



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 01:24 am BST

PDB ID : 3H8B
Title : A combined crystallographic and molecular dynamics study of cathepsin-L retro-binding inhibitors(compound 9)
Authors : Tulsidas, S.R.; Chowdhury, S.F.; Kumar, S.; Joseph, L.; Purisima, E.O.; Sivaraman, J.
Deposited on : 2009-04-29
Resolution : 1.80 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 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 : 2.11
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) : 2.11

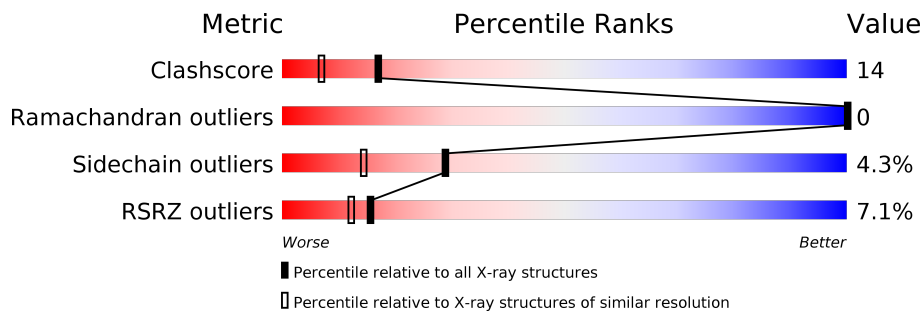
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 on 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	220	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 80%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">4% 80% 17% ..</p>
1	B	220	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 79%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 18%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">5% 79% 18% ..</p>
1	C	220	<div style="display: flex; align-items: center;"> <div style="width: 6%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 74%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">6% 74% 23% .</p>
1	D	220	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 79%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 18%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">5% 79% 18% .</p>
1	E	220	<div style="display: flex; align-items: center;"> <div style="width: 9%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 73%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 24%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">9% 73% 24% ..</p>
1	F	220	<div style="display: flex; align-items: center;"> <div style="width: 13%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">13% 75% 22% .</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NSY	A	300	-	X	-	-
2	NSY	B	400	-	X	-	-
2	NSY	C	500	-	X	-	-
2	NSY	D	600	-	X	-	-
2	NSY	E	700	-	X	-	-
2	NSY	F	800	-	X	-	-

2 Entry composition [i](#)

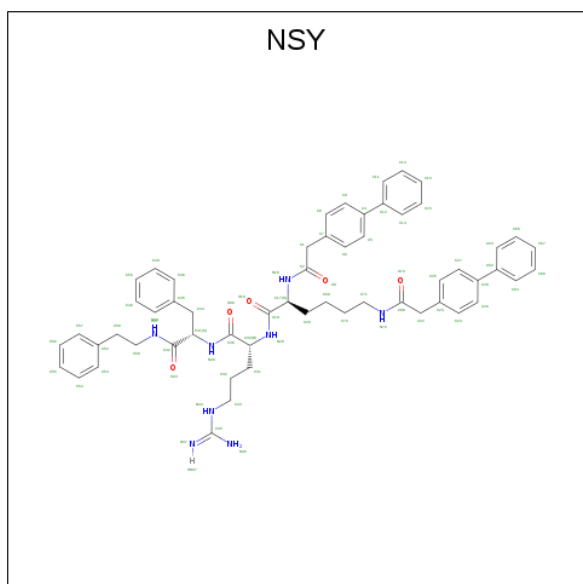
There are 3 unique types of molecules in this entry. The entry contains 10935 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cathepsin L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	Total 1659	C 1041	N 275	O 330	S 13	0	0	0
1	B	215	Total 1659	C 1041	N 275	O 330	S 13	0	0	0
1	C	215	Total 1659	C 1041	N 275	O 330	S 13	0	0	0
1	D	215	Total 1659	C 1041	N 275	O 330	S 13	0	0	0
1	E	215	Total 1659	C 1041	N 275	O 330	S 13	0	0	0
1	F	215	Total 1658	C 1041	N 275	O 329	S 13	0	0	0

- Molecule 2 is N 2 ,N 6 -bis(biphenyl-4-ylacetyl)-L-lysyl-D-arginyl-N-(2-phenylethyl)-L-phenylalaninamide (three-letter code: NSY) (formula: C₅₇H₆₄N₈O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			70	57	8	5		
2	B	1	Total	C	N	O	0	0
			70	57	8	5		
2	C	1	Total	C	N	O	0	0
			70	57	8	5		
2	D	1	Total	C	N	O	0	0
			70	57	8	5		
2	E	1	Total	C	N	O	0	0
			70	57	8	5		
2	F	1	Total	C	N	O	0	0
			70	57	8	5		

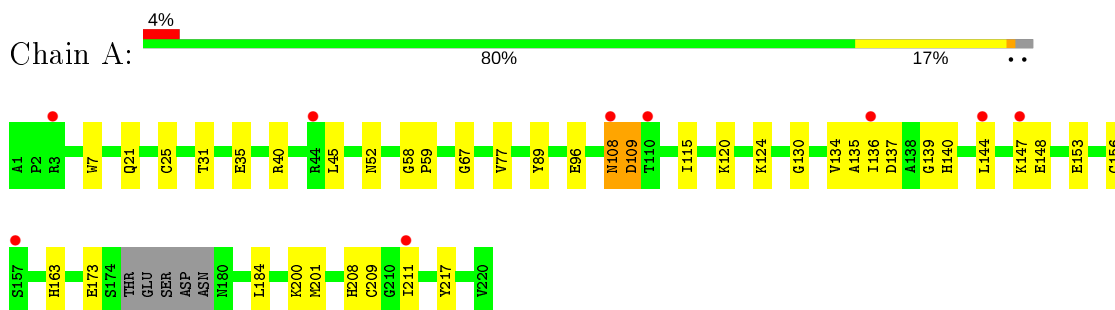
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	111	Total	O	0	0
			111	111		
3	B	124	Total	O	0	0
			124	124		
3	C	93	Total	O	0	0
			93	93		
3	D	88	Total	O	0	0
			88	88		
3	E	75	Total	O	0	0
			75	75		
3	F	71	Total	O	0	0
			71	71		

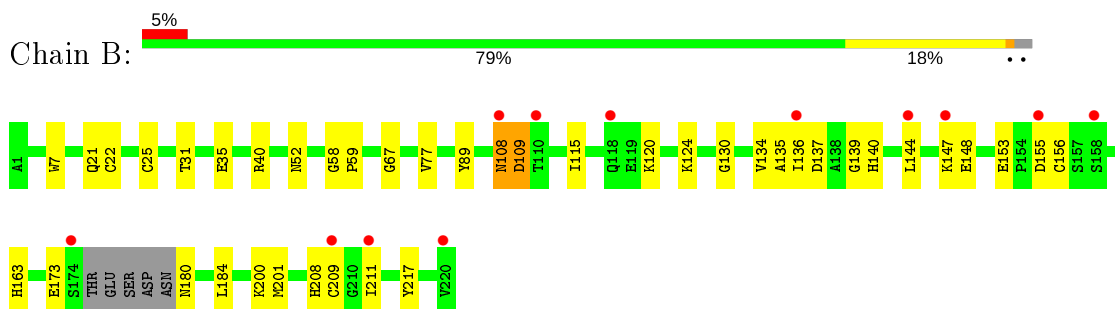
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

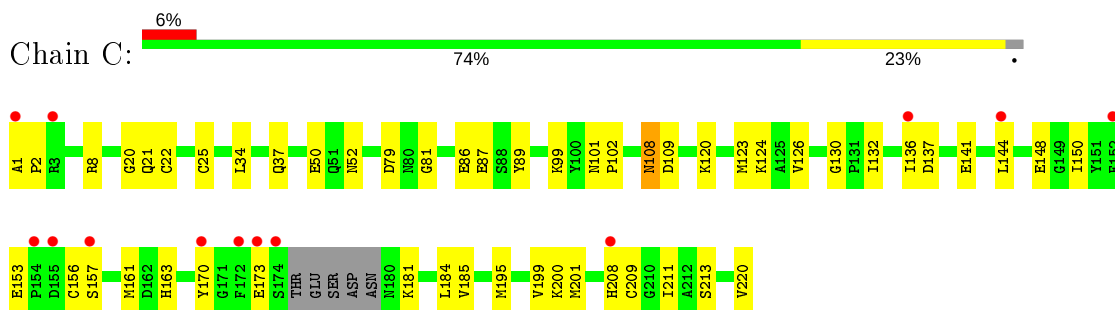
- Molecule 1: Cathepsin L1



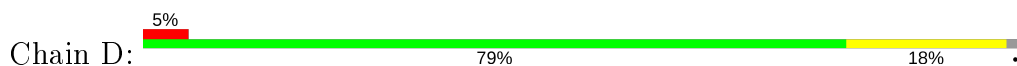
- Molecule 1: Cathepsin L1

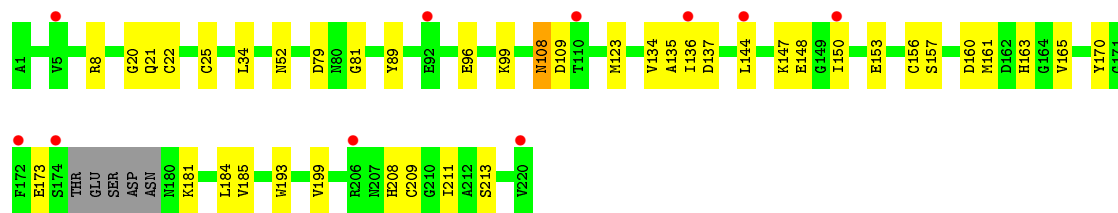


- Molecule 1: Cathepsin L1

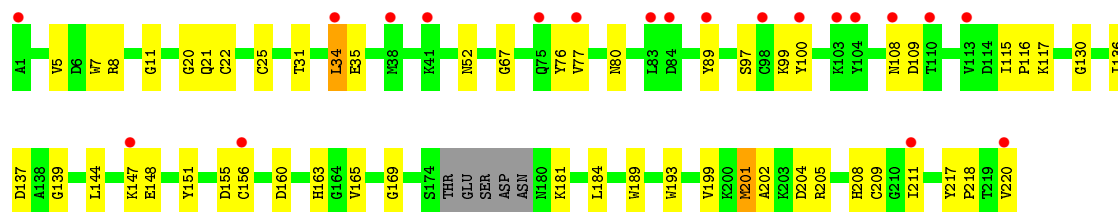
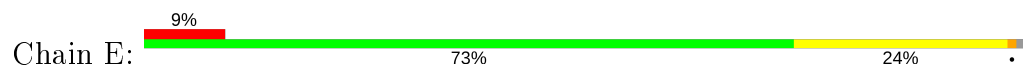


- Molecule 1: Cathepsin L1

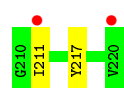
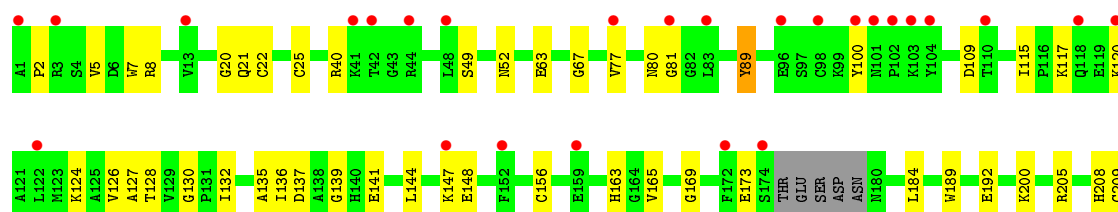
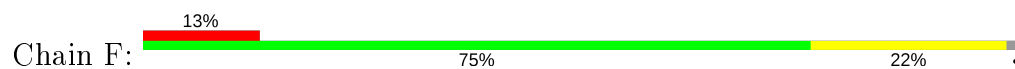




- Molecule 1: Cathepsin L1



- Molecule 1: Cathepsin L1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	61.99Å 99.23Å 206.46Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	45.00 – 1.80 48.24 – 1.79	Depositor EDS
% Data completeness (in resolution range)	94.2 (45.00-1.80) 97.2 (48.24-1.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.39 (at 1.79Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.250 0.236 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.8	Xtrriage
Anisotropy	0.373	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 25.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.479 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10935	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.60	0/1700	0.66	0/2296
1	B	0.60	0/1700	0.65	0/2296
1	C	0.55	0/1700	0.67	0/2296
1	D	0.55	0/1700	0.67	0/2296
1	E	0.54	1/1700 (0.1%)	0.64	1/2296 (0.0%)
1	F	0.52	0/1699	0.64	0/2296
All	All	0.56	1/10199 (0.0%)	0.65	1/13776 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	201	MET	CG-SD	-6.24	1.65	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	201	MET	CA-CB-CG	-5.60	103.78	113.30

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	1659	0	1542	41	0
1	B	1659	0	1542	41	0
1	C	1659	0	1542	59	0
1	D	1659	0	1542	44	0
1	E	1659	0	1542	58	0
1	F	1658	0	1542	57	0
2	A	70	0	58	6	0
2	B	70	0	60	9	0
2	C	70	0	58	10	0
2	D	70	0	58	6	0
2	E	70	0	60	14	0
2	F	70	0	58	13	0
3	A	111	0	0	5	0
3	B	124	0	0	4	0
3	C	93	0	0	7	0
3	D	88	0	0	6	0
3	E	75	0	0	6	0
3	F	71	0	0	12	0
All	All	10935	0	9604	280	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 14.

All (280) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:144:LEU:HD22	2:F:800:NSY:H26	1.22	1.14
1:E:144:LEU:HD22	2:E:700:NSY:H26	1.20	1.10
1:D:144:LEU:HD22	2:D:600:NSY:H26	1.30	1.10
1:C:126:VAL:HG22	1:C:132:ILE:HD13	1.40	1.03
1:C:144:LEU:HD22	2:C:500:NSY:H26	1.42	1.01
1:C:144:LEU:HD21	1:F:144:LEU:HD21	1.46	0.98
1:D:144:LEU:HD21	1:E:144:LEU:HD21	1.53	0.89
1:F:2:PRO:HD2	3:F:472:HOH:O	1.75	0.86
1:E:144:LEU:CD2	2:E:700:NSY:H26	2.07	0.84
1:D:163:HIS:HA	3:D:221:HOH:O	1.78	0.83
1:B:135:ALA:C	1:B:136:ILE:HD12	2.00	0.82
1:E:181:LYS:NZ	1:E:204:ASP:HB2	1.94	0.82
1:E:144:LEU:HD22	2:E:700:NSY:C26	2.08	0.82
1:C:99:LYS:HE2	1:D:99:LYS:HE2	1.63	0.80
1:A:135:ALA:C	1:A:136:ILE:HD12	2.02	0.80
1:C:144:LEU:HD21	1:F:144:LEU:CD2	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:HIS:HA	3:C:222:HOH:O	1.84	0.77
1:C:200:LYS:HE2	3:C:347:HOH:O	1.85	0.77
2:C:500:NSY:H27	1:F:21:GLN:HG2	1.66	0.76
1:E:163:HIS:HA	3:E:238:HOH:O	1.84	0.76
1:B:108:ASN:OD1	1:D:81:GLY:N	2.18	0.75
2:D:600:NSY:H27	1:E:21:GLN:HG2	1.68	0.75
1:A:108:ASN:OD1	1:C:81:GLY:N	2.19	0.74
1:F:163:HIS:HA	3:F:247:HOH:O	1.85	0.74
1:F:144:LEU:CD2	2:F:800:NSY:H26	2.12	0.74
1:F:144:LEU:HD22	2:F:800:NSY:C26	2.10	0.73
1:B:163:HIS:HA	3:B:221:HOH:O	1.88	0.73
1:E:25:CYS:SG	3:E:238:HOH:O	2.46	0.73
1:E:208:HIS:O	1:E:211:ILE:HG13	1.90	0.72
1:C:20:GLY:HA2	1:F:141:GLU:OE1	1.90	0.71
1:E:144:LEU:HD23	2:E:700:NSY:H63	1.74	0.70
1:C:120:LYS:HD3	1:C:124:LYS:HE3	1.74	0.70
1:D:144:LEU:HD21	1:E:144:LEU:CD2	2.22	0.70
1:E:181:LYS:HZ1	1:E:204:ASP:HB2	1.55	0.69
1:F:115:ILE:HD11	1:F:217:TYR:HE1	1.57	0.69
1:F:136:ILE:HG23	1:F:209:CYS:HB3	1.74	0.69
1:C:144:LEU:HD11	1:F:144:LEU:HD23	1.75	0.69
1:A:115:ILE:HD11	1:A:217:TYR:HE1	1.57	0.68
1:C:126:VAL:HA	1:C:132:ILE:HD11	1.74	0.68
1:A:163:HIS:HA	3:A:221:HOH:O	1.94	0.68
1:B:115:ILE:HD11	1:B:217:TYR:HE1	1.57	0.68
1:F:208:HIS:O	1:F:211:ILE:HG13	1.94	0.68
1:F:25:CYS:SG	3:F:247:HOH:O	2.52	0.67
1:F:135:ALA:C	1:F:136:ILE:HD12	2.15	0.67
1:B:136:ILE:HG23	1:B:209:CYS:HB3	1.77	0.66
1:E:25:CYS:SG	3:E:221:HOH:O	2.36	0.65
1:C:195:MET:SD	3:C:347:HOH:O	2.53	0.65
1:C:144:LEU:HD21	1:F:144:LEU:CG	2.28	0.64
1:C:144:LEU:CD2	2:C:500:NSY:H26	2.24	0.64
1:A:136:ILE:HG23	1:A:209:CYS:HB3	1.78	0.64
1:A:115:ILE:HD11	1:A:217:TYR:CE1	2.32	0.64
1:B:115:ILE:HD11	1:B:217:TYR:CE1	2.32	0.64
1:F:136:ILE:HG22	1:F:137:ASP:N	2.11	0.64
1:F:115:ILE:HD11	1:F:217:TYR:CE1	2.33	0.63
1:A:21:GLN:HA	2:A:300:NSY:H6	1.80	0.62
1:C:130:GLY:O	1:C:132:ILE:HD12	1.99	0.62
1:C:150:ILE:HD12	1:C:150:ILE:N	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:108:ASN:HD22	1:D:109:ASP:H	1.48	0.62
1:C:126:VAL:CG2	1:C:132:ILE:HD13	2.25	0.62
1:A:136:ILE:HG22	1:A:137:ASP:N	2.15	0.61
1:C:120:LYS:HD2	1:C:120:LYS:C	2.20	0.61
1:F:136:ILE:HG23	1:F:209:CYS:CB	2.30	0.61
1:D:135:ALA:C	1:D:136:ILE:HD12	2.21	0.60
1:C:144:LEU:HD11	1:F:144:LEU:CD2	2.30	0.60
1:B:136:ILE:HG22	1:B:137:ASP:N	2.17	0.60
1:C:132:ILE:N	1:C:132:ILE:HD12	2.17	0.60
1:F:144:LEU:HD23	2:F:800:NSY:H63	1.84	0.60
1:C:144:LEU:HD23	2:C:500:NSY:H63	1.83	0.60
1:E:8:ARG:NH1	3:E:369:HOH:O	2.24	0.60
1:D:8:ARG:HA	3:D:402:HOH:O	2.02	0.59
1:C:123:MET:HG3	1:C:170:TYR:CE2	2.38	0.59
1:D:96:GLU:HG3	3:D:408:HOH:O	2.01	0.59
1:C:108:ASN:HD22	1:C:109:ASP:H	1.51	0.59
1:D:123:MET:HG3	1:D:170:TYR:CE2	2.38	0.58
1:E:136:ILE:HG22	1:E:137:ASP:N	2.19	0.58
1:B:108:ASN:ND2	1:B:109:ASP:H	2.01	0.58
1:B:208:HIS:O	1:B:211:ILE:HG13	2.03	0.58
1:E:151:TYR:HB3	1:E:201:MET:HG3	1.84	0.58
1:D:136:ILE:HG23	1:D:209:CYS:HB3	1.86	0.57
1:E:144:LEU:CD2	2:E:700:NSY:H63	2.34	0.57
1:D:147:LYS:HG2	1:E:147:LYS:NZ	2.19	0.57
1:A:108:ASN:ND2	1:A:109:ASP:H	2.03	0.56
1:E:108:ASN:ND2	1:E:109:ASP:H	2.03	0.56
1:A:208:HIS:O	1:A:211:ILE:HG13	2.05	0.56
1:A:120:LYS:HD3	1:A:124:LYS:HE3	1.87	0.56
1:D:136:ILE:HD11	1:D:211:ILE:HG23	1.86	0.56
1:F:136:ILE:CG2	1:F:137:ASP:N	2.67	0.56
1:B:120:LYS:HD3	1:B:124:LYS:HE3	1.87	0.56
1:C:150:ILE:HD11	1:C:173:GLU:CD	2.25	0.56
1:D:161:MET:CE	1:D:213:SER:HB2	2.36	0.56
1:D:144:LEU:HD21	1:E:144:LEU:CG	2.36	0.56
1:B:139:GLY:HA2	2:B:400:NSY:H22A	1.88	0.56
3:A:563:HOH:O	1:E:117:LYS:HE2	2.05	0.55
1:D:96:GLU:HG3	3:D:223:HOH:O	2.07	0.55
1:C:25:CYS:SG	3:C:222:HOH:O	2.38	0.55
1:B:21:GLN:HA	2:B:400:NSY:H6	1.87	0.55
1:F:8:ARG:NH1	3:F:242:HOH:O	2.28	0.55
1:F:136:ILE:HD11	1:F:211:ILE:HG23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:VAL:HG21	3:F:472:HOH:O	2.07	0.54
1:C:130:GLY:O	1:C:132:ILE:CD1	2.55	0.54
1:D:136:ILE:CG2	1:D:137:ASP:N	2.70	0.54
1:B:136:ILE:N	1:B:136:ILE:HD12	2.23	0.54
1:F:7:TRP:CE2	1:F:130:GLY:HA2	2.42	0.54
1:A:25:CYS:SG	3:A:271:HOH:O	2.59	0.54
1:C:144:LEU:HD22	2:C:500:NSY:C26	2.29	0.53
1:D:21:GLN:HG2	2:E:700:NSY:H27	1.88	0.53
1:F:205:ARG:NH1	3:F:266:HOH:O	2.39	0.53
1:A:96:GLU:HG3	3:A:403:HOH:O	2.06	0.53
1:E:7:TRP:CE2	1:E:130:GLY:HA2	2.42	0.53
1:A:136:ILE:CG2	1:A:137:ASP:N	2.71	0.53
1:C:136:ILE:HG22	1:C:137:ASP:N	2.22	0.53
1:F:144:LEU:CD2	2:F:800:NSY:H63	2.39	0.52
1:B:136:ILE:CG2	1:B:137:ASP:N	2.72	0.52
1:A:40:ARG:HG3	1:A:40:ARG:HH11	1.74	0.52
1:B:40:ARG:HH11	1:B:40:ARG:HG3	1.74	0.52
1:E:80:ASN:ND2	1:E:100:TYR:CD2	2.77	0.52
1:E:151:TYR:HB3	1:E:201:MET:CG	2.39	0.52
1:D:25:CYS:SG	3:D:221:HOH:O	2.37	0.52
1:E:181:LYS:HZ1	1:E:204:ASP:CB	2.22	0.52
1:C:120:LYS:O	1:C:120:LYS:HD2	2.10	0.51
1:C:136:ILE:HD11	1:C:211:ILE:HG23	1.92	0.51
1:A:108:ASN:OD1	1:C:79:ASP:C	2.48	0.51
1:C:150:ILE:HD11	1:C:173:GLU:OE1	2.10	0.51
1:D:20:GLY:O	2:E:700:NSY:H66	2.09	0.51
1:D:136:ILE:HG22	1:D:137:ASP:N	2.24	0.51
1:F:127:ALA:HB2	3:F:472:HOH:O	2.10	0.51
1:D:208:HIS:O	1:D:211:ILE:HG13	2.10	0.51
1:F:126:VAL:HG22	1:F:132:ILE:HG12	1.93	0.51
1:A:136:ILE:N	1:A:136:ILE:HD12	2.26	0.51
1:E:202:ALA:HB1	1:E:205:ARG:HG3	1.93	0.51
1:B:180:ASN:N	3:B:288:HOH:O	2.44	0.51
1:F:77:VAL:HB	1:F:109:ASP:OD2	2.11	0.50
1:E:136:ILE:HD12	1:E:165:VAL:HG21	1.94	0.50
1:B:58:GLY:N	1:B:59:PRO:CD	2.74	0.50
1:E:136:ILE:HG23	1:E:209:CYS:CB	2.41	0.50
1:B:21:GLN:HA	2:B:400:NSY:C6	2.41	0.50
1:F:81:GLY:HA2	3:F:464:HOH:O	2.10	0.50
1:E:115:ILE:HD11	1:E:217:TYR:CD1	2.46	0.50
1:C:185:VAL:HB	1:C:199:VAL:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:ILE:HG21	1:A:201:MET:CE	2.42	0.50
1:B:108:ASN:OD1	1:D:79:ASP:C	2.50	0.50
1:C:21:GLN:HG2	2:F:800:NSY:H27	1.93	0.50
1:B:136:ILE:HD11	1:B:211:ILE:HG23	1.92	0.49
1:F:117:LYS:NZ	3:F:238:HOH:O	2.45	0.49
1:A:40:ARG:NH1	1:A:40:ARG:HG3	2.27	0.49
1:B:40:ARG:HG3	1:B:40:ARG:NH1	2.27	0.49
1:D:185:VAL:HB	1:D:199:VAL:HG13	1.95	0.49
1:A:58:GLY:N	1:A:59:PRO:CD	2.76	0.49
1:F:22:CYS:N	2:F:800:NSY:H6	2.28	0.49
1:E:136:ILE:HD11	1:E:211:ILE:HG23	1.94	0.49
1:E:136:ILE:CG2	1:E:137:ASP:N	2.75	0.49
2:D:600:NSY:H66	1:E:20:GLY:O	2.13	0.49
1:F:67:GLY:HA2	2:F:800:NSY:O39	2.13	0.48
1:D:25:CYS:SG	3:D:299:HOH:O	2.60	0.48
1:F:136:ILE:CG2	1:F:209:CYS:HB3	2.41	0.48
1:B:136:ILE:HG21	1:B:201:MET:CE	2.44	0.48
1:B:134:VAL:HG23	1:B:136:ILE:CD1	2.44	0.48
1:B:155:ASP:HB2	3:B:565:HOH:O	2.13	0.48
1:C:8:ARG:HA	3:C:455:HOH:O	2.14	0.48
1:B:22:CYS:N	2:B:400:NSY:H6	2.29	0.48
1:F:136:ILE:N	1:F:136:ILE:HD12	2.29	0.48
1:A:136:ILE:HD11	1:A:211:ILE:HG23	1.94	0.48
1:E:22:CYS:N	2:E:700:NSY:H6	2.29	0.47
1:E:136:ILE:HG23	1:E:209:CYS:HB3	1.95	0.47
1:C:208:HIS:O	1:C:211:ILE:HG13	2.13	0.47
1:B:153:GLU:O	1:B:208:HIS:HE1	1.96	0.47
1:B:77:VAL:HB	1:B:109:ASP:OD2	2.15	0.47
1:E:136:ILE:HG12	1:E:211:ILE:HG12	1.97	0.47
1:F:80:ASN:ND2	1:F:100:TYR:CD2	2.78	0.47
1:C:87:GLU:HG2	3:C:305:HOH:O	2.14	0.47
1:F:5:VAL:CG2	3:F:472:HOH:O	2.62	0.47
1:C:20:GLY:O	2:F:800:NSY:H66	2.15	0.47
1:A:77:VAL:HB	1:A:109:ASP:OD2	2.15	0.47
1:C:22:CYS:N	2:C:500:NSY:H6	2.30	0.47
1:E:115:ILE:HG23	1:E:116:PRO:HD2	1.96	0.47
1:A:120:LYS:CD	1:A:124:LYS:HE3	2.45	0.46
1:C:161:MET:CE	1:C:213:SER:HB2	2.45	0.46
1:D:157:SER:HB3	1:D:160:ASP:OD1	2.16	0.46
1:A:136:ILE:HG21	1:A:201:MET:HE1	1.97	0.46
1:F:80:ASN:ND2	1:F:100:TYR:CE2	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:ILE:HD12	1:D:150:ILE:N	2.31	0.46
1:A:21:GLN:HA	2:A:300:NSY:C6	2.45	0.46
1:A:139:GLY:HA2	2:A:300:NSY:C22	2.45	0.46
1:A:31:THR:O	1:A:35:GLU:HG3	2.16	0.46
1:B:173:GLU:OE2	1:B:200:LYS:NZ	2.48	0.46
1:F:49:SER:OG	1:F:89:TYR:HB3	2.16	0.46
1:A:136:ILE:HG23	1:A:209:CYS:CB	2.46	0.45
1:B:135:ALA:O	1:B:136:ILE:HD12	2.16	0.45
1:C:150:ILE:N	1:C:150:ILE:CD1	2.79	0.45
1:D:144:LEU:HD21	1:E:144:LEU:HD11	1.96	0.45
1:E:31:THR:O	1:E:35:GLU:HG3	2.17	0.45
1:E:34:LEU:HG	1:E:218:PRO:HG3	1.97	0.45
1:F:173:GLU:OE2	1:F:200:LYS:NZ	2.50	0.45
1:A:173:GLU:OE2	1:A:200:LYS:NZ	2.48	0.45
1:B:120:LYS:CD	1:B:124:LYS:HE3	2.45	0.45
1:E:181:LYS:HB2	1:E:181:LYS:HZ2	1.80	0.45
1:C:157:SER:HB2	3:C:551:HOH:O	2.17	0.45
2:C:500:NSY:H67	1:F:189:TRP:CD1	2.51	0.45
1:E:77:VAL:HG12	1:E:108:ASN:HD22	1.82	0.45
1:F:127:ALA:CB	3:F:472:HOH:O	2.63	0.45
1:F:211:ILE:H	1:F:211:ILE:HG13	1.55	0.45
1:B:136:ILE:HG21	1:B:201:MET:HE1	1.99	0.45
1:F:5:VAL:O	1:F:169:GLY:HA3	2.17	0.45
1:C:144:LEU:CD2	2:C:500:NSY:H63	2.45	0.44
1:E:139:GLY:HA2	2:E:700:NSY:C22	2.47	0.44
1:B:7:TRP:CE2	1:B:130:GLY:HA2	2.52	0.44
1:D:144:LEU:CD2	1:E:144:LEU:HG	2.47	0.44
1:D:144:LEU:CD2	2:D:600:NSY:H63	2.47	0.44
1:E:193:TRP:CH2	1:E:199:VAL:HB	2.53	0.44
1:B:144:LEU:HD23	2:B:400:NSY:H26	1.98	0.44
1:C:126:VAL:HA	1:C:132:ILE:CD1	2.43	0.44
1:D:181:LYS:HZ3	1:D:181:LYS:HB2	1.83	0.44
1:A:7:TRP:CE2	1:A:130:GLY:HA2	2.52	0.44
1:A:135:ALA:O	1:A:136:ILE:HD12	2.18	0.44
1:A:153:GLU:O	1:A:208:HIS:HE1	1.99	0.44
2:C:500:NSY:H66	1:F:20:GLY:O	2.18	0.44
1:F:124:LYS:O	1:F:128:THR:HG23	2.18	0.44
1:C:144:LEU:CD2	1:F:144:LEU:HD21	2.32	0.44
1:F:120:LYS:HD3	1:F:124:LYS:HE3	1.99	0.44
1:A:25:CYS:SG	3:A:221:HOH:O	2.43	0.44
1:D:144:LEU:CD2	1:E:144:LEU:CG	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:ASP:OD2	1:B:140:HIS:HE1	2.01	0.43
1:A:137:ASP:OD2	1:A:140:HIS:HE1	2.01	0.43
1:D:147:LYS:HG2	1:E:147:LYS:HZ2	1.82	0.43
1:D:153:GLU:O	1:D:208:HIS:HE1	2.01	0.43
1:E:139:GLY:HA2	2:E:700:NSY:H22A	2.01	0.43
1:A:67:GLY:HA2	2:A:300:NSY:O39	2.18	0.43
1:E:11:GLY:N	3:E:247:HOH:O	2.51	0.43
1:E:67:GLY:HA2	2:E:700:NSY:O39	2.19	0.43
1:D:161:MET:HE3	1:D:213:SER:HB2	2.00	0.43
1:C:37:GLN:HB3	1:C:220:VAL:CG2	2.49	0.43
1:D:150:ILE:HD11	1:D:173:GLU:CD	2.39	0.42
1:D:22:CYS:N	2:D:600:NSY:H6	2.34	0.42
1:F:136:ILE:HD13	1:F:165:VAL:CG2	2.50	0.42
1:F:63:GLU:HG2	2:F:800:NSY:H55	2.00	0.42
1:B:31:THR:O	1:B:35:GLU:HG3	2.20	0.42
2:D:600:NSY:H67	1:E:189:TRP:CD1	2.54	0.42
1:A:134:VAL:HG23	1:A:136:ILE:CD1	2.49	0.42
1:A:144:LEU:HD23	2:A:300:NSY:H26	2.00	0.42
1:B:25:CYS:SG	3:B:245:HOH:O	2.62	0.42
1:C:136:ILE:CG2	1:C:137:ASP:N	2.83	0.42
1:C:136:ILE:HG23	1:C:209:CYS:CB	2.49	0.42
1:D:193:TRP:CH2	1:D:199:VAL:HB	2.54	0.42
1:F:40:ARG:HG3	1:F:40:ARG:HH11	1.84	0.42
1:F:139:GLY:HA2	2:F:800:NSY:C22	2.50	0.42
1:B:136:ILE:HG23	1:B:209:CYS:CB	2.46	0.42
1:C:1:ALA:HA	1:C:2:PRO:HD3	1.88	0.42
1:E:220:VAL:HG23	1:E:220:VAL:OXT	2.19	0.42
1:E:211:ILE:H	1:E:211:ILE:HG13	1.58	0.42
1:E:21:GLN:HA	2:E:700:NSY:C6	2.50	0.42
1:C:120:LYS:CD	1:C:120:LYS:C	2.88	0.42
1:D:181:LYS:HB2	1:D:181:LYS:NZ	2.35	0.41
1:D:134:VAL:HG23	1:D:136:ILE:CD1	2.49	0.41
1:D:136:ILE:HG23	1:D:209:CYS:CB	2.50	0.41
1:B:144:LEU:HA	1:B:144:LEU:HD12	1.93	0.41
1:B:67:GLY:HA2	2:B:400:NSY:O39	2.19	0.41
1:C:153:GLU:O	1:C:208:HIS:HE1	2.03	0.41
1:D:136:ILE:HD13	1:D:165:VAL:CG2	2.50	0.41
2:E:700:NSY:H17	3:E:238:HOH:O	2.21	0.41
1:B:144:LEU:CD2	2:B:400:NSY:H26	2.51	0.41
1:E:5:VAL:O	1:E:169:GLY:HA3	2.20	0.41
1:E:21:GLN:HA	2:E:700:NSY:H6	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:TYR:CE1	1:E:80:ASN:HB2	2.56	0.41
1:C:108:ASN:HD22	1:C:109:ASP:N	2.17	0.41
1:E:97:SER:O	1:E:99:LYS:HG3	2.21	0.41
1:F:192:GLU:OE2	1:F:192:GLU:HA	2.21	0.41
1:A:45:LEU:HB3	1:E:160:ASP:HB3	2.02	0.41
1:B:139:GLY:HA2	2:B:400:NSY:C22	2.50	0.41
1:C:181:LYS:HB2	1:C:181:LYS:NZ	2.36	0.41
2:B:400:NSY:H14	2:B:400:NSY:H5	1.87	0.40
1:A:108:ASN:OD1	1:C:79:ASP:O	2.39	0.40
1:C:144:LEU:HG	1:F:144:LEU:HG	2.03	0.40
1:A:144:LEU:HD12	1:A:144:LEU:HA	1.90	0.40
1:A:144:LEU:CD2	2:A:300:NSY:H26	2.51	0.40
1:C:99:LYS:NZ	1:D:99:LYS:NZ	2.70	0.40
1:F:21:GLN:HA	2:F:800:NSY:C6	2.51	0.40
2:F:800:NSY:H17	3:F:247:HOH:O	2.21	0.40
2:C:500:NSY:H5	2:C:500:NSY:H14	1.89	0.40
1:C:101:ASN:HA	1:C:102:PRO:HD3	1.96	0.40
1:C:50:GLU:OE1	1:C:86:GLU:OE1	2.40	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	211/220 (96%)	207 (98%)	4 (2%)	0	100	100
1	B	211/220 (96%)	208 (99%)	3 (1%)	0	100	100
1	C	211/220 (96%)	204 (97%)	7 (3%)	0	100	100
1	D	211/220 (96%)	206 (98%)	5 (2%)	0	100	100
1	E	211/220 (96%)	200 (95%)	11 (5%)	0	100	100
1	F	211/220 (96%)	204 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1266/1320 (96%)	1229 (97%)	37 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	174/179 (97%)	166 (95%)	8 (5%)	27	13
1	B	174/179 (97%)	166 (95%)	8 (5%)	27	13
1	C	174/179 (97%)	165 (95%)	9 (5%)	23	10
1	D	174/179 (97%)	167 (96%)	7 (4%)	31	16
1	E	174/179 (97%)	167 (96%)	7 (4%)	31	16
1	F	174/179 (97%)	168 (97%)	6 (3%)	37	22
All	All	1044/1074 (97%)	999 (96%)	45 (4%)	29	14

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	89	TYR
1	A	108	ASN
1	A	109	ASP
1	A	147	LYS
1	A	148	GLU
1	A	156	CYS
1	A	184	LEU
1	B	52	ASN
1	B	89	TYR
1	B	108	ASN
1	B	109	ASP
1	B	147	LYS
1	B	148	GLU

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Mol	Chain	Res	Type
1	B	156	CYS
1	B	184	LEU
1	C	34	LEU
1	C	52	ASN
1	C	89	TYR
1	C	108	ASN
1	C	141	GLU
1	C	148	GLU
1	C	156	CYS
1	C	184	LEU
1	C	201	MET
1	D	34	LEU
1	D	52	ASN
1	D	89	TYR
1	D	108	ASN
1	D	148	GLU
1	D	156	CYS
1	D	184	LEU
1	E	34	LEU
1	E	52	ASN
1	E	89	TYR
1	E	148	GLU
1	E	155	ASP
1	E	156	CYS
1	E	184	LEU
1	F	52	ASN
1	F	89	TYR
1	F	147	LYS
1	F	148	GLU
1	F	156	CYS
1	F	184	LEU

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

Mol	Chain	Res	Type
1	B	118	GLN
1	C	108	ASN
1	D	108	ASN
1	E	108	ASN
1	F	75	GLN
1	F	78	GLN
1	F	108	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	NSY	A	300	-	75,75,75	5.72	57 (76%)	96,97,97	2.32	31 (32%)
2	NSY	C	500	-	75,75,75	5.79	58 (77%)	96,97,97	2.30	32 (33%)
2	NSY	E	700	-	75,75,75	5.73	56 (74%)	96,97,97	2.33	36 (37%)
2	NSY	F	800	-	75,75,75	5.74	57 (76%)	96,97,97	2.31	35 (36%)
2	NSY	D	600	-	75,75,75	5.80	58 (77%)	96,97,97	2.30	33 (34%)
2	NSY	B	400	-	75,75,75	5.71	57 (76%)	96,97,97	2.36	31 (32%)

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	NSY	A	300	-	-	14/65/65/65	0/6/6/6
2	NSY	C	500	-	-	12/65/65/65	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NSY	E	700	-	-	16/65/65/65	0/6/6/6
2	NSY	F	800	-	-	16/65/65/65	0/6/6/6
2	NSY	D	600	-	-	12/65/65/65	0/6/6/6
2	NSY	B	400	-	-	15/65/65/65	0/6/6/6

All (343) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600	NSY	C14-C12	15.39	1.72	1.39
2	C	500	NSY	C14-C12	15.18	1.71	1.39
2	F	800	NSY	C14-C12	13.87	1.68	1.39
2	E	700	NSY	C14-C12	13.71	1.68	1.39
2	A	300	NSY	C22-C23	-13.42	1.29	1.51
2	A	300	NSY	C14-C12	13.34	1.67	1.39
2	B	400	NSY	C14-C12	13.29	1.67	1.39
2	B	400	NSY	C22-C23	-12.91	1.30	1.51
2	C	500	NSY	C22-C23	-12.73	1.30	1.51
2	D	600	NSY	C22-C23	-12.60	1.31	1.51
2	F	800	NSY	C22-C23	-12.38	1.31	1.51
2	E	700	NSY	C22-C23	-12.01	1.32	1.51
2	D	600	NSY	C53-C52	11.61	1.63	1.38
2	C	500	NSY	C53-C52	11.50	1.63	1.38
2	E	700	NSY	C53-C52	11.29	1.63	1.38
2	A	300	NSY	C53-C52	11.19	1.63	1.38
2	F	800	NSY	C53-C52	11.05	1.62	1.38
2	B	400	NSY	C53-C52	11.01	1.62	1.38
2	B	400	NSY	C8-C7	10.93	1.62	1.38
2	C	500	NSY	C8-C7	10.92	1.62	1.38
2	D	600	NSY	C8-C7	10.91	1.62	1.38
2	A	300	NSY	C8-C7	10.89	1.62	1.38
2	D	600	NSY	C47-C45	10.88	1.62	1.38
2	C	500	NSY	C47-C45	10.68	1.61	1.38
2	F	800	NSY	C47-C45	10.60	1.61	1.38
2	F	800	NSY	C8-C7	10.60	1.61	1.38
2	B	400	NSY	C47-C45	10.54	1.61	1.38
2	A	300	NSY	C47-C45	10.45	1.61	1.38
2	E	700	NSY	C47-C45	10.40	1.61	1.38
2	E	700	NSY	C8-C7	10.37	1.61	1.38
2	D	600	NSY	C5-C4	9.62	1.59	1.39
2	C	500	NSY	C5-C4	9.59	1.59	1.39
2	B	400	NSY	C13-C11	9.54	1.59	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	NSY	C13-C11	9.25	1.58	1.38
2	F	800	NSY	C1-C2	-8.93	1.32	1.51
2	D	600	NSY	C9-C8	8.93	1.55	1.38
2	E	700	NSY	C1-C2	-8.87	1.32	1.51
2	A	300	NSY	C5-C4	8.78	1.58	1.39
2	C	500	NSY	C9-C8	8.78	1.54	1.38
2	C	500	NSY	C1-C2	-8.71	1.32	1.51
2	F	800	NSY	C5-C4	8.56	1.57	1.39
2	E	700	NSY	C5-C4	8.54	1.57	1.39
2	A	300	NSY	C1-C2	-8.54	1.33	1.51
2	D	600	NSY	C1-C2	-8.43	1.33	1.51
2	B	400	NSY	C1-C2	-8.39	1.33	1.51
2	E	700	NSY	C13-C11	8.30	1.56	1.38
2	F	800	NSY	C13-C11	8.27	1.56	1.38
2	B	400	NSY	C9-C8	8.25	1.53	1.38
2	E	700	NSY	C11-C12	8.17	1.56	1.39
2	B	400	NSY	C5-C4	8.16	1.56	1.39
2	D	600	NSY	C11-C12	8.13	1.56	1.39
2	C	500	NSY	C11-C12	8.12	1.56	1.39
2	B	400	NSY	C63-C62	8.09	1.56	1.39
2	F	800	NSY	C11-C12	8.09	1.56	1.39
2	F	800	NSY	C35-N34	8.03	1.49	1.33
2	B	400	NSY	C9-C4	7.94	1.56	1.39
2	A	300	NSY	C11-C12	7.92	1.56	1.39
2	B	400	NSY	C35-N34	7.90	1.48	1.33
2	A	300	NSY	C9-C8	7.83	1.53	1.38
2	D	600	NSY	C63-C62	7.82	1.56	1.39
2	C	500	NSY	C6-C7	7.75	1.55	1.38
2	D	600	NSY	C6-C7	7.74	1.55	1.38
2	A	300	NSY	C63-C62	7.73	1.55	1.39
2	B	400	NSY	C11-C12	7.72	1.55	1.39
2	F	800	NSY	C9-C8	7.70	1.52	1.38
2	E	700	NSY	C18-N29	7.69	1.51	1.34
2	A	300	NSY	C35-N34	7.68	1.48	1.33
2	C	500	NSY	C18-N29	7.61	1.50	1.34
2	F	800	NSY	C42-N60	7.60	1.50	1.33
2	E	700	NSY	C35-N34	7.60	1.48	1.33
2	A	300	NSY	C9-C4	7.58	1.55	1.39
2	E	700	NSY	C42-N60	7.58	1.50	1.33
2	E	700	NSY	C9-C4	7.57	1.55	1.39
2	E	700	NSY	C9-C8	7.51	1.52	1.38
2	A	300	NSY	C54-C53	7.51	1.54	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	800	NSY	C9-C4	7.50	1.55	1.39
2	E	700	NSY	C54-C53	7.48	1.54	1.38
2	E	700	NSY	C6-C7	7.47	1.54	1.38
2	C	500	NSY	C13-C11	7.43	1.54	1.38
2	D	600	NSY	C35-N34	7.41	1.47	1.33
2	C	500	NSY	C63-C62	7.41	1.55	1.39
2	E	700	NSY	C27-C28	7.41	1.55	1.39
2	C	500	NSY	C2-N16	7.40	1.49	1.34
2	F	800	NSY	C6-C7	7.35	1.54	1.38
2	B	400	NSY	C27-C25	7.34	1.52	1.38
2	E	700	NSY	C65-C63	7.32	1.54	1.38
2	D	600	NSY	C2-N16	7.31	1.49	1.34
2	D	600	NSY	C13-C10	7.30	1.57	1.38
2	C	500	NSY	C9-C4	7.28	1.54	1.39
2	C	500	NSY	C35-N34	7.28	1.47	1.33
2	D	600	NSY	C13-C11	7.27	1.54	1.38
2	F	800	NSY	C18-N29	7.26	1.50	1.34
2	B	400	NSY	C54-C53	7.25	1.54	1.38
2	F	800	NSY	C65-C63	7.22	1.54	1.38
2	D	600	NSY	C9-C4	7.21	1.54	1.39
2	C	500	NSY	C13-C10	7.20	1.57	1.38
2	D	600	NSY	C54-C53	7.15	1.54	1.38
2	E	700	NSY	C50-C48	7.15	1.57	1.38
2	D	600	NSY	C18-N29	7.10	1.49	1.34
2	F	800	NSY	C50-C48	7.10	1.56	1.38
2	C	500	NSY	C54-C53	7.09	1.53	1.38
2	F	800	NSY	C27-C28	7.08	1.54	1.39
2	A	300	NSY	C27-C25	7.07	1.51	1.38
2	D	600	NSY	C42-N60	7.05	1.49	1.33
2	B	400	NSY	C6-C7	7.03	1.54	1.38
2	A	300	NSY	C18-N29	7.01	1.49	1.34
2	E	700	NSY	C27-C25	6.99	1.51	1.38
2	A	300	NSY	C6-C7	6.98	1.53	1.38
2	F	800	NSY	C54-C53	6.98	1.53	1.38
2	F	800	NSY	C27-C25	6.96	1.51	1.38
2	B	400	NSY	C18-N29	6.94	1.49	1.34
2	E	700	NSY	C63-C62	6.91	1.54	1.39
2	B	400	NSY	C27-C28	6.86	1.54	1.39
2	C	500	NSY	C50-C48	6.86	1.56	1.38
2	E	700	NSY	C46-C45	6.86	1.53	1.38
2	B	400	NSY	C46-C45	6.85	1.53	1.38
2	B	400	NSY	C64-C62	6.85	1.53	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600	NSY	C65-C63	6.85	1.53	1.38
2	D	600	NSY	C50-C48	6.84	1.56	1.38
2	F	800	NSY	C2-N16	6.82	1.48	1.34
2	A	300	NSY	C64-C62	6.82	1.53	1.39
2	C	500	NSY	C46-C45	6.81	1.53	1.38
2	A	300	NSY	C2-N16	6.80	1.48	1.34
2	A	300	NSY	C50-C48	6.80	1.56	1.38
2	E	700	NSY	C2-N16	6.80	1.48	1.34
2	C	500	NSY	C65-C63	6.79	1.53	1.38
2	C	500	NSY	C27-C25	6.76	1.51	1.38
2	B	400	NSY	C50-C48	6.75	1.55	1.38
2	F	800	NSY	C63-C62	6.74	1.53	1.39
2	F	800	NSY	C13-C10	6.73	1.55	1.38
2	F	800	NSY	C46-C45	6.73	1.53	1.38
2	E	700	NSY	C48-C46	6.72	1.53	1.38
2	A	300	NSY	C27-C28	6.72	1.53	1.39
2	E	700	NSY	C15-C10	6.71	1.55	1.38
2	E	700	NSY	C13-C10	6.66	1.55	1.38
2	F	800	NSY	C15-C10	6.65	1.55	1.38
2	C	500	NSY	C42-N60	6.65	1.48	1.33
2	A	300	NSY	C46-C45	6.65	1.53	1.38
2	B	400	NSY	C42-N60	6.57	1.47	1.33
2	C	500	NSY	C64-C62	6.57	1.53	1.39
2	B	400	NSY	C15-C10	6.56	1.55	1.38
2	D	600	NSY	C46-C45	6.54	1.53	1.38
2	B	400	NSY	C2-N16	6.53	1.48	1.34
2	A	300	NSY	C15-C10	6.47	1.55	1.38
2	F	800	NSY	C48-C46	6.47	1.52	1.38
2	D	600	NSY	C27-C28	6.46	1.53	1.39
2	D	600	NSY	C64-C62	6.44	1.53	1.39
2	A	300	NSY	C42-N60	6.43	1.47	1.33
2	A	300	NSY	C13-C10	6.39	1.55	1.38
2	D	600	NSY	C15-C10	6.37	1.54	1.38
2	D	600	NSY	C27-C25	6.35	1.50	1.38
2	C	500	NSY	C15-C10	6.33	1.54	1.38
2	E	700	NSY	C22-C68	-6.27	1.38	1.51
2	C	500	NSY	C48-C46	6.27	1.52	1.38
2	A	300	NSY	C31-C30	6.26	1.68	1.53
2	B	400	NSY	C65-C63	6.25	1.52	1.38
2	F	800	NSY	C22-C68	-6.24	1.38	1.51
2	D	600	NSY	C22-C68	-6.24	1.38	1.51
2	F	800	NSY	C64-C62	6.17	1.52	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	NSY	C48-C46	6.15	1.51	1.38
2	A	300	NSY	C48-C46	6.15	1.51	1.38
2	C	500	NSY	C22-C68	-6.14	1.38	1.51
2	B	400	NSY	C13-C10	6.13	1.54	1.38
2	B	400	NSY	C31-C30	6.10	1.67	1.53
2	A	300	NSY	C65-C63	6.07	1.51	1.38
2	C	500	NSY	C27-C28	6.07	1.52	1.39
2	D	600	NSY	C48-C46	6.02	1.51	1.38
2	E	700	NSY	C64-C62	6.00	1.52	1.39
2	E	700	NSY	C25-C23	5.95	1.51	1.38
2	A	300	NSY	C15-C14	5.92	1.51	1.38
2	B	400	NSY	C57-C52	5.88	1.51	1.38
2	A	300	NSY	C56-C57	5.87	1.51	1.38
2	B	400	NSY	C15-C14	5.86	1.51	1.38
2	C	500	NSY	C26-C24	5.80	1.49	1.38
2	D	600	NSY	C26-C24	5.74	1.49	1.38
2	B	400	NSY	C24-C23	5.74	1.51	1.38
2	A	300	NSY	C57-C52	5.74	1.51	1.38
2	E	700	NSY	C57-C52	5.73	1.51	1.38
2	F	800	NSY	C25-C23	5.72	1.51	1.38
2	A	300	NSY	C24-C23	5.71	1.51	1.38
2	B	400	NSY	C56-C57	5.70	1.50	1.38
2	F	800	NSY	C57-C52	5.65	1.51	1.38
2	F	800	NSY	C26-C28	5.57	1.51	1.39
2	E	700	NSY	C56-C57	5.53	1.50	1.38
2	E	700	NSY	C31-C30	5.52	1.66	1.53
2	F	800	NSY	C56-C57	5.42	1.50	1.38
2	F	800	NSY	C31-C30	5.39	1.66	1.53
2	D	600	NSY	C24-C23	5.38	1.50	1.38
2	C	500	NSY	C55-C54	5.36	1.52	1.38
2	C	500	NSY	C26-C28	5.34	1.50	1.39
2	C	500	NSY	C24-C23	5.33	1.50	1.38
2	C	500	NSY	C57-C52	5.28	1.50	1.38
2	E	700	NSY	C26-C28	5.25	1.50	1.39
2	E	700	NSY	C56-C55	5.24	1.51	1.38
2	D	600	NSY	C57-C52	5.23	1.50	1.38
2	F	800	NSY	C56-C55	5.23	1.51	1.38
2	B	400	NSY	C26-C28	5.20	1.50	1.39
2	A	300	NSY	C26-C28	5.20	1.50	1.39
2	D	600	NSY	C56-C57	5.12	1.49	1.38
2	F	800	NSY	C26-C24	5.11	1.48	1.38
2	D	600	NSY	C55-C54	5.10	1.51	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600	NSY	C26-C28	5.09	1.50	1.39
2	E	700	NSY	C26-C24	5.09	1.48	1.38
2	F	800	NSY	C24-C23	5.06	1.49	1.38
2	F	800	NSY	C50-C49	5.05	1.51	1.38
2	C	500	NSY	C56-C57	5.02	1.49	1.38
2	C	500	NSY	C31-C30	5.01	1.65	1.53
2	C	500	NSY	C56-C55	4.98	1.51	1.38
2	A	300	NSY	C56-C55	4.98	1.51	1.38
2	B	400	NSY	C56-C55	4.96	1.51	1.38
2	A	300	NSY	C22-C68	-4.94	1.41	1.51
2	B	400	NSY	C55-C54	4.93	1.51	1.38
2	D	600	NSY	C31-C30	4.92	1.64	1.53
2	E	700	NSY	C24-C23	4.91	1.49	1.38
2	A	300	NSY	C55-C54	4.87	1.50	1.38
2	E	700	NSY	C55-C54	4.80	1.50	1.38
2	B	400	NSY	C49-C47	4.77	1.49	1.38
2	E	700	NSY	C50-C49	4.75	1.50	1.38
2	B	400	NSY	C26-C24	4.74	1.47	1.38
2	B	400	NSY	C22-C68	-4.73	1.41	1.51
2	D	600	NSY	C56-C55	4.73	1.50	1.38
2	E	700	NSY	C15-C14	4.71	1.48	1.38
2	D	600	NSY	C50-C49	4.69	1.50	1.38
2	D	600	NSY	O73-C68	-4.69	1.13	1.23
2	A	300	NSY	C50-C49	4.68	1.50	1.38
2	A	300	NSY	C49-C47	4.67	1.48	1.38
2	F	800	NSY	C15-C14	4.66	1.48	1.38
2	F	800	NSY	C49-C47	4.64	1.48	1.38
2	E	700	NSY	C49-C47	4.63	1.48	1.38
2	E	700	NSY	C66-C64	4.62	1.48	1.38
2	F	800	NSY	C55-C54	4.60	1.50	1.38
2	C	500	NSY	O73-C68	-4.59	1.13	1.23
2	C	500	NSY	C50-C49	4.57	1.50	1.38
2	B	400	NSY	C50-C49	4.55	1.50	1.38
2	F	800	NSY	C59-N60	4.49	1.56	1.46
2	D	600	NSY	C49-C47	4.43	1.48	1.38
2	A	300	NSY	C70-C69	-4.41	1.26	1.51
2	F	800	NSY	C66-C64	4.40	1.48	1.38
2	D	600	NSY	C70-C69	-4.39	1.27	1.51
2	A	300	NSY	C67-C66	4.36	1.49	1.38
2	C	500	NSY	C49-C47	4.35	1.48	1.38
2	A	300	NSY	C26-C24	4.34	1.46	1.38
2	F	800	NSY	O73-C68	-4.34	1.14	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	NSY	C25-C23	4.34	1.48	1.38
2	C	500	NSY	C15-C14	4.33	1.48	1.38
2	C	500	NSY	C70-C69	-4.31	1.27	1.51
2	E	700	NSY	O73-C68	-4.30	1.14	1.23
2	B	400	NSY	C70-C69	-4.28	1.27	1.51
2	B	400	NSY	C67-C66	4.26	1.49	1.38
2	E	700	NSY	C59-N60	4.26	1.55	1.46
2	C	500	NSY	C66-C64	4.26	1.47	1.38
2	D	600	NSY	C15-C14	4.21	1.47	1.38
2	D	600	NSY	C25-C23	4.20	1.47	1.38
2	E	700	NSY	O19-C18	4.20	1.31	1.23
2	B	400	NSY	C25-C23	4.18	1.47	1.38
2	D	600	NSY	C66-C64	4.17	1.47	1.38
2	C	500	NSY	C25-C23	4.13	1.47	1.38
2	C	500	NSY	O19-C18	4.13	1.31	1.23
2	D	600	NSY	O19-C18	4.10	1.31	1.23
2	A	300	NSY	C71-N72	4.07	1.55	1.46
2	F	800	NSY	C70-C69	-4.06	1.28	1.51
2	C	500	NSY	C67-C66	4.05	1.48	1.38
2	B	400	NSY	C71-N72	4.05	1.55	1.46
2	E	700	NSY	C70-C69	-4.04	1.28	1.51
2	D	600	NSY	C67-C66	4.01	1.48	1.38
2	F	800	NSY	O19-C18	3.99	1.31	1.23
2	B	400	NSY	O19-C18	3.90	1.31	1.23
2	A	300	NSY	C20-C17	-3.87	1.44	1.53
2	F	800	NSY	C58-C52	-3.84	1.40	1.51
2	A	300	NSY	O19-C18	3.82	1.31	1.23
2	C	500	NSY	C59-N60	3.82	1.54	1.46
2	C	500	NSY	C6-C5	3.81	1.45	1.38
2	B	400	NSY	C59-N60	3.72	1.54	1.46
2	A	300	NSY	C59-N60	3.70	1.54	1.46
2	D	600	NSY	C6-C5	3.65	1.45	1.38
2	D	600	NSY	C59-N60	3.65	1.54	1.46
2	F	800	NSY	C67-C66	3.65	1.47	1.38
2	A	300	NSY	C58-C52	-3.64	1.41	1.51
2	B	400	NSY	C58-C52	-3.61	1.41	1.51
2	D	600	NSY	C58-C52	-3.57	1.41	1.51
2	E	700	NSY	C58-C52	-3.52	1.41	1.51
2	B	400	NSY	C20-C17	-3.51	1.45	1.53
2	C	500	NSY	C58-C52	-3.51	1.41	1.51
2	C	500	NSY	C67-C65	3.48	1.47	1.38
2	D	600	NSY	C67-C65	3.48	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	NSY	C66-C64	3.47	1.46	1.38
2	A	300	NSY	O73-C68	-3.44	1.16	1.23
2	B	400	NSY	C67-C65	3.44	1.47	1.38
2	D	600	NSY	C20-C17	-3.41	1.45	1.53
2	B	400	NSY	C66-C64	3.39	1.46	1.38
2	E	700	NSY	C67-C65	3.38	1.47	1.38
2	B	400	NSY	O73-C68	-3.36	1.16	1.23
2	C	500	NSY	C20-C17	-3.35	1.45	1.53
2	E	700	NSY	C67-C66	3.35	1.46	1.38
2	F	800	NSY	C20-C17	-3.23	1.46	1.53
2	F	800	NSY	C67-C65	3.22	1.46	1.38
2	A	300	NSY	C67-C65	3.12	1.46	1.38
2	D	600	NSY	C30-C38	-3.10	1.44	1.52
2	F	800	NSY	C44-C45	3.09	1.58	1.51
2	F	800	NSY	C68-N72	-3.09	1.26	1.33
2	F	800	NSY	C6-C5	3.07	1.44	1.38
2	E	700	NSY	C20-C17	-3.05	1.46	1.53
2	E	700	NSY	C6-C5	3.05	1.44	1.38
2	D	600	NSY	C71-N72	3.03	1.53	1.46
2	A	300	NSY	C62-C28	-3.03	1.41	1.49
2	C	500	NSY	C71-N72	3.03	1.53	1.46
2	A	300	NSY	C44-C45	3.03	1.58	1.51
2	F	800	NSY	C41-C42	3.01	1.60	1.52
2	F	800	NSY	C30-C38	-2.98	1.45	1.52
2	E	700	NSY	C44-C45	2.96	1.58	1.51
2	E	700	NSY	C68-N72	-2.96	1.26	1.33
2	E	700	NSY	C41-C42	2.95	1.60	1.52
2	C	500	NSY	C68-N72	-2.92	1.26	1.33
2	B	400	NSY	C62-C28	-2.91	1.41	1.49
2	B	400	NSY	C44-C45	2.91	1.58	1.51
2	D	600	NSY	C68-N72	-2.91	1.26	1.33
2	E	700	NSY	C71-N72	2.88	1.52	1.46
2	A	300	NSY	C6-C5	2.85	1.43	1.38
2	F	800	NSY	C71-N72	2.83	1.52	1.46
2	D	600	NSY	C62-C28	-2.76	1.42	1.49
2	E	700	NSY	C62-C28	-2.75	1.42	1.49
2	C	500	NSY	C62-C28	-2.70	1.42	1.49
2	D	600	NSY	C41-C42	2.69	1.59	1.52
2	C	500	NSY	C44-C45	2.67	1.57	1.51
2	C	500	NSY	C30-C38	-2.64	1.45	1.52
2	B	400	NSY	C68-N72	-2.62	1.27	1.33
2	D	600	NSY	C30-N29	-2.62	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	NSY	C68-N72	-2.57	1.27	1.33
2	D	600	NSY	C44-C45	2.56	1.57	1.51
2	E	700	NSY	C30-C38	-2.54	1.46	1.52
2	C	500	NSY	C41-C42	2.46	1.59	1.52
2	B	400	NSY	C30-C38	-2.46	1.46	1.52
2	F	800	NSY	C62-C28	-2.45	1.42	1.49
2	A	300	NSY	C30-C38	-2.38	1.46	1.52
2	B	400	NSY	C6-C5	2.35	1.43	1.38
2	B	400	NSY	C41-C42	2.34	1.58	1.52
2	C	500	NSY	C30-N29	-2.16	1.41	1.45
2	A	300	NSY	C41-C42	2.14	1.58	1.52
2	B	400	NSY	C30-N29	-2.12	1.41	1.45
2	F	800	NSY	C30-N29	-2.09	1.41	1.45
2	A	300	NSY	C30-N29	-2.09	1.41	1.45
2	C	500	NSY	O3-C2	-2.08	1.19	1.23
2	D	600	NSY	O3-C2	-2.04	1.19	1.23

All (198) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	600	NSY	C1-C7-C6	-7.58	110.04	120.89
2	C	500	NSY	C1-C7-C6	-7.37	110.35	120.89
2	B	400	NSY	C1-C7-C6	-7.17	110.63	120.89
2	A	300	NSY	C1-C7-C6	-7.08	110.76	120.89
2	F	800	NSY	C1-C7-C6	-6.71	111.28	120.89
2	E	700	NSY	C1-C7-C6	-6.68	111.34	120.89
2	E	700	NSY	C59-C58-C52	6.43	127.76	112.87
2	B	400	NSY	C1-C7-C8	5.89	129.32	120.89
2	F	800	NSY	C59-C58-C52	5.80	126.31	112.87
2	D	600	NSY	C1-C7-C8	5.55	128.84	120.89
2	A	300	NSY	C1-C7-C8	5.55	128.83	120.89
2	C	500	NSY	C23-C22-C68	5.48	128.80	112.57
2	C	500	NSY	C1-C7-C8	5.37	128.58	120.89
2	D	600	NSY	C23-C22-C68	5.29	128.26	112.57
2	F	800	NSY	O73-C68-C22	-5.19	110.21	122.03
2	B	400	NSY	C70-C69-C20	5.15	131.85	113.62
2	E	700	NSY	O73-C68-C22	-5.12	110.38	122.03
2	A	300	NSY	C70-C69-C20	5.06	131.52	113.62
2	B	400	NSY	C18-C17-N16	-5.02	97.51	111.16
2	D	600	NSY	O73-C68-C22	-4.99	110.68	122.03
2	C	500	NSY	O73-C68-C22	-4.99	110.68	122.03
2	F	800	NSY	C23-C22-C68	4.96	127.27	112.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	400	NSY	C13-C11-C12	-4.95	114.33	120.56
2	D	600	NSY	C70-C69-C20	4.94	131.11	113.62
2	C	500	NSY	C70-C69-C20	4.94	131.10	113.62
2	A	300	NSY	C13-C11-C12	-4.92	114.37	120.56
2	E	700	NSY	C23-C22-C68	4.91	127.13	112.57
2	E	700	NSY	C70-C69-C20	4.90	130.96	113.62
2	A	300	NSY	C71-N72-C68	-4.83	113.87	122.84
2	F	800	NSY	C18-C17-N16	-4.79	98.11	111.16
2	B	400	NSY	C71-N72-C68	-4.79	113.94	122.84
2	F	800	NSY	C1-C7-C8	4.79	127.74	120.89
2	D	600	NSY	C18-C17-N16	-4.77	98.19	111.16
2	A	300	NSY	C18-C17-N16	-4.75	98.24	111.16
2	F	800	NSY	C70-C69-C20	4.70	130.24	113.62
2	E	700	NSY	C18-C17-N16	-4.68	98.43	111.16
2	C	500	NSY	C18-C17-N16	-4.67	98.44	111.16
2	E	700	NSY	C1-C7-C8	4.67	127.57	120.89
2	A	300	NSY	O73-C68-C22	-4.65	111.46	122.03
2	B	400	NSY	O73-C68-C22	-4.63	111.50	122.03
2	D	600	NSY	C59-C58-C52	4.61	123.56	112.87
2	E	700	NSY	C13-C11-C12	-4.54	114.85	120.56
2	F	800	NSY	C13-C11-C12	-4.50	114.91	120.56
2	B	400	NSY	C59-C58-C52	4.49	123.28	112.87
2	F	800	NSY	C71-N72-C68	-4.37	114.73	122.84
2	E	700	NSY	C71-N72-C68	-4.31	114.83	122.84
2	A	300	NSY	C59-C58-C52	4.29	122.81	112.87
2	C	500	NSY	C59-C58-C52	4.27	122.77	112.87
2	A	300	NSY	C31-C30-N29	4.22	119.40	110.88
2	C	500	NSY	C13-C11-C12	-4.22	115.26	120.56
2	D	600	NSY	C13-C11-C12	-4.21	115.27	120.56
2	C	500	NSY	C71-N72-C68	-4.15	115.14	122.84
2	A	300	NSY	C32-C31-C30	4.13	126.67	113.92
2	B	400	NSY	C10-C13-C11	4.10	126.43	120.19
2	A	300	NSY	C22-C68-N72	4.08	121.70	116.19
2	D	600	NSY	C71-N72-C68	-4.08	115.27	122.84
2	B	400	NSY	C9-C8-C7	-4.03	115.48	121.03
2	B	400	NSY	C22-C68-N72	4.00	121.59	116.19
2	E	700	NSY	C9-C8-C7	-4.00	115.52	121.03
2	F	800	NSY	C9-C8-C7	-3.99	115.53	121.03
2	B	400	NSY	C31-C30-N29	3.98	118.93	110.88
2	B	400	NSY	C23-C22-C68	3.97	124.34	112.57
2	A	300	NSY	C23-C22-C68	3.96	124.31	112.57
2	D	600	NSY	C9-C8-C7	-3.95	115.59	121.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	NSY	C9-C8-C7	-3.95	115.60	121.03
2	C	500	NSY	C9-C8-C7	-3.89	115.67	121.03
2	F	800	NSY	C14-C12-C4	-3.83	114.72	121.36
2	A	300	NSY	C10-C13-C11	3.82	126.01	120.19
2	A	300	NSY	C59-N60-C42	-3.79	115.83	122.59
2	C	500	NSY	C14-C12-C4	-3.74	114.87	121.36
2	E	700	NSY	C14-C12-C4	-3.74	114.87	121.36
2	B	400	NSY	C32-C31-C30	3.72	125.40	113.92
2	B	400	NSY	C17-N16-C2	3.72	131.21	121.65
2	D	600	NSY	C14-C12-C4	-3.71	114.93	121.36
2	F	800	NSY	C17-N16-C2	3.67	131.08	121.65
2	B	400	NSY	C59-N60-C42	-3.60	116.16	122.59
2	E	700	NSY	C17-N16-C2	3.60	130.91	121.65
2	A	300	NSY	C32-C33-N34	3.59	122.49	112.21
2	A	300	NSY	C17-N16-C2	3.59	130.89	121.65
2	C	500	NSY	C10-C13-C11	3.59	125.66	120.19
2	D	600	NSY	C10-C13-C11	3.58	125.64	120.19
2	B	400	NSY	C14-C12-C4	-3.53	115.24	121.36
2	B	400	NSY	C32-C33-N34	3.49	122.19	112.21
2	C	500	NSY	C22-C68-N72	3.46	120.86	116.19
2	F	800	NSY	C10-C13-C11	3.45	125.44	120.19
2	E	700	NSY	C10-C13-C11	3.43	125.42	120.19
2	E	700	NSY	O73-C68-N72	3.42	129.47	123.01
2	A	300	NSY	C14-C12-C4	-3.37	115.52	121.36
2	D	600	NSY	C32-C31-C30	3.36	124.29	113.92
2	D	600	NSY	C22-C68-N72	3.36	120.72	116.19
2	C	500	NSY	C17-N16-C2	3.34	130.25	121.65
2	F	800	NSY	C69-C20-C17	3.34	124.22	113.92
2	F	800	NSY	O73-C68-N72	3.32	129.28	123.01
2	E	700	NSY	C69-C20-C17	3.31	124.13	113.92
2	B	400	NSY	C7-C1-C2	3.31	122.37	112.57
2	E	700	NSY	C32-C31-C30	3.28	124.05	113.92
2	C	500	NSY	C54-C53-C52	-3.27	115.62	120.63
2	F	800	NSY	C32-C31-C30	3.26	123.97	113.92
2	D	600	NSY	C54-C53-C52	-3.25	115.64	120.63
2	E	700	NSY	C59-N60-C42	-3.25	116.79	122.59
2	C	500	NSY	C32-C31-C30	3.20	123.80	113.92
2	F	800	NSY	C22-C68-N72	3.20	120.50	116.19
2	D	600	NSY	C17-N16-C2	3.19	129.87	121.65
2	F	800	NSY	C59-N60-C42	-3.19	116.89	122.59
2	A	300	NSY	C7-C1-C2	3.17	121.96	112.57
2	C	500	NSY	C32-C33-N34	3.16	121.25	112.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	600	NSY	C32-C33-N34	3.12	121.12	112.21
2	C	500	NSY	C69-C20-C17	3.09	123.46	113.92
2	F	800	NSY	C31-C30-N29	3.07	117.08	110.88
2	E	700	NSY	C32-C33-N34	3.05	120.94	112.21
2	F	800	NSY	C32-C33-N34	3.03	120.87	112.21
2	E	700	NSY	C58-C52-C57	-3.01	113.61	121.23
2	D	600	NSY	O73-C68-N72	2.96	128.60	123.01
2	E	700	NSY	C31-C30-N29	2.95	116.83	110.88
2	C	500	NSY	C59-N60-C42	-2.94	117.35	122.59
2	B	400	NSY	C69-C20-C17	2.94	122.98	113.92
2	E	700	NSY	C22-C68-N72	2.93	120.14	116.19
2	B	400	NSY	C70-C71-N72	2.90	120.51	112.21
2	E	700	NSY	C69-C70-C71	2.90	127.28	113.56
2	C	500	NSY	C11-C12-C4	2.89	126.37	121.36
2	D	600	NSY	C69-C20-C17	2.89	122.85	113.92
2	C	500	NSY	O73-C68-N72	2.89	128.46	123.01
2	D	600	NSY	C31-C30-N29	2.87	116.67	110.88
2	F	800	NSY	C69-C70-C71	2.86	127.13	113.56
2	D	600	NSY	C11-C12-C4	2.86	126.31	121.36
2	D	600	NSY	C7-C1-C2	2.84	120.98	112.57
2	A	300	NSY	C54-C53-C52	-2.83	116.28	120.63
2	B	400	NSY	C42-C41-N40	-2.83	103.46	111.16
2	B	400	NSY	C54-C53-C52	-2.82	116.30	120.63
2	D	600	NSY	C59-N60-C42	-2.77	117.65	122.59
2	A	300	NSY	C69-C20-C17	2.76	122.44	113.92
2	E	700	NSY	C54-C53-C52	-2.75	116.42	120.63
2	A	300	NSY	C42-C41-N40	-2.74	103.69	111.16
2	F	800	NSY	C1-C2-N16	-2.73	111.48	115.88
2	F	800	NSY	C54-C53-C52	-2.73	116.44	120.63
2	C	500	NSY	C58-C52-C57	-2.72	114.36	121.23
2	F	800	NSY	C58-C52-C57	-2.71	114.39	121.23
2	D	600	NSY	C31-C30-C38	-2.71	103.88	110.20
2	D	600	NSY	C58-C52-C57	-2.70	114.39	121.23
2	B	400	NSY	C69-C70-C71	2.70	126.36	113.56
2	C	500	NSY	C31-C30-N29	2.70	116.33	110.88
2	C	500	NSY	C69-C70-C71	2.69	126.30	113.56
2	A	300	NSY	C69-C70-C71	2.68	126.25	113.56
2	A	300	NSY	C70-C71-N72	2.67	119.83	112.21
2	D	600	NSY	C69-C70-C71	2.65	126.10	113.56
2	E	700	NSY	C1-C2-N16	-2.64	111.63	115.88
2	C	500	NSY	C57-C52-C53	2.59	122.23	118.17
2	C	500	NSY	C31-C30-C38	-2.55	104.25	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	NSY	C7-C1-C2	2.51	120.02	112.57
2	B	400	NSY	C1-C2-N16	-2.50	111.85	115.88
2	C	500	NSY	C22-C23-C24	2.47	124.43	120.89
2	C	500	NSY	C70-C71-N72	2.47	119.27	112.21
2	D	600	NSY	C70-C71-N72	2.45	119.21	112.21
2	F	800	NSY	C11-C12-C4	2.44	125.59	121.36
2	B	400	NSY	C11-C12-C4	2.41	125.52	121.36
2	F	800	NSY	C66-C64-C62	2.38	123.56	120.56
2	D	600	NSY	C5-C4-C12	-2.38	117.23	121.36
2	C	500	NSY	C5-C4-C12	-2.38	117.24	121.36
2	E	700	NSY	C7-C1-C2	2.38	119.61	112.57
2	D	600	NSY	C57-C52-C53	2.37	121.89	118.17
2	B	400	NSY	C44-C41-N40	2.37	115.78	110.79
2	E	700	NSY	C27-C28-C62	2.37	125.46	121.36
2	F	800	NSY	N36-C35-N37	-2.36	113.01	120.26
2	E	700	NSY	C11-C12-C4	2.31	125.36	121.36
2	A	300	NSY	C1-C2-N16	-2.30	112.17	115.88
2	F	800	NSY	C57-C52-C53	2.28	121.75	118.17
2	F	800	NSY	C27-C28-C62	2.27	125.29	121.36
2	A	300	NSY	N36-C35-N37	-2.27	113.28	120.26
2	B	400	NSY	C57-C52-C53	2.26	121.73	118.17
2	F	800	NSY	C7-C1-C2	2.26	119.28	112.57
2	A	300	NSY	C44-C41-N40	2.26	115.56	110.79
2	F	800	NSY	C5-C4-C12	-2.25	117.46	121.36
2	E	700	NSY	C70-C71-N72	2.25	118.63	112.21
2	D	600	NSY	C22-C23-C24	2.24	124.09	120.89
2	E	700	NSY	N36-C35-N37	-2.23	113.39	120.26
2	B	400	NSY	N36-C35-N37	-2.23	113.41	120.26
2	E	700	NSY	C5-C4-C12	-2.22	117.50	121.36
2	E	700	NSY	C57-C52-C53	2.21	121.64	118.17
2	F	800	NSY	C42-C41-N40	-2.19	105.20	111.16
2	E	700	NSY	C31-C30-C38	-2.19	105.08	110.20
2	E	700	NSY	N36-C35-N34	2.19	124.25	119.19
2	C	500	NSY	N36-C35-N37	-2.17	113.58	120.26
2	F	800	NSY	C31-C30-C38	-2.17	105.13	110.20
2	F	800	NSY	C70-C71-N72	2.16	118.40	112.21
2	F	800	NSY	N36-C35-N34	2.15	124.15	119.19
2	E	700	NSY	C66-C64-C62	2.13	123.24	120.56
2	A	300	NSY	C57-C52-C53	2.11	121.48	118.17
2	D	600	NSY	C45-C44-C41	-2.10	107.58	113.39
2	D	600	NSY	C38-C30-N29	2.10	116.89	111.16
2	E	700	NSY	C42-C41-N40	-2.10	105.44	111.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	600	NSY	N36-C35-N37	-2.10	113.79	120.26
2	B	400	NSY	C58-C52-C57	-2.09	115.94	121.23
2	C	500	NSY	C38-C30-N29	2.07	116.80	111.16
2	A	300	NSY	C11-C12-C4	2.07	124.94	121.36
2	B	400	NSY	O73-C68-N72	2.06	126.90	123.01
2	A	300	NSY	C58-C52-C57	-2.04	116.07	121.23
2	A	300	NSY	O73-C68-N72	2.03	126.84	123.01
2	E	700	NSY	C26-C28-C62	-2.02	117.86	121.36

There are no chirality outliers.

All (85) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NSY	N36-C35-N34-C33
2	A	300	NSY	N37-C35-N34-C33
2	C	500	NSY	N36-C35-N34-C33
2	C	500	NSY	N37-C35-N34-C33
2	E	700	NSY	N36-C35-N34-C33
2	F	800	NSY	N36-C35-N34-C33
2	D	600	NSY	N36-C35-N34-C33
2	D	600	NSY	N37-C35-N34-C33
2	B	400	NSY	N36-C35-N34-C33
2	B	400	NSY	N37-C35-N34-C33
2	A	300	NSY	C20-C69-C70-C71
2	C	500	NSY	C20-C69-C70-C71
2	E	700	NSY	C20-C69-C70-C71
2	F	800	NSY	C20-C69-C70-C71
2	D	600	NSY	C20-C69-C70-C71
2	B	400	NSY	C20-C69-C70-C71
2	A	300	NSY	C18-C17-C20-C69
2	C	500	NSY	C18-C17-C20-C69
2	E	700	NSY	C18-C17-C20-C69
2	F	800	NSY	C18-C17-C20-C69
2	D	600	NSY	C18-C17-C20-C69
2	B	400	NSY	C18-C17-C20-C69
2	A	300	NSY	N16-C17-C20-C69
2	C	500	NSY	N16-C17-C20-C69
2	E	700	NSY	N16-C17-C20-C69
2	F	800	NSY	N16-C17-C20-C69
2	D	600	NSY	N16-C17-C20-C69
2	B	400	NSY	N16-C17-C20-C69
2	C	500	NSY	C38-C30-N29-C18

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Mol	Chain	Res	Type	Atoms
2	E	700	NSY	C18-C17-N16-C2
2	E	700	NSY	C38-C30-N29-C18
2	F	800	NSY	C18-C17-N16-C2
2	F	800	NSY	C38-C30-N29-C18
2	D	600	NSY	C38-C30-N29-C18
2	A	300	NSY	C38-C30-N29-C18
2	B	400	NSY	C38-C30-N29-C18
2	B	400	NSY	C31-C30-N29-C18
2	C	500	NSY	C30-C31-C32-C33
2	A	300	NSY	C31-C30-N29-C18
2	A	300	NSY	C2-C1-C7-C6
2	A	300	NSY	C2-C1-C7-C8
2	B	400	NSY	C2-C1-C7-C8
2	D	600	NSY	C30-C31-C32-C33
2	B	400	NSY	C2-C1-C7-C6
2	F	800	NSY	C38-C30-C31-C32
2	C	500	NSY	C18-C17-N16-C2
2	B	400	NSY	C18-C17-N16-C2
2	C	500	NSY	C2-C1-C7-C6
2	E	700	NSY	C2-C1-C7-C6
2	E	700	NSY	C2-C1-C7-C8
2	F	800	NSY	C2-C1-C7-C6
2	F	800	NSY	C2-C1-C7-C8
2	D	600	NSY	C2-C1-C7-C6
2	D	600	NSY	C2-C1-C7-C8
2	E	700	NSY	C31-C30-N29-C18
2	E	700	NSY	C30-C31-C32-C33
2	F	800	NSY	C30-C31-C32-C33
2	F	800	NSY	C31-C30-N29-C18
2	E	700	NSY	C38-C30-C31-C32
2	C	500	NSY	C31-C30-N29-C18
2	C	500	NSY	C2-C1-C7-C8
2	D	600	NSY	C31-C30-N29-C18
2	A	300	NSY	C18-C17-N16-C2
2	E	700	NSY	N37-C35-N34-C33
2	D	600	NSY	C18-C17-N16-C2
2	C	500	NSY	C38-C30-C31-C32
2	B	400	NSY	C53-C52-C58-C59
2	A	300	NSY	C53-C52-C58-C59
2	B	400	NSY	C57-C52-C58-C59
2	A	300	NSY	C57-C52-C58-C59
2	D	600	NSY	C38-C30-C31-C32

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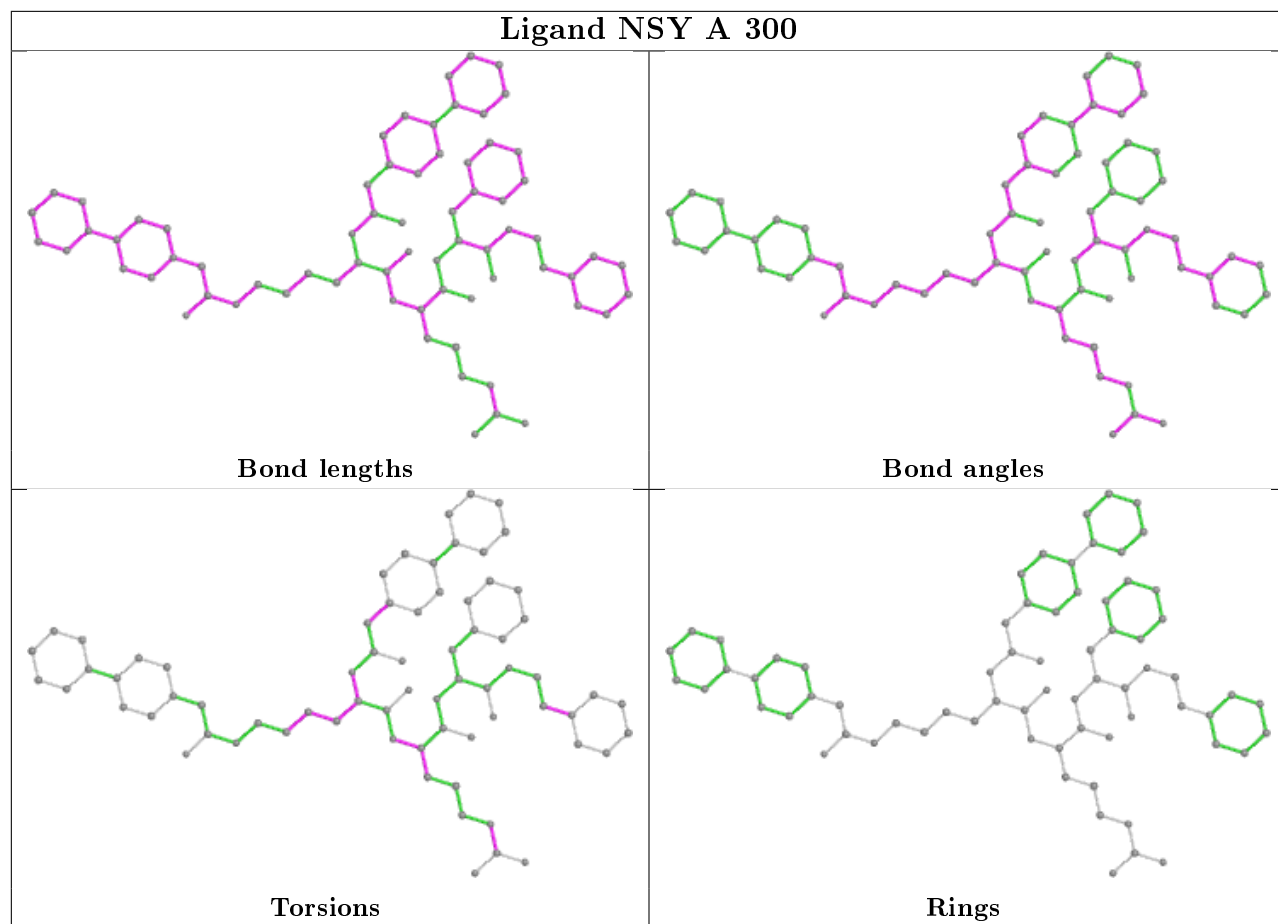
Mol	Chain	Res	Type	Atoms
2	E	700	NSY	C32-C33-N34-C35
2	B	400	NSY	C32-C33-N34-C35
2	A	300	NSY	C38-C30-C31-C32
2	B	400	NSY	C38-C30-C31-C32
2	F	800	NSY	C32-C33-N34-C35
2	F	800	NSY	N29-C30-C31-C32
2	E	700	NSY	C17-C20-C69-C70
2	F	800	NSY	C17-C20-C69-C70
2	A	300	NSY	C17-C20-C69-C70
2	F	800	NSY	N37-C35-N34-C33
2	E	700	NSY	N29-C30-C31-C32
2	E	700	NSY	C20-C17-N16-C2
2	B	400	NSY	C30-C31-C32-C33
2	F	800	NSY	C20-C17-N16-C2

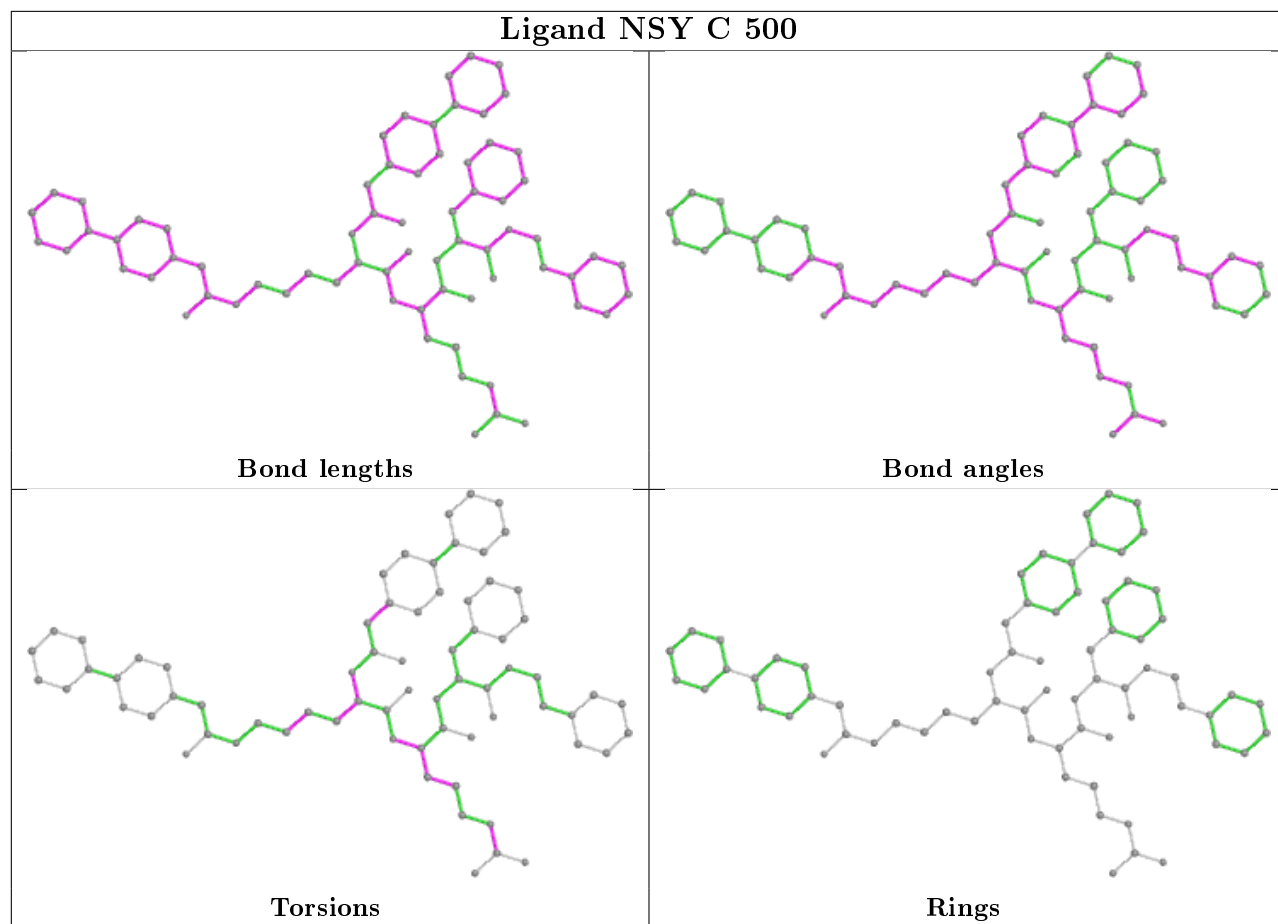
There are no ring outliers.

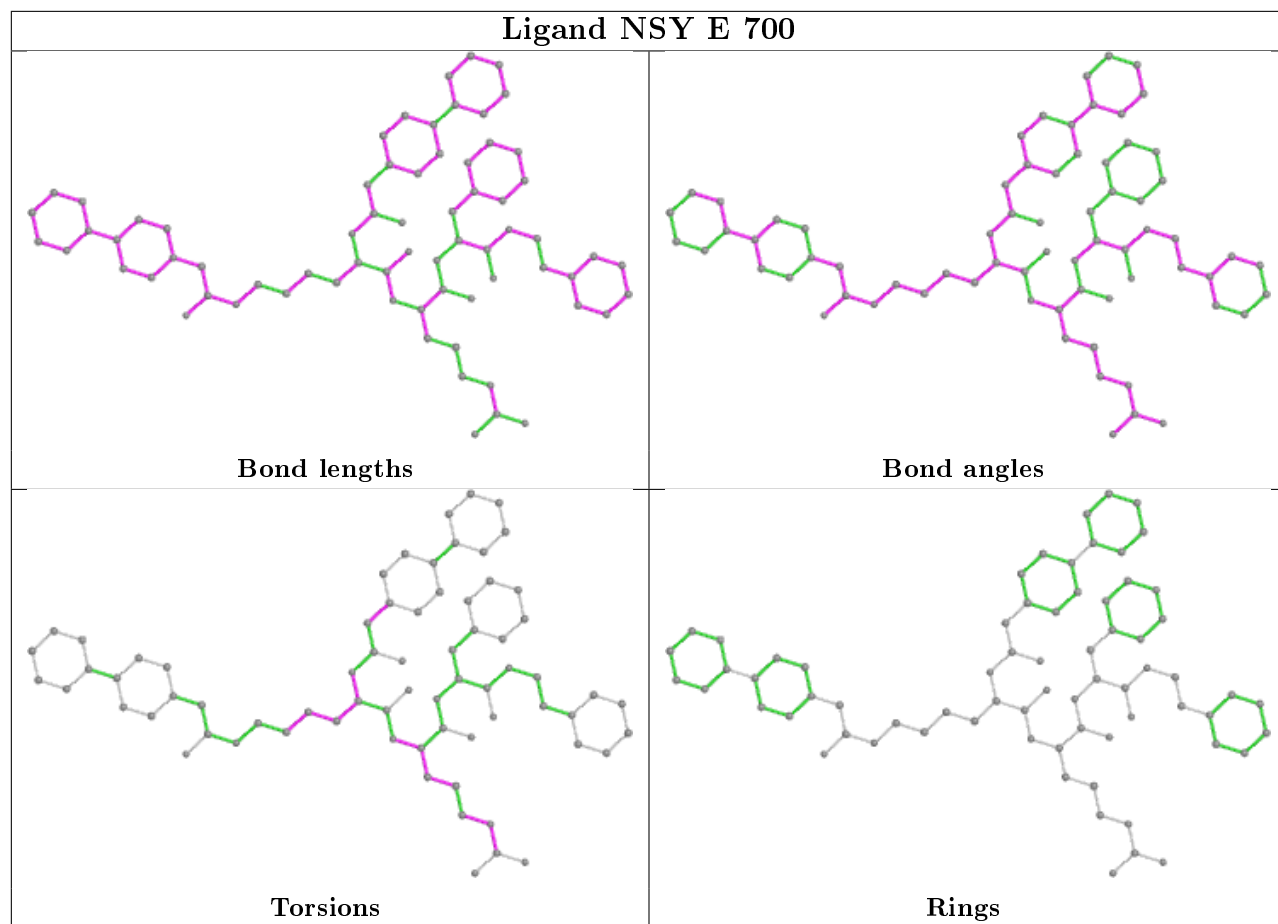
6 monomers are involved in 58 short contacts:

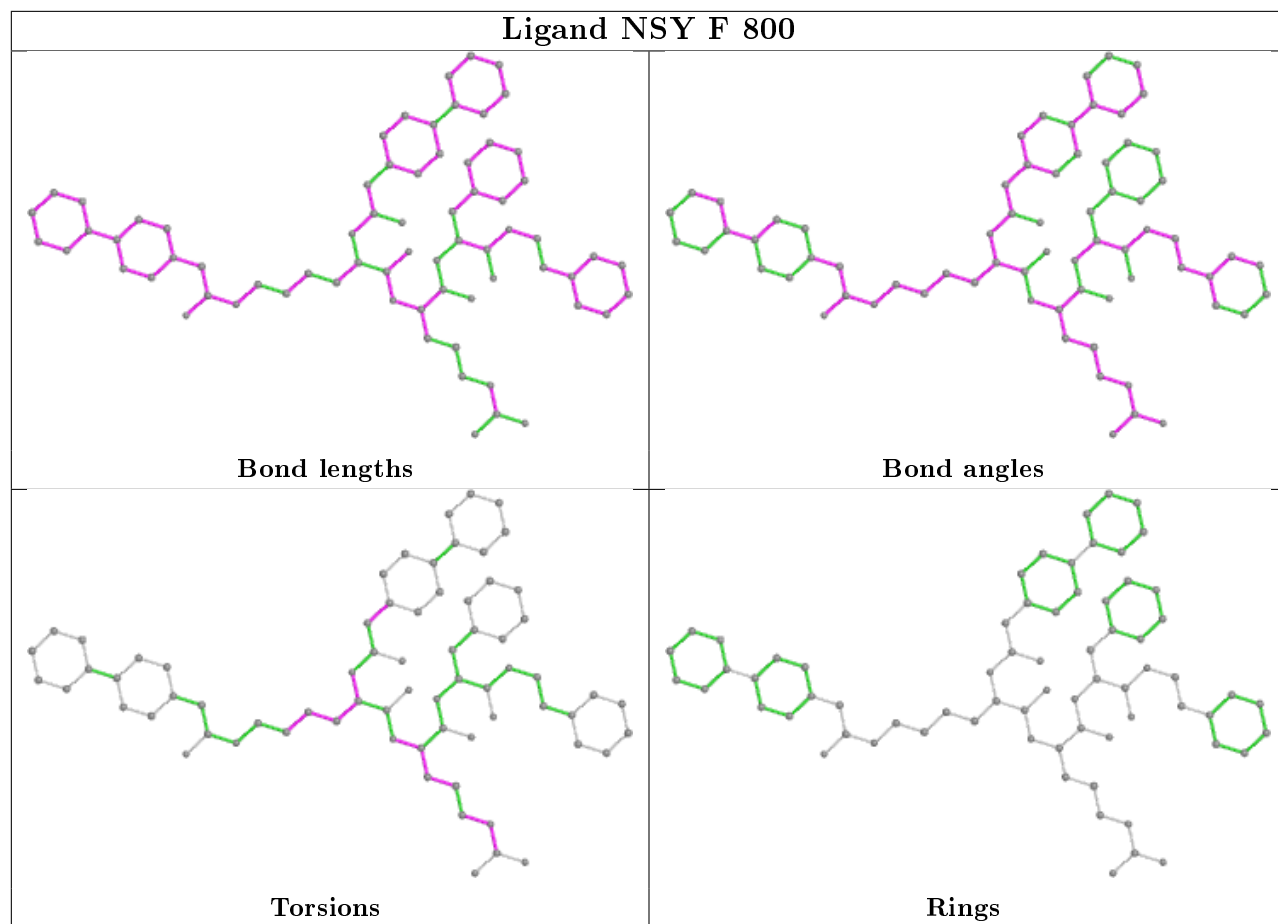
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	300	NSY	6	0
2	C	500	NSY	10	0
2	E	700	NSY	14	0
2	F	800	NSY	13	0
2	D	600	NSY	6	0
2	B	400	NSY	9	0

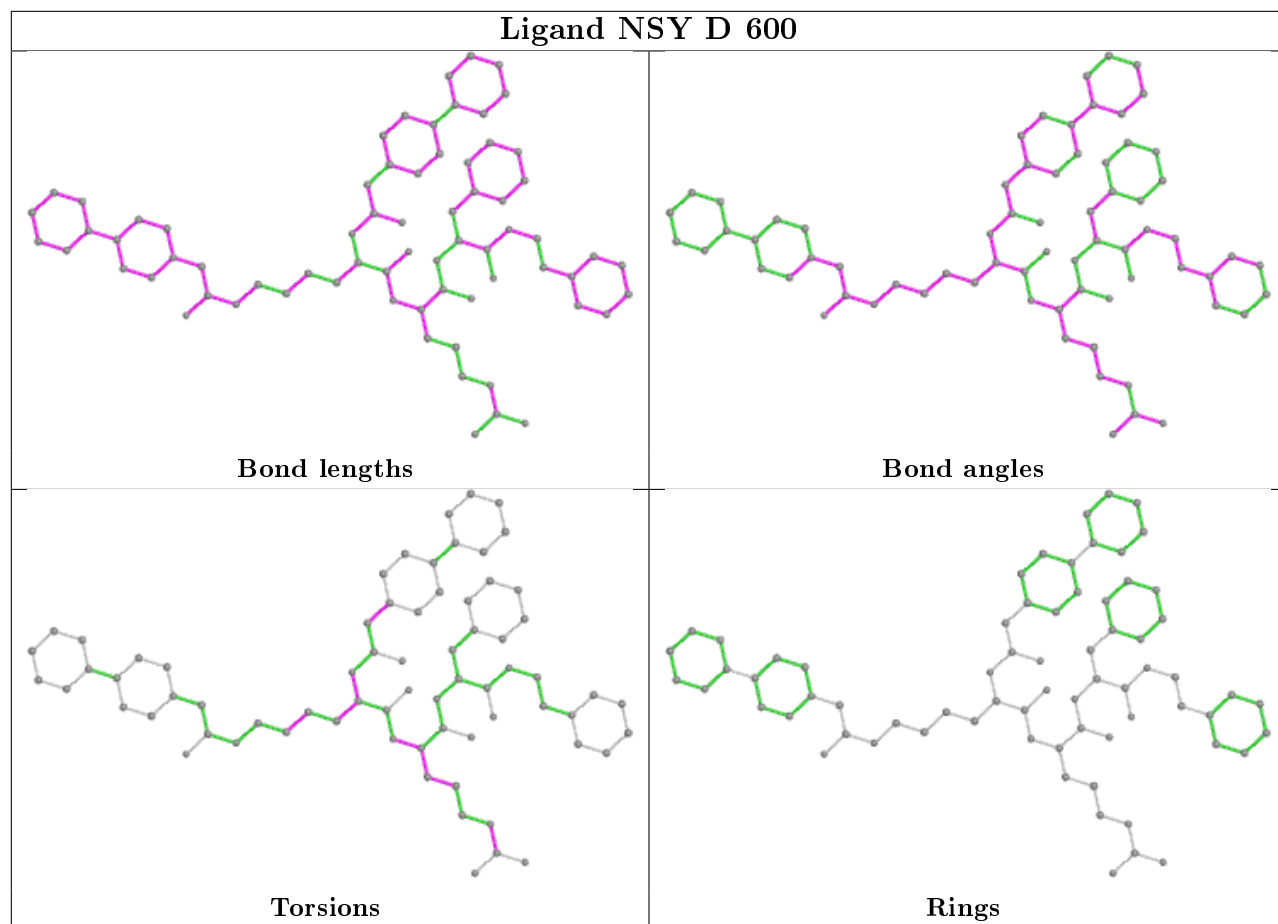
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

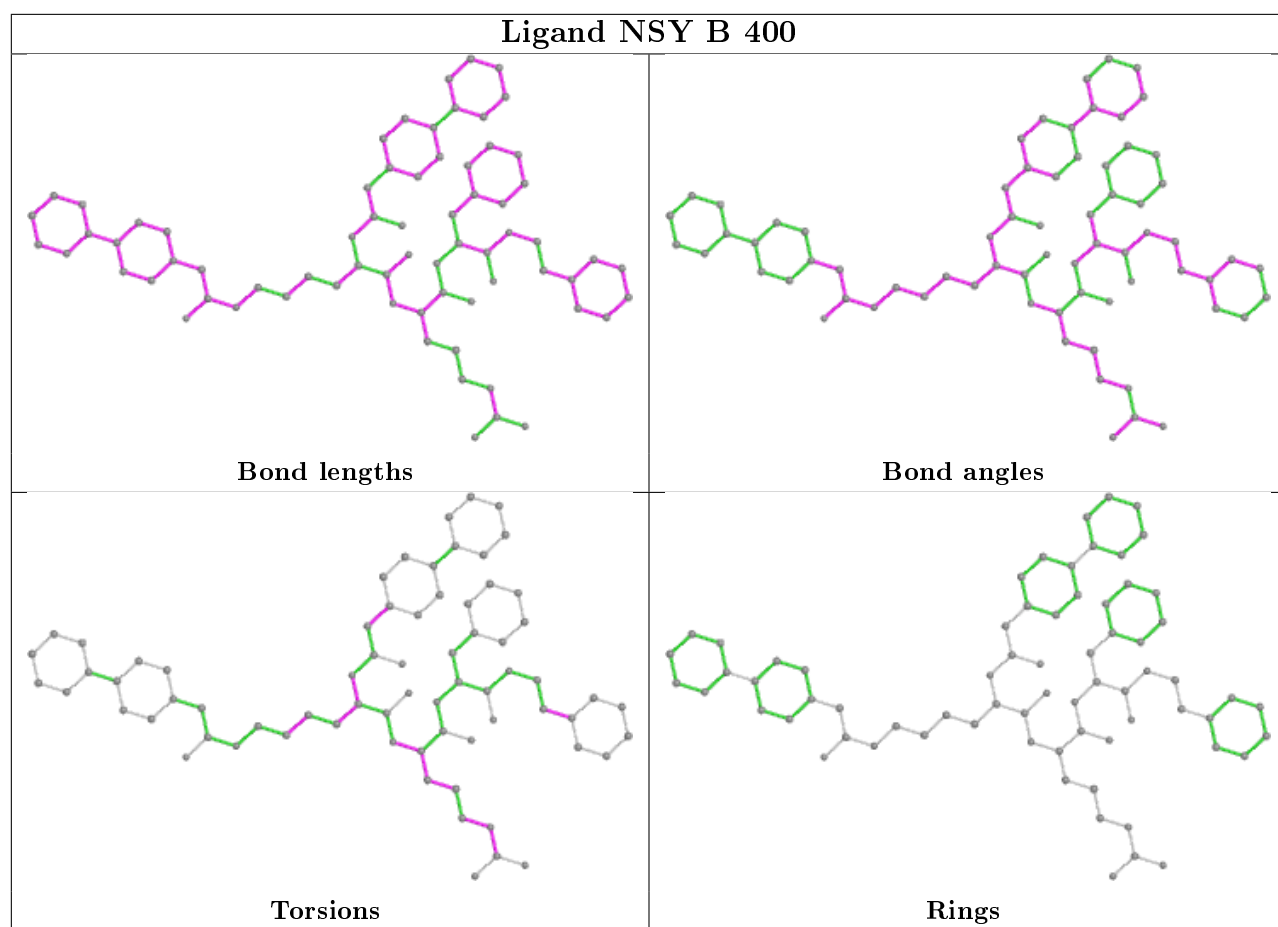












5.7 Other polymers [\(i\)](#)

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	215/220 (97%)	0.34	9 (4%) 36 30	12, 19, 40, 58	0
1	B	215/220 (97%)	0.40	12 (5%) 24 19	12, 19, 40, 57	0
1	C	215/220 (97%)	0.57	13 (6%) 21 17	13, 23, 45, 59	0
1	D	215/220 (97%)	0.45	10 (4%) 31 25	13, 23, 47, 59	0
1	E	215/220 (97%)	0.83	20 (9%) 8 6	13, 28, 54, 72	0
1	F	215/220 (97%)	0.84	28 (13%) 3 2	13, 28, 53, 63	0
All	All	1290/1320 (97%)	0.57	92 (7%) 16 12	12, 23, 49, 72	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	ALA	7.9
1	E	104	TYR	5.3
1	E	211	ILE	4.5
1	E	110	THR	4.5
1	F	103	LYS	4.1
1	F	77	VAL	4.1
1	E	103	LYS	4.1
1	A	211	ILE	4.1
1	E	1	ALA	3.9
1	F	110	THR	3.9
1	A	110	THR	3.8
1	B	174	SER	3.8
1	C	154	PRO	3.7
1	F	104	TYR	3.6
1	B	158	SER	3.5
1	E	98	CYS	3.5
1	C	174	SER	3.4
1	E	83	LEU	3.4
1	E	100	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	84	ASP	3.4
1	A	108	ASN	3.3
1	B	144	LEU	3.2
1	F	122	LEU	3.2
1	A	144	LEU	3.2
1	E	89	TYR	3.2
1	E	77	VAL	3.1
1	E	220	VAL	3.1
1	F	118	GLN	3.1
1	C	152	PHE	3.1
1	C	144	LEU	2.9
1	F	120	LYS	2.9
1	C	208	HIS	2.9
1	D	150	ILE	2.9
1	F	3	ARG	2.9
1	B	108	ASN	2.9
1	A	44	ARG	2.8
1	F	83	LEU	2.8
1	C	172	PHE	2.8
1	F	81	GLY	2.8
1	F	44	ARG	2.8
1	F	98	CYS	2.8
1	D	206	ARG	2.7
1	D	220	VAL	2.7
1	F	1	ALA	2.7
1	B	110	THR	2.7
1	D	174	SER	2.7
1	F	147	LYS	2.6
1	C	136	ILE	2.6
1	D	172	PHE	2.6
1	C	170	TYR	2.6
1	C	155	ASP	2.5
1	E	108	ASN	2.5
1	F	100	TYR	2.4
1	B	147	LYS	2.4
1	C	157	SER	2.4
1	E	41	LYS	2.4
1	F	211	ILE	2.4
1	E	38	MET	2.4
1	E	113	VAL	2.4
1	B	155	ASP	2.3
1	A	136	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	157	SER	2.3
1	D	144	LEU	2.3
1	A	147	LYS	2.2
1	F	152	PHE	2.2
1	F	174	SER	2.2
1	F	13	VAL	2.2
1	F	220	VAL	2.2
1	B	211	ILE	2.2
1	D	110	THR	2.2
1	C	173	GLU	2.2
1	F	102	PRO	2.2
1	F	159	GLU	2.2
1	D	136	ILE	2.1
1	F	42	THR	2.1
1	F	172	PHE	2.1
1	F	48	LEU	2.1
1	B	118	GLN	2.1
1	D	5	VAL	2.1
1	F	101	ASN	2.1
1	E	147	LYS	2.1
1	B	220	VAL	2.1
1	B	136	ILE	2.1
1	E	34	LEU	2.1
1	A	3	ARG	2.0
1	C	3	ARG	2.0
1	F	96	GLU	2.0
1	E	75	GLN	2.0
1	F	41	LYS	2.0
1	B	209	CYS	2.0
1	E	156	CYS	2.0
1	D	92	GLU	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](#)

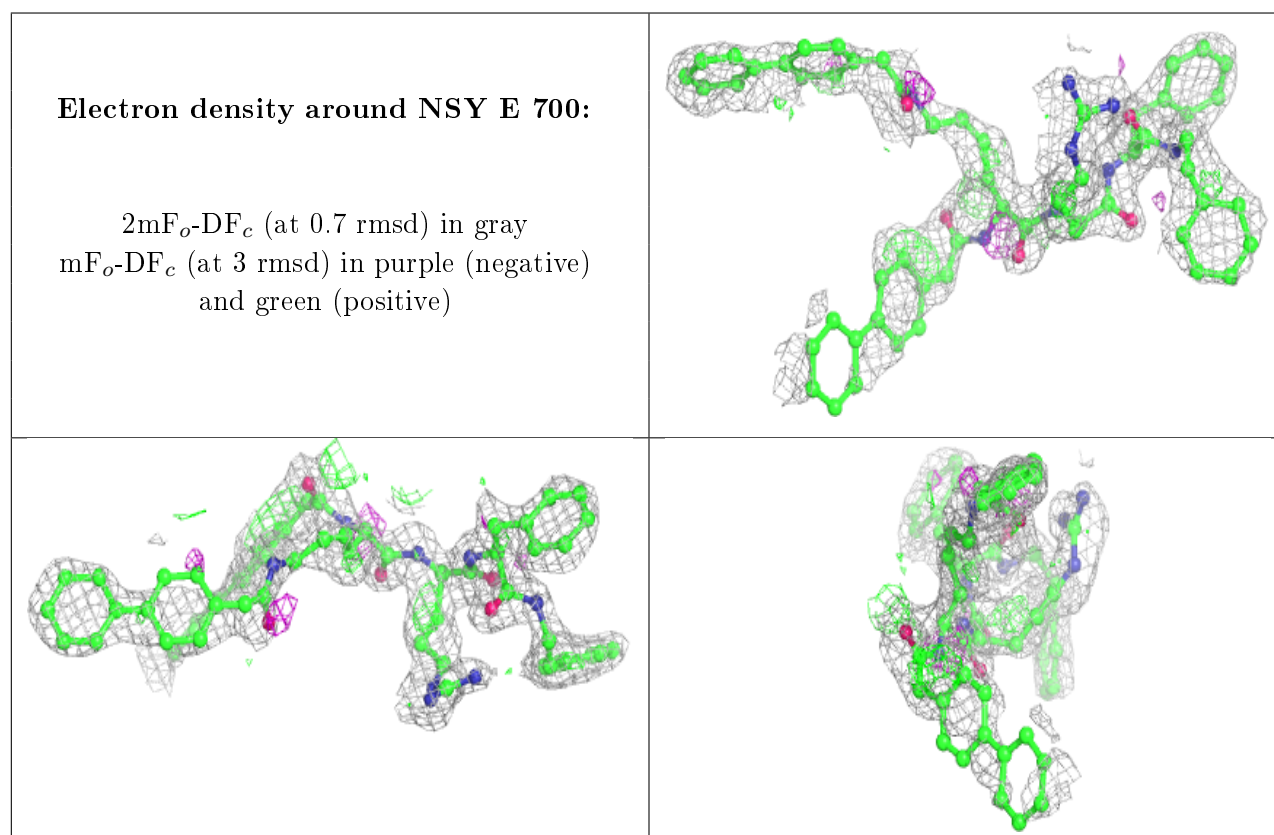
There are no carbohydrates in this entry.

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.

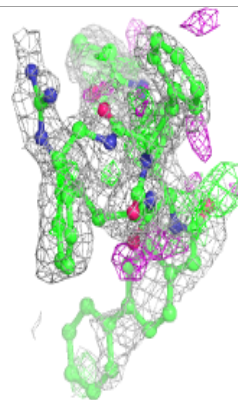
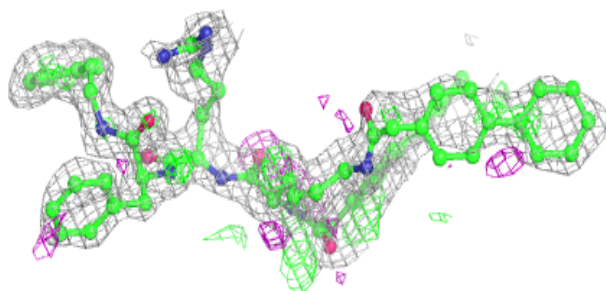
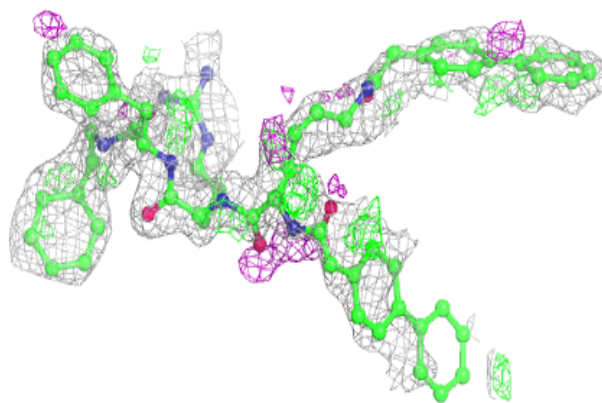
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NSY	E	700	70/70	0.70	0.27	22,43,66,69	0
2	NSY	F	800	70/70	0.70	0.28	22,43,66,69	0
2	NSY	B	400	70/70	0.71	0.27	22,43,66,69	0
2	NSY	C	500	70/70	0.73	0.28	22,43,66,69	0
2	NSY	D	600	70/70	0.75	0.29	22,43,66,69	0
2	NSY	A	300	70/70	0.81	0.26	22,43,66,69	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.

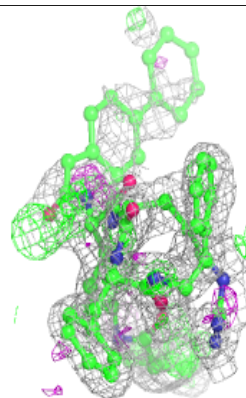
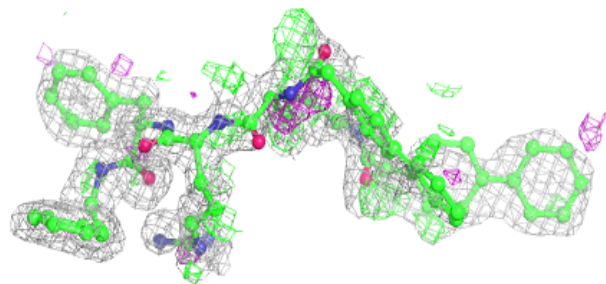
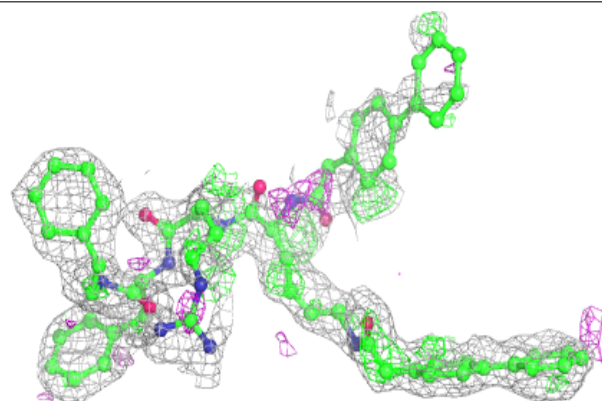


Electron density around NSY F 800:

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

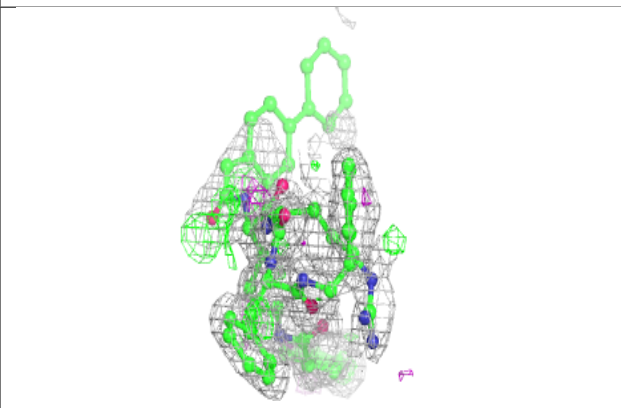
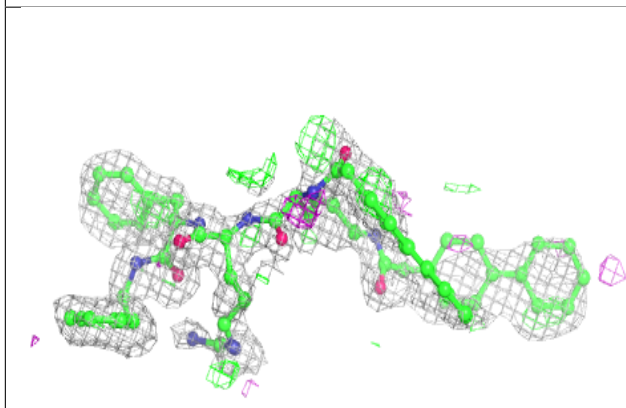
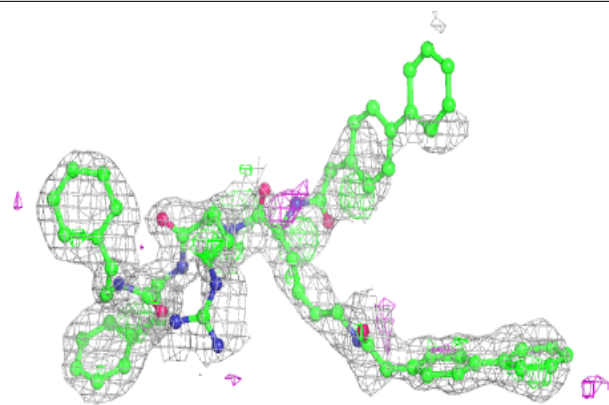
**Electron density around NSY B 400:**

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

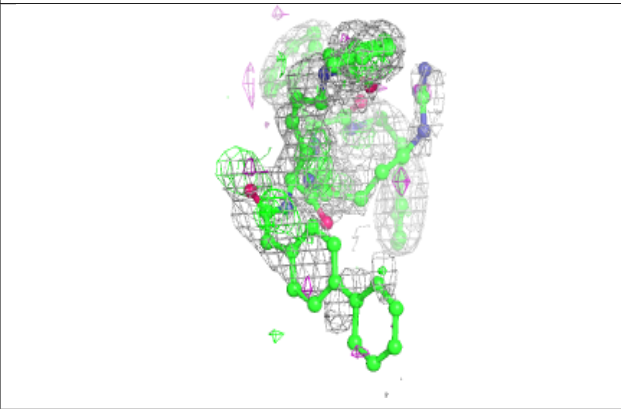
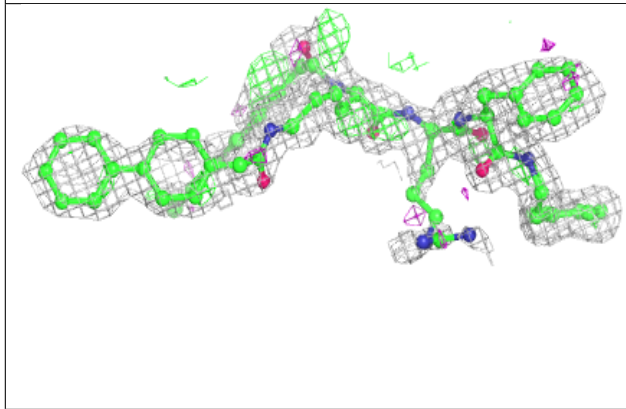
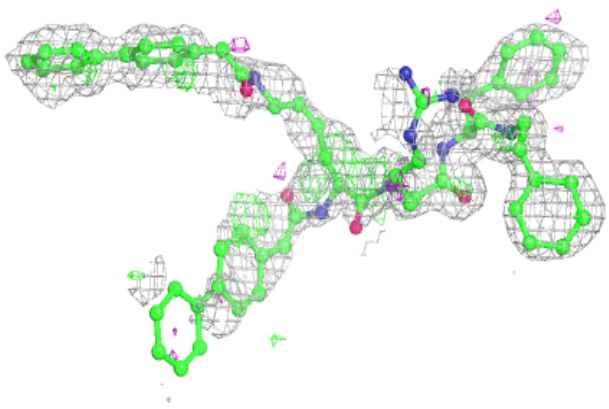


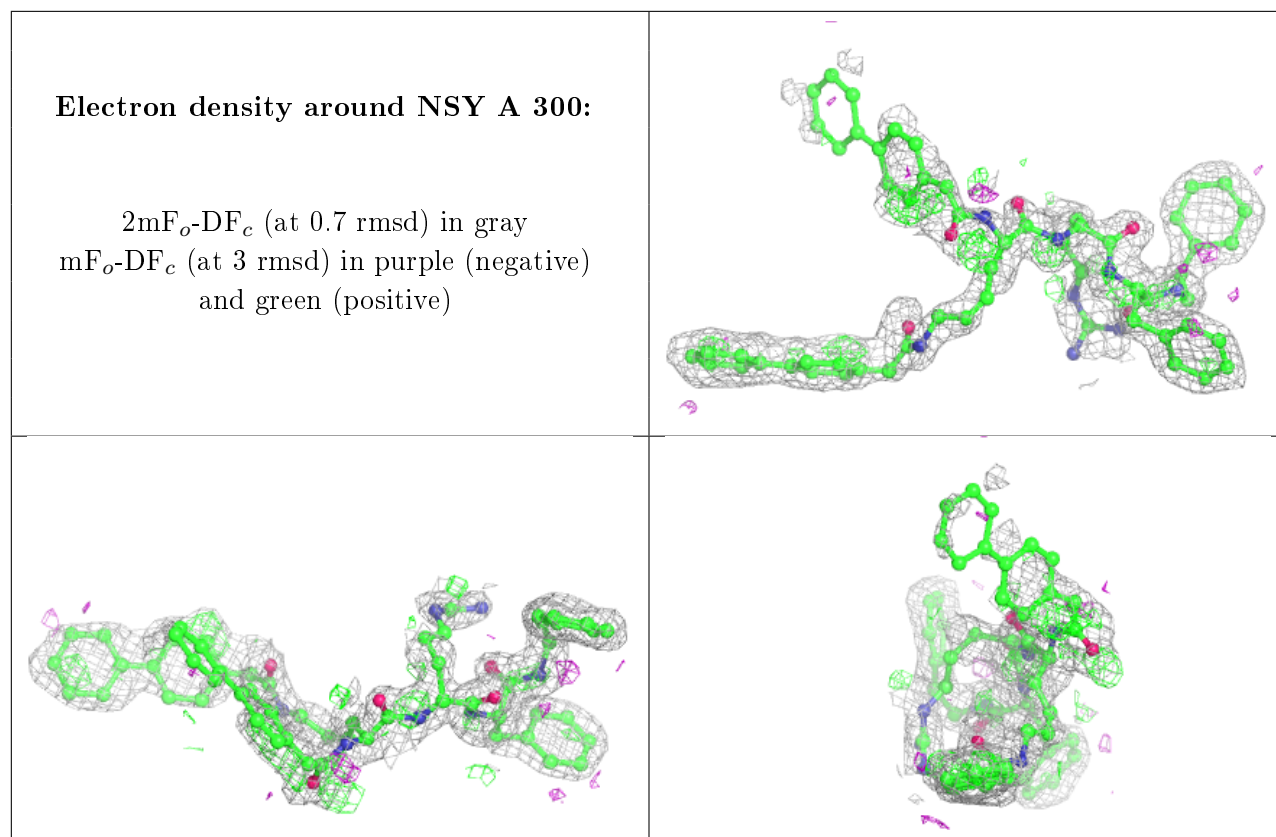
Electron density around NSY C 500:

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

**Electron density around NSY D 600:**

$2mF_o-DF_c$ (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.