%)
3	2M3	H	290	-	26,30,30	2.35	6 (23%)	32,45,45	2.27	13 (40%)

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	NDP	B	300	-	-	11/30/77/77	0/5/5/5
3	2M3	C	4	-	-	2/14/33/33	0/5/5/5
2	NDP	E	300	-	-	5/30/77/77	0/5/5/5
3	2M3	F	290	-	-	0/14/33/33	0/5/5/5
2	NDP	A	300	-	-	9/30/77/77	0/5/5/5
2	NDP	G	300	-	-	6/30/77/77	0/5/5/5
3	2M3	B	1	-	-	0/14/33/33	0/5/5/5
3	2M3	D	3	-	-	1/14/33/33	0/5/5/5
3	2M3	G	8	-	-	2/14/33/33	0/5/5/5
2	NDP	H	300	-	-	8/30/77/77	0/5/5/5
3	2M3	H	290	-	-	0/14/33/33	0/5/5/5
3	2M3	A	2	-	-	0/14/33/33	0/5/5/5
2	NDP	F	300	-	-	10/30/77/77	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDP	D	300	-	-	6/30/77/77	0/5/5/5
2	NDP	C	300	-	-	8/30/77/77	0/5/5/5
3	2M3	E	7	-	-	2/14/33/33	0/5/5/5

All (109) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	290	2M3	C9-C5	6.21	1.47	1.40
3	B	1	2M3	C9-C5	6.09	1.47	1.40
3	A	2	2M3	C9-C5	6.03	1.47	1.40
3	E	7	2M3	C9-C5	5.95	1.47	1.40
3	E	7	2M3	C1-C2	5.92	1.55	1.37
3	H	290	2M3	C1-C2	5.92	1.55	1.37
3	B	1	2M3	C1-C2	5.86	1.54	1.37
3	D	3	2M3	C1-C2	5.85	1.54	1.37
3	G	8	2M3	C1-C2	5.84	1.54	1.37
3	C	4	2M3	C1-C2	5.84	1.54	1.37
3	G	8	2M3	C9-C5	5.78	1.46	1.40
3	F	290	2M3	C1-C2	5.74	1.54	1.37
3	A	2	2M3	C1-C2	5.68	1.54	1.37
2	E	300	NDP	C3B-C2B	-5.67	1.40	1.52
2	F	300	NDP	C3B-C2B	-5.65	1.40	1.52
3	C	4	2M3	C9-C5	5.64	1.46	1.40
2	H	300	NDP	C3B-C2B	-5.55	1.40	1.52
3	D	3	2M3	C9-C5	5.42	1.46	1.40
2	A	300	NDP	C3B-C2B	-5.39	1.40	1.52
2	C	300	NDP	C3B-C2B	-5.25	1.41	1.52
2	G	300	NDP	C3B-C2B	-5.19	1.41	1.52
2	B	300	NDP	C3B-C2B	-5.02	1.41	1.52
3	F	290	2M3	C9-C5	4.83	1.45	1.40
2	C	300	NDP	C6N-C5N	4.63	1.41	1.33
2	D	300	NDP	C3B-C2B	-4.62	1.42	1.52
3	A	2	2M3	C22-C23	4.62	1.50	1.38
2	H	300	NDP	C6N-C5N	4.49	1.41	1.33
3	G	8	2M3	C22-C23	4.49	1.49	1.38
2	E	300	NDP	C6N-C5N	4.48	1.41	1.33
3	C	4	2M3	C22-C23	4.46	1.49	1.38
3	H	290	2M3	C22-C23	4.40	1.49	1.38
3	E	7	2M3	C22-C23	4.31	1.49	1.38
3	D	3	2M3	C22-C23	4.31	1.49	1.38
2	B	300	NDP	C6N-C5N	4.27	1.41	1.33
3	F	290	2M3	C22-C23	4.26	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	300	NDP	C6N-C5N	4.24	1.40	1.33
3	E	7	2M3	C5-C6	4.21	1.54	1.43
3	B	1	2M3	C22-C23	4.20	1.49	1.38
2	D	300	NDP	C6N-C5N	4.19	1.40	1.33
3	B	1	2M3	C5-C6	4.16	1.54	1.43
3	H	290	2M3	C5-C6	4.14	1.53	1.43
2	G	300	NDP	C6N-C5N	4.07	1.40	1.33
2	A	300	NDP	C6N-C5N	4.06	1.40	1.33
3	F	290	2M3	C5-C6	4.03	1.53	1.43
3	A	2	2M3	C5-C6	3.99	1.53	1.43
3	D	3	2M3	C5-C6	3.89	1.53	1.43
3	G	8	2M3	C5-C6	3.88	1.53	1.43
3	C	4	2M3	C5-C6	3.78	1.52	1.43
2	C	300	NDP	C2N-C3N	3.36	1.44	1.34
2	B	300	NDP	C2N-C3N	3.35	1.44	1.34
2	G	300	NDP	C4N-C3N	-3.31	1.43	1.49
2	F	300	NDP	C2N-C3N	3.27	1.44	1.34
2	F	300	NDP	C4N-C5N	-3.26	1.40	1.48
2	H	300	NDP	C4N-C3N	-3.16	1.43	1.49
2	B	300	NDP	C4N-C3N	-3.16	1.43	1.49
2	E	300	NDP	C4N-C5N	-3.14	1.40	1.48
2	E	300	NDP	C8A-N7A	-3.11	1.29	1.34
2	A	300	NDP	C4N-C3N	-3.11	1.43	1.49
2	C	300	NDP	C4N-C3N	-3.06	1.43	1.49
2	H	300	NDP	C2N-C3N	3.06	1.43	1.34
2	B	300	NDP	C4N-C5N	-3.05	1.40	1.48
2	H	300	NDP	C4N-C5N	-3.04	1.41	1.48
2	G	300	NDP	C4N-C5N	-3.03	1.41	1.48
2	F	300	NDP	C8A-N7A	-3.00	1.29	1.34
3	H	290	2M3	C26-C25	-2.98	1.43	1.50
2	E	300	NDP	C2N-C3N	2.98	1.43	1.34
2	E	300	NDP	C4N-C3N	-2.97	1.44	1.49
2	D	300	NDP	C2N-C3N	2.97	1.43	1.34
2	A	300	NDP	C4N-C5N	-2.97	1.41	1.48
2	G	300	NDP	C2N-C3N	2.96	1.43	1.34
3	D	3	2M3	C26-C25	-2.96	1.43	1.50
2	A	300	NDP	C2N-C3N	2.95	1.43	1.34
2	F	300	NDP	C4N-C3N	-2.92	1.44	1.49
3	B	1	2M3	C26-C25	-2.91	1.43	1.50
2	B	300	NDP	C8A-N7A	-2.90	1.29	1.34
3	G	8	2M3	C26-C25	-2.88	1.43	1.50
2	D	300	NDP	C4N-C5N	-2.87	1.41	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	300	NDP	C4N-C5N	-2.86	1.41	1.48
3	F	290	2M3	C26-C25	-2.85	1.43	1.50
3	A	2	2M3	C26-C25	-2.83	1.43	1.50
3	C	4	2M3	C26-C25	-2.83	1.43	1.50
3	E	7	2M3	C26-C25	-2.81	1.43	1.50
2	H	300	NDP	C8A-N7A	-2.78	1.29	1.34
2	A	300	NDP	C8A-N7A	-2.76	1.29	1.34
2	G	300	NDP	C8A-N7A	-2.71	1.29	1.34
2	D	300	NDP	C4N-C3N	-2.68	1.44	1.49
2	C	300	NDP	C8A-N7A	-2.56	1.30	1.34
2	F	300	NDP	P2B-O1X	2.54	1.58	1.50
2	G	300	NDP	P2B-O2B	2.50	1.64	1.59
2	H	300	NDP	P2B-O2B	2.48	1.64	1.59
2	H	300	NDP	C3B-C4B	2.39	1.59	1.53
2	A	300	NDP	C2A-N3A	2.33	1.35	1.32
2	B	300	NDP	C3B-C4B	2.28	1.58	1.53
2	C	300	NDP	P2B-O1X	2.26	1.57	1.50
3	H	290	2M3	C6-N3	-2.26	1.34	1.37
3	F	290	2M3	C6-N3	-2.25	1.34	1.37
2	D	300	NDP	P2B-O1X	2.21	1.57	1.50
2	E	300	NDP	P2B-O1X	2.18	1.57	1.50
2	F	300	NDP	P2B-O2B	2.18	1.63	1.59
2	B	300	NDP	P2B-O2B	2.15	1.63	1.59
2	C	300	NDP	P2B-O2B	2.14	1.63	1.59
2	B	300	NDP	P2B-O1X	2.12	1.57	1.50
3	C	4	2M3	C16-N14	2.11	1.38	1.35
2	A	300	NDP	C3B-C4B	2.09	1.58	1.53
2	F	300	NDP	C3B-C4B	2.07	1.58	1.53
3	F	290	2M3	C24-C19	2.05	1.42	1.39
2	C	300	NDP	C2A-N3A	2.03	1.35	1.32
2	D	300	NDP	C8A-N7A	-2.02	1.31	1.34
2	C	300	NDP	C3B-C4B	2.00	1.58	1.53

All (138) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	300	NDP	N3A-C2A-N1A	-4.86	121.08	128.68
2	E	300	NDP	N3A-C2A-N1A	-4.86	121.08	128.68
3	D	3	2M3	C21-N20-C19	4.83	124.09	117.49
2	D	300	NDP	N3A-C2A-N1A	-4.80	121.18	128.68
3	H	290	2M3	C26-C17-C25	-4.79	56.30	58.33
3	H	290	2M3	C21-N20-C19	4.79	124.04	117.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	300	NDP	N3A-C2A-N1A	-4.77	121.23	128.68
2	C	300	NDP	N3A-C2A-N1A	-4.72	121.30	128.68
3	C	4	2M3	C21-N20-C19	4.72	123.95	117.49
3	F	290	2M3	C26-C17-C25	-4.69	56.35	58.33
3	F	290	2M3	C21-N20-C19	4.65	123.85	117.49
3	E	7	2M3	C21-N20-C19	4.63	123.83	117.49
3	G	8	2M3	C26-C17-C25	-4.62	56.37	58.33
3	B	1	2M3	C26-C17-C25	-4.62	56.38	58.33
2	G	300	NDP	N3A-C2A-N1A	-4.60	121.49	128.68
2	H	300	NDP	N3A-C2A-N1A	-4.55	121.56	128.68
3	A	2	2M3	C21-N20-C19	4.55	123.72	117.49
3	B	1	2M3	C21-N20-C19	4.53	123.69	117.49
3	C	4	2M3	C2-N3-C6	4.51	122.16	116.60
3	G	8	2M3	C21-N20-C19	4.50	123.65	117.49
3	D	3	2M3	C2-N3-C6	4.48	122.13	116.60
3	A	2	2M3	C2-N3-C6	4.45	122.09	116.60
3	G	8	2M3	C2-N3-C6	4.41	122.04	116.60
3	D	3	2M3	C26-C17-C25	-4.36	56.48	58.33
3	H	290	2M3	C2-N3-C6	4.34	121.95	116.60
3	B	1	2M3	C2-N3-C6	4.33	121.94	116.60
2	D	300	NDP	C3B-C2B-C1B	4.20	110.79	102.89
3	A	2	2M3	C26-C17-C25	-4.20	56.55	58.33
3	C	4	2M3	C26-C17-C25	-4.19	56.56	58.33
3	F	290	2M3	C2-N3-C6	4.16	121.73	116.60
2	A	300	NDP	N3A-C2A-N1A	-4.14	122.20	128.68
3	E	7	2M3	C26-C17-C25	-4.14	56.58	58.33
3	E	7	2M3	C2-N3-C6	4.08	121.63	116.60
2	H	300	NDP	C3B-C2B-C1B	4.07	110.53	102.89
2	F	300	NDP	C3B-C2B-C1B	3.99	110.39	102.89
2	G	300	NDP	C3B-C2B-C1B	3.95	110.32	102.89
2	B	300	NDP	C3B-C2B-C1B	3.86	110.15	102.89
3	A	2	2M3	C12-C13-N14	3.85	107.83	103.28
2	B	300	NDP	O4B-C1B-C2B	-3.73	100.11	106.59
3	E	7	2M3	C12-C13-N14	3.71	107.67	103.28
3	G	8	2M3	C19-C17-C16	-3.60	107.68	114.25
3	C	4	2M3	C12-C13-N14	3.56	107.48	103.28
2	C	300	NDP	C3B-C2B-C1B	3.55	109.56	102.89
2	E	300	NDP	C3B-C2B-C1B	3.45	109.38	102.89
3	H	290	2M3	C17-C16-N14	3.36	123.22	118.60
3	H	290	2M3	C12-C13-N14	3.36	107.25	103.28
2	A	300	NDP	C3B-C2B-C1B	3.35	109.18	102.89
3	B	1	2M3	C12-C13-N14	3.25	107.13	103.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	8	2M3	C13-C12-C11	-3.25	100.38	105.73
3	F	290	2M3	C12-C13-N14	3.25	107.12	103.28
2	C	300	NDP	O4B-C1B-C2B	-3.15	101.13	106.59
3	D	3	2M3	C12-C13-N14	3.14	106.99	103.28
3	E	7	2M3	C12-C11-C9	-3.06	109.70	115.08
2	F	300	NDP	O4B-C1B-C2B	-3.05	101.29	106.59
3	G	8	2M3	C26-C17-C19	3.05	122.36	117.28
3	B	1	2M3	C19-C17-C16	-3.01	108.76	114.25
2	G	300	NDP	O4B-C1B-C2B	-2.98	101.42	106.59
3	A	2	2M3	C10-C8-C9	-2.97	124.17	129.79
3	C	4	2M3	C19-C17-C16	-2.97	108.84	114.25
3	H	290	2M3	C10-C8-C9	-2.92	124.27	129.79
3	B	1	2M3	C10-C8-C9	-2.90	124.31	129.79
3	G	8	2M3	C12-C13-N14	2.87	106.67	103.28
2	H	300	NDP	O4B-C1B-C2B	-2.86	101.63	106.59
2	D	300	NDP	O4B-C1B-C2B	-2.85	101.65	106.59
3	B	1	2M3	C26-C17-C19	2.84	122.00	117.28
3	F	290	2M3	C10-C8-C9	-2.84	124.42	129.79
3	D	3	2M3	C13-C12-C11	-2.82	101.09	105.73
3	D	3	2M3	C17-C16-N14	2.81	122.46	118.60
3	F	290	2M3	C19-C17-C16	-2.79	109.16	114.25
3	F	290	2M3	C26-C17-C19	2.78	121.90	117.28
3	E	7	2M3	C19-C17-C16	-2.76	109.22	114.25
3	E	7	2M3	C10-C8-C9	-2.75	124.59	129.79
3	D	3	2M3	C10-C8-C9	-2.75	124.59	129.79
3	G	8	2M3	C10-C8-C9	-2.74	124.60	129.79
3	H	290	2M3	C26-C17-C16	2.71	121.76	115.48
3	G	8	2M3	C26-C17-C16	2.70	121.75	115.48
2	E	300	NDP	O4B-C1B-C2B	-2.70	101.91	106.59
3	C	4	2M3	C10-C8-C9	-2.65	124.77	129.79
3	A	2	2M3	C12-C11-C9	-2.65	110.42	115.08
3	C	4	2M3	C26-C17-C16	2.62	121.55	115.48
2	A	300	NDP	O4B-C1B-C2B	-2.61	102.05	106.59
3	E	7	2M3	C26-C17-C16	2.61	121.53	115.48
3	H	290	2M3	C19-C17-C16	-2.58	109.54	114.25
3	G	8	2M3	C17-C16-N14	2.58	122.15	118.60
3	B	1	2M3	C26-C17-C16	2.55	121.40	115.48
3	A	2	2M3	C17-C16-N14	2.55	122.10	118.60
3	A	2	2M3	C19-C17-C16	-2.51	109.67	114.25
3	F	290	2M3	C26-C17-C16	2.48	121.24	115.48
3	E	7	2M3	C17-C16-N14	2.48	122.00	118.60
3	C	4	2M3	C26-C17-C19	2.47	121.38	117.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	300	NDP	C3N-C2N-N1N	-2.42	119.64	123.10
3	B	1	2M3	C12-C11-C9	-2.42	110.82	115.08
3	B	1	2M3	C17-C16-N14	2.38	121.88	118.60
3	A	2	2M3	C26-C17-C19	2.37	121.22	117.28
3	F	290	2M3	C13-C12-C11	-2.37	101.84	105.73
3	E	7	2M3	C26-C17-C19	2.36	121.21	117.28
3	D	3	2M3	C26-C17-C16	2.36	120.96	115.48
3	C	4	2M3	C13-C12-C11	-2.36	101.86	105.73
2	F	300	NDP	C3N-C2N-N1N	-2.32	119.78	123.10
3	H	290	2M3	C26-C25-C17	2.32	61.96	60.84
3	A	2	2M3	C26-C17-C16	2.32	120.86	115.48
2	D	300	NDP	C3N-C2N-N1N	-2.31	119.79	123.10
2	B	300	NDP	C3N-C2N-N1N	-2.31	119.80	123.10
3	G	8	2M3	C25-C17-C16	2.30	120.83	115.48
3	G	8	2M3	C25-C26-C17	2.30	61.95	60.84
3	H	290	2M3	C13-C12-C11	-2.30	101.95	105.73
3	E	7	2M3	C25-C26-C17	2.30	61.95	60.84
3	F	290	2M3	C17-C16-N14	2.28	121.73	118.60
3	D	3	2M3	C22-C21-N20	-2.24	119.77	123.43
3	H	290	2M3	C26-C17-C19	2.23	121.00	117.28
2	C	300	NDP	C3N-C2N-N1N	-2.23	119.91	123.10
3	D	3	2M3	C26-C17-C19	2.23	120.98	117.28
3	H	290	2M3	C22-C21-N20	-2.22	119.81	123.43
2	D	300	NDP	C2A-N1A-C6A	2.19	122.51	118.75
2	D	300	NDP	O4D-C1D-N1N	2.18	112.32	108.06
3	G	8	2M3	C22-C21-N20	-2.17	119.88	123.43
3	D	3	2M3	C19-C17-C16	-2.16	110.31	114.25
3	C	4	2M3	C22-C21-N20	-2.14	119.93	123.43
3	C	4	2M3	C17-C16-N14	2.13	121.52	118.60
2	A	300	NDP	C3N-C2N-N1N	-2.12	120.06	123.10
2	A	300	NDP	O4D-C1D-N1N	2.12	112.21	108.06
3	F	290	2M3	C26-C25-C17	2.12	61.86	60.84
3	C	4	2M3	C1-C2-N3	-2.12	120.70	123.94
3	G	8	2M3	C9-C5-C6	-2.09	103.64	106.47
3	B	1	2M3	C26-C25-C17	2.09	61.85	60.84
3	A	2	2M3	C22-C21-N20	-2.08	120.02	123.43
3	D	3	2M3	C9-C5-C6	-2.08	103.65	106.47
3	B	1	2M3	C9-C5-C6	-2.08	103.66	106.47
3	E	7	2M3	C1-C2-N3	-2.06	120.78	123.94
3	E	7	2M3	C9-C5-C6	-2.06	103.68	106.47
3	F	290	2M3	C9-C5-C6	-2.05	103.70	106.47
3	A	2	2M3	C9-C5-C6	-2.05	103.70	106.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	2M3	C1-C2-N3	-2.04	120.82	123.94
3	B	1	2M3	C13-N14-C15	-2.04	106.29	111.55
3	E	7	2M3	C22-C21-N20	-2.03	120.12	123.43
3	H	290	2M3	C9-C5-C6	-2.03	103.73	106.47
3	B	1	2M3	C22-C21-N20	-2.01	120.14	123.43
3	G	8	2M3	C1-C2-N3	-2.01	120.86	123.94

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NDP	C2B-O2B-P2B-O2X
2	A	300	NDP	C5D-O5D-PN-O1N
2	A	300	NDP	C5D-O5D-PN-O2N
2	B	300	NDP	C5B-O5B-PA-O3
2	B	300	NDP	O4B-C4B-C5B-O5B
2	B	300	NDP	C2B-O2B-P2B-O1X
2	C	300	NDP	C2B-O2B-P2B-O1X
2	D	300	NDP	C2B-O2B-P2B-O1X
2	D	300	NDP	C5D-O5D-PN-O1N
2	E	300	NDP	C2B-O2B-P2B-O2X
2	F	300	NDP	C5B-O5B-PA-O1A
2	F	300	NDP	C5B-O5B-PA-O3
2	F	300	NDP	C2B-O2B-P2B-O1X
2	G	300	NDP	C2B-O2B-P2B-O1X
2	G	300	NDP	C5D-O5D-PN-O3
2	G	300	NDP	C5D-O5D-PN-O2N
2	H	300	NDP	C2B-O2B-P2B-O2X
2	H	300	NDP	C5D-O5D-PN-O1N
2	H	300	NDP	C5D-O5D-PN-O2N
3	C	4	2M3	C26-C17-C19-N20
2	D	300	NDP	O4D-C1D-N1N-C6N
2	B	300	NDP	C3B-C4B-C5B-O5B
2	F	300	NDP	O4B-C4B-C5B-O5B
2	A	300	NDP	O4D-C1D-N1N-C6N
2	C	300	NDP	O4D-C1D-N1N-C6N
2	E	300	NDP	O4D-C1D-N1N-C6N
2	F	300	NDP	O4D-C1D-N1N-C6N
2	D	300	NDP	O4B-C4B-C5B-O5B
2	F	300	NDP	C3B-C4B-C5B-O5B
2	B	300	NDP	O4D-C1D-N1N-C6N
2	G	300	NDP	O4D-C1D-N1N-C6N

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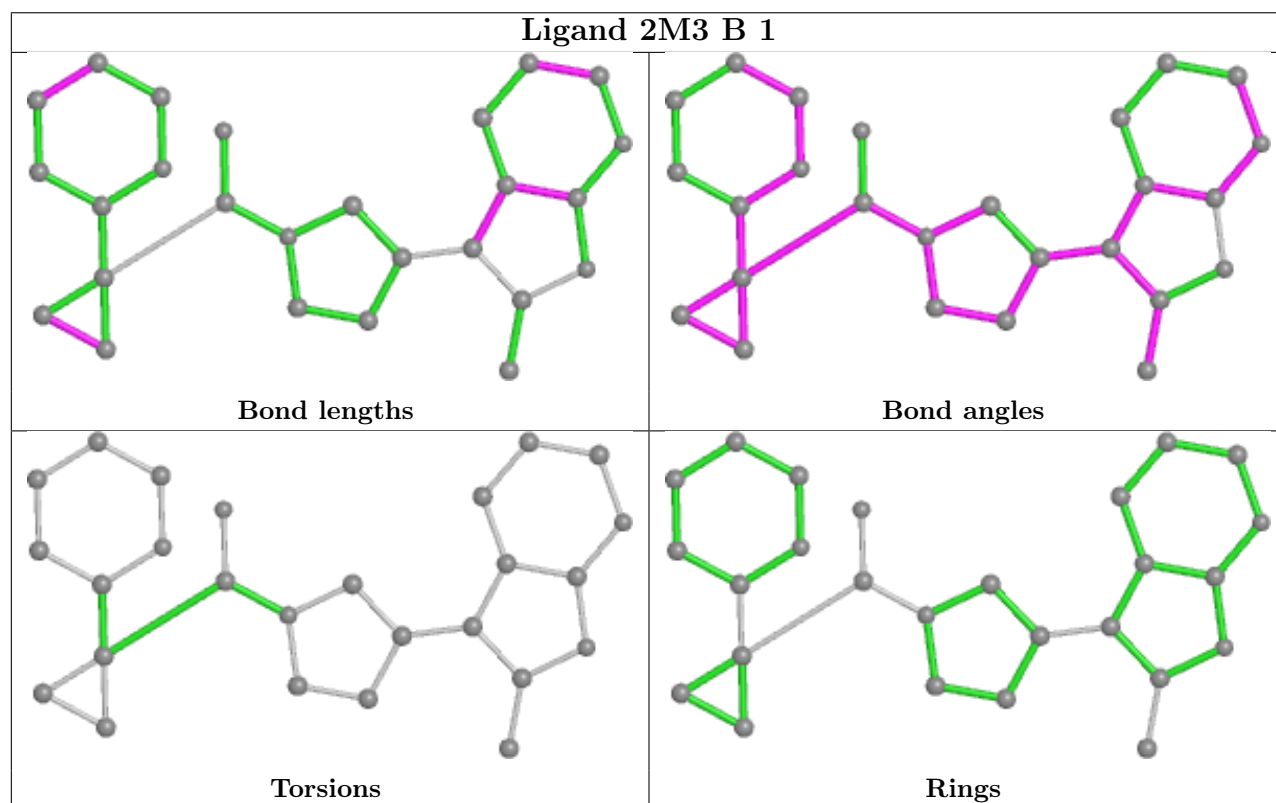
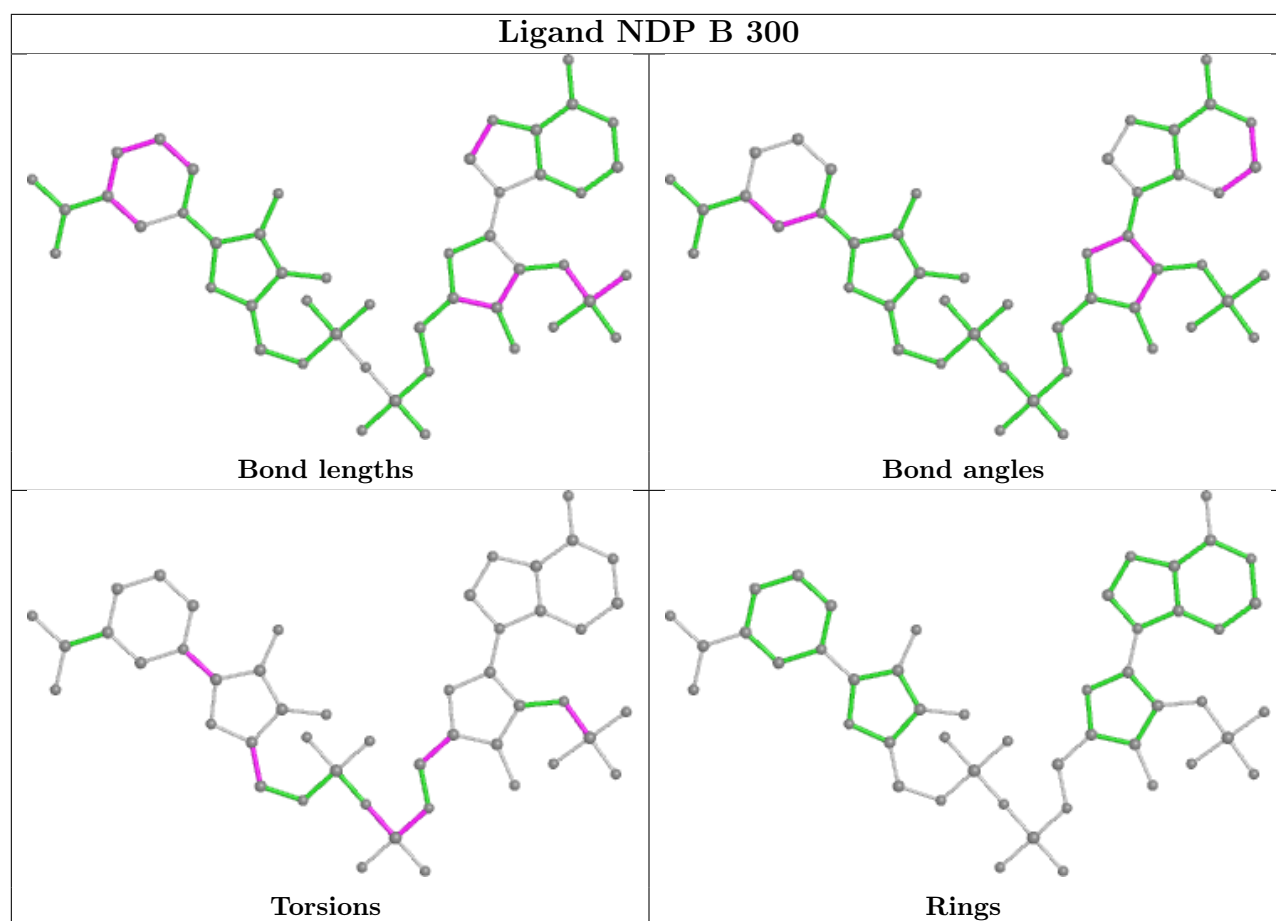
Mol	Chain	Res	Type	Atoms
2	H	300	NDP	O4D-C1D-N1N-C6N
3	C	4	2M3	C26-C17-C19-C24
3	E	7	2M3	C26-C17-C19-C24
3	G	8	2M3	C26-C17-C19-C24
2	B	300	NDP	O4D-C4D-C5D-O5D
2	H	300	NDP	C2B-O2B-P2B-O1X
2	C	300	NDP	C2B-O2B-P2B-O2X
2	D	300	NDP	C5D-O5D-PN-O3
2	F	300	NDP	C2B-O2B-P2B-O2X
2	G	300	NDP	C2B-O2B-P2B-O2X
2	H	300	NDP	C5D-O5D-PN-O3
2	B	300	NDP	PN-O3-PA-O1A
2	F	300	NDP	PN-O3-PA-O1A
2	H	300	NDP	PA-O3-PN-O1N
2	B	300	NDP	C5B-O5B-PA-O1A
2	B	300	NDP	C5B-O5B-PA-O2A
2	D	300	NDP	C5D-O5D-PN-O2N
2	C	300	NDP	C1B-C2B-O2B-P2B
2	C	300	NDP	O4D-C4D-C5D-O5D
2	H	300	NDP	O4B-C4B-C5B-O5B
2	E	300	NDP	PN-O3-PA-O1A
3	D	3	2M3	C26-C17-C19-C24
2	C	300	NDP	PN-O3-PA-O1A
2	B	300	NDP	C3D-C4D-C5D-O5D
2	C	300	NDP	C3D-C4D-C5D-O5D
3	E	7	2M3	C26-C17-C19-N20
3	G	8	2M3	C26-C17-C19-N20
2	A	300	NDP	C5D-O5D-PN-O3
2	F	300	NDP	C5D-O5D-PN-O3
2	G	300	NDP	O4B-C4B-C5B-O5B
2	A	300	NDP	PA-O3-PN-O1N
2	B	300	NDP	PN-O3-PA-O2A
2	E	300	NDP	PN-O3-PA-O2A
2	A	300	NDP	C2N-C3N-C7N-N7N
2	F	300	NDP	C5D-O5D-PN-O2N
2	A	300	NDP	O4B-C4B-C5B-O5B
2	C	300	NDP	O4B-C4B-C5B-O5B
2	E	300	NDP	O4B-C4B-C5B-O5B
2	A	300	NDP	C1B-C2B-O2B-P2B

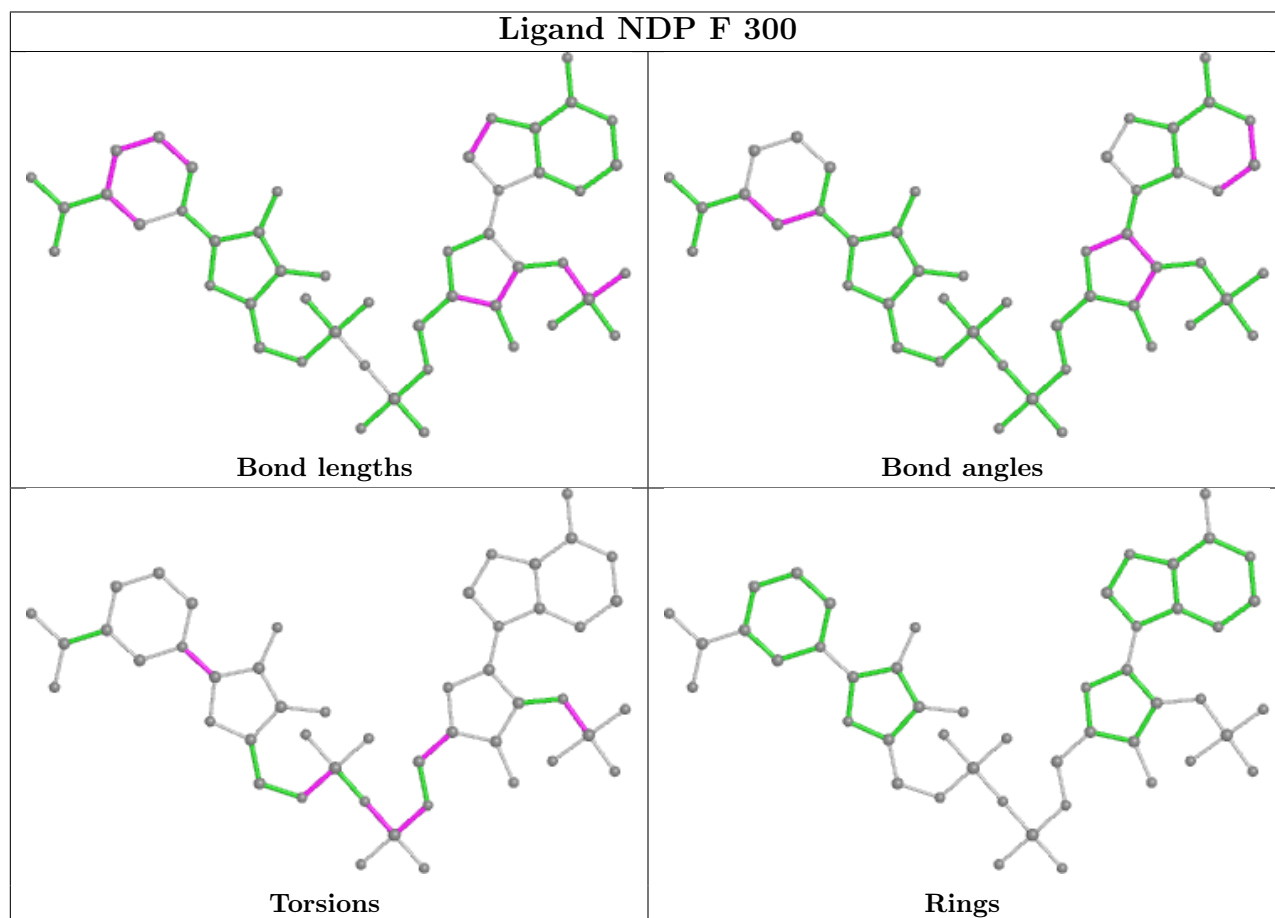
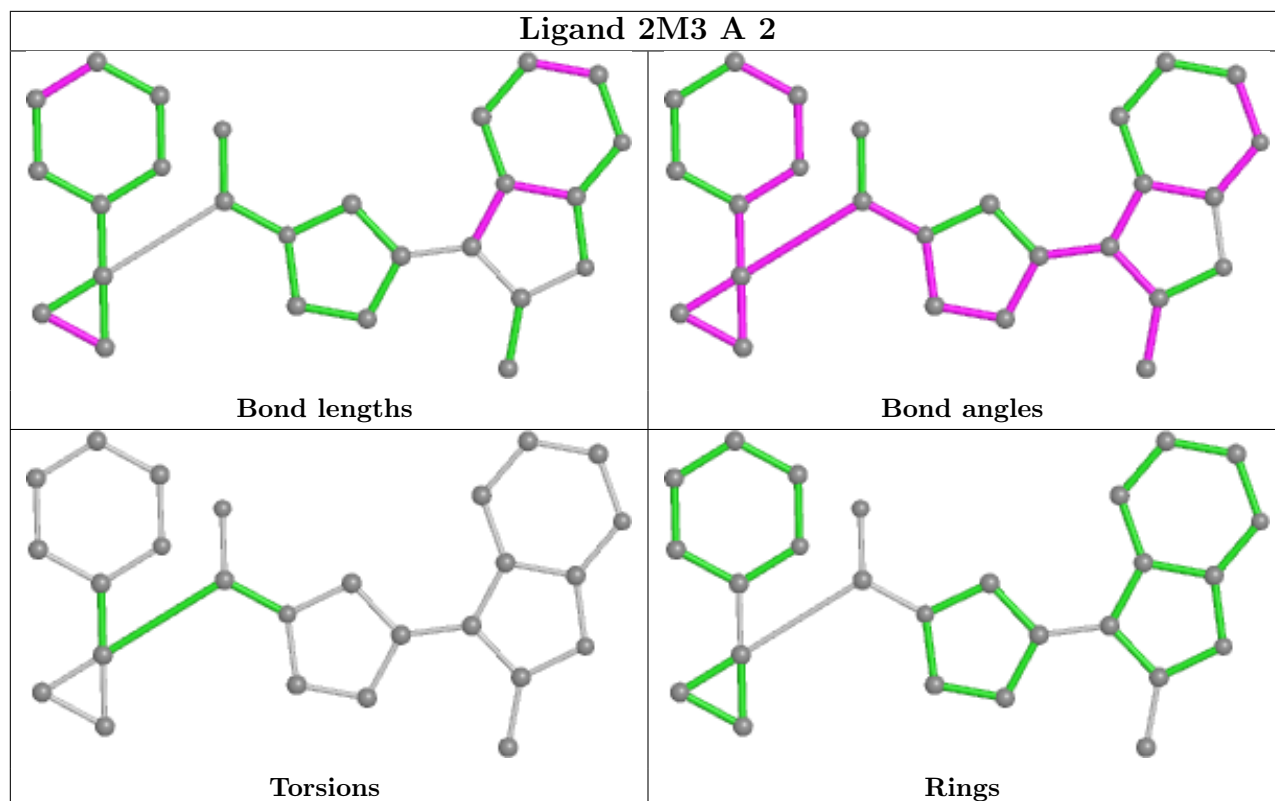
There are no ring outliers.

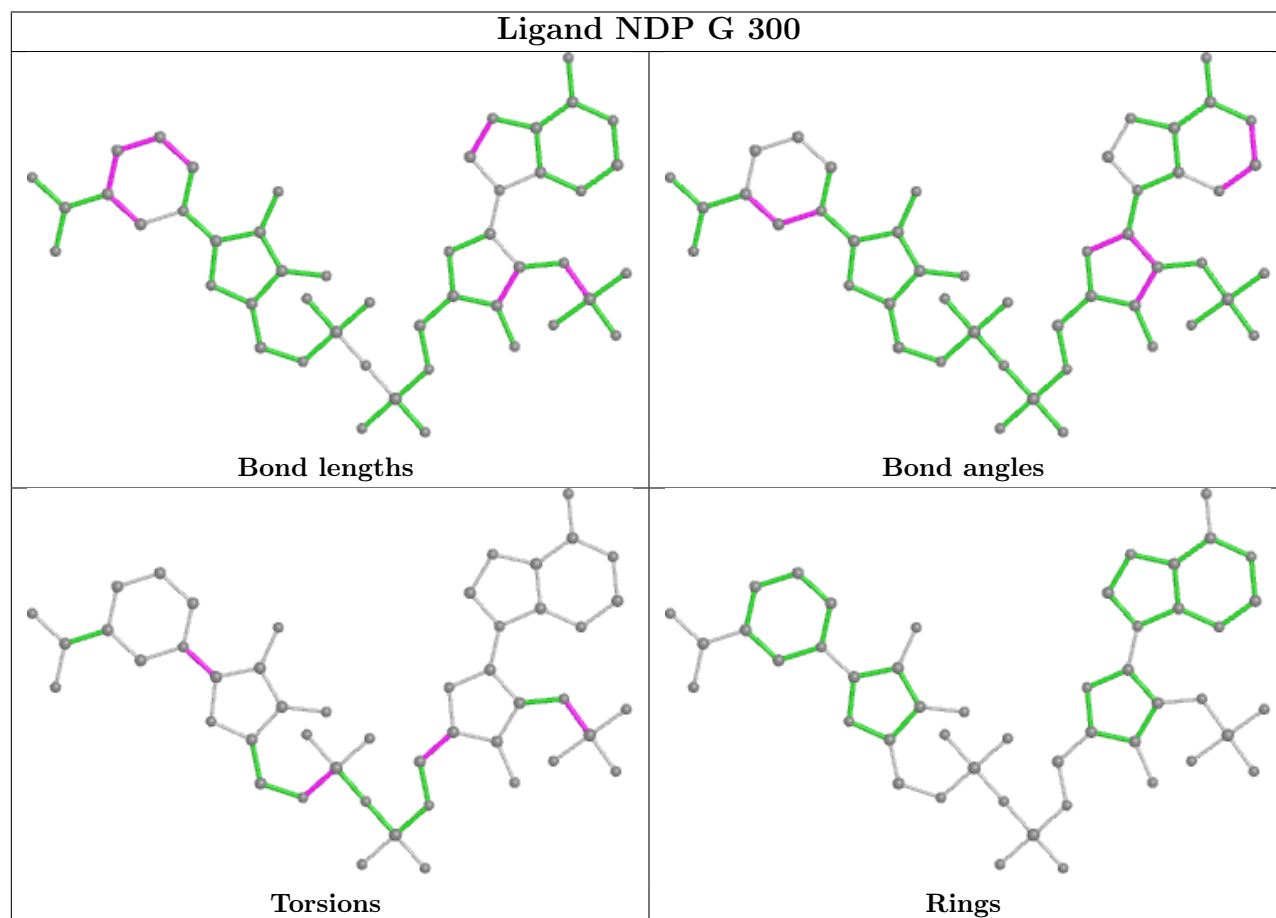
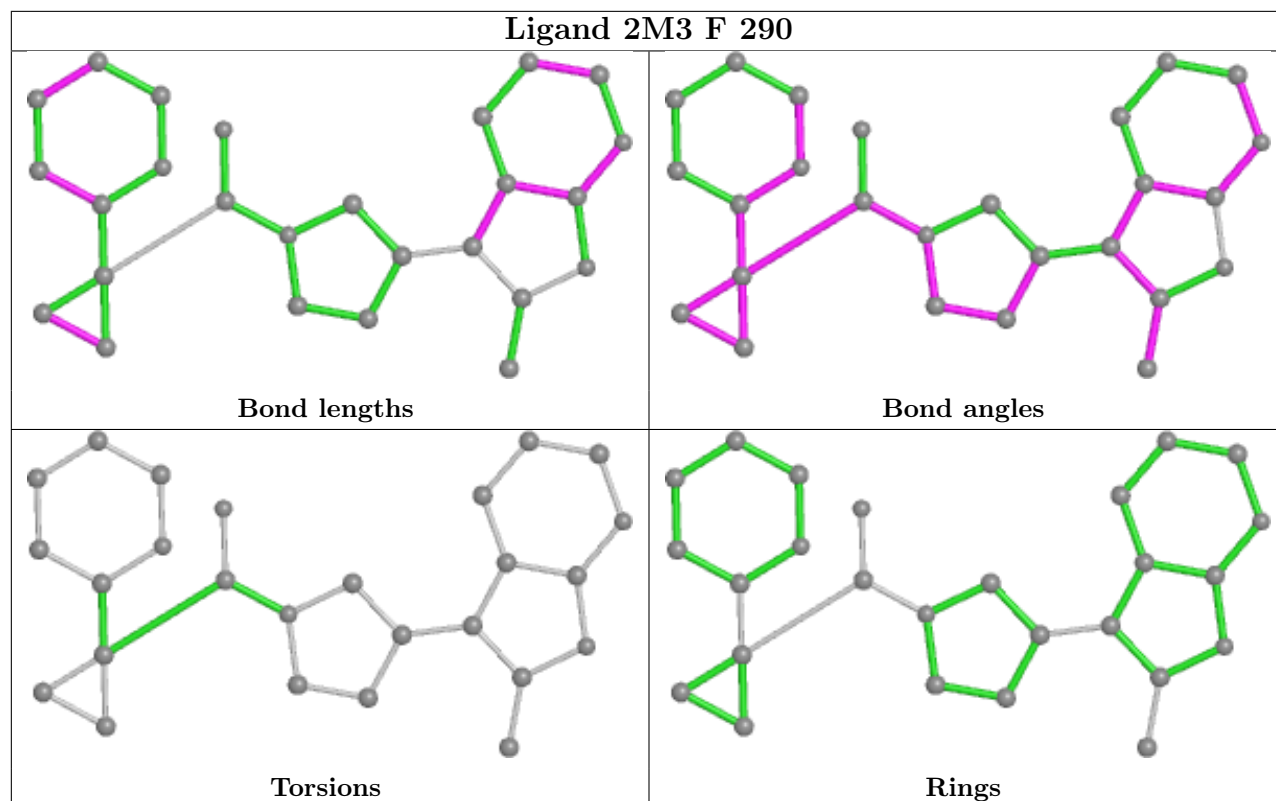
17 monomers are involved in 40 short contacts:

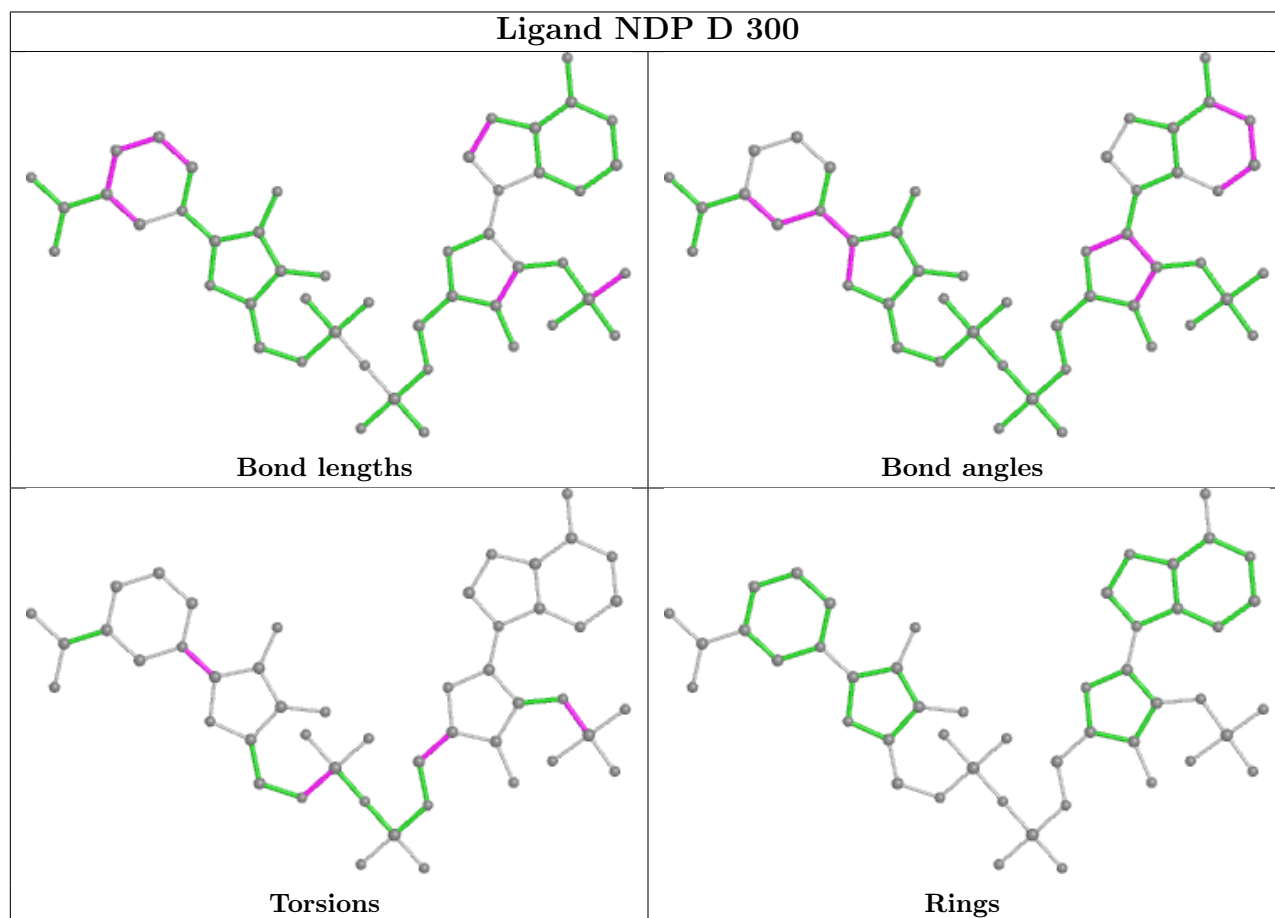
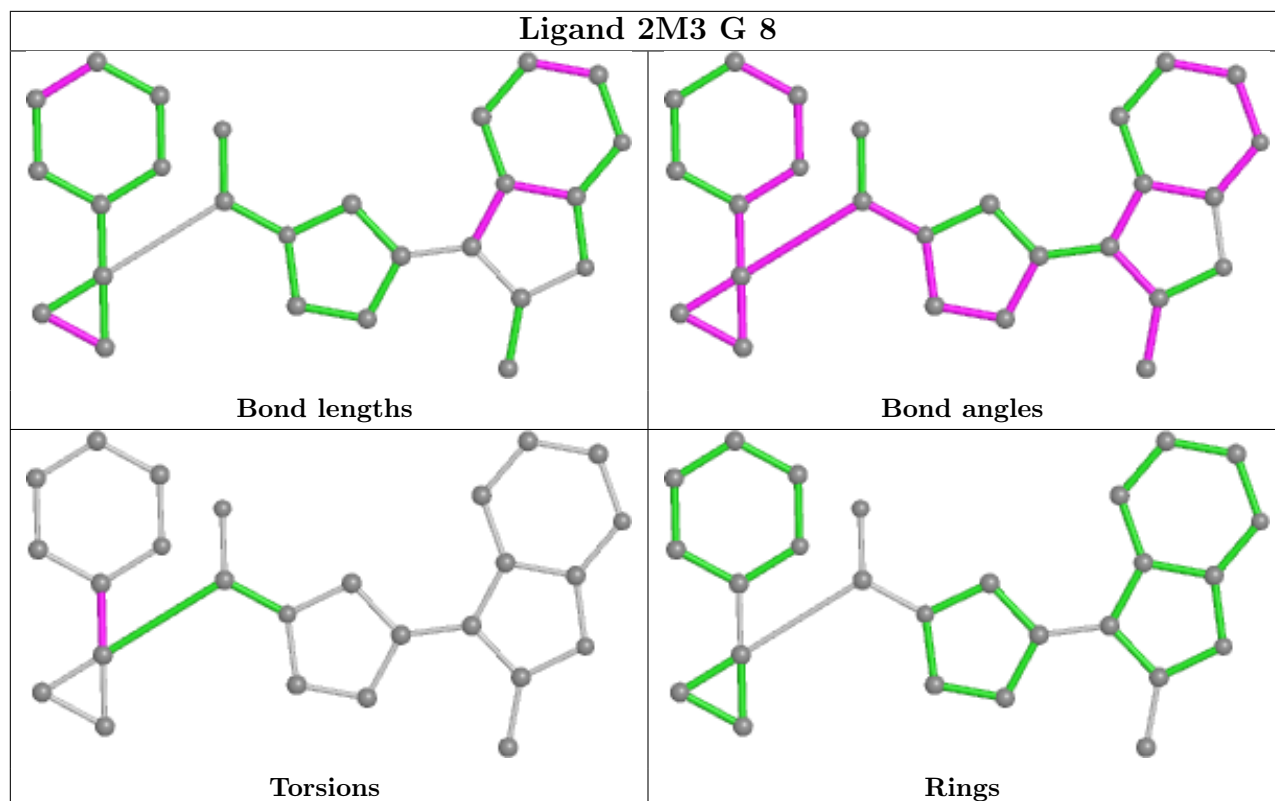
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	300	NDP	2	0
3	B	1	2M3	5	0
2	F	300	NDP	3	0
3	F	290	2M3	4	0
2	G	300	NDP	4	0
3	G	8	2M3	2	0
2	D	300	NDP	3	0
3	C	4	2M3	5	0
4	E	4	SO4	1	0
3	D	3	2M3	3	0
4	C	8	SO4	1	0
2	E	300	NDP	4	0
2	A	300	NDP	2	0
2	H	300	NDP	2	0
4	B	2	SO4	1	0
3	E	7	2M3	3	0
3	H	290	2M3	1	0

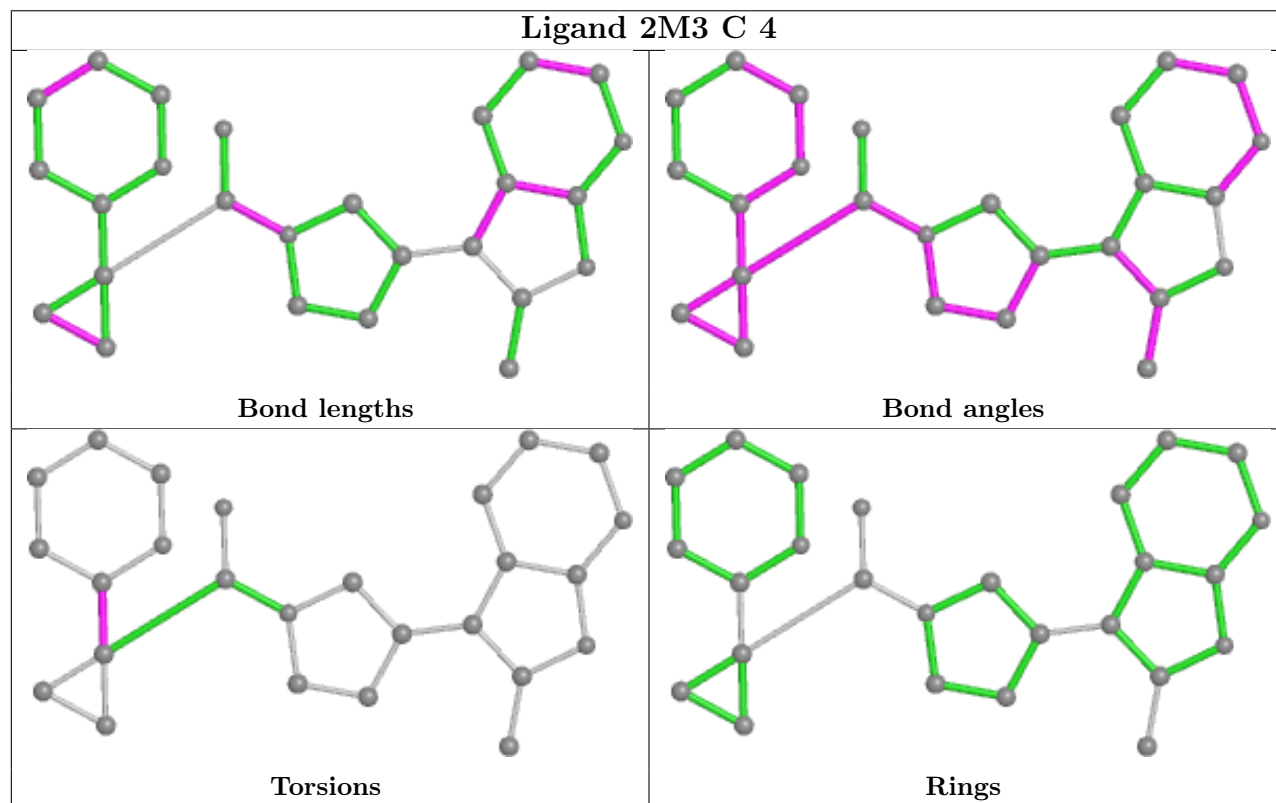
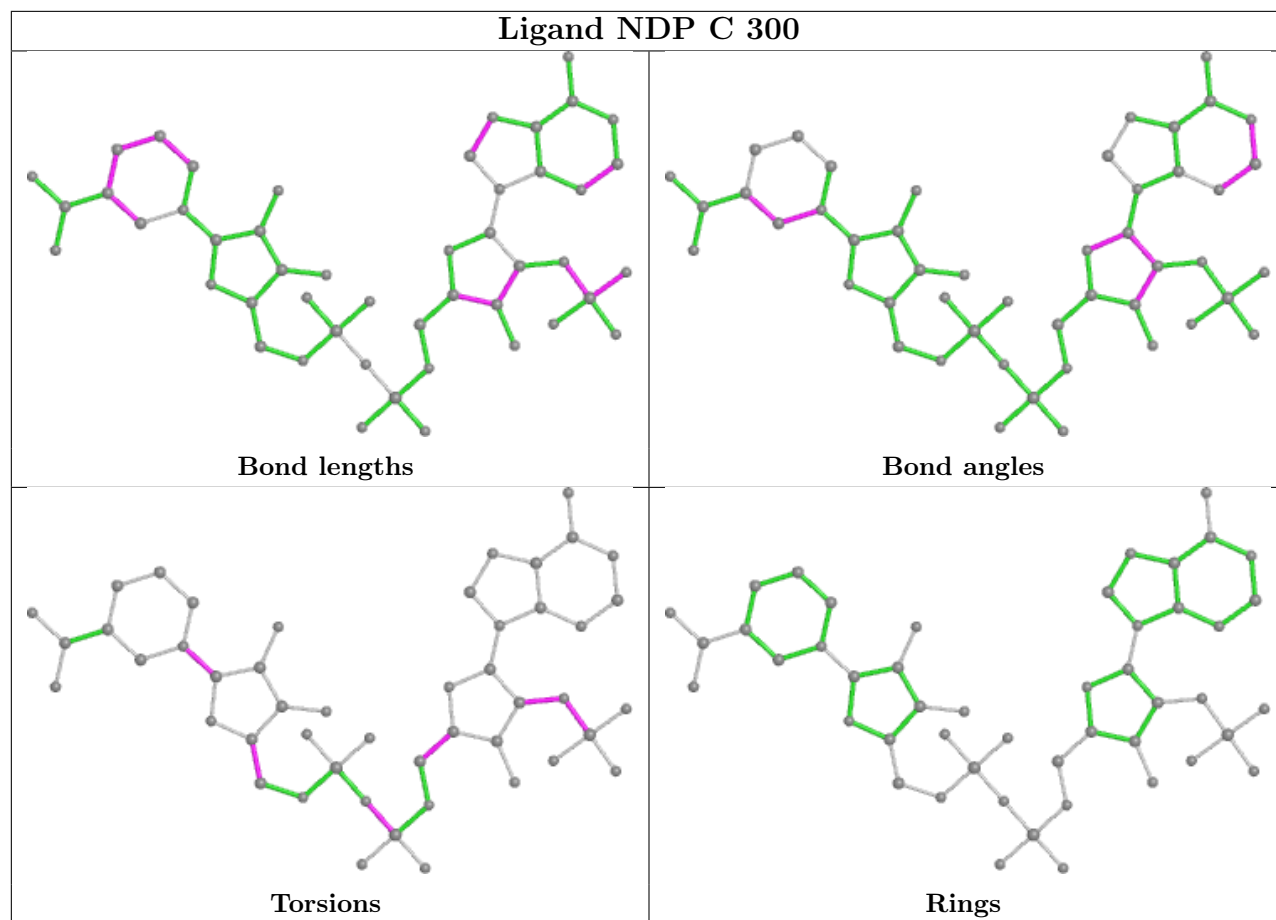
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

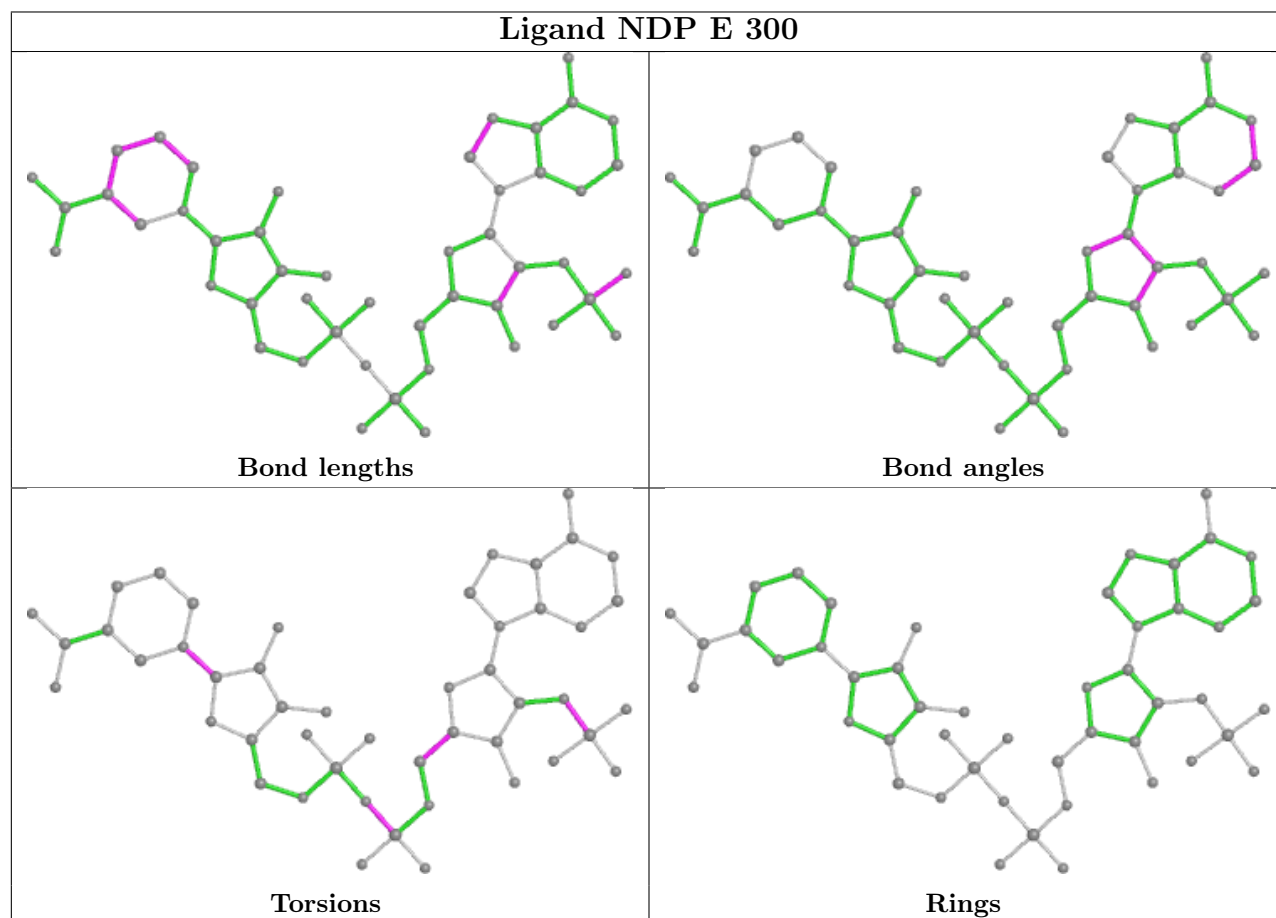
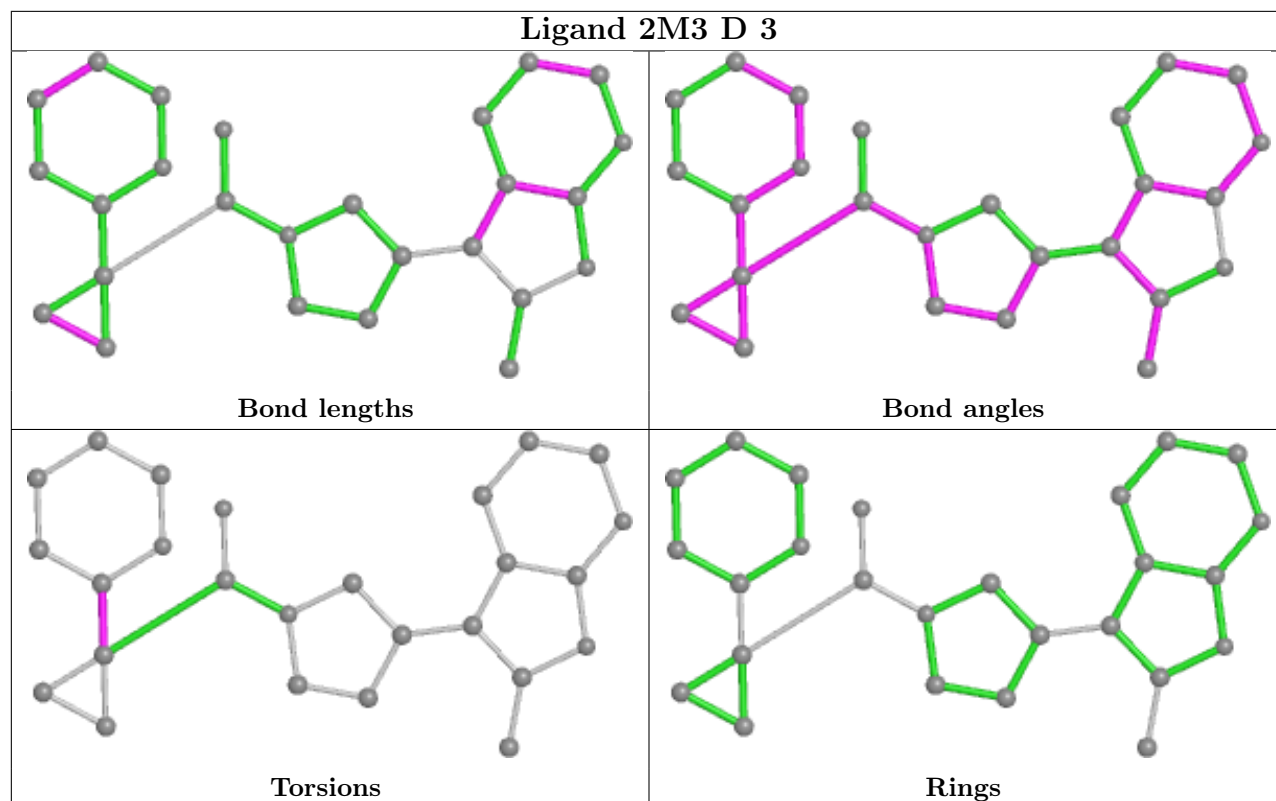


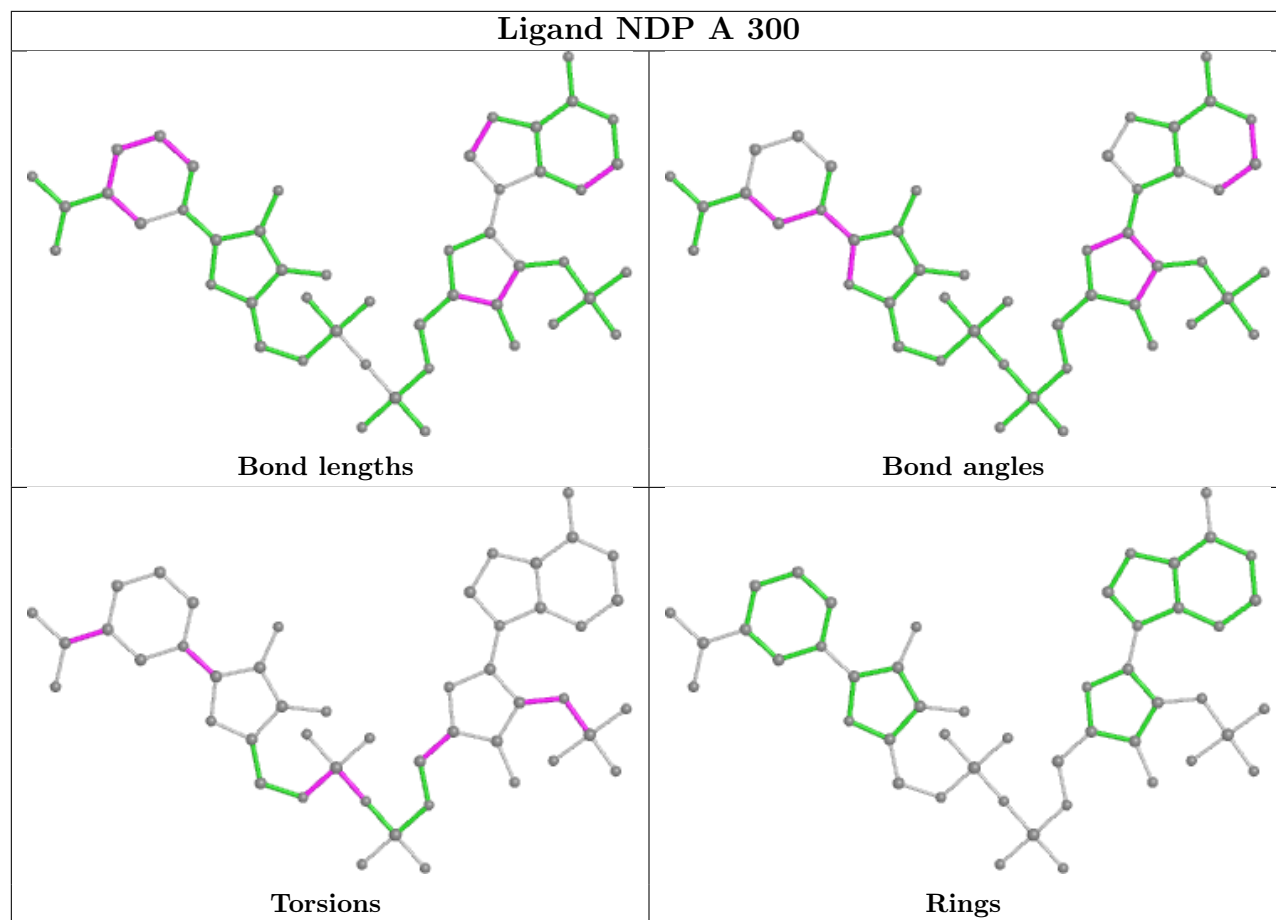


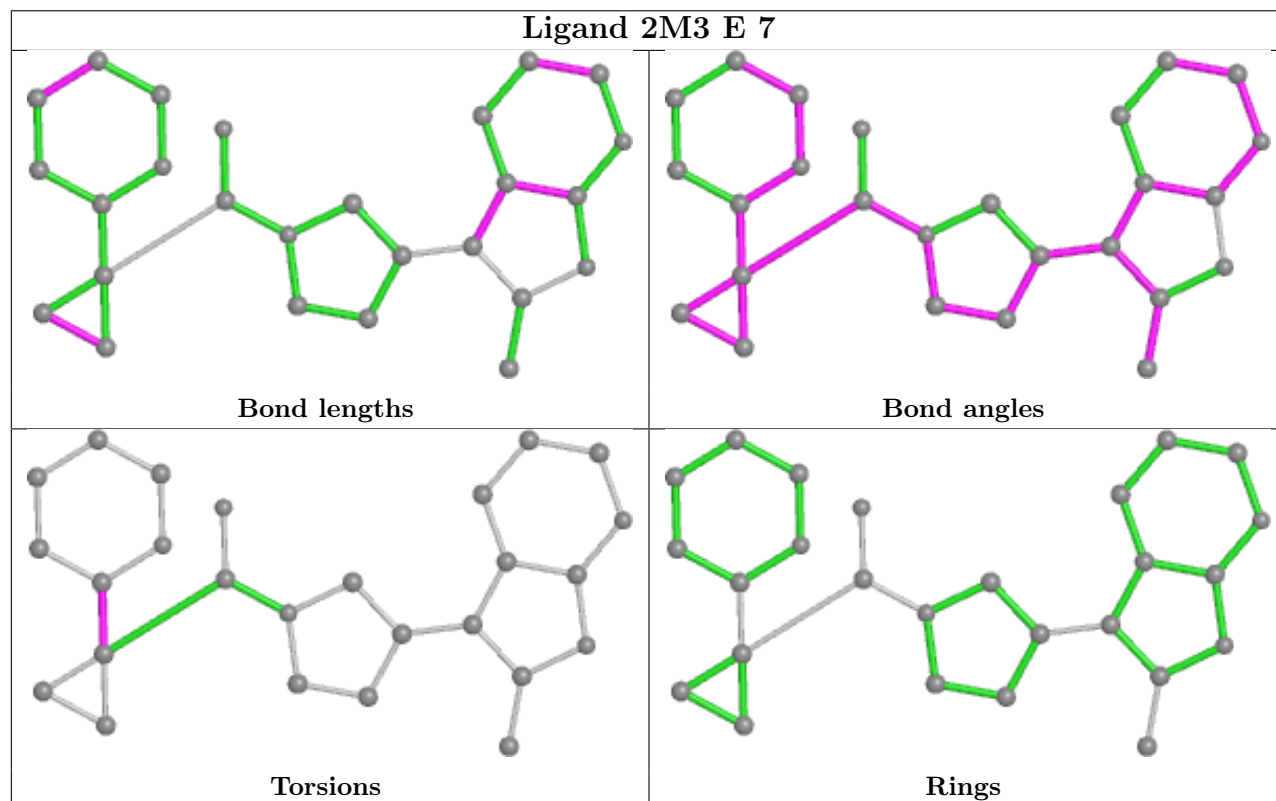
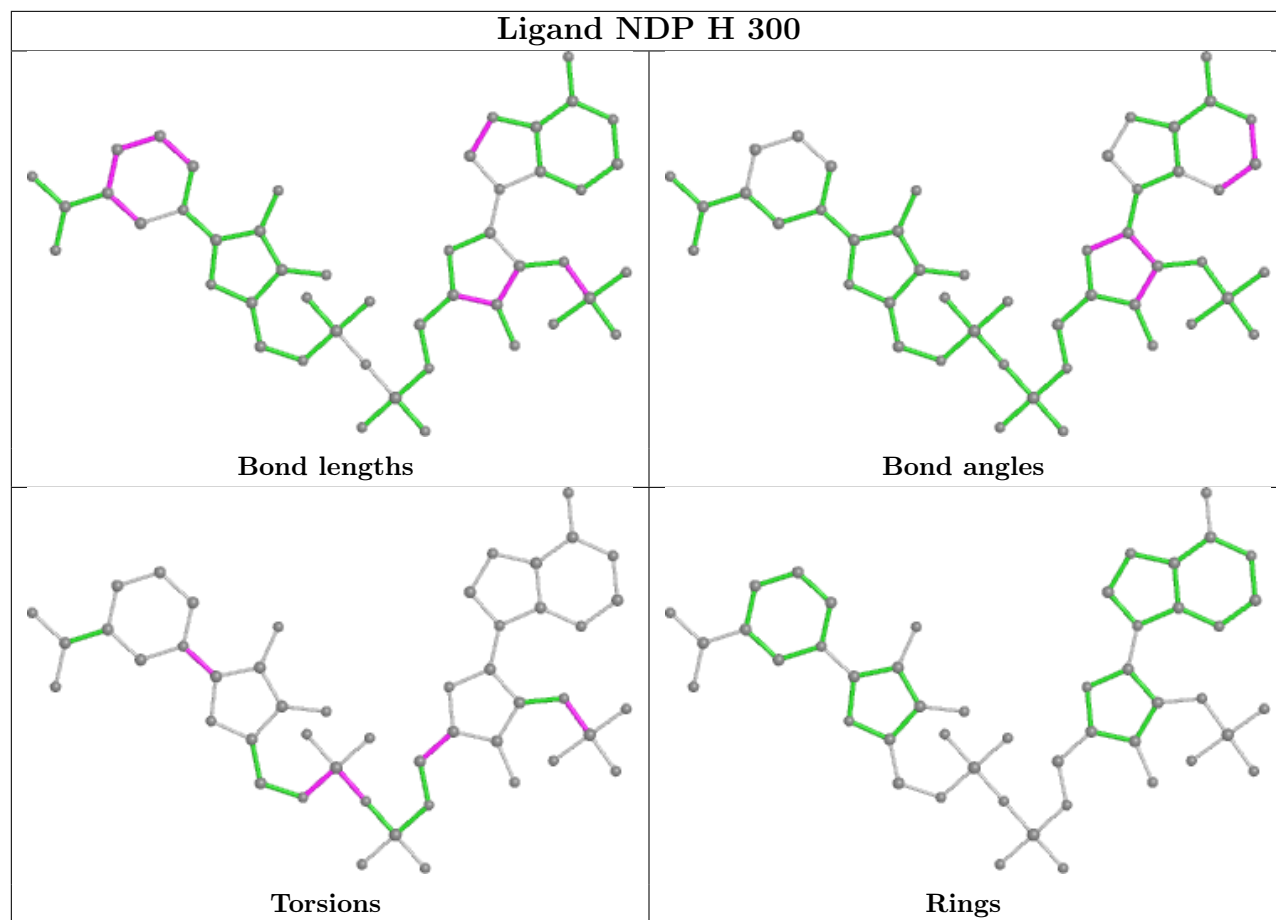


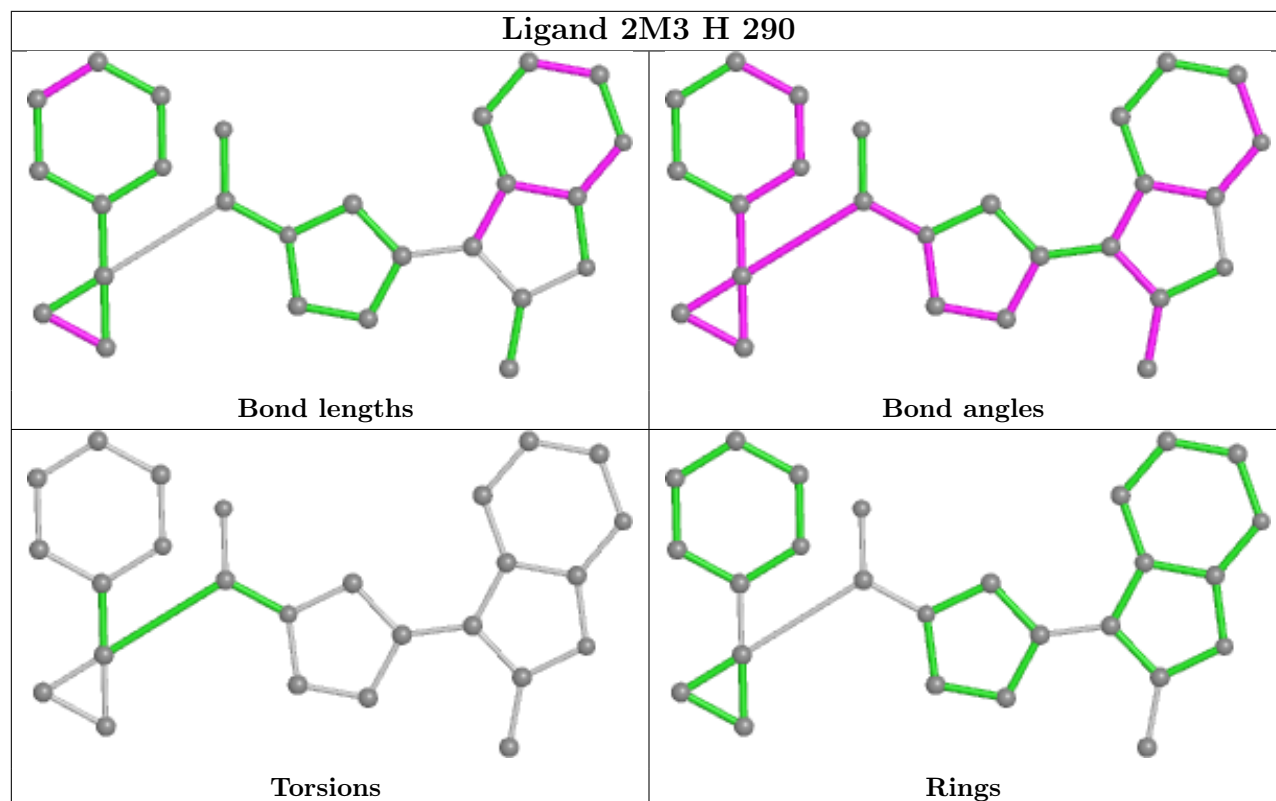












5.7 Other polymers [i](#)

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	264/264 (100%)	0.13	4 (1%) 73 78	17, 30, 49, 71	6 (2%)
1	B	264/264 (100%)	0.31	9 (3%) 45 50	19, 30, 53, 58	9 (3%)
1	C	264/264 (100%)	-0.22	2 (0%) 86 89	5, 18, 40, 56	5 (1%)
1	D	264/264 (100%)	-0.20	5 (1%) 66 72	5, 18, 45, 58	7 (2%)
1	E	264/264 (100%)	-0.14	3 (1%) 80 84	8, 20, 43, 72	5 (1%)
1	F	263/264 (99%)	-0.15	4 (1%) 73 78	7, 20, 44, 57	2 (0%)
1	G	264/264 (100%)	0.03	0 100 100	14, 27, 48, 58	8 (3%)
1	H	264/264 (100%)	0.12	5 (1%) 66 72	15, 28, 53, 69	6 (2%)
All	All	2111/2112 (99%)	-0.02	32 (1%) 73 78	5, 25, 48, 72	48 (2%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	263	LEU	7.0
1	B	264	THR	4.7
1	H	262	PRO	4.0
1	A	289	PHE	3.7
1	B	266	ILE	3.4
1	B	283	TYR	3.3
1	B	262	PRO	3.1
1	B	265	PRO	2.9
1	D	289	PHE	2.9
1	C	278	PHE	2.8
1	F	202	TYR	2.6
1	A	278	PHE	2.6
1	H	234	GLN	2.5
1	H	265	PRO	2.5
1	E	263	LEU	2.4
1	F	278	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	266	ILE	2.4
1	B	269	GLY	2.4
1	E	289	PHE	2.4
1	D	281	LEU	2.3
1	D	267	LEU	2.3
1	F	262	PRO	2.3
1	E	283	TYR	2.2
1	F	265	PRO	2.2
1	H	289	PHE	2.2
1	H	261	SER	2.2
1	D	133	ILE	2.1
1	B	32	LEU	2.1
1	D	265	PRO	2.1
1	A	65	ALA	2.1
1	C	288	MET	2.1
1	B	278	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 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
3	2M3	B	1	26/26	0.84	0.25	44,51,54,55	0
3	2M3	H	290	26/26	0.88	0.21	39,42,44,44	0
3	2M3	F	290	26/26	0.89	0.20	32,42,43,44	0
3	2M3	A	2	26/26	0.90	0.19	29,31,35,36	0
3	2M3	D	3	26/26	0.92	0.15	27,31,34,36	0
3	2M3	E	7	26/26	0.92	0.17	19,24,28,29	0
4	SO4	H	3	5/5	0.92	0.13	57,57,58,59	0

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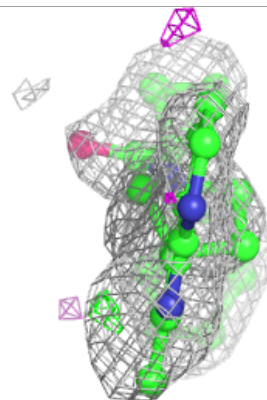
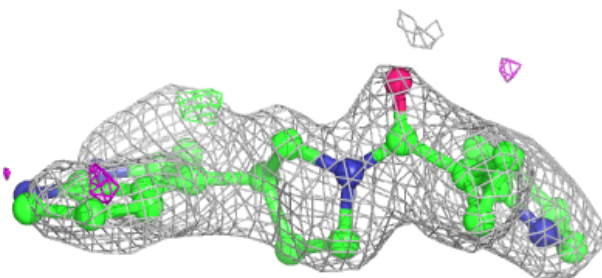
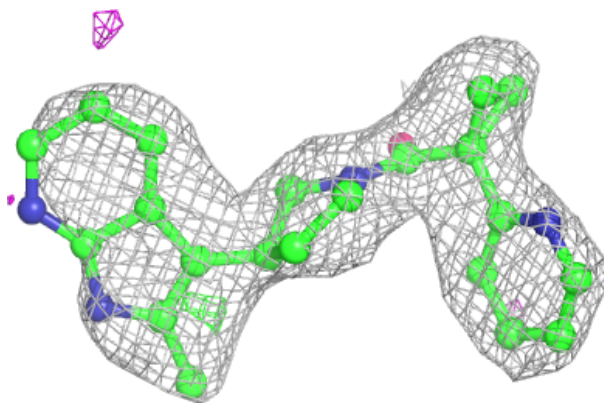
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	G	9	5/5	0.93	0.14	48,49,51,51	0
3	2M3	G	8	26/26	0.93	0.17	26,29,30,31	0
4	SO4	E	4	5/5	0.95	0.14	46,47,47,48	0
3	2M3	C	4	26/26	0.95	0.19	14,22,23,24	0
2	NDP	G	300	48/48	0.95	0.12	19,28,30,31	0
2	NDP	H	300	48/48	0.96	0.11	16,29,33,36	0
2	NDP	B	300	48/48	0.96	0.11	24,28,31,34	0
2	NDP	A	300	48/48	0.96	0.12	17,27,33,34	0
4	SO4	H	6	5/5	0.96	0.19	60,60,61,61	0
2	NDP	F	300	48/48	0.97	0.11	9,14,18,20	0
4	SO4	B	2	5/5	0.97	0.12	48,48,49,50	0
2	NDP	D	300	48/48	0.97	0.11	5,13,19,21	0
4	SO4	D	1	5/5	0.98	0.13	34,36,36,36	0
2	NDP	C	300	48/48	0.98	0.10	11,14,20,20	0
4	SO4	F	5	5/5	0.98	0.11	27,30,31,32	0
2	NDP	E	300	48/48	0.98	0.10	11,15,19,19	0
4	SO4	C	7	5/5	0.98	0.10	48,49,49,50	0
4	SO4	C	8	5/5	0.98	0.13	35,37,37,37	0

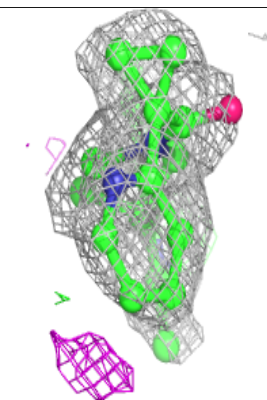
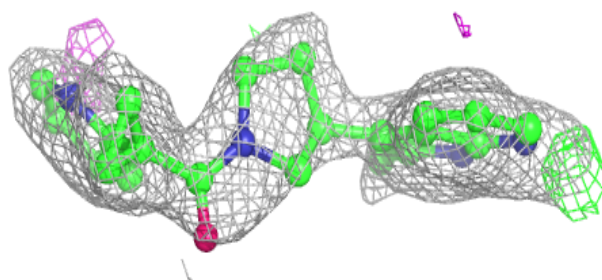
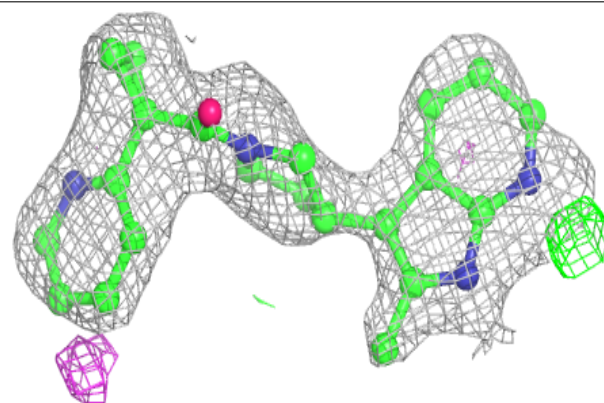
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 2M3 B 1:

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

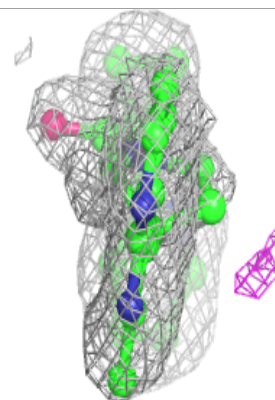
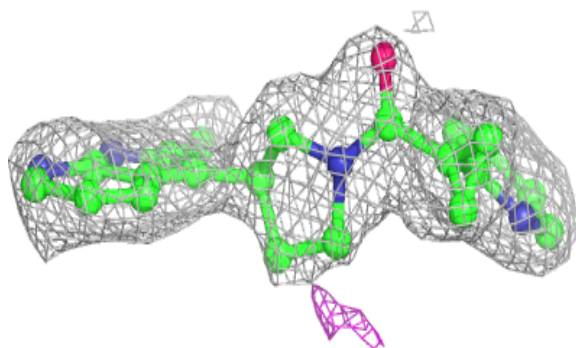
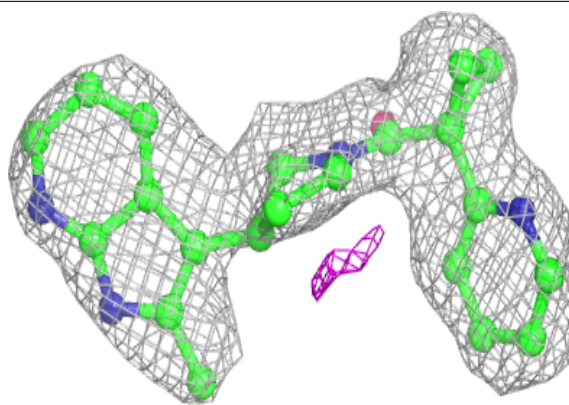
**Electron density around 2M3 H 290:**

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

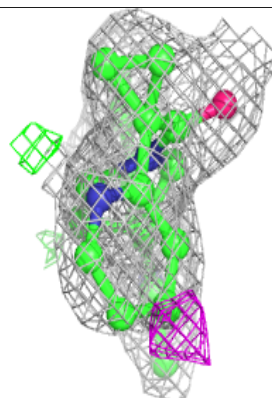
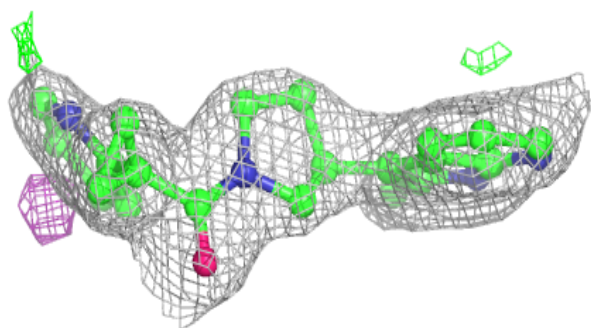
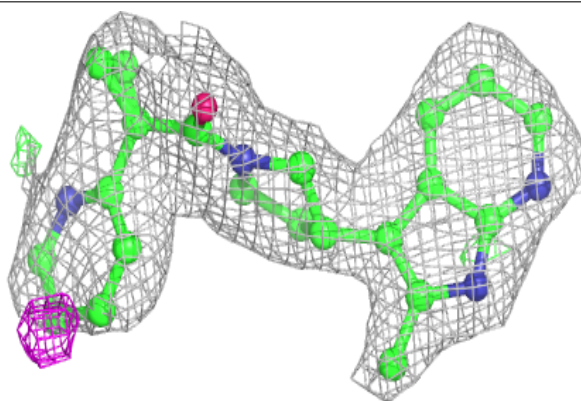


Electron density around 2M3 F 290:

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

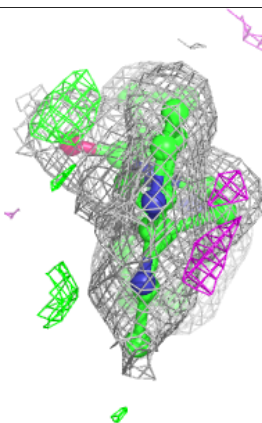
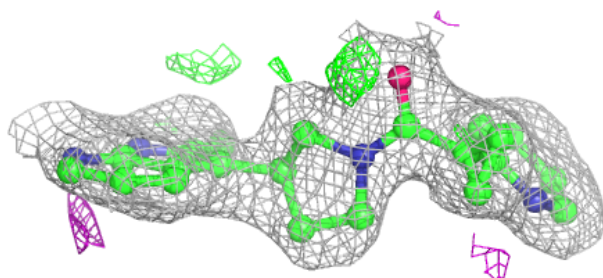
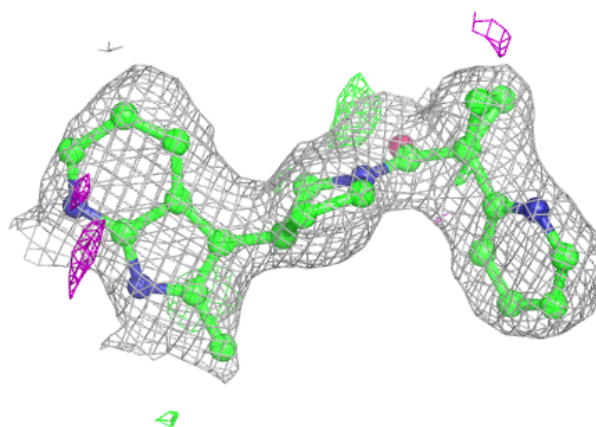
**Electron density around 2M3 A 2:**

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

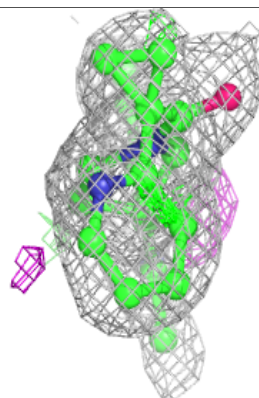
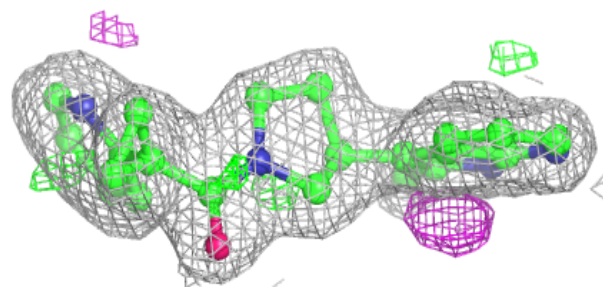
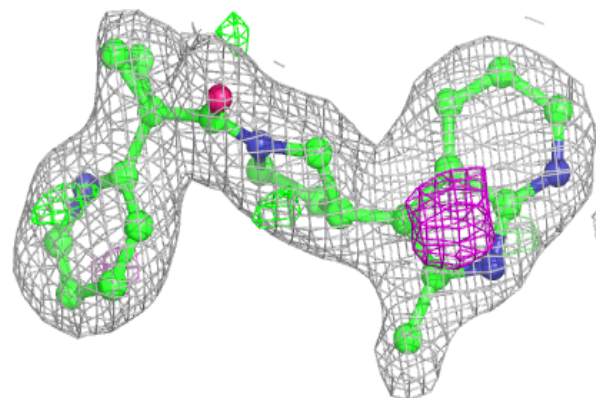


Electron density around 2M3 D 3:

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

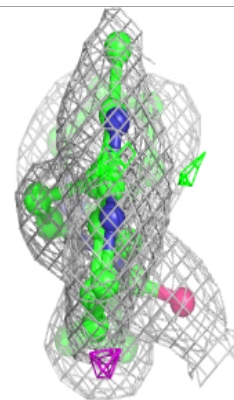
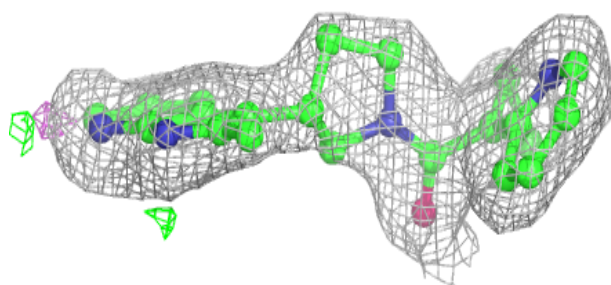
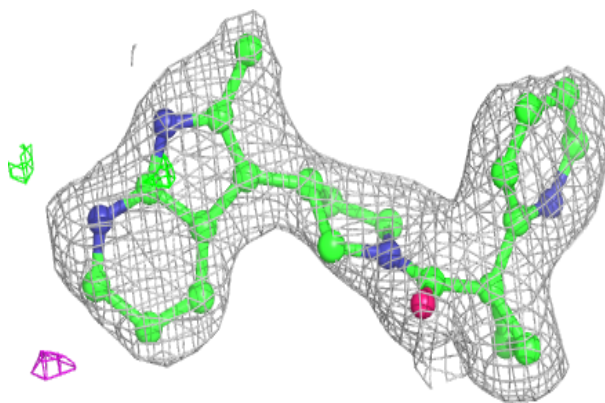
**Electron density around 2M3 E 7:**

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

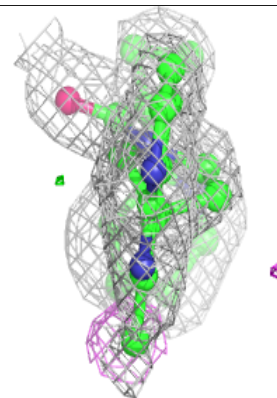
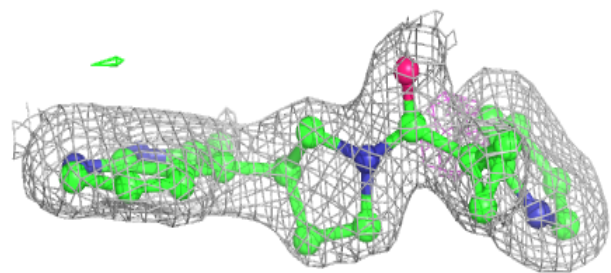
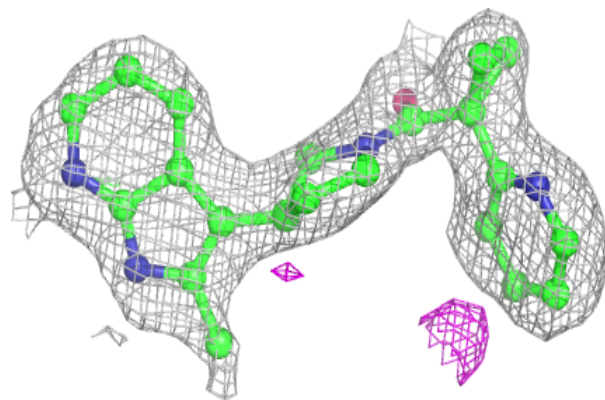


Electron density around 2M3 G 8:

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

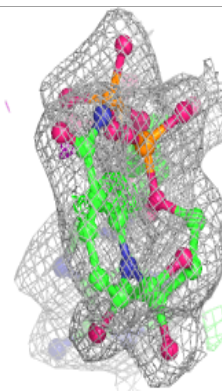
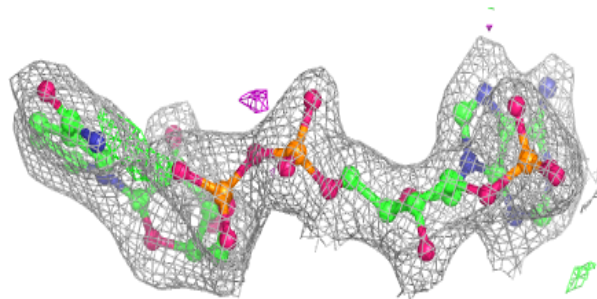
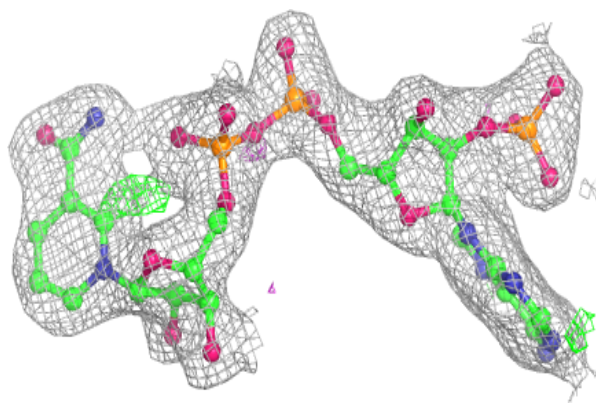
**Electron density around 2M3 C 4:**

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

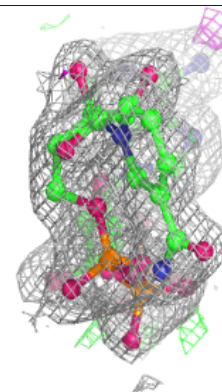
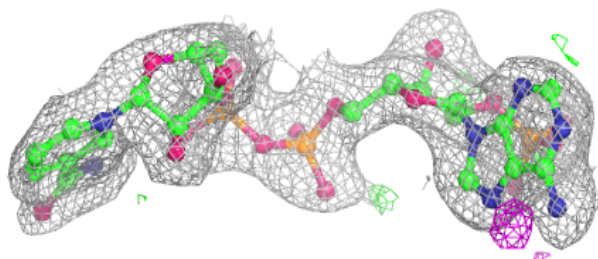
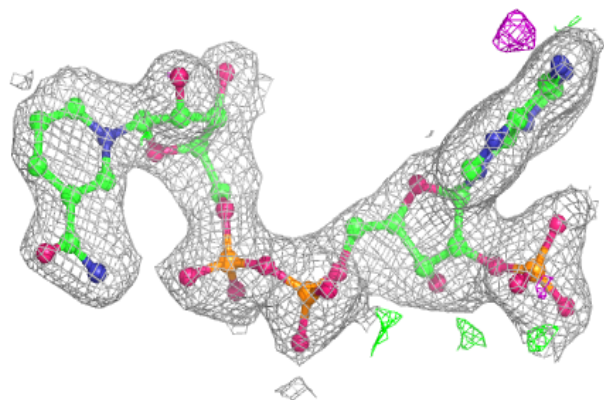


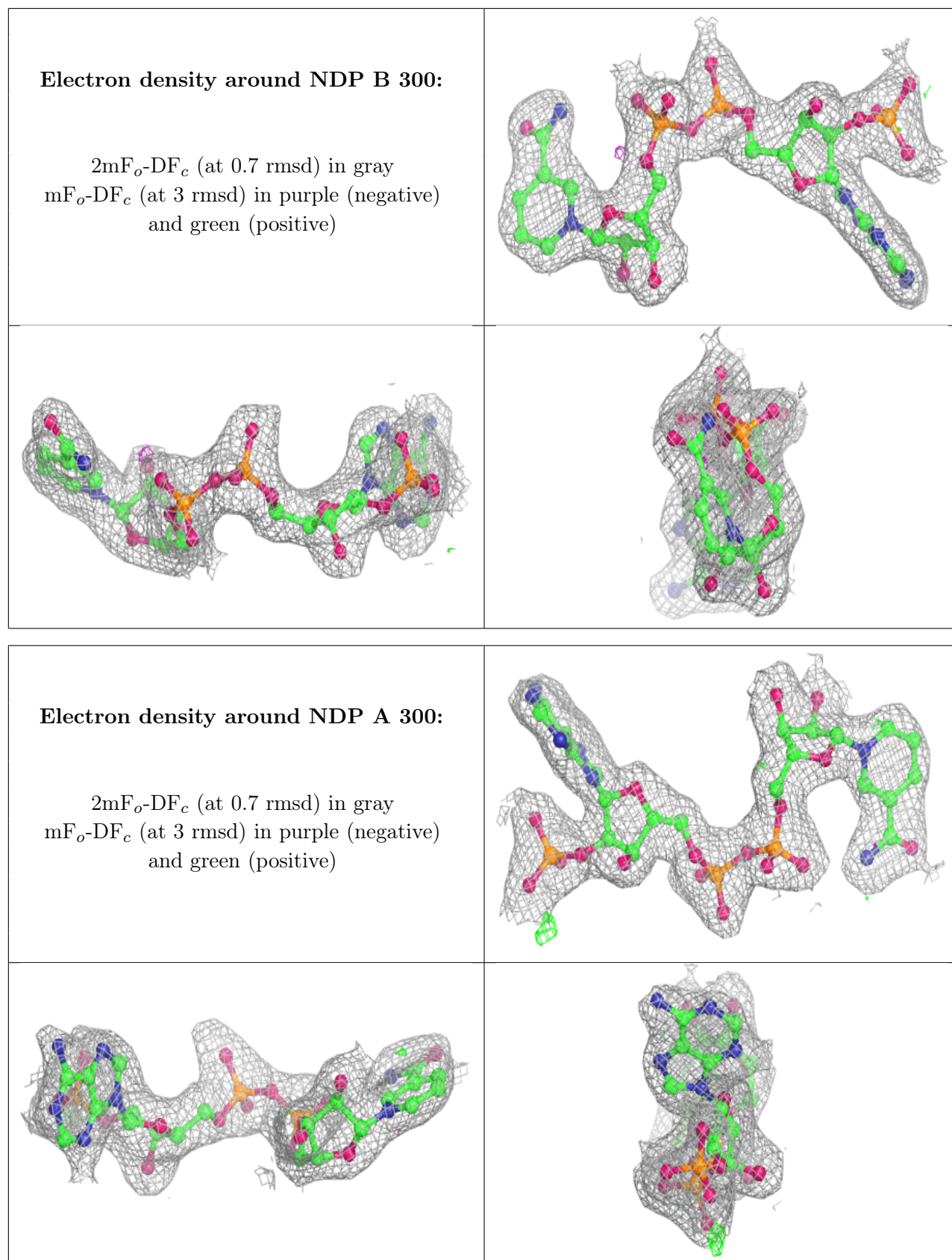
Electron density around NDP G 300:

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

**Electron density around NDP H 300:**

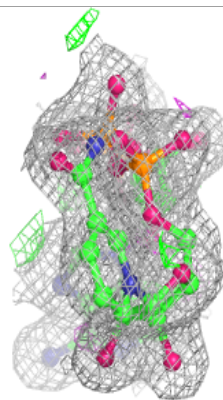
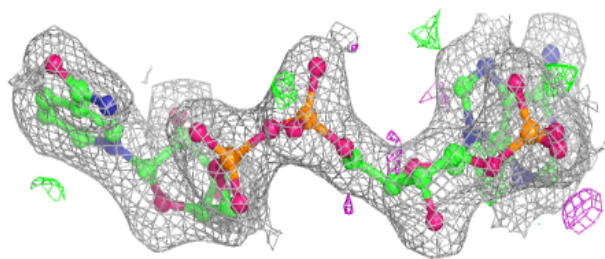
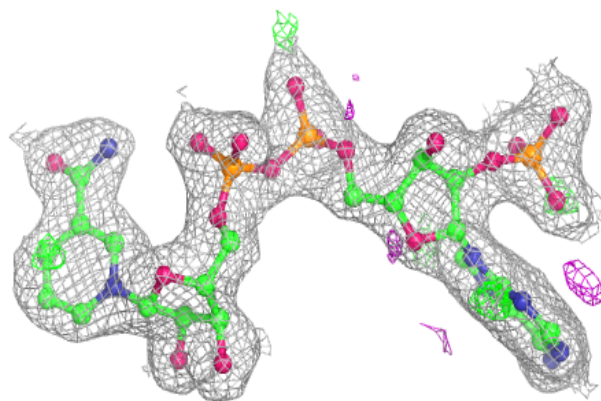
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



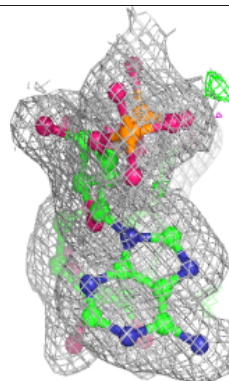
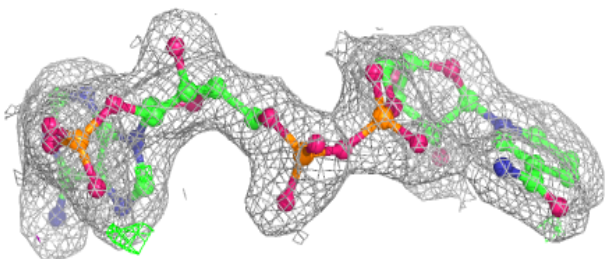
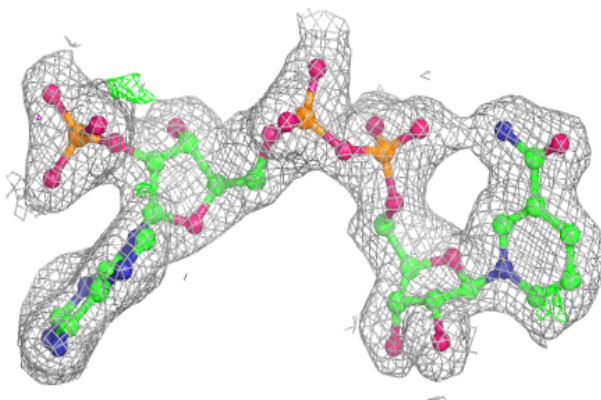


Electron density around NDP F 300:

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

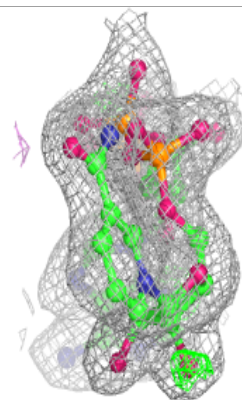
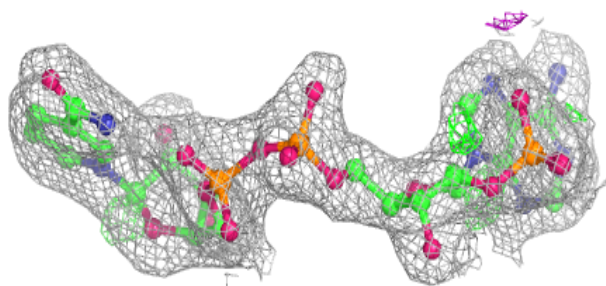
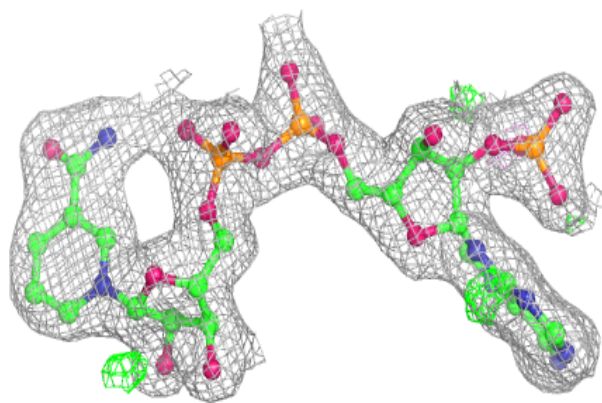
**Electron density around NDP D 300:**

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

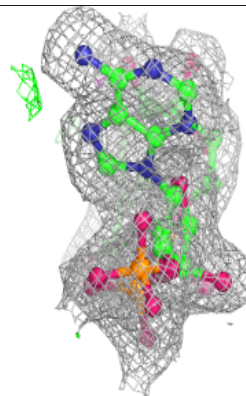
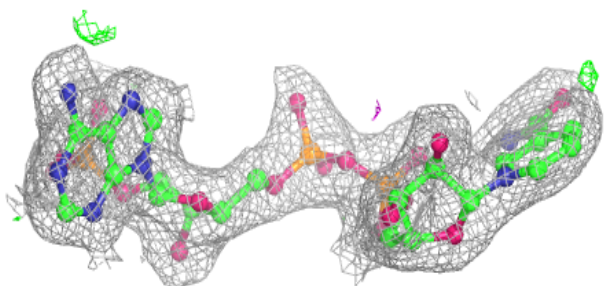
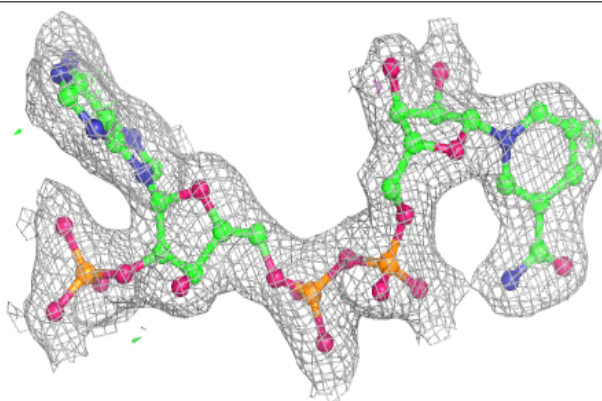


Electron density around NDP C 300:

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

**Electron density around NDP E 300:**

$2mF_o-DF_c$ (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.