



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:41 PM UTC

PDB ID : 3GMD / pdb_00003gmd
Title : Structure-based design of 7-Azaindole-pyrrolidines as inhibitors of 11 β -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	:	4-5-2 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

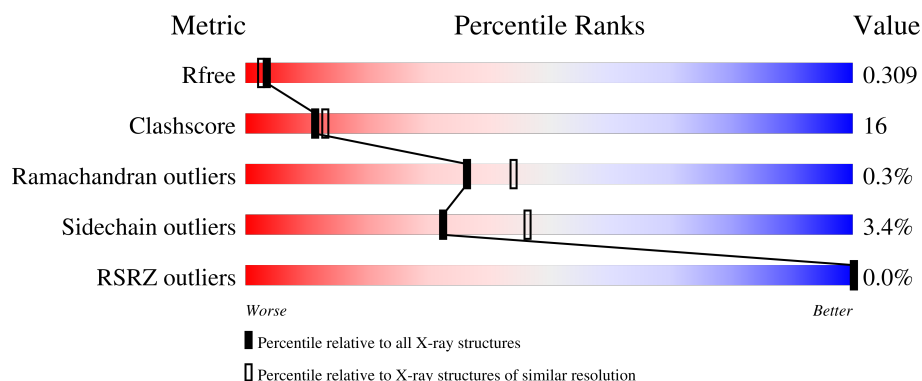
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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}	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (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	 63% 36% .
1	B	264	 57% 40% .
1	C	264	 74% 23% .
1	D	264	 74% 25% .

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Mol	Chain	Length	Quality of chain
1	E	264	 66% 32% •
1	F	264	 67% 30% •
1	G	264	 62% 36% •
1	H	264	 68% 31% •

2 Entry composition

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
1	A	264	Total	C	N	O	S	27	0	0
			2025	1297	337	374	17			
1	B	264	Total	C	N	O	S	10	0	0
			2025	1297	337	374	17			
1	C	264	Total	C	N	O	S	17	0	0
			2025	1297	337	374	17			
1	D	264	Total	C	N	O	S	29	0	0
			2025	1297	337	374	17			
1	E	264	Total	C	N	O	S	23	0	0
			2025	1297	337	374	17			
1	F	264	Total	C	N	O	S	15	0	0
			2025	1297	337	374	17			
1	G	264	Total	C	N	O	S	30	0	0
			2025	1297	337	374	17			
1	H	264	Total	C	N	O	S	25	0	0
			2025	1297	337	374	17			

There are 48 discrepancies between the modelled and reference sequences:

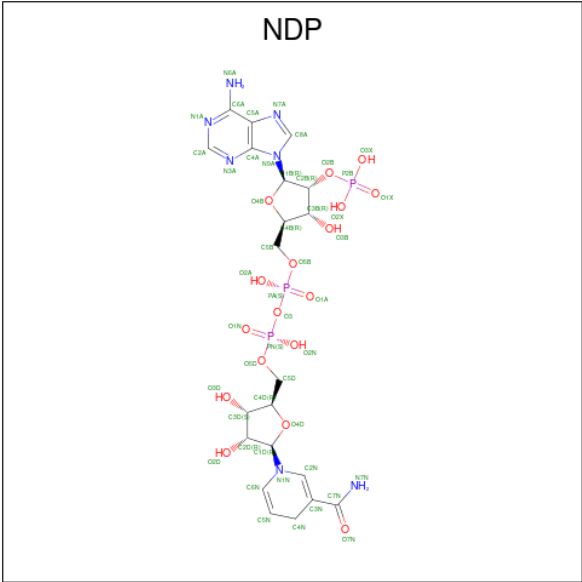
Chain	Residue	Modelled	Actual	Comment	Reference
A	175	VAL	MET	engineered mutation	UNP P50172
A	177	TYR	GLN	engineered mutation	UNP P50172
A	180	VAL	ILE	engineered mutation	UNP P50172
A	226	ALA	GLU	engineered mutation	UNP P50172
A	227	VAL	ILE	engineered mutation	UNP P50172
A	231	VAL	ILE	engineered mutation	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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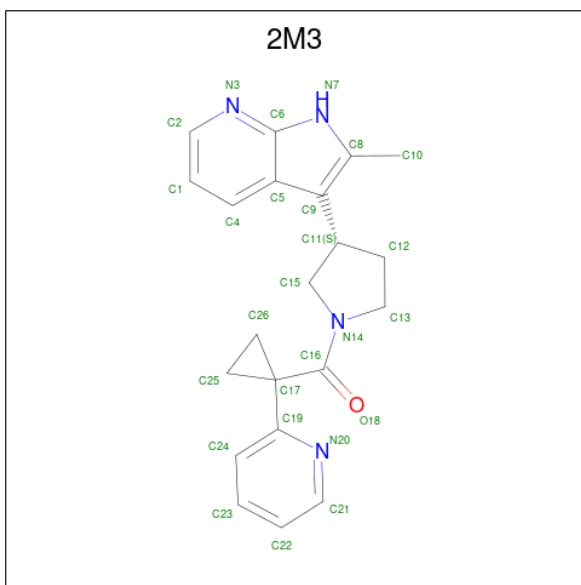
Chain	Residue	Modelled	Actual	Comment	Reference
C	177	TYR	GLN	engineered mutation	UNP P50172
C	180	VAL	ILE	engineered mutation	UNP P50172
C	226	ALA	GLU	engineered mutation	UNP P50172
C	227	VAL	ILE	engineered mutation	UNP P50172
C	231	VAL	ILE	engineered mutation	UNP P50172
D	175	VAL	MET	engineered mutation	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 (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



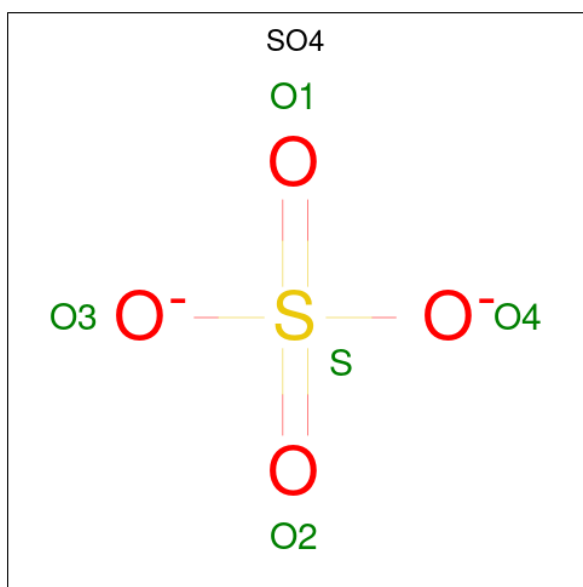
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G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

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



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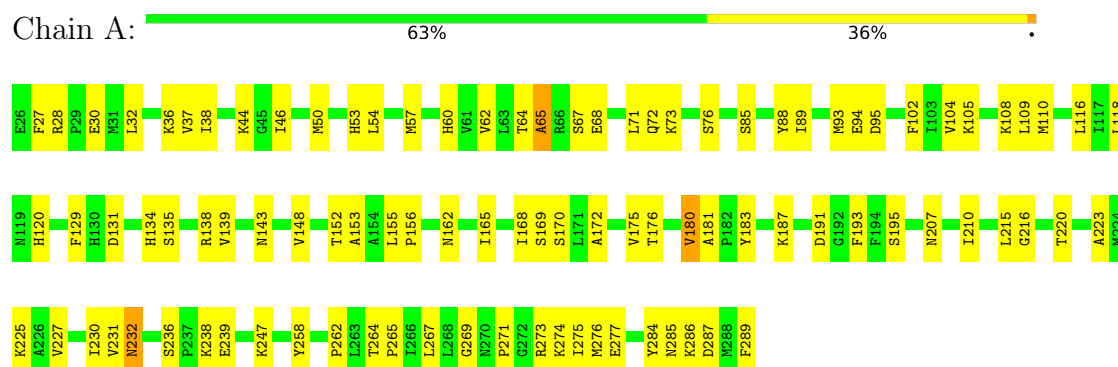
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	70	Total 70	O 70	0	0
5	E	71	Total 71	O 71	0	0
5	F	61	Total 61	O 61	0	0
5	G	64	Total 64	O 64	0	0
5	H	47	Total 47	O 47	0	0

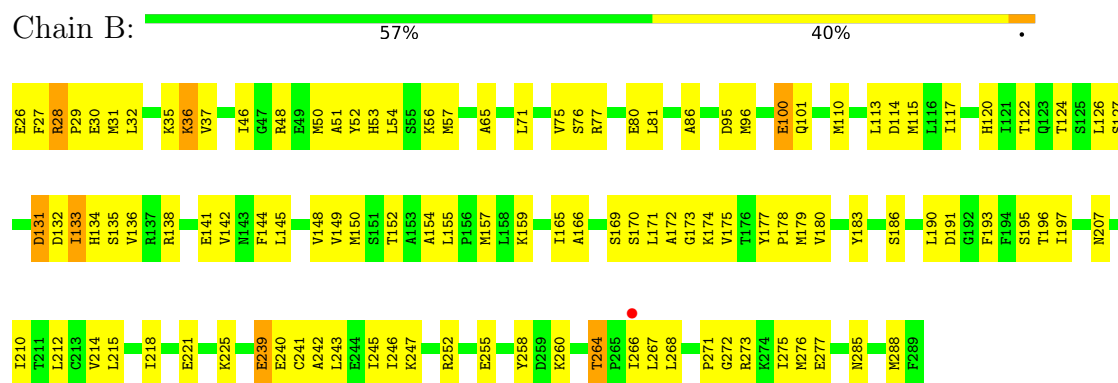
3 Residue-property plots

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.

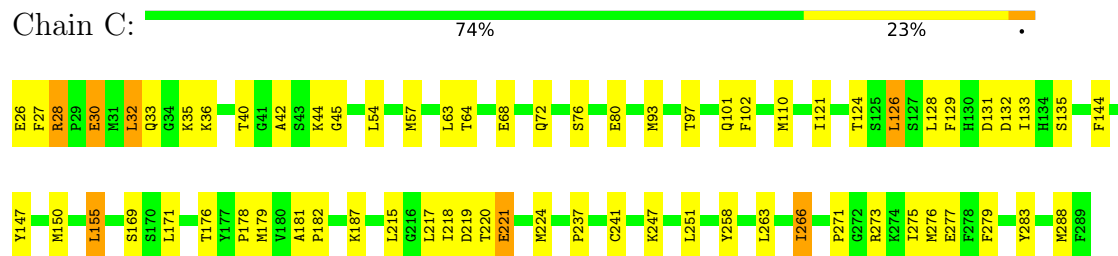
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



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



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



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

Chain D:  74% 25% .



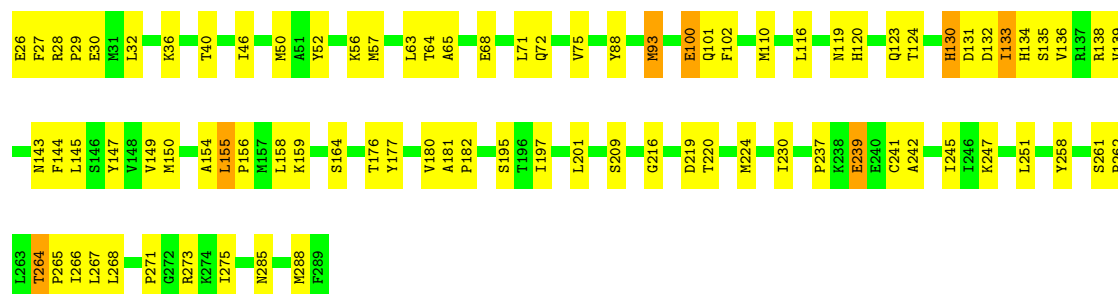
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1

Chain E:  66% 32% .



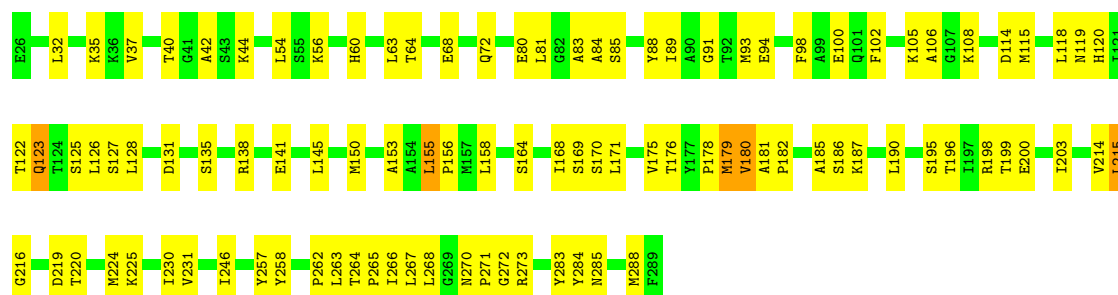
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1

Chain F:  67% 30% .



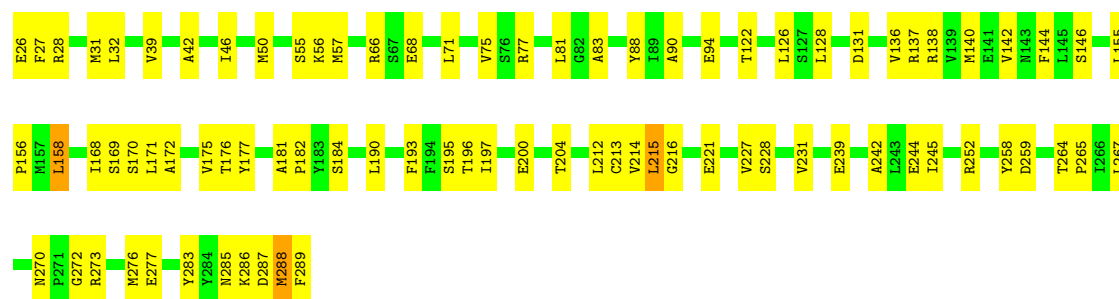
- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1

Chain G:  62% 36% .



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

Chain H: 68% 31%



4 Data and refinement statistics

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 70.00 – 2.28	Depositor EDS
% Data completeness (in resolution range)	95.4 (70.00-2.28) 95.9 (70.00-2.28)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.29Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.252 , 0.306 0.261 , 0.309	Depositor DCC
R_{free} test set	1260 reflections (1.17%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	1.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 32.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.160 for h,-k,-l 0.006 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17364	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage'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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, SO4, 2M3

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	0.41	0/2059	0.80	0/2775
1	B	0.40	0/2059	0.80	0/2775
1	C	0.48	0/2059	0.80	2/2775 (0.1%)
1	D	0.48	0/2059	0.83	0/2775
1	E	0.48	0/2059	0.83	0/2775
1	F	0.46	0/2059	0.81	1/2775 (0.0%)
1	G	0.42	0/2059	0.79	0/2775
1	H	0.43	0/2059	0.80	0/2775
All	All	0.45	0/16472	0.81	3/22200 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	28	ARG	CA-C-N	5.17	125.46	119.47
1	C	28	ARG	C-N-CA	5.17	125.46	119.47
1	F	130	HIS	N-CA-C	5.12	115.77	107.32

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	2025	0	2092	77	0
1	B	2025	0	2092	108	0
1	C	2025	0	2092	54	0
1	D	2025	0	2092	62	0
1	E	2025	0	2092	71	0
1	F	2025	0	2092	65	0
1	G	2025	0	2092	84	0
1	H	2025	0	2092	71	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	5	0
2	H	48	0	26	2	0
3	A	26	0	22	0	0
3	B	26	0	22	3	0
3	C	26	0	22	3	0
3	D	26	0	22	1	0
3	E	26	0	22	2	0
3	F	26	0	22	3	0
3	G	26	0	22	1	0
3	H	26	0	22	0	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	538	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 16.

All (538) 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:E:126:LEU:HB3	1:E:179:MET:HE2	1.53	0.90
1:B:36:LYS:HG3	1:B:110:MET:HB3	1.54	0.90
1:F:46:ILE:HG22	1:F:50:MET:HE2	1.53	0.87
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: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:46:ILE:HG22	1:B:50:MET:HE2	1.68	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:A:232:ASN:C	1:A:232:ASN:HD22	1.97	0.72
1:H:50:MET:HG2	1:H:242:ALA:HB1	1.73	0.71
1:A:276:MET:HE1	1:B:268:LEU:HG	1.71	0.70
1:C:179:MET:HE1	1:D:288:MET:HE2	1.73	0.70
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ILE:HG12	1:B:288:MET:HE2	1.71	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:B:120:HIS:HE1	1:B:150:MET:HE1	1.58	0.68
1:A:273:ARG:O	1:A:277:GLU:HG3	1.93	0.68
1:F:30:GLU:CD	1:F:30:GLU:H	2.00	0.68
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:C:263:LEU:HA	1:C:266:ILE:HD11	1.77	0.67
1:D:126:LEU:HB3	1:D:179:MET:HE2	1.76	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: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: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:C:179:MET:CE	1:D:288:MET:HE2	2.29	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:B:141:GLU:CD	1:B:145:LEU:HD22	2.24	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:94:GLU:CD	1:A:138:ARG:HH11	2.09	0.60
1:B:120:HIS:CE1	1:B:150:MET:HE1	2.36	0.60
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: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: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:C:276:MET:HE3	1:D:267:LEU:HD13	1.87	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:F:93:MET:HE3	1:F:150:MET:SD	2.46	0.56
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: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:232:ASN:C	1:A:232:ASN:ND2	2.64	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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: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:A:276:MET:HE3	1:B:175:VAL:HG11	1.92	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:H:168:ILE:HD11	1:H:245:ILE:HG21	1.93	0.51
1:B:239:GLU:CD	1:B:239:GLU:H	2.18	0.51
1:C:221:GLU:HG2	4:C:8:SO4:O3	2.11	0.51
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:A:46:ILE:HG22	1:A:50:MET:HE2	1.93	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: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: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:F:120:HIS:CE1	1:F:150:MET:HE1	2.47	0.49
1:A:60:HIS:ND1	1:A:85:SER:HB2	2.27	0.49
1:F:180:VAL:O	1:F:180:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:52:TYR:O	1:B:56:LYS:HG3	2.13	0.48
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: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: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:E:162:ASN:CG	1:E:207:ASN:HD22	2.20	0.48
1:G:89:ILE:HB	1:G:102:PHE:CE1	2.49	0.48
1:G:120:HIS:HE1	1:G:150:MET:HE1	1.77	0.48
1:G:122:THR:O	1:G:123:GLN:C	2.57	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:B:53:HIS:O	1:B:57:MET:HE3	2.13	0.47
1:C:237:PRO:HD3	1:E:240:GLU:OE2	2.14	0.47
1:C:288:MET:HE2	1:C:288:MET:HA	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:H:270:ASN:C	1:H:270:ASN:HD22	2.22	0.46
1:D:138:ARG:O	1:D:142:VAL:HG23	2.15	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:F:120:HIS:HE1	1:F:150:MET:HE1	1.80	0.46
1:G:32:LEU:HD21	1:G:115:MET:HE1	1.98	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: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:B:95:ASP:C	1:B:95:ASP:OD1	2.58	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:H:287:ASP:C	1:H:289:PHE:H	2.24	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:191:ASP:CG	1:B:273:ARG:HH22	2.23	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:D:276:MET:HE2	1:D:276:MET:HB3	1.89	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
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: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:A:180:VAL:O	1:A:180:VAL:HG13	2.17	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:94:GLU:CD	1:H:138:ARG:HG3	2.42	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:G:83:ALA:O	1:G:84:ALA:C	2.60	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:54:LEU:HA	1:C:57:MET:HE3	2.00	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:G:44:LYS:HZ2	2:G:300:NDP:H3B	1.81	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:F:239:GLU:CD	1:F:239:GLU:H	2.26	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:B:174:LYS:NZ	1:B:191:ASP:OD2	2.45	0.43
1:D:264:THR:HB	1:D:265:PRO:HD3	2.00	0.43
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:H:239:GLU:CD	1:H:239:GLU:H	2.26	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: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:E:62:VAL:CG2	1:E:110:MET:HE2	2.48	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: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:A:95:ASP:OD1	1:A:95:ASP:C	2.60	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:G:105:LYS:O	1:G:106:ALA:C	2.62	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:62:VAL:HG23	1:E:110:MET:HE2	2.01	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
1:D:179:MET:HE1	1:D:230:ILE:HG21	2.00	0.42
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: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:B:171:LEU:HD23	1:B:214:VAL:CG1	2.50	0.42
1:D:130:HIS:O	1:D:131:ASP:C	2.62	0.42
1:D:206:VAL:HG12	1:D:208:VAL:HG23	2.01	0.42
1:E:276:MET:HE2	1:E:276:MET:HB3	1.80	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:F:30:GLU:CD	1:F:30:GLU:N	2.76	0.42
1:G:35:LYS:HD2	1:G:114:ASP:CG	2.45	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:H:285:ASN:ND2	1:H:285:ASN:C	2.77	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:E:44:LYS:HE2	2:E:300:NDP:H3B	2.01	0.41
1:E:120:HIS:CE1	1:E:150:MET:HE1	2.55	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
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:A:262:PRO:C	1:A:264:THR:H	2.27	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
1:A:60:HIS:ND1	1:A:85:SER:CB	2.84	0.41
1:A:170:SER:C	1:A:172:ALA:N	2.78	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:131:ASP:HB3	1:G:135:SER:HB3	2.03	0.41
1:H:227:VAL:O	1:H:228:SER:C	2.63	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:C:93:MET:HE1	1:C:150:MET:SD	2.61	0.41
1:E:288:MET:SD	1:F:230:ILE:HG23	2.61	0.41
1:H:142:VAL:O	1:H:146:SER:OG	2.34	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:F:124:THR:HG22	3:F:290:2M3:H10A	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: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
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:C:121:ILE:HD12	1:C:121:ILE:C	2.47	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: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: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:E:64:THR:OG1	1:E:89:ILE:O	2.36	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:217:LEU:C	1:C:218:ILE:HD13	2.47	0.40
1:D:126:LEU:CB	1:D:179:MET:HE2	2.49	0.40
1:D:234:GLN:CD	1:D:260:LYS:NZ	2.79	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%)	30	36
1	B	262/264 (99%)	247 (94%)	13 (5%)	2 (1%)	16	18
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%)	30	36
1	G	262/264 (99%)	246 (94%)	14 (5%)	2 (1%)	16	18
1	H	262/264 (99%)	249 (95%)	12 (5%)	1 (0%)	30	36
All	All	2096/2112 (99%)	1990 (95%)	99 (5%)	7 (0%)	36	44

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

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Mol	Chain	Res	Type
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%)	39	55
1	B	222/222 (100%)	216 (97%)	6 (3%)	39	55
1	C	222/222 (100%)	214 (96%)	8 (4%)	31	44
1	D	222/222 (100%)	214 (96%)	8 (4%)	31	44
1	E	222/222 (100%)	214 (96%)	8 (4%)	31	44
1	F	222/222 (100%)	212 (96%)	10 (4%)	24	35
1	G	222/222 (100%)	212 (96%)	10 (4%)	24	35
1	H	222/222 (100%)	217 (98%)	5 (2%)	44	60
All	All	1776/1776 (100%)	1715 (97%)	61 (3%)	32	46

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LYS
1	A	73	LYS
1	A	134	HIS
1	A	180	VAL
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	B	239	GLU
1	B	260	LYS

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Mol	Chain	Res	Type
1	C	30	GLU
1	C	32	LEU
1	C	126	LEU
1	C	131	ASP
1	C	155	LEU
1	C	215	LEU
1	C	221	GLU
1	C	266	ILE
1	D	35	LYS
1	D	138	ARG
1	D	155	LEU
1	D	174	LYS
1	D	203	ILE
1	D	215	LEU
1	D	276	MET
1	D	280	SER
1	E	126	LEU
1	E	155	LEU
1	E	158	LEU
1	E	210	ILE
1	E	215	LEU
1	E	266	ILE
1	E	276	MET
1	E	277	GLU
1	F	26	GLU
1	F	32	LEU
1	F	75	VAL
1	F	93	MET
1	F	100	GLU
1	F	123	GLN
1	F	133	ILE
1	F	155	LEU
1	F	158	LEU
1	F	239	GLU
1	G	80	GLU
1	G	100	GLU
1	G	123	GLN
1	G	125	SER
1	G	126	LEU
1	G	155	LEU
1	G	158	LEU
1	G	180	VAL

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Mol	Chain	Res	Type
1	G	215	LEU
1	G	225	LYS
1	H	158	LEU
1	H	184	SER
1	H	215	LEU
1	H	221	GLU
1	H	288	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	72	GLN
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	87	HIS
1	D	162	ASN
1	E	120	HIS
1	E	207	ASN
1	F	101	GLN
1	F	130	HIS
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
1	G	134	HIS
1	H	101	GLN
1	H	162	ASN
1	H	232	ASN
1	H	270	ASN
1	H	285	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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
4	SO4	C	7	-	4,4,4	0.38	0	6,6,6	0.08	0
4	SO4	H	3	-	4,4,4	0.39	0	6,6,6	0.10	0
4	SO4	B	2	-	4,4,4	0.37	0	6,6,6	0.08	0
4	SO4	C	8	-	4,4,4	0.39	0	6,6,6	0.11	0
3	2M3	H	290	-	30,30,30	2.93	7 (23%)	35,45,45	3.17	18 (51%)
2	NDP	H	300	-	51,52,52	1.61	8 (15%)	71,80,80	1.60	11 (15%)
3	2M3	B	1	-	30,30,30	2.83	6 (20%)	35,45,45	3.15	18 (51%)
3	2M3	G	8	-	30,30,30	2.82	6 (20%)	35,45,45	3.19	18 (51%)
2	NDP	B	300	-	51,52,52	1.60	9 (17%)	71,80,80	1.65	13 (18%)
4	SO4	G	9	-	4,4,4	0.39	0	6,6,6	0.09	0
3	2M3	D	3	-	30,30,30	2.84	7 (23%)	35,45,45	3.08	18 (51%)
4	SO4	D	1	-	4,4,4	0.36	0	6,6,6	0.07	0
3	2M3	F	290	-	30,30,30	2.82	6 (20%)	35,45,45	3.17	19 (54%)
2	NDP	A	300	-	51,52,52	1.59	8 (15%)	71,80,80	1.58	12 (16%)
4	SO4	F	5	-	4,4,4	0.38	0	6,6,6	0.07	0
2	NDP	C	300	-	51,52,52	1.58	10 (19%)	71,80,80	1.62	12 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NDP	D	300	-	51,52,52	1.48	8 (15%)	71,80,80	1.67	14 (19%)
2	NDP	E	300	-	51,52,52	1.58	7 (13%)	71,80,80	1.63	13 (18%)
2	NDP	F	300	-	51,52,52	1.63	10 (19%)	71,80,80	1.58	12 (16%)
3	2M3	E	7	-	30,30,30	2.87	6 (20%)	35,45,45	3.04	18 (51%)
4	SO4	H	6	-	4,4,4	0.38	0	6,6,6	0.12	0
2	NDP	G	300	-	51,52,52	1.60	9 (17%)	71,80,80	1.61	12 (16%)
3	2M3	A	2	-	30,30,30	2.83	6 (20%)	35,45,45	3.07	17 (48%)
3	2M3	C	4	-	30,30,30	2.79	7 (23%)	35,45,45	3.05	19 (54%)
4	SO4	E	4	-	4,4,4	0.38	0	6,6,6	0.11	0

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	F	300	-	-	8/34/77/77	0/5/5/5
3	2M3	E	7	-	-	4/19/33/33	0/5/5/5
3	2M3	D	3	-	-	2/19/33/33	0/5/5/5
2	NDP	H	300	-	-	9/34/77/77	0/5/5/5
3	2M3	B	1	-	-	3/19/33/33	0/5/5/5
3	2M3	G	8	-	-	4/19/33/33	0/5/5/5
2	NDP	G	300	-	-	6/34/77/77	0/5/5/5
3	2M3	A	2	-	-	3/19/33/33	0/5/5/5
3	2M3	F	290	-	-	2/19/33/33	0/5/5/5
2	NDP	A	300	-	-	8/34/77/77	0/5/5/5
3	2M3	H	290	-	-	2/19/33/33	0/5/5/5
3	2M3	C	4	-	-	3/19/33/33	0/5/5/5
2	NDP	B	300	-	-	11/34/77/77	0/5/5/5
2	NDP	C	300	-	-	7/34/77/77	0/5/5/5
2	NDP	D	300	-	-	6/34/77/77	0/5/5/5
2	NDP	E	300	-	-	4/34/77/77	0/5/5/5

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	7	2M3	C5-C6	11.63	1.54	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	2M3	C5-C6	11.52	1.54	1.41
3	H	290	2M3	C5-C6	11.46	1.53	1.41
3	F	290	2M3	C5-C6	11.21	1.53	1.41
3	A	2	2M3	C5-C6	11.11	1.53	1.41
3	D	3	2M3	C5-C6	10.87	1.53	1.41
3	G	8	2M3	C5-C6	10.83	1.53	1.41
3	C	4	2M3	C5-C6	10.59	1.52	1.41
3	E	7	2M3	C1-C2	6.13	1.55	1.37
3	H	290	2M3	C1-C2	6.12	1.55	1.37
3	B	1	2M3	C1-C2	6.07	1.54	1.37
3	D	3	2M3	C1-C2	6.05	1.54	1.37
3	G	8	2M3	C1-C2	6.04	1.54	1.37
3	C	4	2M3	C1-C2	6.04	1.54	1.37
3	F	290	2M3	C1-C2	5.93	1.54	1.37
3	A	2	2M3	C1-C2	5.88	1.54	1.37
2	E	300	NDP	C3B-C2B	-5.80	1.40	1.53
2	F	300	NDP	C3B-C2B	-5.78	1.40	1.53
2	H	300	NDP	C3B-C2B	-5.68	1.40	1.53
2	A	300	NDP	C3B-C2B	-5.51	1.40	1.53
3	A	2	2M3	C22-C23	5.46	1.50	1.38
2	C	300	NDP	C3B-C2B	-5.38	1.41	1.53
3	G	8	2M3	C22-C23	5.31	1.49	1.38
2	G	300	NDP	C3B-C2B	-5.31	1.41	1.53
3	C	4	2M3	C22-C23	5.28	1.49	1.38
3	H	290	2M3	C22-C23	5.20	1.49	1.38
2	B	300	NDP	C3B-C2B	-5.13	1.41	1.53
3	E	7	2M3	C22-C23	5.09	1.49	1.38
3	D	3	2M3	C22-C23	5.09	1.49	1.38
3	F	290	2M3	C22-C23	5.04	1.49	1.38
3	B	1	2M3	C22-C23	4.96	1.49	1.38
2	B	300	NDP	C1B-N9A	-4.86	1.32	1.46
2	E	300	NDP	C1B-N9A	-4.73	1.33	1.46
2	D	300	NDP	C3B-C2B	-4.73	1.42	1.53
2	F	300	NDP	C1B-N9A	-4.64	1.33	1.46
2	A	300	NDP	C1B-N9A	-4.53	1.33	1.46
2	G	300	NDP	C1B-N9A	-4.52	1.33	1.46
2	H	300	NDP	C1B-N9A	-4.48	1.34	1.46
2	C	300	NDP	C1B-N9A	-4.41	1.34	1.46
2	D	300	NDP	C1B-N9A	-4.20	1.34	1.46
3	G	8	2M3	C8-N7	-4.07	1.32	1.37
3	D	3	2M3	C8-N7	-4.07	1.32	1.37
3	F	290	2M3	C8-N7	-3.93	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	4	2M3	C8-N7	-3.64	1.32	1.37
2	G	300	NDP	C4N-C3N	-3.48	1.43	1.50
3	B	1	2M3	C8-N7	-3.37	1.33	1.37
2	C	300	NDP	C2N-C3N	3.33	1.44	1.35
2	H	300	NDP	C4N-C3N	-3.33	1.43	1.50
2	F	300	NDP	C4N-C5N	-3.33	1.40	1.49
2	B	300	NDP	C4N-C3N	-3.32	1.43	1.50
2	B	300	NDP	C2N-C3N	3.32	1.44	1.35
2	A	300	NDP	C4N-C3N	-3.27	1.43	1.50
2	F	300	NDP	C2N-C3N	3.24	1.44	1.35
3	H	290	2M3	C8-N7	-3.23	1.33	1.37
3	E	7	2M3	C8-N7	-3.23	1.33	1.37
2	C	300	NDP	C4N-C3N	-3.22	1.43	1.50
3	A	2	2M3	C8-N7	-3.22	1.33	1.37
2	E	300	NDP	C4N-C5N	-3.21	1.40	1.49
2	E	300	NDP	C4N-C3N	-3.13	1.44	1.50
2	B	300	NDP	C4N-C5N	-3.12	1.40	1.49
2	H	300	NDP	C4N-C5N	-3.10	1.41	1.49
2	G	300	NDP	C4N-C5N	-3.10	1.41	1.49
2	F	300	NDP	C4N-C3N	-3.07	1.44	1.50
2	A	300	NDP	C4N-C5N	-3.03	1.41	1.49
2	H	300	NDP	C2N-C3N	3.02	1.43	1.35
3	H	290	2M3	C17-C16	2.98	1.59	1.52
3	H	290	2M3	C26-C25	-2.96	1.43	1.50
2	A	300	NDP	C5A-N7A	-2.94	1.33	1.39
2	E	300	NDP	C2N-C3N	2.94	1.43	1.35
3	D	3	2M3	C26-C25	-2.94	1.43	1.50
2	D	300	NDP	C4N-C5N	-2.93	1.41	1.49
2	D	300	NDP	C2N-C3N	2.93	1.43	1.35
2	C	300	NDP	C4N-C5N	-2.93	1.41	1.49
2	G	300	NDP	C2N-C3N	2.93	1.43	1.35
2	A	300	NDP	C2N-C3N	2.91	1.43	1.35
3	B	1	2M3	C26-C25	-2.89	1.43	1.50
3	C	4	2M3	C17-C16	2.87	1.58	1.52
3	G	8	2M3	C26-C25	-2.86	1.43	1.50
3	F	290	2M3	C26-C25	-2.83	1.43	1.50
2	D	300	NDP	C4N-C3N	-2.83	1.44	1.50
3	A	2	2M3	C26-C25	-2.81	1.43	1.50
3	C	4	2M3	C26-C25	-2.80	1.43	1.50
3	D	3	2M3	C17-C16	2.79	1.58	1.52
3	E	7	2M3	C26-C25	-2.78	1.43	1.50
2	C	300	NDP	C6N-C5N	2.78	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	300	NDP	C6N-C5N	2.71	1.41	1.33
2	E	300	NDP	C6N-C5N	2.70	1.41	1.33
3	H	290	2M3	C11-C9	2.69	1.54	1.49
3	A	2	2M3	C17-C16	2.68	1.58	1.52
2	F	300	NDP	P2B-O1X	2.66	1.58	1.50
3	F	290	2M3	C17-C16	2.62	1.58	1.52
2	B	300	NDP	C6N-C5N	2.58	1.41	1.33
2	G	300	NDP	P2B-O2B	2.56	1.64	1.59
2	F	300	NDP	C6N-C5N	2.56	1.40	1.33
2	H	300	NDP	P2B-O2B	2.55	1.64	1.59
3	E	7	2M3	C17-C16	2.54	1.58	1.52
2	D	300	NDP	C6N-C5N	2.53	1.40	1.33
2	G	300	NDP	C6N-C5N	2.46	1.40	1.33
2	A	300	NDP	C6N-C5N	2.46	1.40	1.33
2	H	300	NDP	C3B-C4B	2.41	1.59	1.53
2	C	300	NDP	P2B-O1X	2.37	1.57	1.50
2	D	300	NDP	P2B-O1X	2.31	1.57	1.50
2	B	300	NDP	C3B-C4B	2.30	1.58	1.53
2	E	300	NDP	P2B-O1X	2.29	1.57	1.50
2	D	300	NDP	C5A-C4A	2.29	1.43	1.39
2	B	300	NDP	P2B-O1X	2.22	1.57	1.50
2	F	300	NDP	P2B-O2B	2.22	1.63	1.59
2	B	300	NDP	P2B-O2B	2.19	1.63	1.59
2	C	300	NDP	P2B-O2B	2.18	1.63	1.59
2	G	300	NDP	C5A-N7A	-2.18	1.35	1.39
3	G	8	2M3	C17-C16	2.17	1.57	1.52
3	B	1	2M3	C17-C16	2.17	1.57	1.52
2	C	300	NDP	C5A-N7A	-2.13	1.35	1.39
2	A	300	NDP	C3B-C4B	2.11	1.58	1.53
2	F	300	NDP	C3B-C4B	2.09	1.58	1.53
3	C	4	2M3	C16-N14	2.08	1.38	1.35
2	G	300	NDP	C5A-C4A	2.07	1.42	1.39
2	F	300	NDP	C6A-N6A	2.03	1.39	1.34
3	D	3	2M3	C11-C9	2.03	1.53	1.49
2	C	300	NDP	C3B-C4B	2.02	1.58	1.53

All (244) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	2M3	C10-C8-C9	-7.79	124.17	131.16
3	H	290	2M3	C10-C8-C9	-7.68	124.27	131.16
3	B	1	2M3	C10-C8-C9	-7.63	124.31	131.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	290	2M3	C10-C8-C9	-7.51	124.42	131.16
3	E	7	2M3	C10-C8-C9	-7.33	124.59	131.16
3	D	3	2M3	C10-C8-C9	-7.32	124.59	131.16
3	G	8	2M3	C10-C8-C9	-7.31	124.60	131.16
3	C	4	2M3	C10-C8-C9	-7.12	124.77	131.16
3	F	290	2M3	C9-C8-N7	6.86	112.69	109.07
3	B	1	2M3	C9-C8-N7	6.77	112.64	109.07
3	H	290	2M3	C9-C8-N7	6.59	112.55	109.07
3	G	8	2M3	C9-C8-N7	6.43	112.46	109.07
3	D	3	2M3	C9-C8-N7	6.39	112.44	109.07
3	A	2	2M3	C9-C8-N7	6.24	112.36	109.07
3	E	7	2M3	C9-C8-N7	6.22	112.35	109.07
3	C	4	2M3	C9-C8-N7	6.18	112.33	109.07
3	H	290	2M3	C26-C17-C16	5.35	121.76	114.50
3	A	2	2M3	C5-C6-N3	-5.34	119.83	126.31
3	G	8	2M3	C26-C17-C16	5.34	121.75	114.50
3	B	1	2M3	C5-C6-N3	-5.30	119.89	126.31
3	D	3	2M3	C5-C6-N3	-5.25	119.95	126.31
3	F	290	2M3	C5-C6-N3	-5.24	119.96	126.31
3	B	1	2M3	C13-N14-C15	-5.22	106.29	112.38
3	C	4	2M3	C26-C17-C16	5.20	121.55	114.50
3	E	7	2M3	C26-C17-C16	5.18	121.53	114.50
3	D	3	2M3	C21-N20-C19	5.10	124.09	117.48
3	B	1	2M3	C26-C17-C16	5.08	121.40	114.50
3	H	290	2M3	C5-C6-N3	-5.08	120.15	126.31
3	H	290	2M3	C21-N20-C19	5.06	124.04	117.48
2	C	300	NDP	C5A-C4A-N3A	-5.05	119.77	126.72
3	C	4	2M3	C5-C6-N3	-5.02	120.22	126.31
3	C	4	2M3	C21-N20-C19	4.99	123.95	117.48
2	G	300	NDP	C5A-C4A-N3A	-4.99	119.85	126.72
3	F	290	2M3	C26-C17-C16	4.97	121.24	114.50
2	H	300	NDP	C5A-C4A-N3A	-4.97	119.88	126.72
3	E	7	2M3	C5-C6-N3	-4.96	120.30	126.31
2	B	300	NDP	N3A-C2A-N1A	-4.96	121.08	128.58
2	E	300	NDP	N3A-C2A-N1A	-4.96	121.08	128.58
3	G	8	2M3	C5-C6-N3	-4.95	120.31	126.31
3	F	290	2M3	C13-N14-C15	-4.93	106.62	112.38
3	F	290	2M3	C21-N20-C19	4.91	123.85	117.48
3	E	7	2M3	C21-N20-C19	4.90	123.83	117.48
2	D	300	NDP	N3A-C2A-N1A	-4.89	121.18	128.58
2	F	300	NDP	N3A-C2A-N1A	-4.86	121.23	128.58
2	D	300	NDP	C5A-C4A-N3A	-4.84	120.05	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	NDP	C5A-C4A-N3A	-4.82	120.08	126.72
2	C	300	NDP	N3A-C2A-N1A	-4.81	121.30	128.58
3	A	2	2M3	C21-N20-C19	4.81	123.72	117.48
2	E	300	NDP	C5A-C4A-N3A	-4.80	120.11	126.72
3	B	1	2M3	C21-N20-C19	4.78	123.69	117.48
3	H	290	2M3	C26-C17-C25	-4.77	56.30	58.45
3	D	3	2M3	C26-C17-C16	4.76	120.96	114.50
3	G	8	2M3	C21-N20-C19	4.76	123.65	117.48
2	B	300	NDP	C5A-C4A-N3A	-4.74	120.19	126.72
3	G	8	2M3	C13-N14-C15	-4.70	106.89	112.38
3	A	2	2M3	C26-C17-C16	4.69	120.86	114.50
2	G	300	NDP	N3A-C2A-N1A	-4.68	121.49	128.58
3	F	290	2M3	C26-C17-C25	-4.68	56.35	58.45
3	G	8	2M3	C25-C17-C16	4.66	120.83	114.50
3	B	1	2M3	N7-C6-N3	4.65	134.73	125.32
2	H	300	NDP	N3A-C2A-N1A	-4.64	121.56	128.58
3	G	8	2M3	C26-C17-C25	-4.61	56.37	58.45
3	B	1	2M3	C26-C17-C25	-4.61	56.38	58.45
3	A	2	2M3	N7-C6-N3	4.55	134.52	125.32
2	F	300	NDP	C5A-C4A-N3A	-4.54	120.46	126.72
3	D	3	2M3	N7-C6-N3	4.53	134.48	125.32
3	H	290	2M3	C13-N14-C15	-4.51	107.11	112.38
3	F	290	2M3	N7-C6-N3	4.51	134.44	125.32
3	D	3	2M3	C13-N14-C15	-4.50	107.12	112.38
3	C	4	2M3	N7-C6-N3	4.49	134.42	125.32
3	E	7	2M3	N7-C6-N3	4.48	134.38	125.32
3	H	290	2M3	N7-C6-N3	4.47	134.37	125.32
3	G	8	2M3	N7-C6-N3	4.45	134.33	125.32
2	A	300	NDP	N3A-C4A-N9A	4.43	134.70	127.17
2	C	300	NDP	N3A-C4A-N9A	4.43	134.70	127.17
3	A	2	2M3	C13-N14-C15	-4.41	107.23	112.38
3	D	3	2M3	C26-C17-C25	-4.37	56.48	58.45
2	G	300	NDP	N3A-C4A-N9A	4.36	134.59	127.17
2	H	300	NDP	N3A-C4A-N9A	4.36	134.58	127.17
3	E	7	2M3	C13-N14-C15	-4.33	107.32	112.38
2	B	300	NDP	N3A-C4A-N9A	4.33	134.53	127.17
3	C	4	2M3	C13-N14-C15	-4.30	107.36	112.38
2	E	300	NDP	N3A-C4A-N9A	4.29	134.46	127.17
3	A	2	2M3	C26-C17-C25	-4.22	56.55	58.45
2	A	300	NDP	N3A-C2A-N1A	-4.21	122.20	128.58
3	C	4	2M3	C26-C17-C25	-4.21	56.56	58.45
2	F	300	NDP	N3A-C4A-N9A	4.19	134.29	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	300	NDP	C3B-C2B-C1B	4.17	110.79	102.81
3	E	7	2M3	C26-C17-C25	-4.16	56.58	58.45
3	C	4	2M3	C25-C17-C16	4.10	120.07	114.50
2	D	300	NDP	N3A-C4A-N9A	4.09	134.13	127.17
2	H	300	NDP	C3B-C2B-C1B	4.04	110.53	102.81
3	D	3	2M3	C25-C17-C16	4.01	119.95	114.50
2	F	300	NDP	C3B-C2B-C1B	3.96	110.39	102.81
2	G	300	NDP	C3B-C2B-C1B	3.93	110.32	102.81
3	H	290	2M3	C25-C17-C16	3.88	119.76	114.50
3	A	2	2M3	C25-C17-C16	3.86	119.74	114.50
3	B	1	2M3	C25-C17-C16	3.84	119.71	114.50
3	F	290	2M3	C25-C17-C16	3.84	119.71	114.50
2	B	300	NDP	C3B-C2B-C1B	3.83	110.15	102.81
3	A	2	2M3	C12-C13-N14	3.81	107.83	102.93
3	G	8	2M3	C13-C12-C11	-3.77	100.38	105.80
2	B	300	NDP	O4B-C1B-C2B	-3.76	100.11	106.59
2	H	300	NDP	C5A-N7A-C8A	3.72	109.30	103.45
2	A	300	NDP	C5A-N7A-C8A	3.71	109.29	103.45
2	E	300	NDP	C5A-N7A-C8A	3.71	109.28	103.45
3	E	7	2M3	C25-C17-C16	3.69	119.51	114.50
3	E	7	2M3	C12-C13-N14	3.68	107.67	102.93
2	D	300	NDP	C2A-N3A-C4A	3.66	120.76	111.83
2	D	300	NDP	C5A-N7A-C8A	3.66	109.19	103.45
2	E	300	NDP	C2A-N3A-C4A	3.63	120.69	111.83
2	A	300	NDP	C2B-C1B-N9A	3.60	119.67	113.75
2	H	300	NDP	C2A-N3A-C4A	3.59	120.59	111.83
2	C	300	NDP	C2A-N3A-C4A	3.56	120.53	111.83
3	C	4	2M3	C12-C13-N14	3.54	107.48	102.93
2	B	300	NDP	C2A-N3A-C4A	3.53	120.46	111.83
2	C	300	NDP	C3B-C2B-C1B	3.53	109.56	102.81
2	G	300	NDP	C2A-N3A-C4A	3.52	120.43	111.83
2	F	300	NDP	C2A-N3A-C4A	3.51	120.42	111.83
2	C	300	NDP	C5A-N7A-C8A	3.50	108.95	103.45
2	B	300	NDP	C5A-N7A-C8A	3.49	108.94	103.45
2	G	300	NDP	C5A-N7A-C8A	3.46	108.89	103.45
2	E	300	NDP	C3B-C2B-C1B	3.43	109.38	102.81
2	F	300	NDP	C5A-N7A-C8A	3.38	108.76	103.45
3	H	290	2M3	C12-C13-N14	3.36	107.25	102.93
2	A	300	NDP	C3B-C2B-C1B	3.33	109.18	102.81
3	D	3	2M3	C13-C12-C11	-3.28	101.09	105.80
3	B	1	2M3	C12-C13-N14	3.26	107.13	102.93
3	F	290	2M3	C12-C13-N14	3.26	107.12	102.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	8	2M3	C26-C17-C19	3.21	122.36	117.30
2	A	300	NDP	C2A-N3A-C4A	3.18	119.60	111.83
2	C	300	NDP	O4B-C1B-C2B	-3.17	101.13	106.59
3	D	3	2M3	C12-C13-N14	3.15	106.99	102.93
3	A	2	2M3	C10-C8-N7	3.14	123.47	120.00
2	F	300	NDP	O4B-C1B-C2B	-3.08	101.29	106.59
2	G	300	NDP	O4B-C1B-C2B	-3.00	101.42	106.59
2	D	300	NDP	C2B-C1B-N9A	2.99	118.67	113.75
3	B	1	2M3	C26-C17-C19	2.98	122.00	117.30
3	F	290	2M3	C26-C17-C19	2.92	121.90	117.30
2	D	300	NDP	C6N-N1N-C2N	2.91	122.44	119.32
3	G	8	2M3	C12-C13-N14	2.91	106.67	102.93
3	H	290	2M3	C10-C8-N7	2.89	123.19	120.00
2	H	300	NDP	O4B-C1B-C2B	-2.88	101.63	106.59
2	D	300	NDP	O4B-C1B-C2B	-2.87	101.65	106.59
2	H	300	NDP	C4A-C5A-N7A	-2.84	107.33	110.58
2	E	300	NDP	C2B-C1B-N9A	2.80	118.36	113.75
2	F	300	NDP	N9A-C8A-N7A	-2.79	109.98	113.94
3	C	4	2M3	C2-N3-C6	2.78	122.16	116.74
2	E	300	NDP	C4A-C5A-N7A	-2.78	107.40	110.58
2	E	300	NDP	N9A-C8A-N7A	-2.78	109.99	113.94
3	E	7	2M3	C10-C8-N7	2.78	123.06	120.00
3	D	3	2M3	C2-N3-C6	2.77	122.13	116.74
3	B	1	2M3	C10-C8-N7	2.76	123.05	120.00
3	F	290	2M3	C13-C12-C11	-2.76	101.84	105.80
3	A	2	2M3	C2-N3-C6	2.75	122.09	116.74
3	C	4	2M3	C13-C12-C11	-2.75	101.86	105.80
2	D	300	NDP	C4A-C5A-N7A	-2.73	107.45	110.58
3	G	8	2M3	C2-N3-C6	2.72	122.04	116.74
2	E	300	NDP	O4B-C1B-C2B	-2.72	101.91	106.59
3	D	3	2M3	C10-C8-N7	2.69	122.97	120.00
3	H	290	2M3	C13-C12-C11	-2.68	101.95	105.80
3	H	290	2M3	C2-N3-C6	2.68	121.95	116.74
3	B	1	2M3	C2-N3-C6	2.67	121.94	116.74
3	G	8	2M3	C19-C17-C16	-2.67	107.68	114.97
2	G	300	NDP	C6N-N1N-C2N	2.67	122.17	119.32
3	G	8	2M3	C10-C8-N7	2.67	122.94	120.00
3	F	290	2M3	C4-C5-C6	2.66	119.81	117.16
2	A	300	NDP	C6N-N1N-C2N	2.64	122.15	119.32
2	A	300	NDP	O4B-C1B-C2B	-2.63	102.05	106.59
3	C	4	2M3	C10-C8-N7	2.63	122.90	120.00
3	F	290	2M3	C10-C8-N7	2.62	122.89	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	300	NDP	C6N-N1N-C2N	2.62	122.12	119.32
2	D	300	NDP	N9A-C8A-N7A	-2.62	110.22	113.94
2	C	300	NDP	C6N-N1N-C2N	2.61	122.11	119.32
3	H	290	2M3	C26-C25-C17	2.61	61.96	60.78
2	B	300	NDP	N9A-C8A-N7A	-2.59	110.25	113.94
2	G	300	NDP	C4A-C5A-N7A	-2.59	107.62	110.58
3	C	4	2M3	C26-C17-C19	2.59	121.38	117.30
2	E	300	NDP	C6N-N1N-C2N	2.59	122.09	119.32
3	G	8	2M3	C25-C26-C17	2.59	61.95	60.78
3	E	7	2M3	C25-C26-C17	2.58	61.95	60.78
3	F	290	2M3	C2-N3-C6	2.56	121.73	116.74
2	C	300	NDP	C4A-C5A-N7A	-2.56	107.65	110.58
2	H	300	NDP	N9A-C8A-N7A	-2.54	110.33	113.94
3	E	7	2M3	C2-N3-C6	2.51	121.63	116.74
3	A	2	2M3	C26-C17-C19	2.49	121.22	117.30
3	E	7	2M3	C26-C17-C19	2.48	121.21	117.30
2	A	300	NDP	N9A-C8A-N7A	-2.45	110.46	113.94
2	B	300	NDP	C4A-C5A-N7A	-2.44	107.79	110.58
2	C	300	NDP	N9A-C8A-N7A	-2.44	110.47	113.94
2	G	300	NDP	C3N-C2N-N1N	-2.43	119.64	123.20
3	D	3	2M3	C4-C5-C6	2.41	119.56	117.16
3	F	290	2M3	C26-C25-C17	2.39	61.86	60.78
3	B	1	2M3	C4-C5-C6	2.38	119.53	117.16
3	E	7	2M3	C4-C5-C6	2.38	119.53	117.16
2	G	300	NDP	C2B-C1B-N9A	2.36	117.64	113.75
3	B	1	2M3	C26-C25-C17	2.36	61.85	60.78
2	H	300	NDP	C6N-N1N-C2N	2.35	121.83	119.32
3	H	290	2M3	C26-C17-C19	2.34	121.00	117.30
3	D	3	2M3	C26-C17-C19	2.33	120.98	117.30
2	F	300	NDP	C3N-C2N-N1N	-2.33	119.78	123.20
2	D	300	NDP	C3N-C2N-N1N	-2.32	119.79	123.20
2	C	300	NDP	C2B-C1B-N9A	2.32	117.58	113.75
2	B	300	NDP	C3N-C2N-N1N	-2.32	119.80	123.20
3	D	3	2M3	C22-C21-N20	-2.30	119.77	123.42
3	E	7	2M3	C13-C12-C11	-2.30	102.49	105.80
2	D	300	NDP	C2A-N1A-C6A	2.30	122.51	118.73
2	F	300	NDP	C6N-N1N-C2N	2.30	121.78	119.32
3	H	290	2M3	C4-C5-C6	2.30	119.45	117.16
3	A	2	2M3	C4-C5-C6	2.28	119.44	117.16
3	H	290	2M3	C22-C21-N20	-2.28	119.81	123.42
3	B	1	2M3	C19-C17-C16	-2.27	108.76	114.97
3	C	4	2M3	C4-C5-C6	2.26	119.41	117.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	300	NDP	N9A-C8A-N7A	-2.25	110.74	113.94
3	C	4	2M3	C19-C17-C16	-2.24	108.84	114.97
2	C	300	NDP	C3N-C2N-N1N	-2.24	119.91	123.20
3	D	3	2M3	C26-C25-C17	2.24	61.79	60.78
3	G	8	2M3	C22-C21-N20	-2.24	119.88	123.42
3	F	290	2M3	C25-C26-C17	2.24	61.79	60.78
2	B	300	NDP	C2B-C1B-N9A	2.23	117.42	113.75
2	D	300	NDP	O4D-C1D-N1N	2.22	112.32	108.08
3	C	4	2M3	C22-C21-N20	-2.20	119.93	123.42
3	B	1	2M3	C25-C26-C17	2.20	61.78	60.78
2	A	300	NDP	O4D-C1D-N1N	2.16	112.21	108.08
2	F	300	NDP	C4A-C5A-N7A	-2.16	108.11	110.58
3	G	8	2M3	C4-C5-C6	2.15	119.31	117.16
3	A	2	2M3	C22-C21-N20	-2.15	120.02	123.42
2	A	300	NDP	C3N-C2N-N1N	-2.14	120.06	123.20
3	C	4	2M3	C25-C26-C17	2.13	61.75	60.78
3	F	290	2M3	C19-C17-C16	-2.13	109.16	114.97
3	A	2	2M3	C26-C25-C17	2.13	61.74	60.78
3	H	290	2M3	C25-C26-C17	2.11	61.73	60.78
3	E	7	2M3	C19-C17-C16	-2.11	109.22	114.97
3	E	7	2M3	C22-C21-N20	-2.09	120.12	123.42
2	E	300	NDP	C2A-N1A-C6A	2.08	122.15	118.73
3	D	3	2M3	C25-C26-C17	2.08	61.72	60.78
3	B	1	2M3	C22-C21-N20	-2.07	120.14	123.42
2	B	300	NDP	C2A-N1A-C6A	2.07	122.13	118.73
2	E	300	NDP	C4A-N9A-C8A	2.05	107.89	105.74
2	F	300	NDP	C4A-N9A-C8A	2.05	107.89	105.74
3	A	2	2M3	C25-C26-C17	2.04	61.70	60.78
3	F	290	2M3	C24-C19-N20	-2.04	119.87	122.33
3	C	4	2M3	C26-C25-C17	2.03	61.70	60.78
2	H	300	NDP	O4D-C1D-N1N	2.02	111.94	108.08

There are no chirality outliers.

All (82) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NDP	C5D-O5D-PN-O3
2	A	300	NDP	C5D-O5D-PN-O1N
2	A	300	NDP	C5D-O5D-PN-O2N
2	B	300	NDP	O4B-C4B-C5B-O5B
2	D	300	NDP	C5D-O5D-PN-O1N
2	F	300	NDP	C5B-O5B-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	F	300	NDP	C5B-O5B-PA-O3
2	G	300	NDP	C5D-O5D-PN-O3
2	G	300	NDP	C5D-O5D-PN-O2N
2	H	300	NDP	C5D-O5D-PN-O3
2	H	300	NDP	C5D-O5D-PN-O1N
2	H	300	NDP	C5D-O5D-PN-O2N
3	B	1	2M3	C16-C17-C19-C24
3	C	4	2M3	C26-C17-C19-N20
3	F	290	2M3	C16-C17-C19-C24
3	H	290	2M3	C16-C17-C19-C24
2	D	300	NDP	O4D-C1D-N1N-C6N
2	B	300	NDP	C3B-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	F	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
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	H	300	NDP	O4D-C1D-N1N-C6N
2	D	300	NDP	O4B-C4B-C5B-O5B
2	B	300	NDP	O4D-C4D-C5D-O5D
3	D	3	2M3	C26-C17-C19-C24
2	B	300	NDP	PN-O3-PA-O1A
2	F	300	NDP	PN-O3-PA-O1A
2	H	300	NDP	PA-O3-PN-O1N
3	A	2	2M3	C15-C11-C9-C5
3	B	1	2M3	C15-C11-C9-C5
3	E	7	2M3	C15-C11-C9-C5
3	G	8	2M3	C15-C11-C9-C5
2	C	300	NDP	O4D-C4D-C5D-O5D
2	B	300	NDP	C5B-O5B-PA-O1A
2	B	300	NDP	C5B-O5B-PA-O2A
2	B	300	NDP	C5B-O5B-PA-O3
2	D	300	NDP	C5D-O5D-PN-O3
2	D	300	NDP	C5D-O5D-PN-O2N
2	C	300	NDP	C1B-C2B-O2B-P2B
3	A	2	2M3	C26-C17-C19-C24

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Mol	Chain	Res	Type	Atoms
3	B	1	2M3	C26-C17-C19-C24
3	F	290	2M3	C26-C17-C19-C24
3	H	290	2M3	C26-C17-C19-C24
2	E	300	NDP	PN-O3-PA-O1A
2	A	300	NDP	C2B-O2B-P2B-O2X
2	C	300	NDP	C2B-O2B-P2B-O2X
2	E	300	NDP	C2B-O2B-P2B-O2X
2	G	300	NDP	C2B-O2B-P2B-O2X
2	H	300	NDP	C2B-O2B-P2B-O2X
2	A	300	NDP	C2N-C3N-C7N-N7N
2	C	300	NDP	C2B-O2B-P2B-O1X
2	D	300	NDP	C2B-O2B-P2B-O1X
2	G	300	NDP	C2B-O2B-P2B-O1X
2	H	300	NDP	C2B-O2B-P2B-O1X
2	C	300	NDP	PN-O3-PA-O1A
3	A	2	2M3	C16-C17-C19-C24
3	C	4	2M3	C16-C17-C19-C24
3	D	3	2M3	C16-C17-C19-C24
3	E	7	2M3	C16-C17-C19-C24
3	G	8	2M3	C16-C17-C19-C24
2	H	300	NDP	O4B-C4B-C5B-O5B
3	E	7	2M3	C26-C17-C19-N20
3	G	8	2M3	C26-C17-C19-N20
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	B	300	NDP	C3D-C4D-C5D-O5D
2	C	300	NDP	C3D-C4D-C5D-O5D
2	B	300	NDP	C2B-O2B-P2B-O1X
2	F	300	NDP	C2B-O2B-P2B-O1X
2	A	300	NDP	C1B-C2B-O2B-P2B
2	F	300	NDP	PN-O3-PA-O2A
2	G	300	NDP	PA-O3-PN-O2N
2	H	300	NDP	PA-O3-PN-O2N

There are no ring outliers.

16 monomers are involved in 31 short contacts:

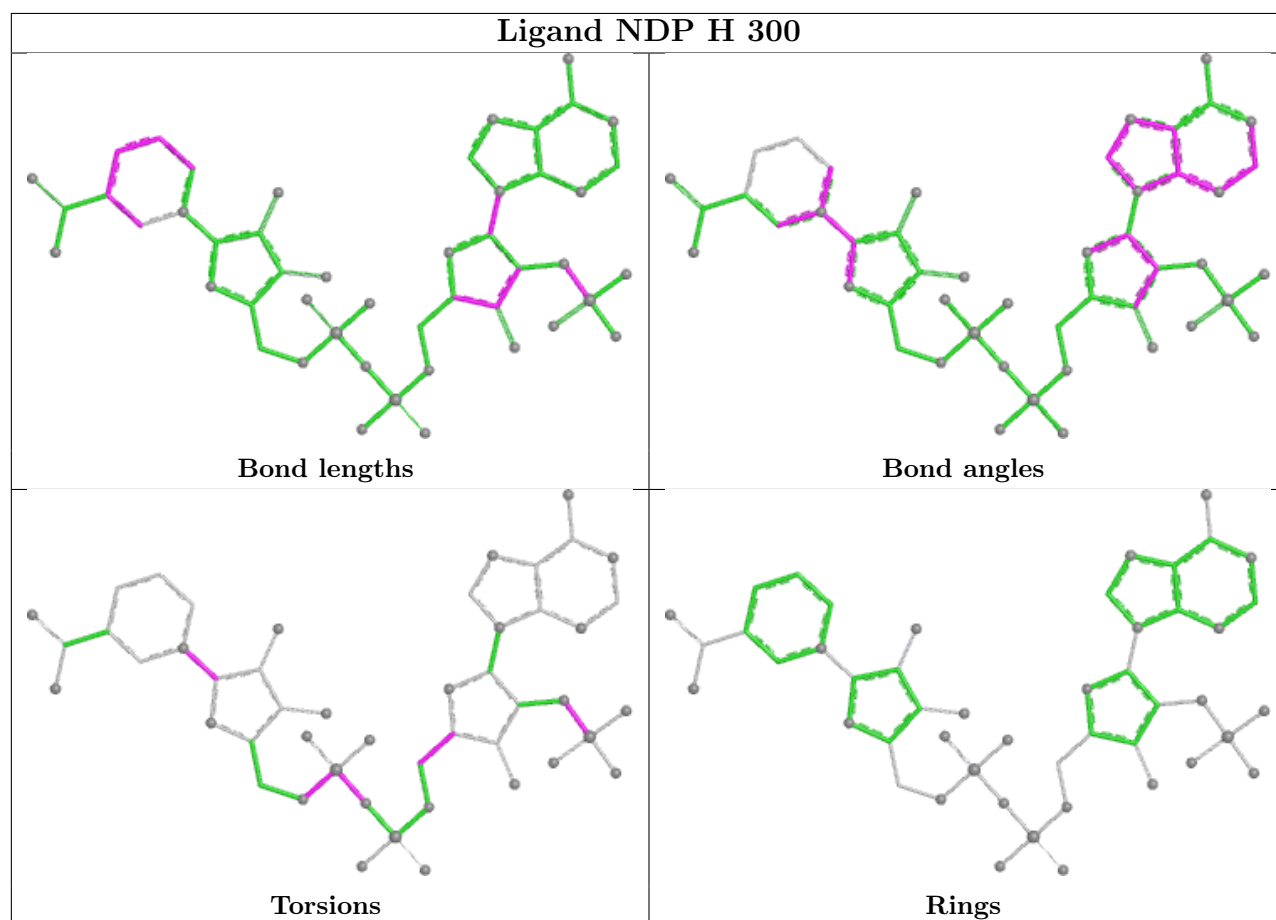
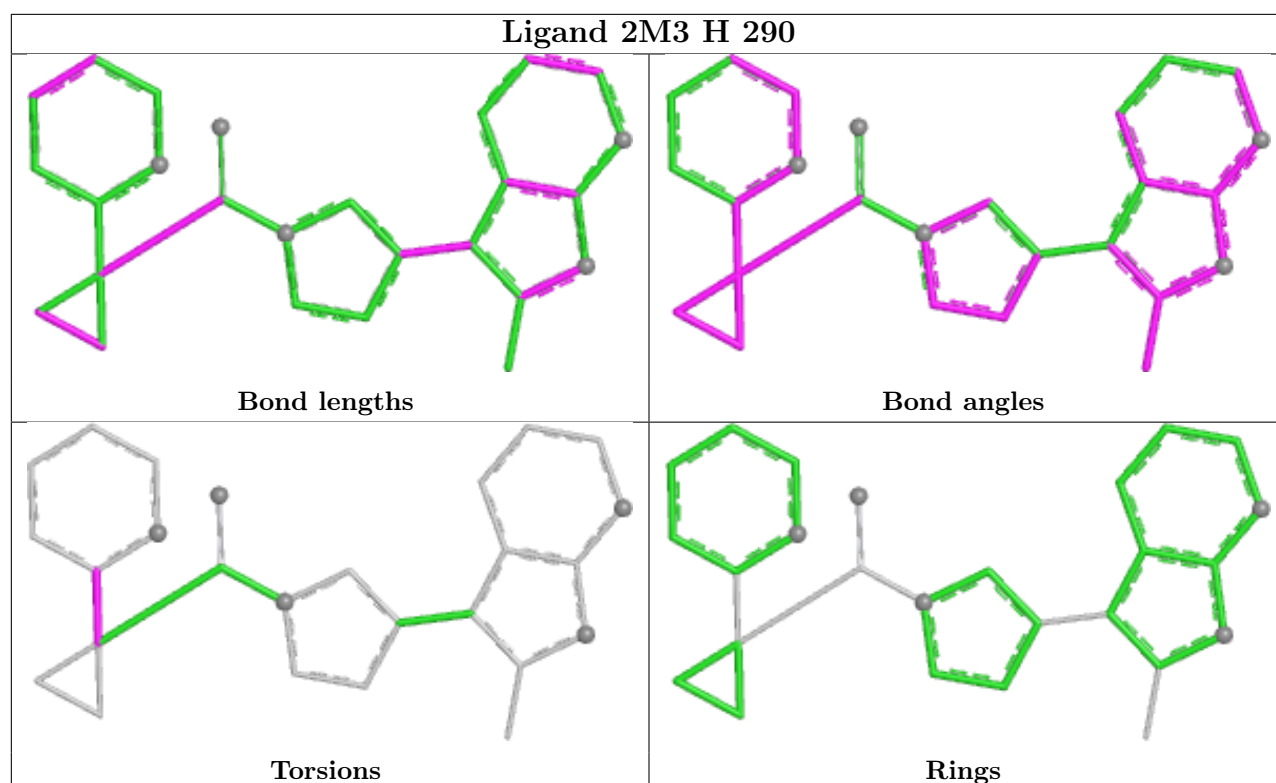
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2	SO4	1	0
4	C	8	SO4	1	0
2	H	300	NDP	2	0

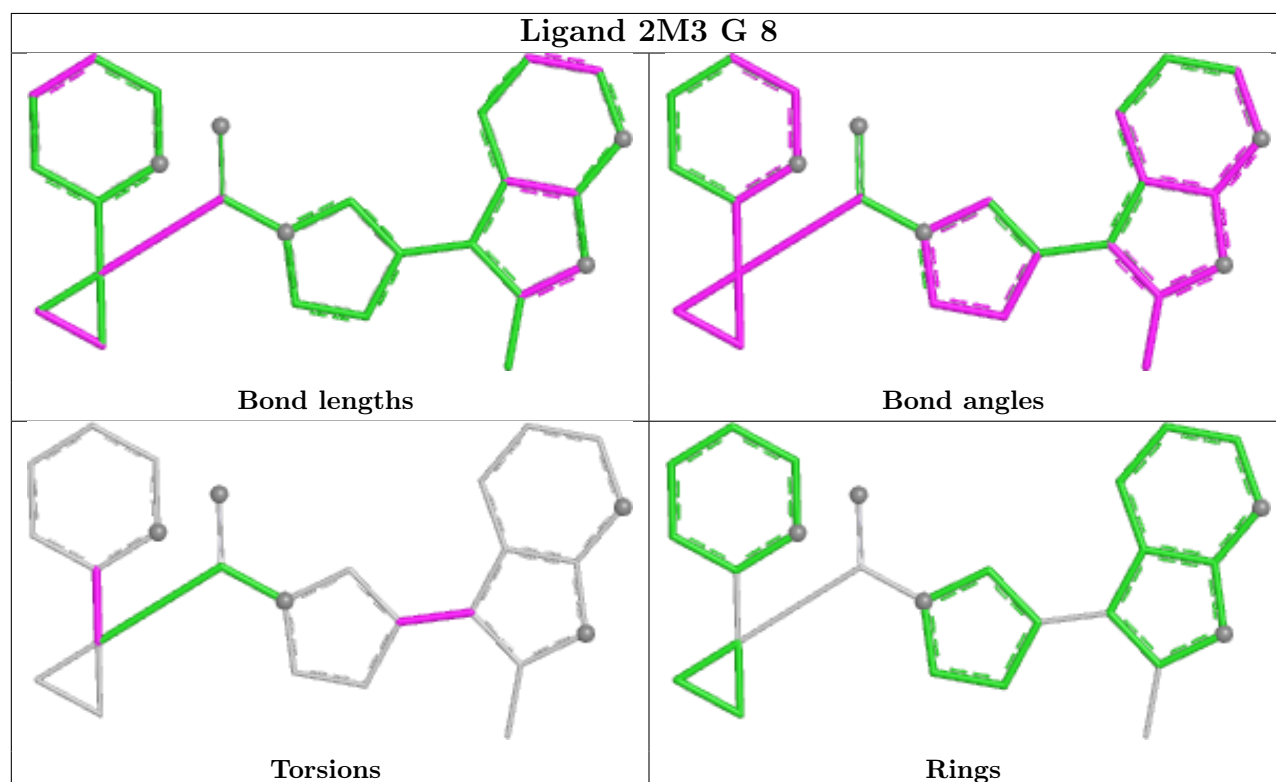
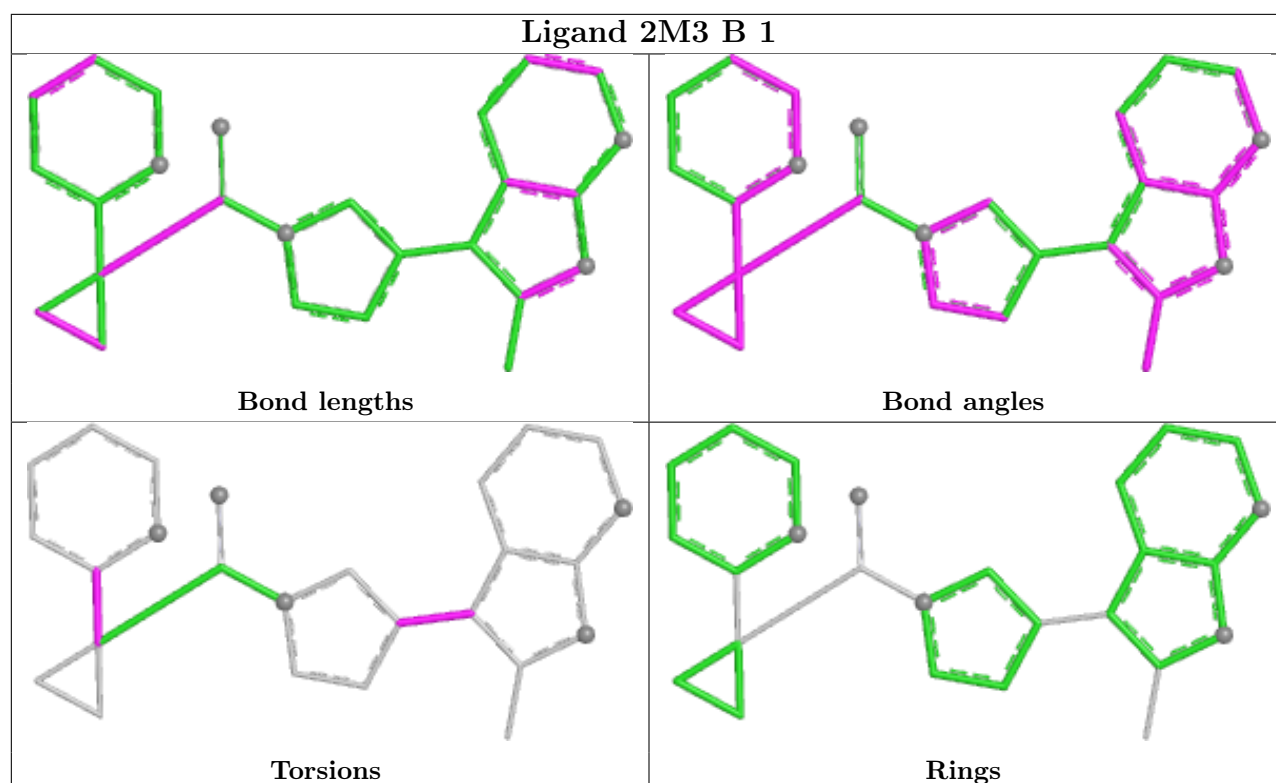
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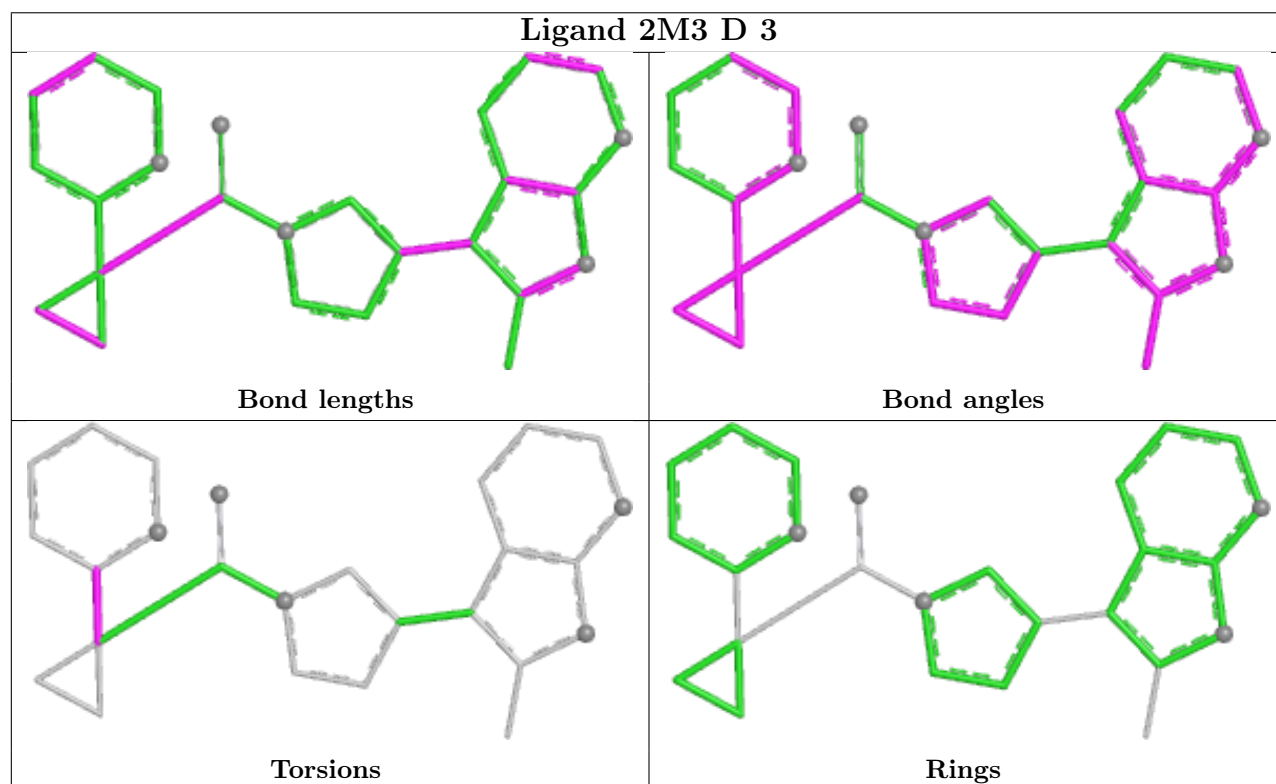
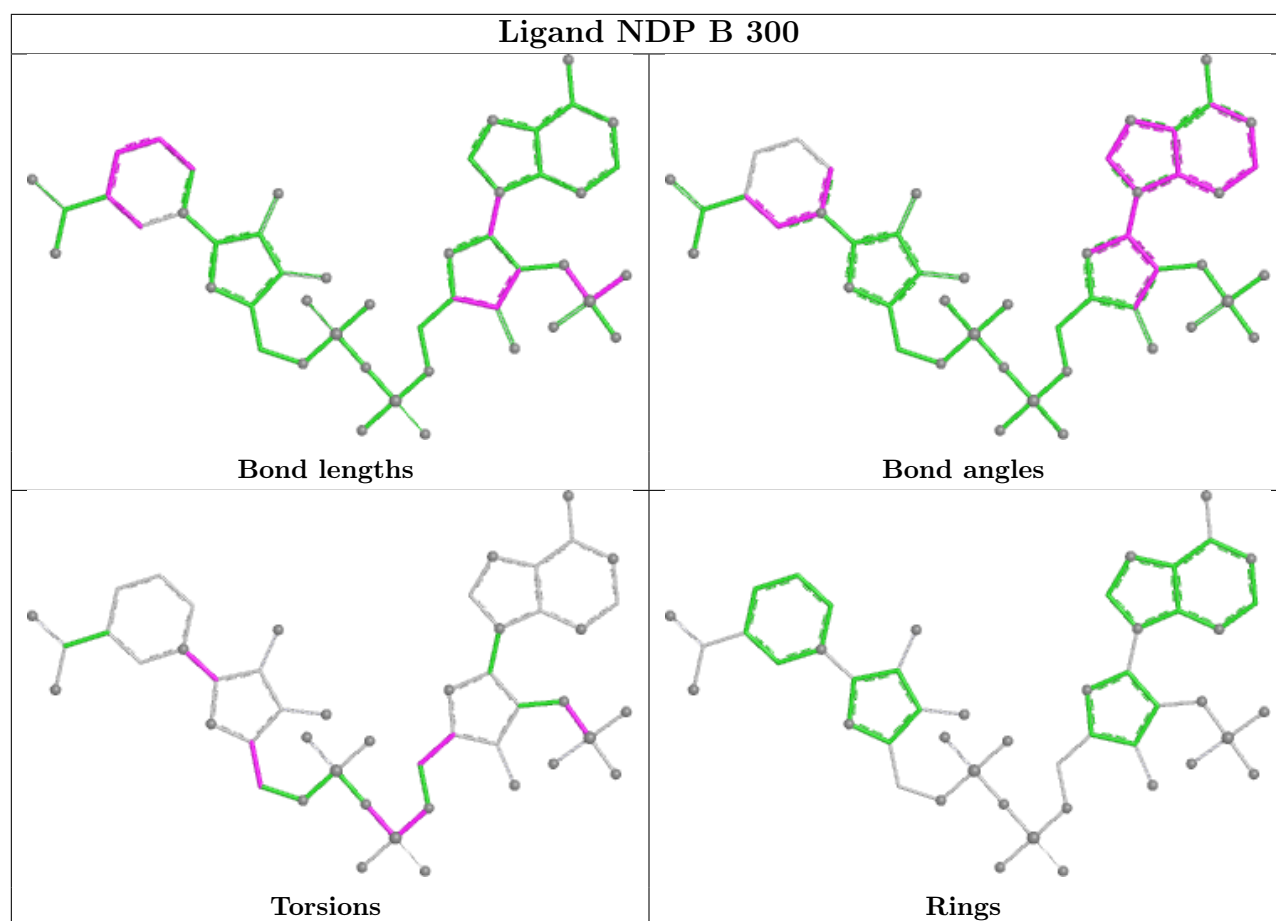
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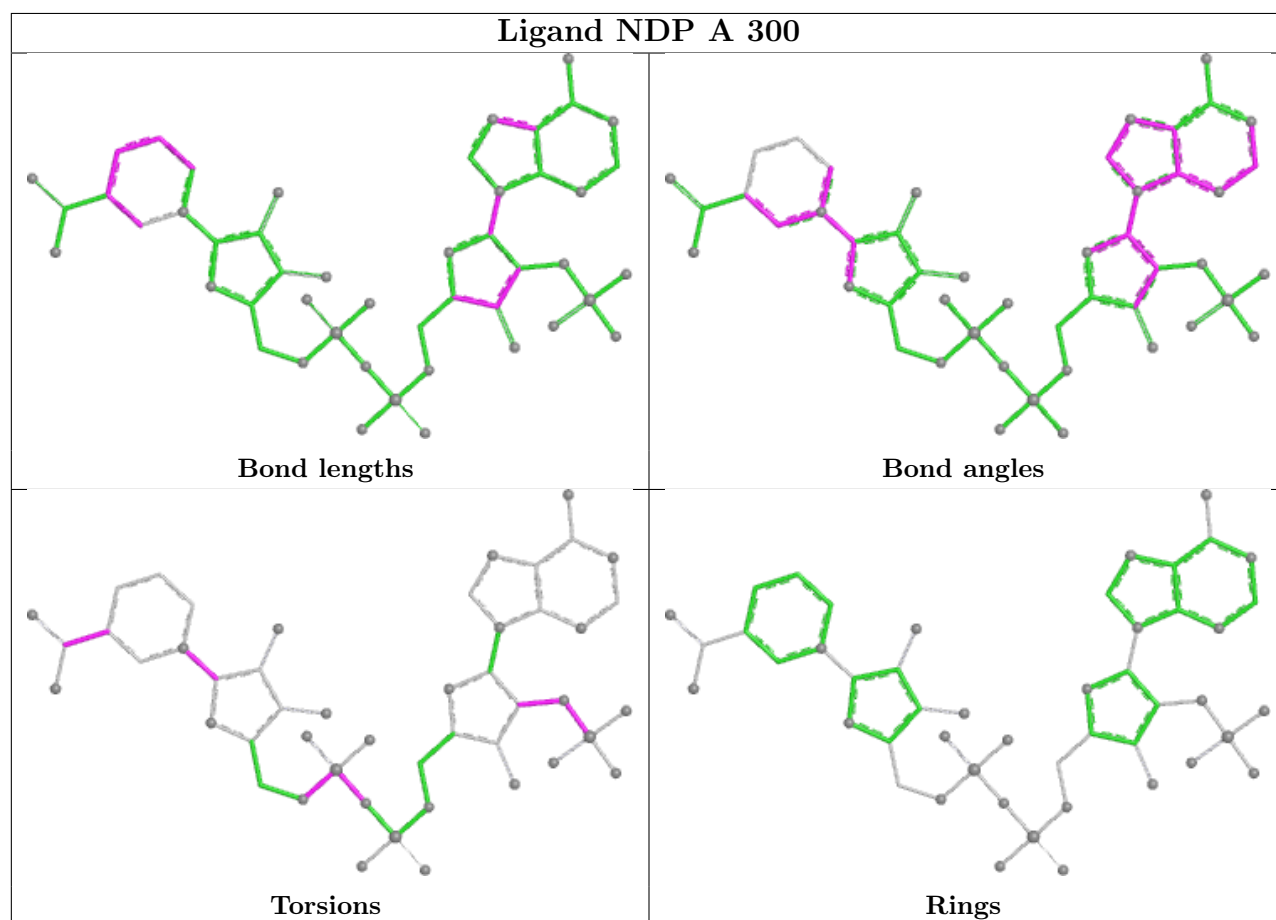
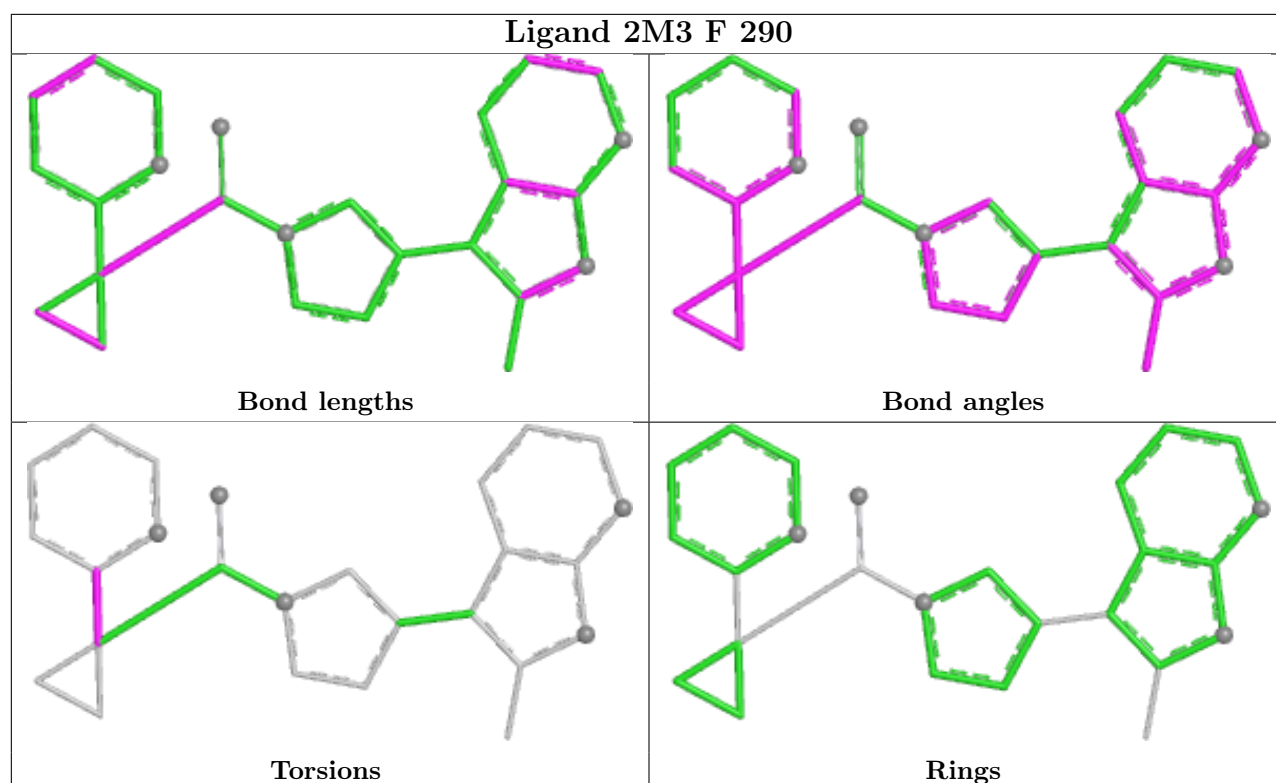
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1	2M3	3	0
3	G	8	2M3	1	0
2	B	300	NDP	2	0
3	D	3	2M3	1	0
3	F	290	2M3	3	0
2	A	300	NDP	2	0
2	D	300	NDP	3	0
2	E	300	NDP	4	0
2	F	300	NDP	3	0
3	E	7	2M3	2	0
2	G	300	NDP	5	0
3	C	4	2M3	3	0
4	E	4	SO4	1	0

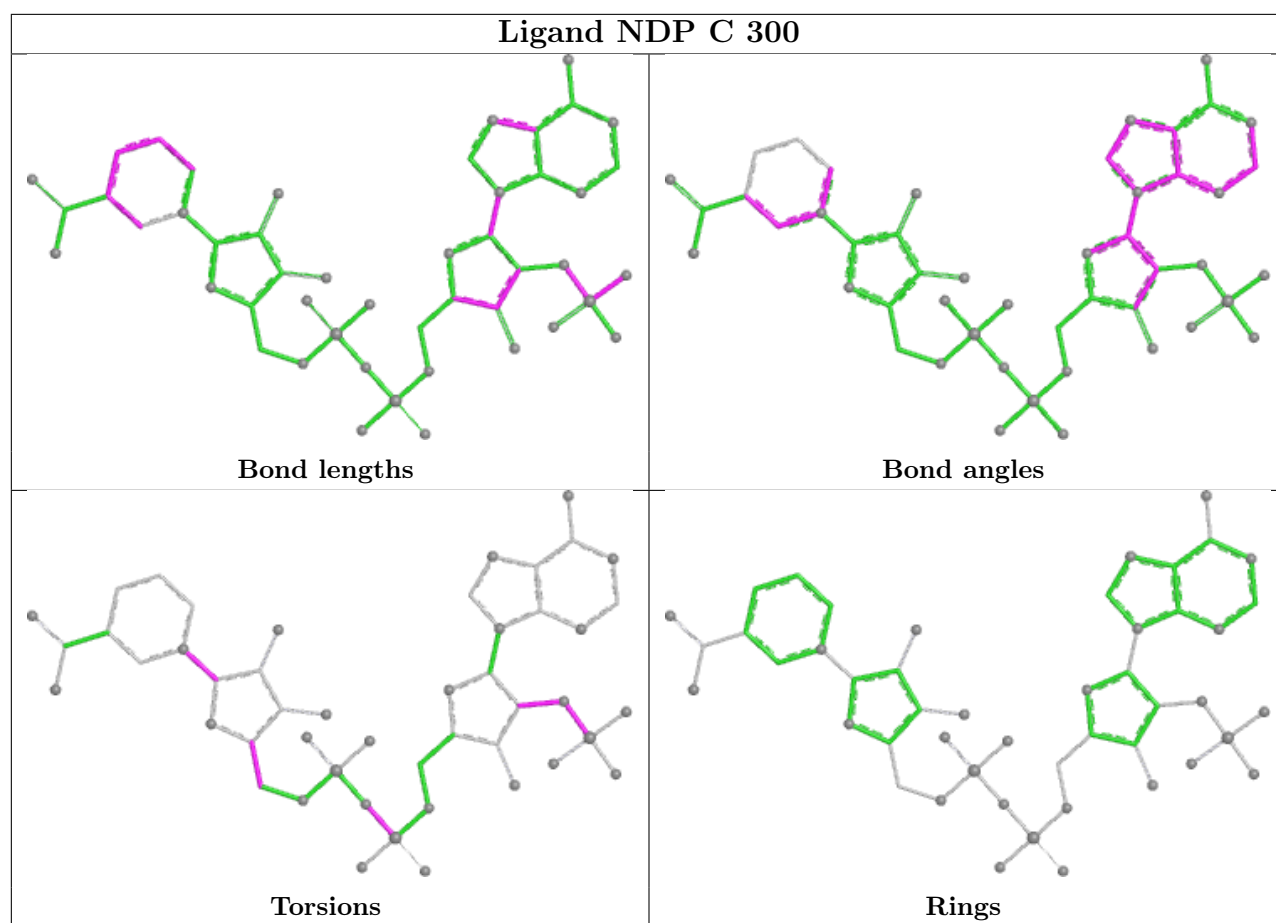
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

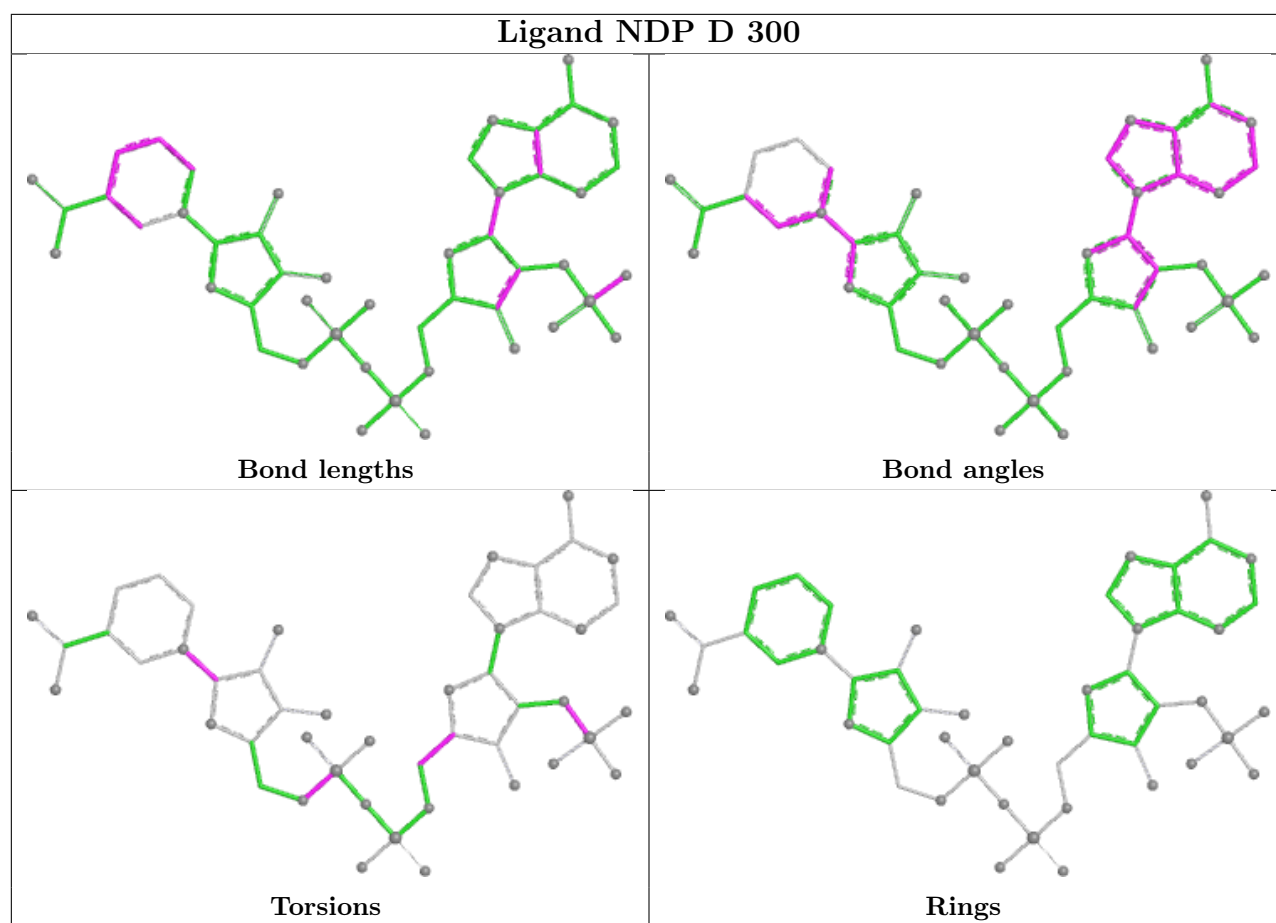


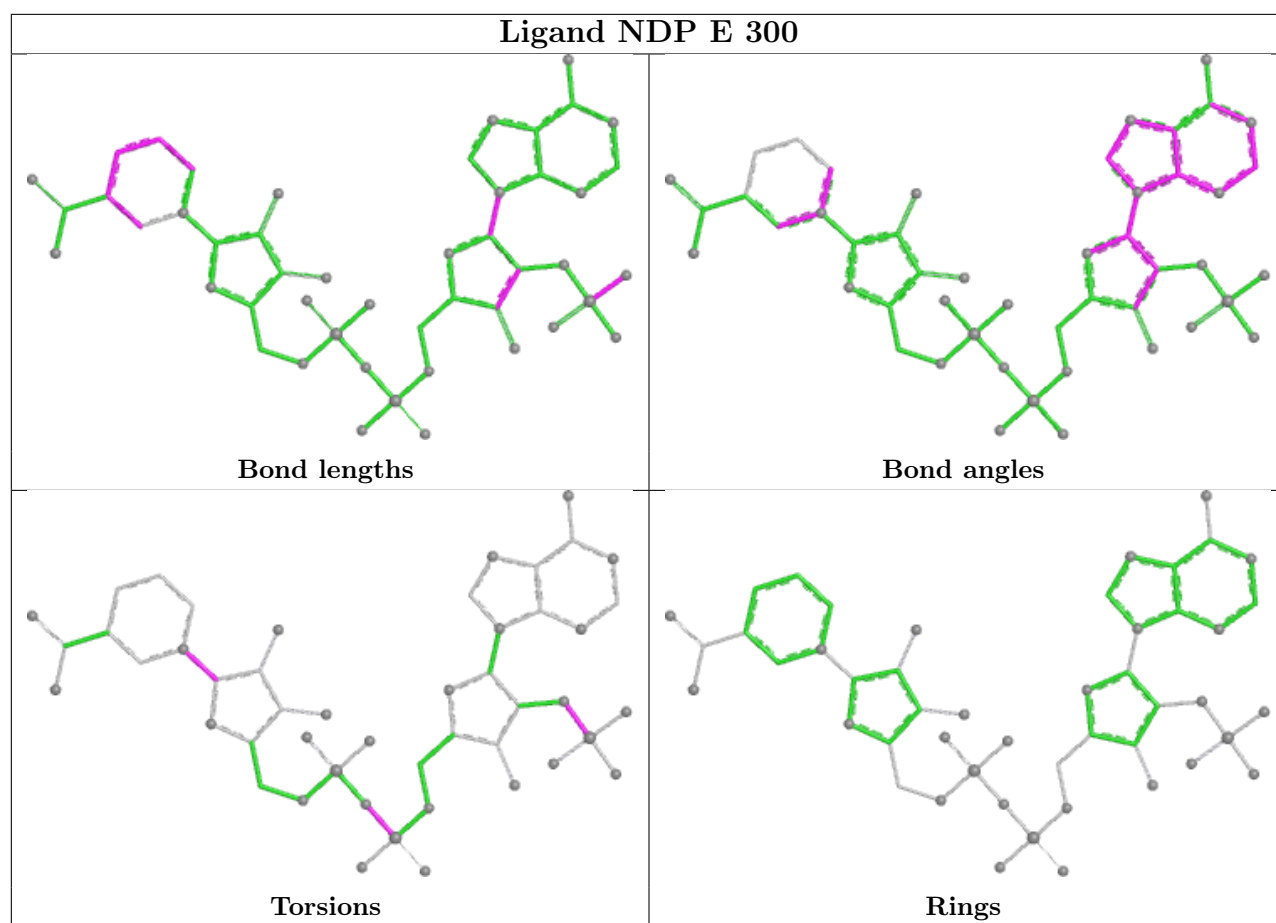


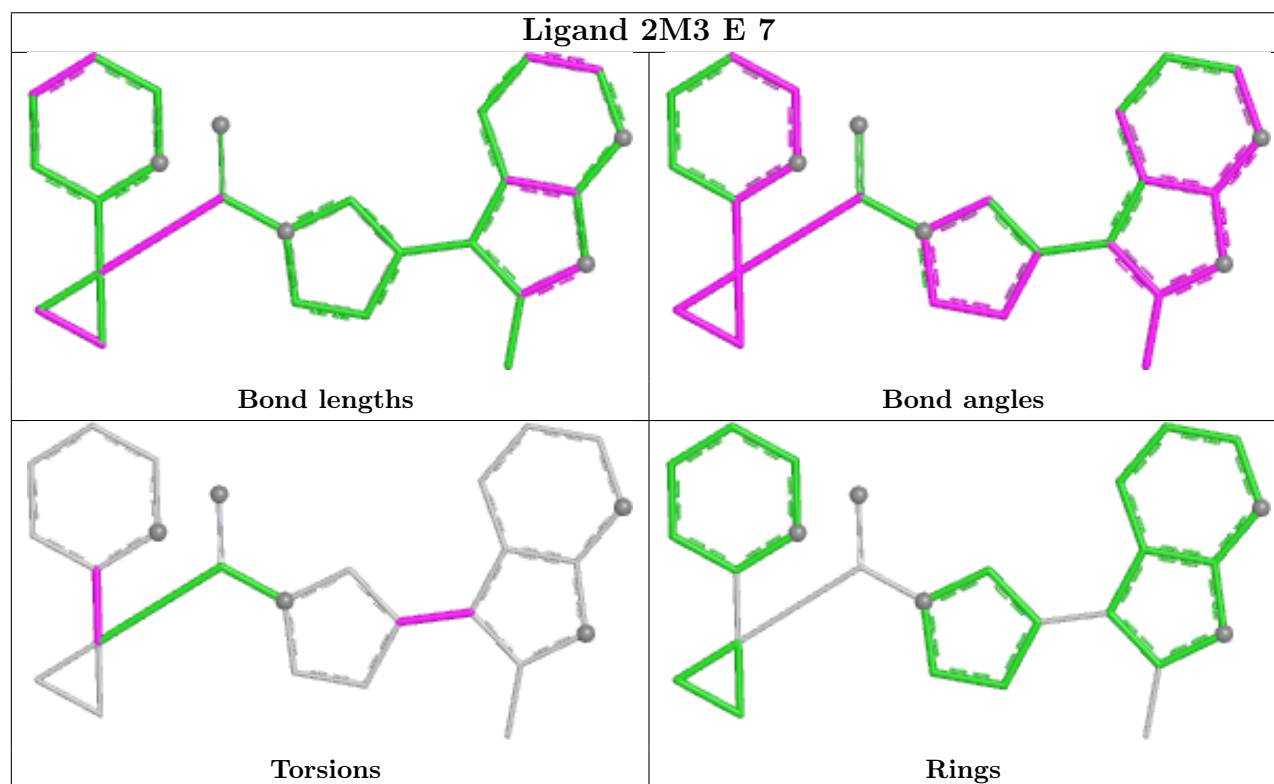
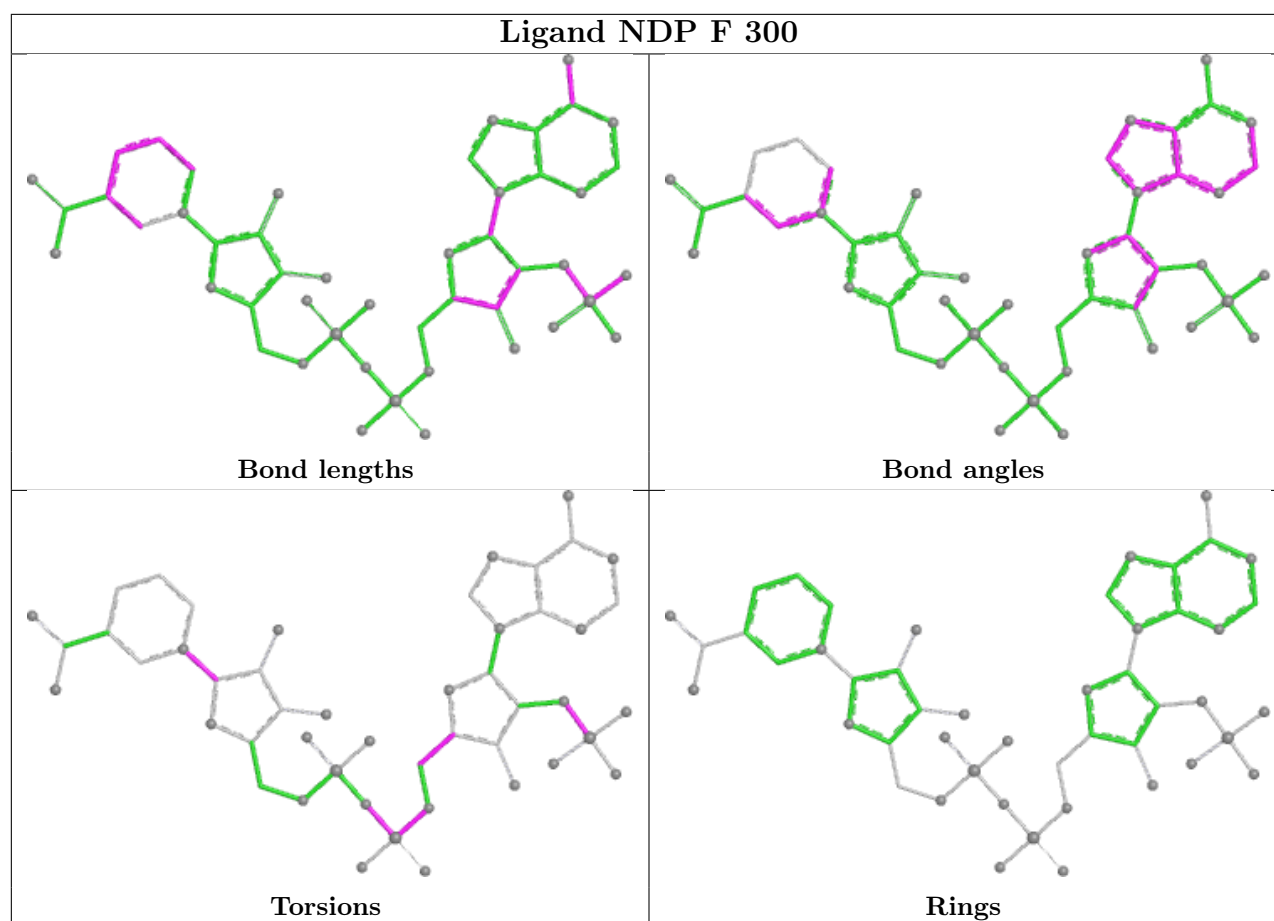


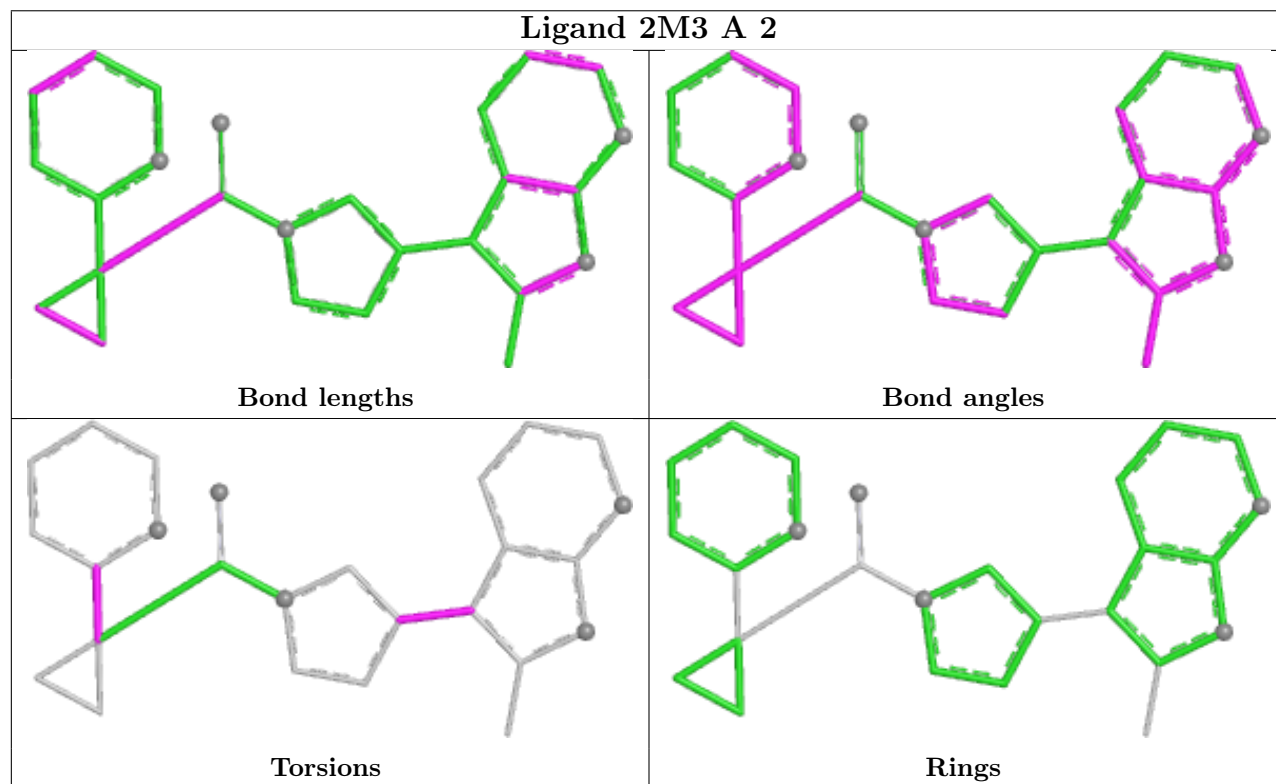
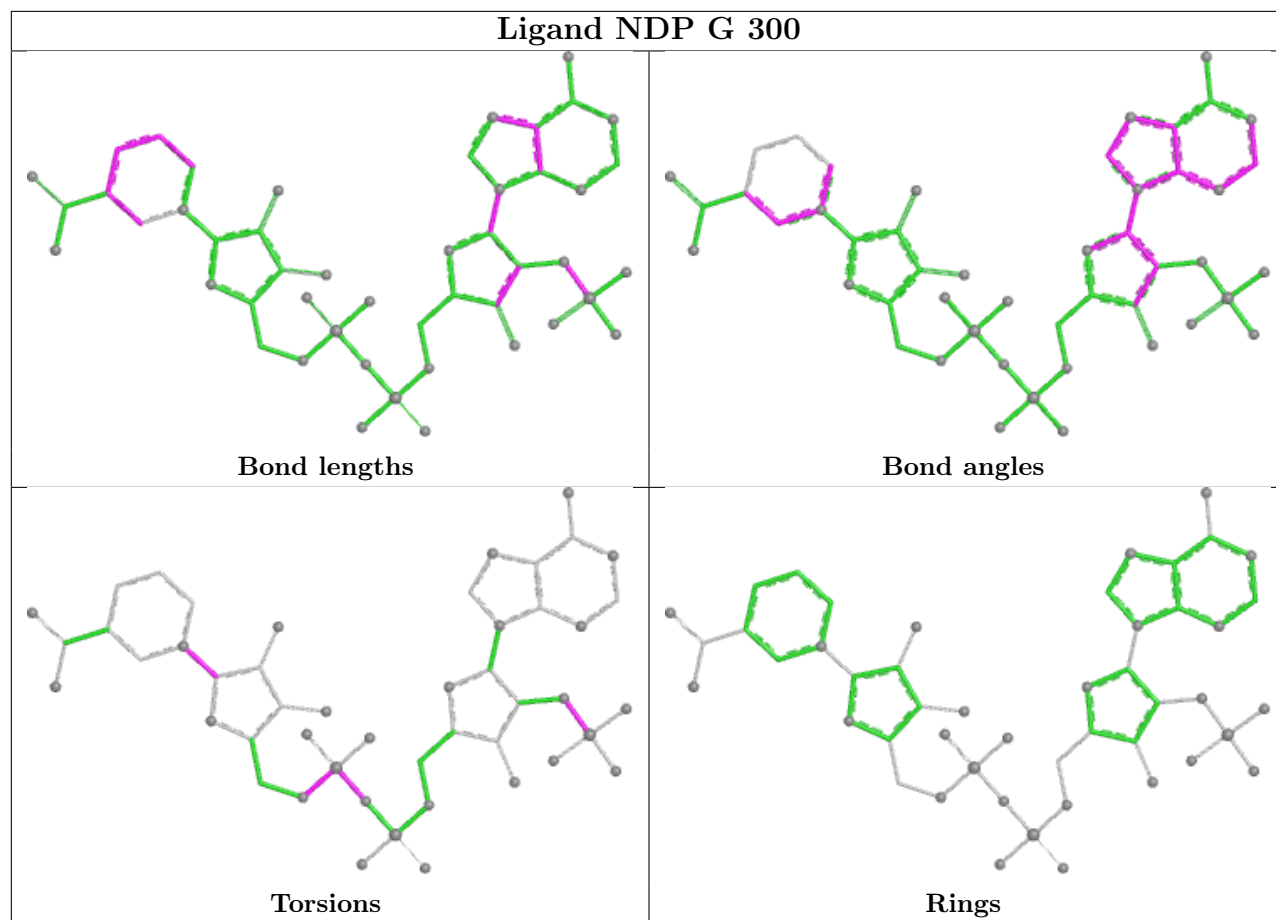


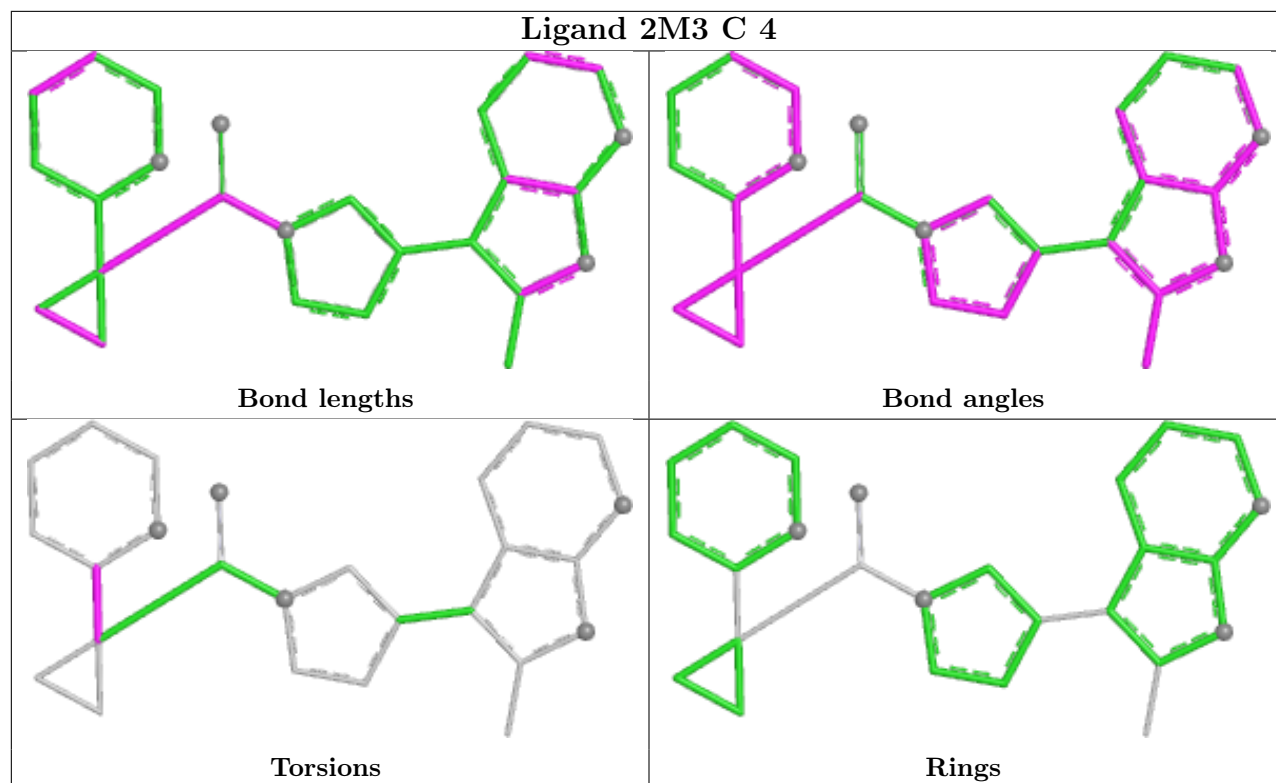












5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	-1.24	0 100 100	15, 29, 48, 71	6 (2%)
1	B	264/264 (100%)	-1.21	1 (0%) 88 89	15, 30, 51, 58	9 (3%)
1	C	264/264 (100%)	-1.43	0 100 100	5, 18, 40, 56	5 (1%)
1	D	264/264 (100%)	-1.43	0 100 100	5, 18, 45, 58	7 (2%)
1	E	264/264 (100%)	-1.41	0 100 100	8, 20, 43, 72	5 (1%)
1	F	263/264 (99%)	-1.40	0 100 100	7, 19, 44, 57	2 (0%)
1	G	264/264 (100%)	-1.30	0 100 100	12, 27, 48, 58	8 (3%)
1	H	264/264 (100%)	-1.28	0 100 100	15, 28, 53, 69	6 (2%)
All	All	2111/2112 (99%)	-1.34	1 (0%) 100 100	5, 24, 48, 72	48 (2%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	266	ILE	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,

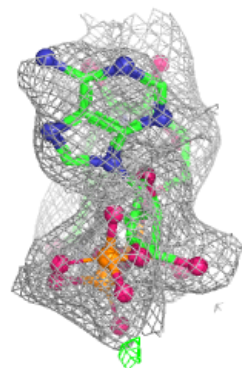
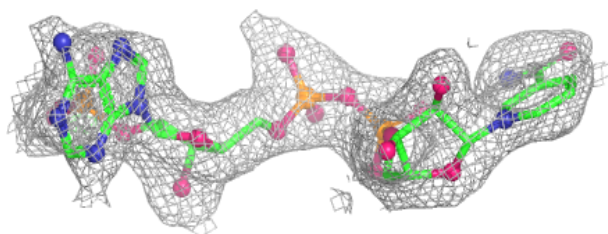
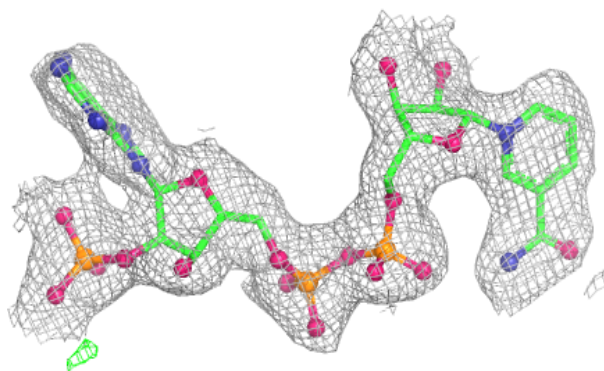
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NDP	A	300	48/48	0.99	0.03	17,27,33,34	0
2	NDP	B	300	48/48	0.99	0.03	24,28,31,34	0
2	NDP	G	300	48/48	0.99	0.03	19,28,30,31	0
2	NDP	H	300	48/48	0.99	0.03	16,29,33,36	0
3	2M3	A	2	26/26	0.99	0.03	29,31,35,36	0
3	2M3	B	1	26/26	0.99	0.05	44,51,54,55	0
3	2M3	C	4	26/26	0.99	0.03	14,22,23,24	0
3	2M3	D	3	26/26	0.99	0.04	27,31,34,36	0
3	2M3	E	7	26/26	0.99	0.04	19,24,28,29	0
3	2M3	F	290	26/26	0.99	0.04	32,42,43,44	0
3	2M3	G	8	26/26	0.99	0.04	26,29,30,31	0
3	2M3	H	290	26/26	0.99	0.04	39,42,44,44	0
4	SO4	B	2	5/5	0.99	0.04	48,48,49,50	0
4	SO4	C	7	5/5	0.99	0.04	48,49,49,50	0
4	SO4	C	8	5/5	0.99	0.04	35,37,37,37	0
4	SO4	E	4	5/5	0.99	0.05	46,47,47,48	0
4	SO4	G	9	5/5	0.99	0.05	48,49,51,51	0
4	SO4	H	3	5/5	0.99	0.05	57,57,58,59	0
4	SO4	H	6	5/5	0.99	0.05	60,60,61,61	0
4	SO4	D	1	5/5	1.00	0.05	34,36,36,36	0
2	NDP	D	300	48/48	1.00	0.02	5,13,19,21	0
4	SO4	F	5	5/5	1.00	0.02	27,30,31,32	0
2	NDP	E	300	48/48	1.00	0.02	11,15,19,19	0
2	NDP	F	300	48/48	1.00	0.02	9,14,18,20	0
2	NDP	C	300	48/48	1.00	0.02	11,14,20,20	0

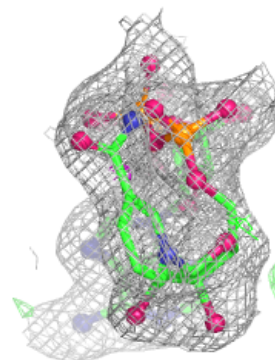
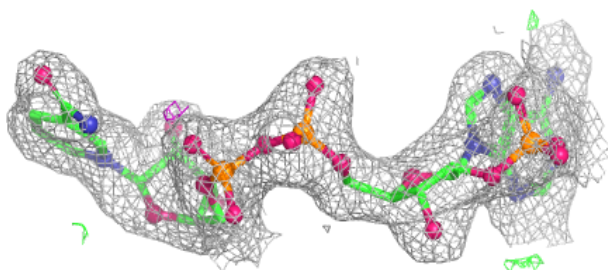
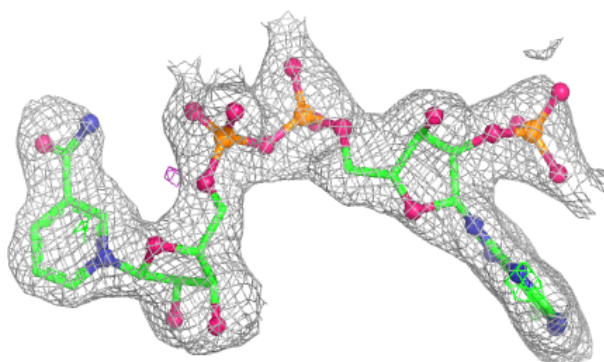
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NDP A 300:

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

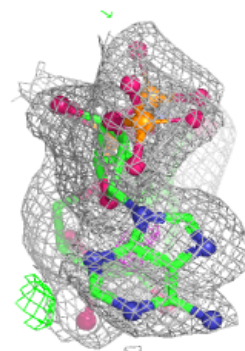
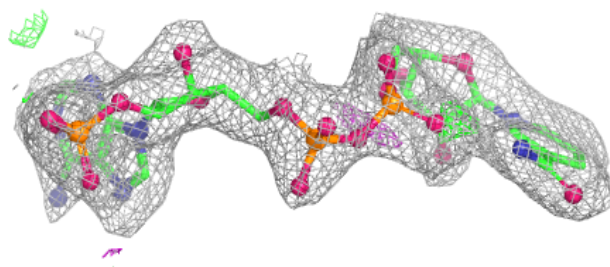
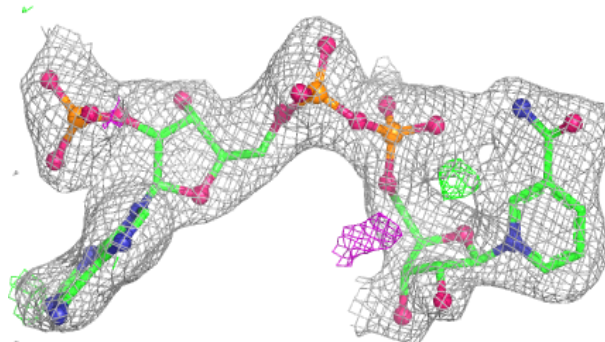
**Electron density around NDP B 300:**

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

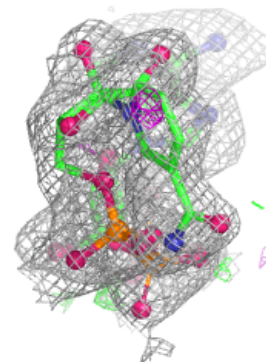
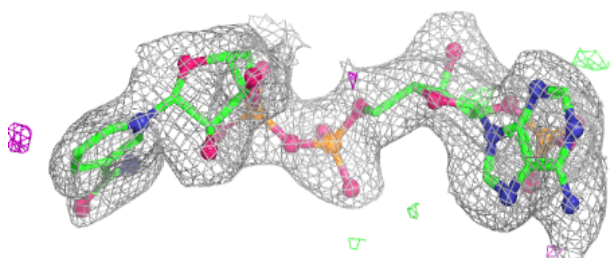
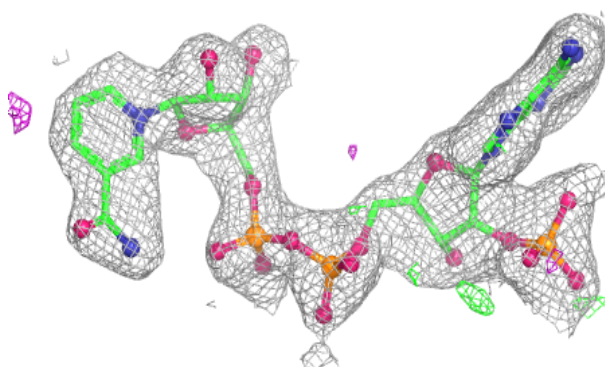


Electron density around NDP G 300:

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

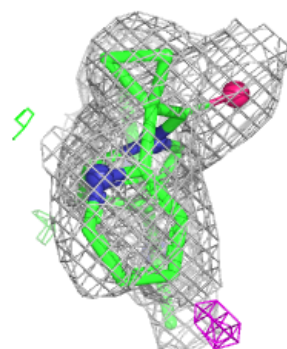
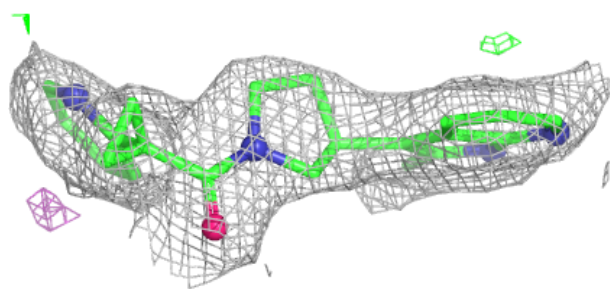
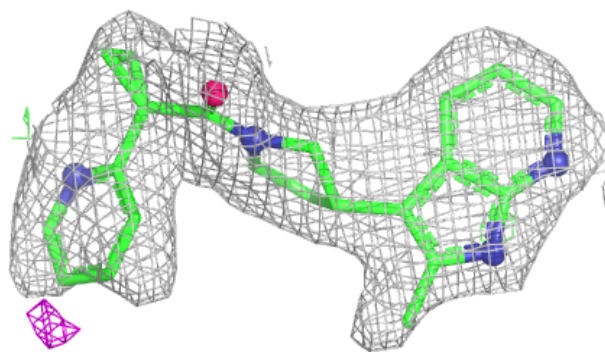
**Electron density around NDP H 300:**

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

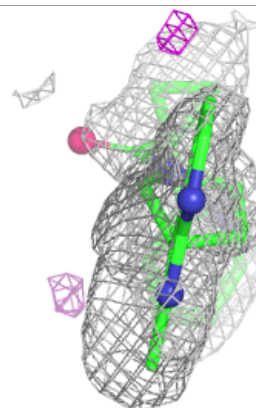
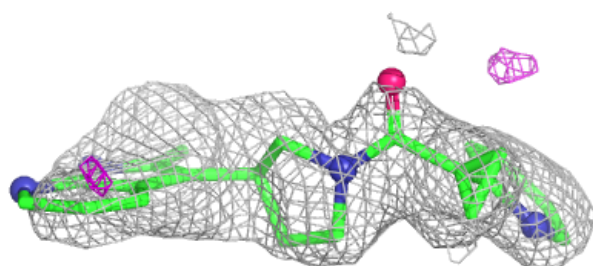
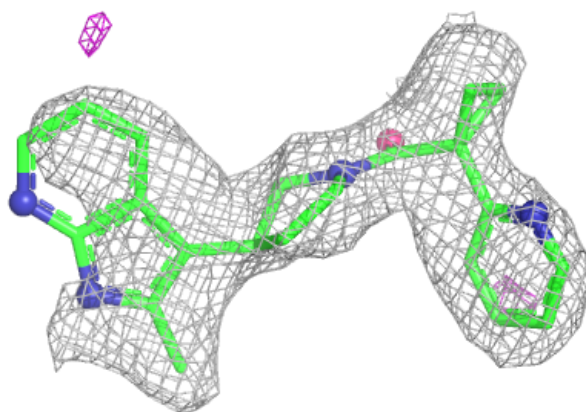


Electron density around 2M3 A 2:

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

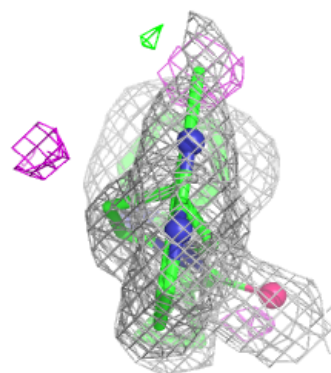
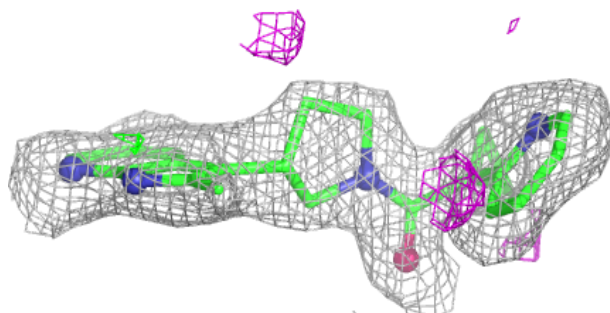
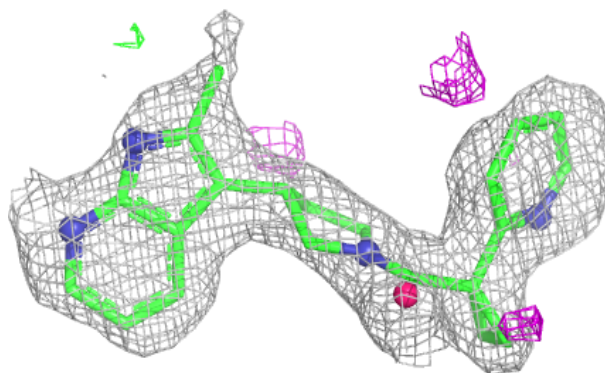
**Electron density around 2M3 B 1:**

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

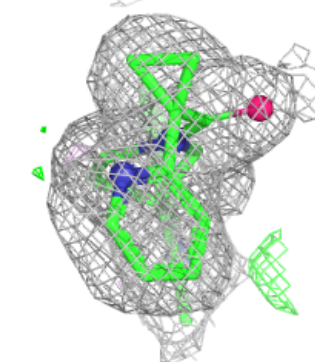
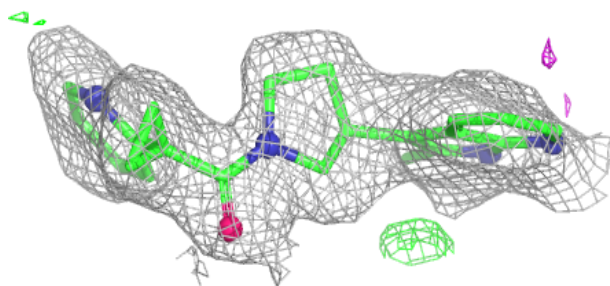
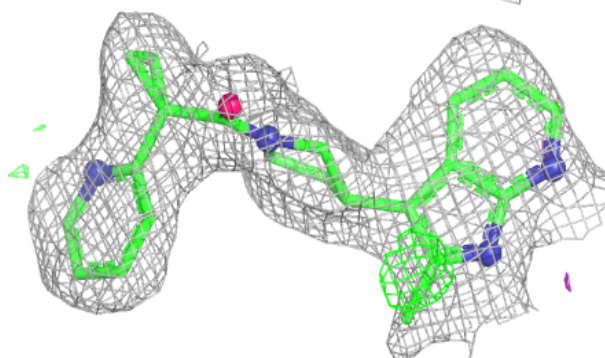


Electron density around 2M3 C 4:

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

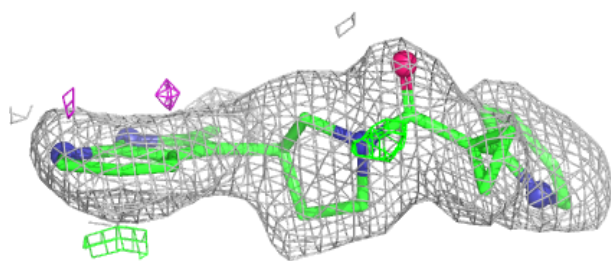
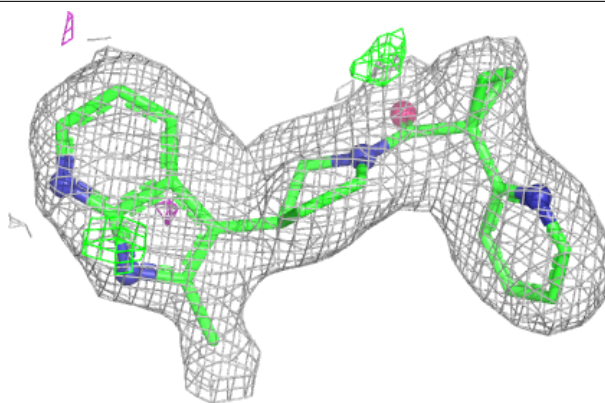
**Electron density around 2M3 D 3:**

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

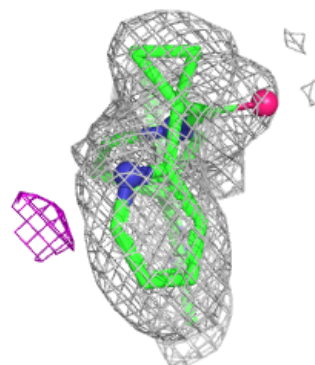
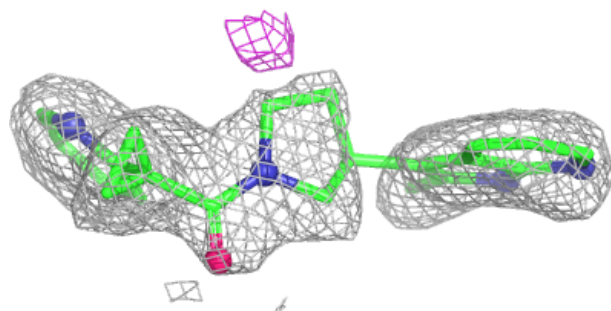
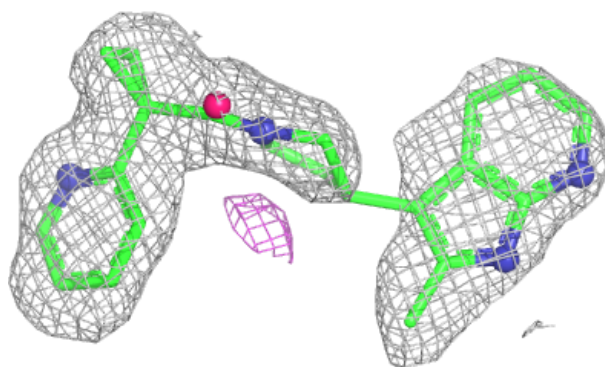


Electron density around 2M3 E 7:

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

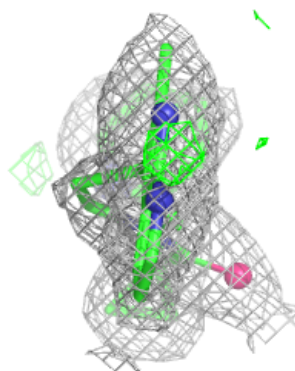
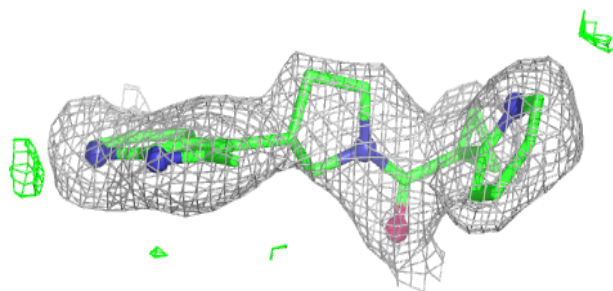
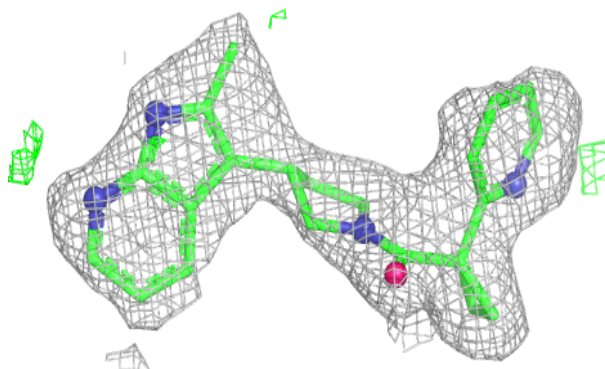
**Electron density around 2M3 F 290:**

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

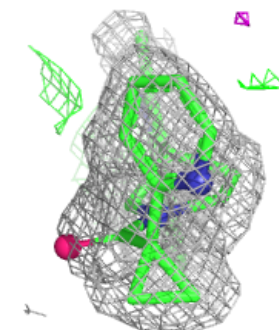
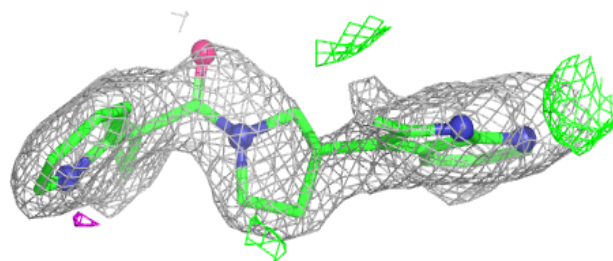
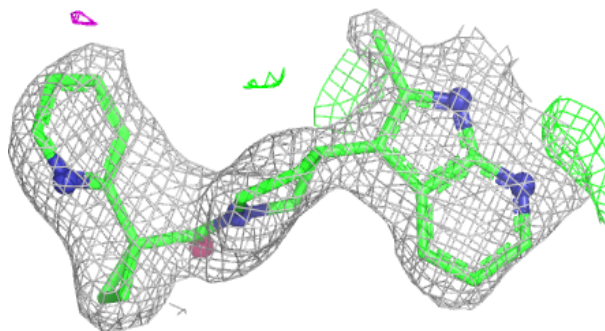


Electron density around 2M3 G 8:

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

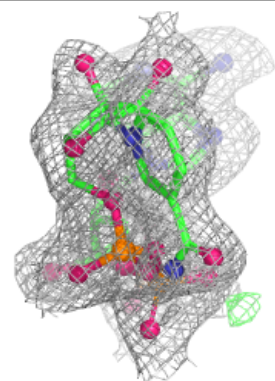
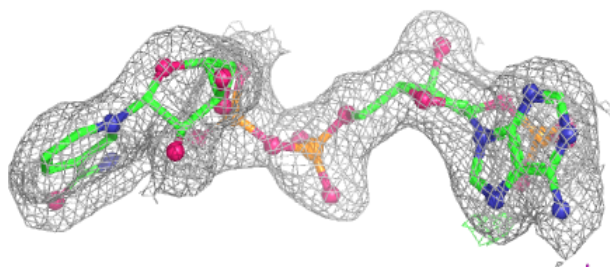
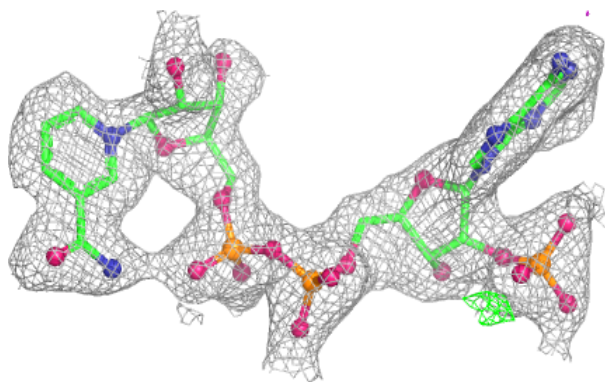
**Electron density around 2M3 H 290:**

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

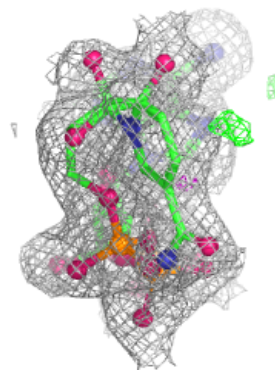
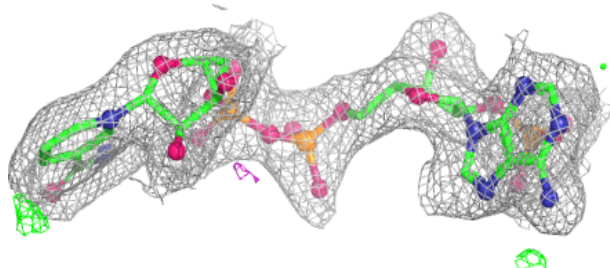
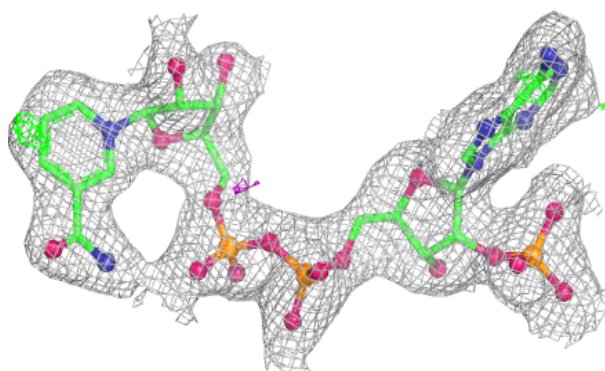


Electron density around NDP D 300:

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

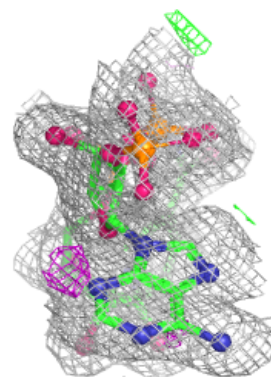
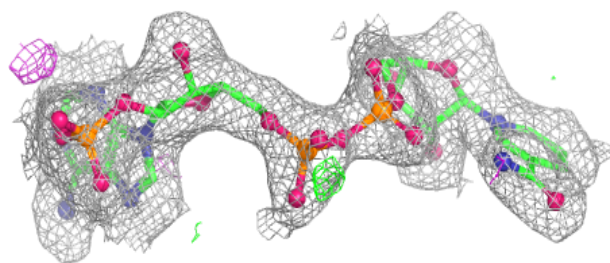
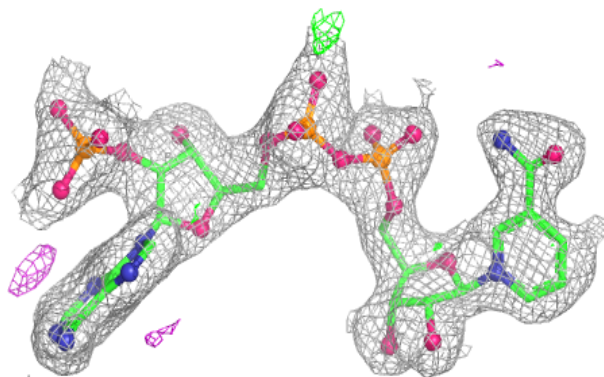
**Electron density around NDP E 300:**

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

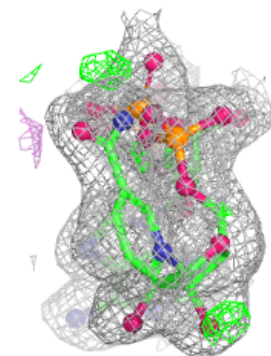
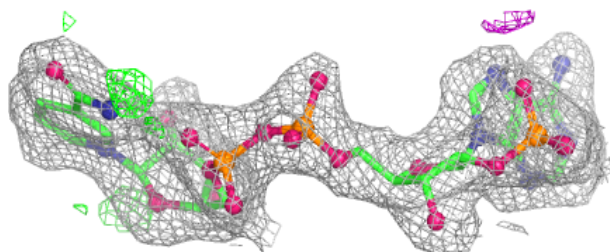
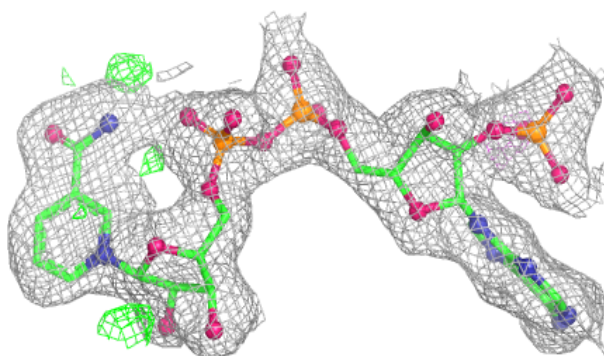


Electron density around NDP F 300:

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

**Electron density around NDP 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.