



wwPDB X-ray Structure Validation Summary Report

May 14, 2020 – 11:57 am BST

PDB ID : 3B2C
Title : Crystal structure of the collagen triple helix model [$\{\text{PRO-HYP(R)-GLY}\}_4\text{-}\{\text{HYP(S)-Pro-GLY}\}_2\text{-}\{\text{PRO-HYP(R)-GLY}\}_4$] $_3$
Authors : Motooka, D.; Kawahara, K.; Nakamura, S.; Doi, M.; Nishi, Y.; Nishiuchi, Y.; Nakazawa, T.; Yoshida, T.; Ohkubo, T.; Kobayashi, Y.; Kang, Y.K.; Uchiyama, S.
Deposited on : 2011-07-26
Resolution : 1.36 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

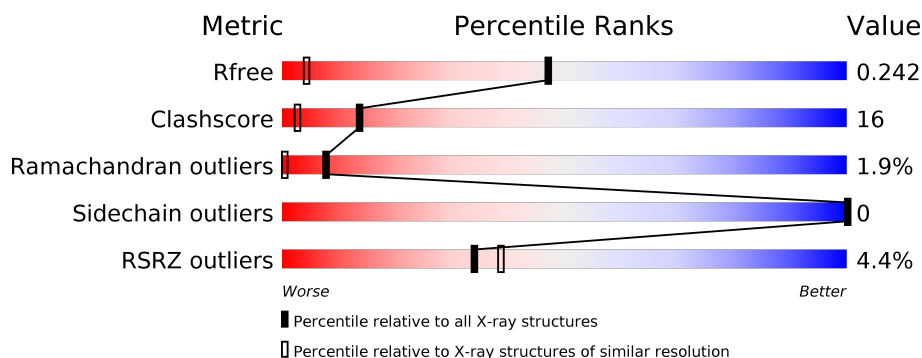
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.36 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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	30	
1	B	30	
1	C	30	
1	D	30	
1	E	30	
1	F	30	

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Mol	Chain	Length	Quality of chain
1	G	30	
1	H	30	
1	I	30	

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
1	HYP	B	29[G]	-	-	X	-
1	HYP	C	29[B]	-	-	X	-
1	HYP	C	29[C]	-	-	X	-
1	HYP	C	2[B]	-	-	X	-
1	HYP	C	2[C]	-	-	X	-
1	HYP	C	5[D]	-	-	X	-
1	HYP	C	8[D]	-	-	X	-
1	HYP	D	2[D]	-	-	X	-
1	HYP	D	5[D]	-	-	X	-
1	HYP	E	26[G]	-	-	X	-
1	HYP	E	29[A]	-	-	X	-
1	HYP	E	8[G]	-	-	X	-
1	HYP	G	2[A]	-	-	X	-
1	HYP	G	2[B]	-	-	X	-
1	HYP	G	2[D]	-	-	X	-
1	HYP	H	23[G]	-	-	X	-
1	HYP	H	29[A]	-	-	X	-
1	HYP	H	29[E]	-	-	X	-
1	HYP	H	5[C]	-	-	X	-
1	HYP	H	5[D]	-	-	X	-
1	HYP	I	26[A]	-	-	X	-
1	HYP	I	29[E]	-	-	X	-
1	HYP	I	29[F]	-	-	X	-

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 12591 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 Collagen-like peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	30	1330	840	210	280	0	30	0
1	B	30	1330	840	210	280	0	30	0
1	C	30	1330	840	210	280	0	30	0
1	D	30	1330	840	210	280	0	30	0
1	E	30	1330	840	210	280	0	30	0
1	F	30	1330	840	210	280	0	30	0
1	G	30	1330	840	210	280	0	30	0
1	H	30	1330	840	210	280	0	30	0
1	I	30	1330	840	210	280	0	30	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	56	Total 56	O 56	0	0
2	B	79	Total 79	O 79	0	0
2	C	63	Total 63	O 63	0	0
2	D	79	Total 79	O 79	0	0
2	E	69	Total 69	O 69	0	0

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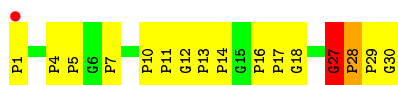
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	F	81	Total O 81 81	0	0
2	G	53	Total O 53 53	0	0
2	H	76	Total O 76 76	0	0
2	I	65	Total O 65 65	0	0

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.

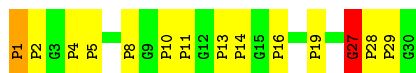
- Molecule 1: Collagen-like peptide



- Molecule 1: Collagen-like peptide



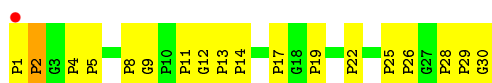
- Molecule 1: Collagen-like peptide



- Molecule 1: Collagen-like peptide



- Molecule 1: Collagen-like peptide



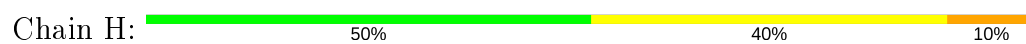
- Molecule 1: Collagen-like peptide



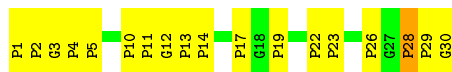
- Molecule 1: Collagen-like peptide



- Molecule 1: Collagen-like peptide



- Molecule 1: Collagen-like peptide



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.80Å 26.15Å 84.74Å 90.00° 92.48° 90.00°	Depositor
Resolution (Å)	10.00 – 1.36 9.97 – 1.36	Depositor EDS
% Data completeness (in resolution range)	98.8 (10.00-1.36) 98.8 (9.97-1.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.94 (at 1.36Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.203 , 0.248 0.203 , 0.242	Depositor DCC
R_{free} test set	1942 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	6.9	Xtrriage
Anisotropy	0.283	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 92.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.99	EDS
Total number of atoms	12591	wwPDB-VP
Average B, all atoms (Å ²)	8.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 74.64 % 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 1.4721e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: HYP, HZP

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	0.53	0/763	0.66	0/938
1	B	0.48	0/763	0.67	0/938
1	C	0.62	0/763	0.66	0/938
1	D	0.59	0/763	0.62	0/938
1	E	0.51	0/763	0.72	0/938
1	F	0.47	0/763	0.63	0/938
1	G	0.61	0/763	0.60	0/938
1	H	0.49	0/763	0.63	0/938
1	I	0.63	0/763	0.68	0/938
All	All	0.55	0/6867	0.65	0/8442

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
1	C	0	4
1	D	0	5
1	E	0	4
1	F	0	4
1	G	0	7
1	H	0	6
1	I	0	4
All	All	0	38

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27[E]	GLY	Mainchain
1	A	27[F]	GLY	Mainchain
1	A	27[G]	GLY	Mainchain
1	B	4[D]	PRO	Mainchain
1	C	1[B]	PRO	Mainchain

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	1330	0	1204	72	0
1	B	1330	0	1204	42	0
1	C	1330	0	1204	60	0
1	D	1330	0	1204	67	2
1	E	1330	0	1204	75	0
1	F	1330	0	1203	83	0
1	G	1330	0	1204	84	0
1	H	1330	0	1204	86	0
1	I	1330	0	1204	94	0
2	A	56	0	0	0	2
2	B	79	0	0	4	3
2	C	63	0	0	0	2
2	D	79	0	0	15	1
2	E	69	0	0	4	1
2	F	81	0	0	4	1
2	G	53	0	0	0	4
2	H	76	0	0	0	1
2	I	65	0	0	0	3
All	All	12591	0	10835	362	10

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.

The worst 5 of 362 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:29[A]:HYP:HA	1:F:28[A]:PRO:CG	1.20	1.61
1:E:29[A]:HYP:CA	1:F:28[A]:PRO:HG2	1.09	1.52
1:E:29[A]:HYP:CA	1:F:28[A]:PRO:CG	1.86	1.33
1:E:29[A]:HYP:OD1	1:F:28[A]:PRO:HG3	1.27	1.28
1:B:29[G]:HYP:HA	1:C:28[G]:PRO:HD2	1.27	1.13

The worst 5 of 10 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:502:HOH:O	2:I:319:HOH:O[2_655]	1.26	0.94
2:A:274:HOH:O	2:B:511:HOH:O[2_555]	1.34	0.86
2:G:523:HOH:O	2:I:561:HOH:O[2_645]	1.87	0.33
2:B:585:HOH:O	2:D:613:HOH:O[2_555]	1.94	0.26
2:F:212:HOH:O	2:H:611:HOH:O[2_645]	2.02	0.18

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	126/30 (420%)	112 (89%)	0	14 (11%)	0 0
1	B	126/30 (420%)	126 (100%)	0	0	100 100
1	C	126/30 (420%)	119 (94%)	0	7 (6%)	2 0
1	D	126/30 (420%)	126 (100%)	0	0	100 100
1	E	126/30 (420%)	119 (94%)	7 (6%)	0	100 100
1	F	126/30 (420%)	119 (94%)	7 (6%)	0	100 100
1	G	126/30 (420%)	126 (100%)	0	0	100 100
1	H	126/30 (420%)	126 (100%)	0	0	100 100
1	I	126/30 (420%)	126 (100%)	0	0	100 100
All	All	1134/270 (420%)	1099 (97%)	14 (1%)	21 (2%)	8 0

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28[A]	PRO
1	A	28[B]	PRO
1	A	28[C]	PRO
1	A	28[D]	PRO
1	A	28[E]	PRO

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	70/10 (700%)	70 (100%)	0	100	100
1	B	70/10 (700%)	70 (100%)	0	100	100
1	C	70/10 (700%)	70 (100%)	0	100	100
1	D	70/10 (700%)	70 (100%)	0	100	100
1	E	70/10 (700%)	70 (100%)	0	100	100
1	F	70/10 (700%)	70 (100%)	0	100	100
1	G	70/10 (700%)	70 (100%)	0	100	100
1	H	70/10 (700%)	70 (100%)	0	100	100
1	I	70/10 (700%)	70 (100%)	0	100	100
All	All	630/90 (700%)	630 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

630 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	HYP	G	5[B]	1	6,8,9	0.58	0	5,10,12	1.76	2 (40%)
1	HYP	C	23[G]	1	6,8,9	0.64	0	5,10,12	2.06	2 (40%)
1	HZP	A	16[E]	1	6,8,9	0.65	0	5,10,12	6.75	3 (60%)
1	HYP	C	23[E]	1	6,8,9	0.55	0	5,10,12	0.80	0
1	HYP	A	5[B]	1	6,8,9	0.62	0	5,10,12	1.31	1 (20%)
1	HYP	C	20[C]	1	6,8,9	0.44	0	5,10,12	2.34	2 (40%)
1	HZP	F	13[B]	1	6,8,9	0.80	0	5,10,12	6.46	3 (60%)
1	HYP	B	23[F]	1	6,8,9	0.73	0	5,10,12	0.92	0
1	HYP	B	23[G]	1	6,8,9	0.74	0	5,10,12	0.93	0
1	HYP	B	11[A]	1	6,8,9	0.57	0	5,10,12	1.55	1 (20%)
1	HYP	C	11[E]	1	6,8,9	0.62	0	5,10,12	1.77	2 (40%)
1	HYP	A	5[F]	1	6,8,9	0.59	0	5,10,12	1.15	0
1	HYP	C	20[G]	1	6,8,9	0.53	0	5,10,12	0.80	0
1	HYP	B	11[C]	1	6,8,9	0.68	0	5,10,12	1.10	0
1	HYP	C	11[G]	1	6,8,9	0.54	0	5,10,12	1.74	1 (20%)
1	HYP	I	5[F]	1	6,8,9	0.66	0	5,10,12	0.88	0
1	HYP	C	11[A]	1	6,8,9	0.59	0	5,10,12	1.76	2 (40%)
1	HYP	A	26[E]	1	6,8,9	0.63	0	5,10,12	1.58	1 (20%)
1	HYP	C	11[C]	1	6,8,9	0.61	0	5,10,12	1.35	1 (20%)
1	HYP	G	29[B]	1	6,8,9	0.61	0	5,10,12	1.32	1 (20%)
1	HYP	A	2[F]	1	6,8,9	0.61	0	5,10,12	1.60	2 (40%)
1	HYP	A	26[A]	1	6,8,9	0.61	0	5,10,12	1.02	0
1	HYP	H	2[D]	1	6,8,9	0.56	0	5,10,12	1.29	0
1	HYP	D	5[F]	1	6,8,9	0.67	0	5,10,12	1.27	0
1	HYP	F	23[G]	1	6,8,9	0.62	0	5,10,12	1.51	0
1	HYP	G	29[F]	1	6,8,9	0.64	0	5,10,12	1.97	2 (40%)
1	HZP	F	13[F]	1	6,8,9	0.59	0	5,10,12	5.17	3 (60%)
1	HYP	F	23[B]	1	6,8,9	0.62	0	5,10,12	1.40	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	B	26[A]	1	6,8,9	0.73	0	5,10,12	0.86	0
1	HYP	I	8[C]	1	6,8,9	0.64	0	5,10,12	0.93	0
1	HYP	H	29[E]	1	6,8,9	0.66	0	5,10,12	1.58	2 (40%)
1	HYP	I	8[A]	1	6,8,9	0.46	0	5,10,12	1.77	2 (40%)
1	HYP	B	23[B]	1	6,8,9	0.60	0	5,10,12	1.23	0
1	HYP	G	2[G]	1	6,8,9	0.64	0	5,10,12	1.41	1 (20%)
1	HYP	B	26[E]	1	6,8,9	0.74	0	5,10,12	0.85	0
1	HYP	I	29[E]	1	6,8,9	0.75	0	5,10,12	1.65	1 (20%)
1	HYP	G	23[F]	1	6,8,9	0.63	0	5,10,12	1.45	1 (20%)
1	HYP	G	2[C]	1	6,8,9	0.62	0	5,10,12	1.68	1 (20%)
1	HYP	D	5[D]	1	6,8,9	0.58	0	5,10,12	1.16	0
1	HYP	B	29[B]	1	6,8,9	0.52	0	5,10,12	1.93	2 (40%)
1	HYP	G	2[A]	1	6,8,9	0.59	0	5,10,12	1.69	1 (20%)
1	HYP	C	29[D]	1	6,8,9	0.65	0	5,10,12	1.93	2 (40%)
1	HYP	B	29[D]	1	6,8,9	0.71	0	5,10,12	0.88	0
1	HZP	D	16[A]	1	6,8,9	0.58	0	5,10,12	3.97	3 (60%)
1	HYP	I	11[A]	1	6,8,9	0.72	0	5,10,12	1.42	0
1	HYP	B	20[F]	1	6,8,9	0.62	0	5,10,12	1.27	0
1	HYP	D	2[A]	1	6,8,9	0.60	0	5,10,12	1.17	0
1	HYP	B	20[B]	1	6,8,9	0.46	0	5,10,12	2.04	2 (40%)
1	HYP	D	2[B]	1	6,8,9	0.60	0	5,10,12	1.18	0
1	HZP	D	16[B]	1	6,8,9	0.58	0	5,10,12	3.98	3 (60%)
1	HYP	H	11[D]	1	6,8,9	0.70	0	5,10,12	0.78	0
1	HYP	D	11[C]	1	6,8,9	0.69	0	5,10,12	0.91	0
1	HYP	E	5[E]	1	6,8,9	0.57	0	5,10,12	1.45	1 (20%)
1	HYP	C	20[D]	1	6,8,9	0.42	0	5,10,12	2.34	2 (40%)
1	HYP	G	11[A]	1	6,8,9	0.59	0	5,10,12	1.53	1 (20%)
1	HYP	I	5[B]	1	6,8,9	0.70	0	5,10,12	2.22	2 (40%)
1	HYP	G	11[C]	1	6,8,9	0.60	0	5,10,12	1.53	1 (20%)
1	HYP	G	11[E]	1	6,8,9	0.65	0	5,10,12	1.44	1 (20%)
1	HYP	G	11[G]	1	6,8,9	0.65	0	5,10,12	1.42	1 (20%)
1	HYP	F	2[A]	1	6,8,9	0.62	0	5,10,12	1.34	0
1	HZP	B	16[D]	1	6,8,9	0.64	0	5,10,12	2.83	5 (100%)
1	HZP	F	16[C]	1	6,8,9	0.55	0	5,10,12	5.20	3 (60%)
1	HYP	C	20[B]	1	6,8,9	0.43	0	5,10,12	2.34	2 (40%)
1	HYP	A	20[A]	1	6,8,9	0.66	0	5,10,12	1.42	1 (20%)
1	HYP	C	5[F]	1	6,8,9	0.59	0	5,10,12	1.42	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HZP	C	16[E]	1	6,8,9	0.61	0	5,10,12	5.80	3 (60%)
1	HZP	C	16[D]	1	6,8,9	0.63	0	5,10,12	3.01	3 (60%)
1	HYP	E	20[F]	1	6,8,9	0.60	0	5,10,12	1.11	0
1	HZP	H	13[E]	1	6,8,9	0.64	0	5,10,12	5.59	3 (60%)
1	HYP	H	20[F]	1	6,8,9	0.51	0	5,10,12	1.39	0
1	HYP	A	20[E]	1	6,8,9	0.65	0	5,10,12	1.32	1 (20%)
1	HYP	E	20[D]	1	6,8,9	0.64	0	5,10,12	1.92	2 (40%)
1	HYP	H	26[B]	1	6,8,9	0.63	0	5,10,12	1.46	1 (20%)
1	HZP	C	16[B]	1	6,8,9	0.64	0	5,10,12	3.02	3 (60%)
1	HYP	E	20[B]	1	6,8,9	0.67	0	5,10,12	1.65	2 (40%)
1	HYP	E	5[A]	1	6,8,9	0.57	0	5,10,12	1.44	1 (20%)
1	HYP	H	26[D]	1	6,8,9	0.50	0	5,10,12	1.52	1 (20%)
1	HYP	H	5[G]	1	6,8,9	0.70	0	5,10,12	0.73	0
1	HYP	E	8[F]	1	6,8,9	0.40	0	5,10,12	1.39	1 (20%)
1	HYP	C	26[G]	1	6,8,9	0.65	0	5,10,12	2.11	2 (40%)
1	HYP	H	26[F]	1	6,8,9	0.71	0	5,10,12	1.36	0
1	HYP	H	5[E]	1	6,8,9	0.72	0	5,10,12	1.38	1 (20%)
1	HYP	A	20[F]	1	6,8,9	0.64	0	5,10,12	1.34	1 (20%)
1	HYP	C	26[B]	1	6,8,9	0.53	0	5,10,12	0.80	0
1	HYP	E	11[D]	1	6,8,9	0.61	0	5,10,12	0.80	0
1	HYP	B	8[D]	1	6,8,9	0.68	0	5,10,12	0.77	0
1	HYP	E	23[B]	1	6,8,9	0.62	0	5,10,12	1.07	0
1	HYP	E	23[G]	1	6,8,9	0.61	0	5,10,12	1.24	0
1	HZP	C	16[G]	1	6,8,9	0.78	0	5,10,12	7.23	3 (60%)
1	HYP	C	23[D]	1	6,8,9	0.60	0	5,10,12	1.16	0
1	HYP	A	20[D]	1	6,8,9	0.82	0	5,10,12	0.98	0
1	HYP	F	29[F]	1	6,8,9	0.66	0	5,10,12	1.81	1 (20%)
1	HYP	C	23[B]	1	6,8,9	0.60	0	5,10,12	1.16	0
1	HYP	F	29[G]	1	6,8,9	0.61	0	5,10,12	1.65	1 (20%)
1	HYP	B	5[B]	1	6,8,9	0.69	0	5,10,12	0.84	0
1	HYP	F	29[A]	1	6,8,9	0.68	0	5,10,12	1.82	1 (20%)
1	HYP	F	29[B]	1	6,8,9	0.69	0	5,10,12	1.34	1 (20%)
1	HYP	I	5[C]	1	6,8,9	0.68	0	5,10,12	2.23	2 (40%)
1	HYP	F	29[C]	1	6,8,9	0.69	0	5,10,12	1.33	1 (20%)
1	HYP	E	2[G]	1	6,8,9	0.52	0	5,10,12	1.13	0
1	HYP	D	23[E]	1	6,8,9	0.52	0	5,10,12	1.86	2 (40%)
1	HYP	D	23[F]	1	6,8,9	0.54	0	5,10,12	1.85	2 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	I	2[D]	1	6,8,9	0.52	0	5,10,12	1.74	1 (20%)
1	HYP	D	23[G]	1	6,8,9	0.56	0	5,10,12	1.86	2 (40%)
1	HYP	E	2[C]	1	6,8,9	0.66	0	5,10,12	2.05	2 (40%)
1	HZP	E	13[B]	1	6,8,9	0.54	0	5,10,12	5.17	3 (60%)
1	HYP	E	29[C]	1	6,8,9	0.62	0	5,10,12	1.15	0
1	HYP	D	23[A]	1	6,8,9	0.55	0	5,10,12	0.71	0
1	HYP	I	26[D]	1	6,8,9	0.66	0	5,10,12	0.94	0
1	HYP	D	23[B]	1	6,8,9	0.52	0	5,10,12	0.69	0
1	HYP	G	8[D]	1	6,8,9	0.65	0	5,10,12	1.01	0
1	HYP	D	23[C]	1	6,8,9	0.54	0	5,10,12	0.70	0
1	HYP	I	26[F]	1	6,8,9	0.62	0	5,10,12	1.28	0
1	HZP	E	13[F]	1	6,8,9	0.51	0	5,10,12	4.59	3 (60%)
1	HYP	C	8[A]	1	6,8,9	0.60	0	5,10,12	1.12	0
1	HYP	I	23[C]	1	6,8,9	0.43	0	5,10,12	1.52	1 (20%)
1	HYP	C	8[E]	1	6,8,9	0.59	0	5,10,12	1.11	0
1	HYP	I	2[B]	1	6,8,9	0.47	0	5,10,12	1.72	1 (20%)
1	HYP	I	8[B]	1	6,8,9	0.64	0	5,10,12	0.93	0
1	HYP	H	29[A]	1	6,8,9	0.66	0	5,10,12	1.60	2 (40%)
1	HYP	G	23[G]	1	6,8,9	0.62	0	5,10,12	1.45	0
1	HZP	D	16[F]	1	6,8,9	1.19	0	5,10,12	3.39	1 (20%)
1	HYP	E	11[B]	1	6,8,9	0.38	0	5,10,12	1.42	1 (20%)
1	HYP	I	11[B]	1	6,8,9	0.48	0	5,10,12	1.71	2 (40%)
1	HYP	B	29[E]	1	6,8,9	0.52	0	5,10,12	1.88	2 (40%)
1	HYP	G	29[D]	1	6,8,9	0.64	0	5,10,12	1.45	1 (20%)
1	HYP	B	29[G]	1	6,8,9	1.07	0	5,10,12	2.04	2 (40%)
1	HYP	B	20[E]	1	6,8,9	0.45	0	5,10,12	2.06	2 (40%)
1	HZP	C	13[B]	1	6,8,9	0.53	0	5,10,12	5.46	3 (60%)
1	HYP	D	29[A]	1	6,8,9	0.56	0	5,10,12	1.62	1 (20%)
1	HYP	B	20[G]	1	6,8,9	0.62	0	5,10,12	1.29	0
1	HZP	C	13[G]	1	6,8,9	0.60	0	5,10,12	3.64	2 (40%)
1	HZP	I	16[C]	1	6,8,9	0.56	0	5,10,12	5.42	3 (60%)
1	HYP	B	20[A]	1	6,8,9	0.46	0	5,10,12	2.05	2 (40%)
1	HYP	B	20[C]	1	6,8,9	0.58	0	5,10,12	1.75	2 (40%)
1	HZP	A	13[E]	1	6,8,9	0.59	0	5,10,12	4.45	3 (60%)
1	HZP	I	16[G]	1	6,8,9	0.64	0	5,10,12	5.62	3 (60%)
1	HYP	I	2[F]	1	6,8,9	0.60	0	5,10,12	1.66	1 (20%)
1	HZP	A	13[D]	1	6,8,9	0.50	0	5,10,12	4.67	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	F	11[F]	1	6,8,9	0.53	0	5,10,12	2.12	2 (40%)
1	HYP	D	5[C]	1	6,8,9	0.58	0	5,10,12	1.72	1 (20%)
1	HYP	F	11[B]	1	6,8,9	0.67	0	5,10,12	0.93	0
1	HYP	E	29[A]	1	6,8,9	0.65	0	5,10,12	1.37	1 (20%)
1	HYP	E	29[G]	1	6,8,9	0.62	0	5,10,12	1.94	2 (40%)
1	HYP	B	2[D]	1	6,8,9	0.60	0	5,10,12	1.96	1 (20%)
1	HYP	E	29[E]	1	6,8,9	0.65	0	5,10,12	1.39	1 (20%)
1	HYP	G	20[D]	1	6,8,9	0.66	0	5,10,12	1.65	1 (20%)
1	HYP	E	11[G]	1	6,8,9	0.80	0	5,10,12	2.07	2 (40%)
1	HYP	H	13[F]	1	6,8,9	0.67	0	5,10,12	3.84	3 (60%)
1	HYP	C	5[A]	1	6,8,9	0.58	0	5,10,12	1.44	1 (20%)
1	HYP	B	2[A]	1	6,8,9	0.68	0	5,10,12	1.52	1 (20%)
1	HYP	F	20[B]	1	6,8,9	0.46	0	5,10,12	1.54	1 (20%)
1	HYP	F	2[F]	1	6,8,9	0.60	0	5,10,12	1.35	0
1	HYP	G	5[G]	1	6,8,9	0.62	0	5,10,12	1.04	0
1	HYP	F	5[A]	1	6,8,9	0.57	0	5,10,12	1.26	0
1	HYP	F	20[F]	1	6,8,9	0.64	0	5,10,12	1.41	1 (20%)
1	HYP	F	5[E]	1	6,8,9	0.60	0	5,10,12	1.28	0
1	HYP	I	20[D]	1	6,8,9	0.67	0	5,10,12	1.35	1 (20%)
1	HYP	G	26[G]	1	6,8,9	0.71	0	5,10,12	2.15	3 (60%)
1	HYP	G	26[E]	1	6,8,9	0.70	0	5,10,12	2.15	3 (60%)
1	HYP	G	5[D]	1	6,8,9	0.62	0	5,10,12	1.68	1 (20%)
1	HYP	H	8[D]	1	6,8,9	0.73	0	5,10,12	1.36	1 (20%)
1	HYP	D	26[C]	1	6,8,9	0.52	0	5,10,12	1.94	2 (40%)
1	HYP	A	16[C]	1	6,8,9	0.59	0	5,10,12	4.28	3 (60%)
1	HYP	D	26[B]	1	6,8,9	0.54	0	5,10,12	1.94	2 (40%)
1	HYP	D	11[F]	1	6,8,9	0.73	0	5,10,12	1.35	0
1	HYP	A	16[G]	1	6,8,9	0.69	0	5,10,12	6.75	3 (60%)
1	HYP	B	5[E]	1	6,8,9	0.68	0	5,10,12	0.84	0
1	HYP	B	8[G]	1	6,8,9	0.56	0	5,10,12	1.57	1 (20%)
1	HYP	D	5[A]	1	6,8,9	0.60	0	5,10,12	1.72	1 (20%)
1	HYP	B	5[G]	1	6,8,9	0.68	0	5,10,12	1.42	0
1	HYP	H	8[E]	1	6,8,9	0.68	0	5,10,12	0.72	0
1	HYP	C	20[A]	1	6,8,9	0.61	0	5,10,12	1.09	0
1	HYP	B	5[A]	1	6,8,9	0.68	0	5,10,12	0.84	0
1	HYP	B	8[C]	1	6,8,9	0.68	0	5,10,12	0.78	0
1	HYP	B	23[A]	1	6,8,9	0.62	0	5,10,12	1.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	B	5[C]	1	6,8,9	0.65	0	5,10,12	1.68	1 (20%)
1	HZP	H	16[G]	1	6,8,9	0.64	0	5,10,12	5.79	3 (60%)
1	HYP	C	20[E]	1	6,8,9	0.63	0	5,10,12	1.09	0
1	HYP	B	23[D]	1	6,8,9	0.45	0	5,10,12	2.09	2 (40%)
1	HYP	A	2[A]	1	6,8,9	0.58	0	5,10,12	2.34	2 (40%)
1	HYP	E	2[F]	1	6,8,9	0.54	0	5,10,12	1.14	0
1	HYP	G	2[E]	1	6,8,9	0.64	0	5,10,12	1.41	1 (20%)
1	HYP	A	2[C]	1	6,8,9	0.61	0	5,10,12	2.31	2 (40%)
1	HYP	D	5[G]	1	6,8,9	0.67	0	5,10,12	1.27	0
1	HYP	E	2[B]	1	6,8,9	0.66	0	5,10,12	1.59	1 (20%)
1	HYP	I	26[E]	1	6,8,9	0.62	0	5,10,12	1.27	0
1	HZP	B	13[C]	1	6,8,9	0.81	0	5,10,12	4.80	3 (60%)
1	HYP	I	23[F]	1	6,8,9	0.65	0	5,10,12	0.93	0
1	HYP	H	29[D]	1	6,8,9	0.64	0	5,10,12	1.56	1 (20%)
1	HYP	A	23[B]	1	6,8,9	0.67	0	5,10,12	1.21	1 (20%)
1	HYP	F	23[D]	1	6,8,9	0.61	0	5,10,12	1.39	1 (20%)
1	HYP	B	26[C]	1	6,8,9	0.60	0	5,10,12	1.25	0
1	HYP	I	23[B]	1	6,8,9	0.42	0	5,10,12	1.52	1 (20%)
1	HZP	B	13[D]	1	6,8,9	0.79	0	5,10,12	4.79	3 (60%)
1	HYP	D	5[E]	1	6,8,9	0.67	0	5,10,12	1.26	0
1	HYP	B	26[G]	1	6,8,9	0.54	0	5,10,12	2.79	3 (60%)
1	HYP	F	23[A]	1	6,8,9	0.73	0	5,10,12	0.85	0
1	HYP	A	8[B]	1	6,8,9	0.58	0	5,10,12	1.14	0
1	HYP	H	29[F]	1	6,8,9	0.71	0	5,10,12	2.16	3 (60%)
1	HZP	B	13[B]	1	6,8,9	0.70	0	5,10,12	7.41	3 (60%)
1	HZP	D	16[G]	1	6,8,9	1.17	0	5,10,12	3.41	1 (20%)
1	HYP	G	2[B]	1	6,8,9	0.60	0	5,10,12	1.67	1 (20%)
1	HYP	A	8[G]	1	6,8,9	0.52	0	5,10,12	0.82	0
1	HYP	G	23[D]	1	6,8,9	0.69	0	5,10,12	1.86	2 (40%)
1	HYP	A	8[E]	1	6,8,9	0.51	0	5,10,12	0.83	0
1	HZP	D	16[C]	1	6,8,9	0.58	0	5,10,12	3.96	4 (80%)
1	HYP	I	11[E]	1	6,8,9	0.71	0	5,10,12	1.41	0
1	HYP	I	11[C]	1	6,8,9	0.46	0	5,10,12	1.68	2 (40%)
1	HZP	I	13[G]	1	6,8,9	0.57	0	5,10,12	4.63	3 (60%)
1	HYP	I	29[A]	1	6,8,9	0.76	0	5,10,12	1.64	1 (20%)
1	HYP	D	29[B]	1	6,8,9	0.55	0	5,10,12	1.61	1 (20%)
1	HZP	I	13[E]	1	6,8,9	0.46	0	5,10,12	5.02	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	H	11[B]	1	6,8,9	0.80	0	5,10,12	1.13	0
1	HYP	H	11[A]	1	6,8,9	0.80	0	5,10,12	1.12	0
1	HYP	E	5[D]	1	6,8,9	1.06	0	5,10,12	2.05	2 (40%)
1	HYP	H	11[F]	1	6,8,9	0.60	0	5,10,12	2.40	3 (60%)
1	HYP	H	11[E]	1	6,8,9	0.83	0	5,10,12	1.15	0
1	HYP	D	11[E]	1	6,8,9	0.74	0	5,10,12	1.35	0
1	HYP	D	2[G]	1	6,8,9	0.61	0	5,10,12	1.73	1 (20%)
1	HYP	F	5[F]	1	6,8,9	0.57	0	5,10,12	1.25	0
1	HYP	C	5[C]	1	6,8,9	0.60	0	5,10,12	1.06	0
1	HZP	D	13[B]	1	6,8,9	0.65	0	5,10,12	3.83	3 (60%)
1	HZP	D	13[F]	1	6,8,9	0.63	0	5,10,12	4.62	3 (60%)
1	HYP	E	29[D]	1	6,8,9	0.61	0	5,10,12	1.16	0
1	HYP	F	2[C]	1	6,8,9	0.60	0	5,10,12	2.19	2 (40%)
1	HZP	F	16[A]	1	6,8,9	0.56	0	5,10,12	5.56	3 (60%)
1	HYP	G	20[G]	1	6,8,9	0.71	0	5,10,12	0.68	0
1	HZP	B	16[G]	1	6,8,9	0.76	0	5,10,12	7.69	3 (60%)
1	HYP	E	8[G]	1	6,8,9	0.40	0	5,10,12	1.38	1 (20%)
1	HZP	H	13[G]	1	6,8,9	0.66	0	5,10,12	3.83	3 (60%)
1	HYP	G	20[C]	1	6,8,9	0.69	0	5,10,12	1.85	2 (40%)
1	HYP	E	8[E]	1	6,8,9	0.61	0	5,10,12	0.78	0
1	HZP	F	16[D]	1	6,8,9	0.57	0	5,10,12	5.20	3 (60%)
1	HYP	G	26[B]	1	6,8,9	0.64	0	5,10,12	1.42	1 (20%)
1	HZP	B	16[C]	1	6,8,9	0.62	0	5,10,12	2.83	5 (100%)
1	HZP	H	13[B]	1	6,8,9	0.63	0	5,10,12	5.60	3 (60%)
1	HZP	H	13[C]	1	6,8,9	0.58	0	5,10,12	5.08	3 (60%)
1	HZP	C	16[C]	1	6,8,9	0.66	0	5,10,12	3.02	3 (60%)
1	HZP	A	13[G]	1	6,8,9	0.59	0	5,10,12	4.44	3 (60%)
1	HZP	A	13[F]	1	6,8,9	0.60	0	5,10,12	4.44	3 (60%)
1	HYP	B	11[B]	1	6,8,9	0.57	0	5,10,12	1.55	1 (20%)
1	HYP	C	26[D]	1	6,8,9	0.55	0	5,10,12	0.81	0
1	HYP	E	11[F]	1	6,8,9	0.81	0	5,10,12	2.07	2 (40%)
1	HZP	E	16[E]	1	6,8,9	0.57	0	5,10,12	5.64	3 (60%)
1	HYP	C	26[A]	1	6,8,9	0.65	0	5,10,12	2.40	2 (40%)
1	HYP	E	23[E]	1	6,8,9	0.60	0	5,10,12	1.07	0
1	HZP	E	16[A]	1	6,8,9	0.56	0	5,10,12	5.66	3 (60%)
1	HZP	F	13[G]	1	6,8,9	0.69	0	5,10,12	5.86	3 (60%)
1	HZP	F	13[C]	1	6,8,9	0.82	0	5,10,12	6.45	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	I	20[F]	1	6,8,9	0.44	0	5,10,12	1.66	2 (40%)
1	HYP	E	2[E]	1	6,8,9	0.63	0	5,10,12	1.61	1 (20%)
1	HYP	C	11[F]	1	6,8,9	0.59	0	5,10,12	1.76	2 (40%)
1	HYP	D	8[B]	1	6,8,9	0.67	0	5,10,12	1.27	0
1	HYP	E	2[A]	1	6,8,9	0.63	0	5,10,12	1.60	1 (20%)
1	HYP	A	23[E]	1	6,8,9	0.60	0	5,10,12	1.00	0
1	HYP	C	11[B]	1	6,8,9	0.61	0	5,10,12	1.33	1 (20%)
1	HYP	D	8[F]	1	6,8,9	0.67	0	5,10,12	1.00	0
1	HYP	B	11[F]	1	6,8,9	0.61	0	5,10,12	2.26	2 (40%)
1	HYP	A	23[G]	1	6,8,9	0.62	0	5,10,12	0.99	0
1	HYP	I	23[E]	1	6,8,9	0.65	0	5,10,12	0.92	0
1	HYP	A	26[F]	1	6,8,9	0.67	0	5,10,12	1.57	1 (20%)
1	HYP	A	26[B]	1	6,8,9	0.60	0	5,10,12	1.01	0
1	HYP	E	26[A]	1	6,8,9	0.61	0	5,10,12	1.26	0
1	HYP	I	23[A]	1	6,8,9	0.67	0	5,10,12	0.94	0
1	HYP	E	26[B]	1	6,8,9	0.62	0	5,10,12	1.27	0
1	HYP	D	20[F]	1	6,8,9	0.53	0	5,10,12	0.70	0
1	HYP	E	26[C]	1	6,8,9	0.60	0	5,10,12	1.05	0
1	HYP	E	26[D]	1	6,8,9	0.61	0	5,10,12	1.05	0
1	HYP	F	26[B]	1	6,8,9	0.74	0	5,10,12	0.77	0
1	HYP	H	29[C]	1	6,8,9	0.63	0	5,10,12	1.55	1 (20%)
1	HYP	I	2[A]	1	6,8,9	0.59	0	5,10,12	1.65	1 (20%)
1	HYP	G	23[A]	1	6,8,9	0.69	0	5,10,12	0.69	0
1	HYP	D	20[B]	1	6,8,9	0.65	0	5,10,12	1.75	1 (20%)
1	HYP	B	26[D]	1	6,8,9	0.60	0	5,10,12	1.24	0
1	HYP	I	11[D]	1	6,8,9	0.46	0	5,10,12	1.67	2 (40%)
1	HYP	C	2[E]	1	6,8,9	0.62	0	5,10,12	0.99	0
1	HZP	D	16[D]	1	6,8,9	0.66	0	5,10,12	3.83	3 (60%)
1	HYP	E	5[C]	1	6,8,9	1.07	0	5,10,12	2.04	2 (40%)
1	HZP	C	13[E]	1	6,8,9	0.64	0	5,10,12	3.26	3 (60%)
1	HYP	F	26[F]	1	6,8,9	0.59	0	5,10,12	1.88	2 (40%)
1	HZP	I	16[D]	1	6,8,9	0.60	0	5,10,12	5.43	3 (60%)
1	HYP	C	8[C]	1	6,8,9	0.59	0	5,10,12	1.46	1 (20%)
1	HYP	D	26[F]	1	6,8,9	0.56	0	5,10,12	2.11	1 (20%)
1	HYP	I	29[G]	1	6,8,9	0.66	0	5,10,12	1.65	1 (20%)
1	HYP	D	11[B]	1	6,8,9	0.69	0	5,10,12	0.91	0
1	HYP	C	8[B]	1	6,8,9	0.58	0	5,10,12	1.46	1 (20%)
1	HYP	H	23[E]	1	6,8,9	0.49	0	5,10,12	1.54	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	B	2[F]	1	6,8,9	0.69	0	5,10,12	0.80	0
1	HYP	H	23[F]	1	6,8,9	0.63	0	5,10,12	1.42	1 (20%)
1	HYP	H	23[G]	1	6,8,9	0.63	0	5,10,12	1.43	1 (20%)
1	HZP	E	16[D]	1	6,8,9	0.52	0	5,10,12	5.15	3 (60%)
1	HYP	B	2[C]	1	6,8,9	0.58	0	5,10,12	1.95	1 (20%)
1	HYP	F	2[D]	1	6,8,9	0.57	0	5,10,12	2.20	2 (40%)
1	HYP	I	20[C]	1	6,8,9	0.65	0	5,10,12	1.35	1 (20%)
1	HYP	H	20[G]	1	6,8,9	0.50	0	5,10,12	1.41	0
1	HYP	I	20[A]	1	6,8,9	0.41	0	5,10,12	1.62	1 (20%)
1	HYP	E	20[G]	1	6,8,9	0.61	0	5,10,12	1.10	0
1	HYP	H	20[E]	1	6,8,9	0.44	0	5,10,12	1.34	1 (20%)
1	HYP	E	20[E]	1	6,8,9	0.70	0	5,10,12	1.67	2 (40%)
1	HYP	C	8[G]	1	6,8,9	0.60	0	5,10,12	1.78	2 (40%)
1	HYP	E	20[C]	1	6,8,9	0.64	0	5,10,12	1.95	2 (40%)
1	HYP	A	29[D]	1	6,8,9	0.61	0	5,10,12	1.00	0
1	HYP	D	26[D]	1	6,8,9	0.53	0	5,10,12	0.69	0
1	HYP	E	20[A]	1	6,8,9	0.69	0	5,10,12	1.66	3 (60%)
1	HYP	A	29[B]	1	6,8,9	0.80	0	5,10,12	1.59	1 (20%)
1	HYP	D	26[A]	1	6,8,9	0.53	0	5,10,12	1.94	2 (40%)
1	HYP	C	2[D]	1	6,8,9	0.64	0	5,10,12	1.97	2 (40%)
1	HYP	B	8[E]	1	6,8,9	0.69	0	5,10,12	1.43	0
1	HZP	A	16[D]	1	6,8,9	0.54	0	5,10,12	5.22	3 (60%)
1	HYP	B	8[A]	1	6,8,9	0.69	0	5,10,12	1.41	0
1	HZP	G	13[E]	1	6,8,9	0.71	0	5,10,12	5.22	3 (60%)
1	HYP	B	23[C]	1	6,8,9	0.46	0	5,10,12	2.06	2 (40%)
1	HYP	C	23[C]	1	6,8,9	0.58	0	5,10,12	1.16	0
1	HZP	G	13[G]	1	6,8,9	0.71	0	5,10,12	5.21	3 (60%)
1	HYP	C	23[A]	1	6,8,9	0.53	0	5,10,12	0.81	0
1	HZP	G	13[A]	1	6,8,9	0.49	0	5,10,12	5.46	3 (60%)
1	HZP	G	13[C]	1	6,8,9	0.51	0	5,10,12	5.48	3 (60%)
1	HYP	E	2[D]	1	6,8,9	0.66	0	5,10,12	2.05	2 (40%)
1	HZP	F	13[D]	1	6,8,9	0.80	0	5,10,12	6.48	3 (60%)
1	HYP	A	5[D]	1	6,8,9	0.61	0	5,10,12	2.32	2 (40%)
1	HYP	B	11[E]	1	6,8,9	0.57	0	5,10,12	1.55	1 (20%)
1	HYP	A	2[B]	1	6,8,9	0.60	0	5,10,12	2.34	2 (40%)
1	HYP	B	11[G]	1	6,8,9	0.62	0	5,10,12	2.27	2 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HZP	E	13[A]	1	6,8,9	0.53	0	5,10,12	5.18	3 (60%)
1	HYP	A	2[D]	1	6,8,9	0.43	0	5,10,12	1.33	1 (20%)
1	HYP	I	23[D]	1	6,8,9	0.41	0	5,10,12	1.51	1 (20%)
1	HZP	F	13[E]	1	6,8,9	0.54	0	5,10,12	5.17	3 (60%)
1	HYP	F	23[F]	1	6,8,9	0.74	0	5,10,12	0.86	0
1	HZP	E	13[E]	1	6,8,9	0.52	0	5,10,12	5.18	3 (60%)
1	HYP	H	2[G]	1	6,8,9	0.72	0	5,10,12	1.36	1 (20%)
1	HZP	D	13[A]	1	6,8,9	0.65	0	5,10,12	3.83	3 (60%)
1	HYP	F	23[C]	1	6,8,9	0.62	0	5,10,12	1.40	1 (20%)
1	HYP	G	23[B]	1	6,8,9	0.70	0	5,10,12	0.72	0
1	HYP	H	2[C]	1	6,8,9	0.55	0	5,10,12	1.29	0
1	HYP	I	29[F]	1	6,8,9	0.73	0	5,10,12	1.65	1 (20%)
1	HYP	I	8[G]	1	6,8,9	0.74	0	5,10,12	1.67	1 (20%)
1	HYP	G	2[D]	1	6,8,9	0.56	0	5,10,12	1.61	1 (20%)
1	HYP	I	8[E]	1	6,8,9	0.45	0	5,10,12	1.74	2 (40%)
1	HYP	I	29[B]	1	6,8,9	0.51	0	5,10,12	1.19	0
1	HZP	H	16[B]	1	6,8,9	0.63	0	5,10,12	3.62	3 (60%)
1	HZP	B	13[G]	1	6,8,9	0.62	0	5,10,12	5.15	3 (60%)
1	HYP	D	29[D]	1	6,8,9	0.53	0	5,10,12	1.91	2 (40%)
1	HYP	B	29[F]	1	6,8,9	1.07	0	5,10,12	2.04	2 (40%)
1	HYP	E	5[G]	1	6,8,9	0.61	0	5,10,12	0.77	0
1	HYP	B	20[D]	1	6,8,9	0.56	0	5,10,12	1.77	2 (40%)
1	HYP	H	11[C]	1	6,8,9	0.68	0	5,10,12	0.79	0
1	HYP	G	20[E]	1	6,8,9	0.72	0	5,10,12	0.68	0
1	HYP	H	11[G]	1	6,8,9	0.57	0	5,10,12	2.40	3 (60%)
1	HYP	D	11[G]	1	6,8,9	0.72	0	5,10,12	1.35	0
1	HYP	D	2[E]	1	6,8,9	0.60	0	5,10,12	1.74	1 (20%)
1	HYP	D	2[F]	1	6,8,9	0.60	0	5,10,12	1.74	1 (20%)
1	HYP	C	5[B]	1	6,8,9	0.62	0	5,10,12	1.06	0
1	HZP	D	13[C]	1	6,8,9	0.65	0	5,10,12	3.83	3 (60%)
1	HYP	G	11[B]	1	6,8,9	0.59	0	5,10,12	1.54	1 (20%)
1	HYP	A	20[C]	1	6,8,9	0.66	0	5,10,12	1.44	1 (20%)
1	HYP	C	8[F]	1	6,8,9	0.61	0	5,10,12	1.12	0
1	HYP	G	11[D]	1	6,8,9	0.64	0	5,10,12	0.82	0
1	HZP	D	13[G]	1	6,8,9	0.60	0	5,10,12	4.63	3 (60%)
1	HYP	D	29[C]	1	6,8,9	0.57	0	5,10,12	1.62	1 (20%)
1	HYP	G	11[F]	1	6,8,9	0.66	0	5,10,12	1.44	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HZP	H	16[E]	1	6,8,9	0.61	0	5,10,12	3.61	3 (60%)
1	HZP	D	13[E]	1	6,8,9	0.65	0	5,10,12	4.63	3 (60%)
1	HYP	F	20[C]	1	6,8,9	0.46	0	5,10,12	1.54	1 (20%)
1	HZP	B	16[E]	1	6,8,9	0.65	0	5,10,12	4.74	3 (60%)
1	HYP	C	5[D]	1	6,8,9	0.63	0	5,10,12	1.06	0
1	HYP	G	20[A]	1	6,8,9	0.70	0	5,10,12	1.85	2 (40%)
1	HZP	F	16[B]	1	6,8,9	0.56	0	5,10,12	5.20	3 (60%)
1	HYP	F	20[G]	1	6,8,9	0.75	0	5,10,12	0.75	0
1	HZP	B	16[A]	1	6,8,9	0.66	0	5,10,12	4.73	3 (60%)
1	HYP	F	2[E]	1	6,8,9	0.65	0	5,10,12	1.33	0
1	HZP	G	13[D]	1	6,8,9	0.82	0	5,10,12	6.06	3 (60%)
1	HZP	F	16[G]	1	6,8,9	0.56	0	5,10,12	6.67	3 (60%)
1	HZP	C	16[A]	1	6,8,9	0.62	0	5,10,12	5.81	3 (60%)
1	HYP	H	20[D]	1	6,8,9	0.60	0	5,10,12	1.62	1 (20%)
1	HYP	H	20[B]	1	6,8,9	0.43	0	5,10,12	1.35	1 (20%)
1	HYP	C	26[F]	1	6,8,9	0.65	0	5,10,12	2.40	2 (40%)
1	HYP	H	5[F]	1	6,8,9	0.70	0	5,10,12	0.73	0
1	HYP	E	11[A]	1	6,8,9	0.37	0	5,10,12	1.43	1 (20%)
1	HYP	G	5[E]	1	6,8,9	0.60	0	5,10,12	1.05	0
1	HYP	C	26[C]	1	6,8,9	0.52	0	5,10,12	0.80	0
1	HZP	C	16[F]	1	6,8,9	0.62	0	5,10,12	5.80	3 (60%)
1	HYP	E	11[E]	1	6,8,9	0.37	0	5,10,12	1.43	1 (20%)
1	HYP	E	23[C]	1	6,8,9	0.68	0	5,10,12	1.57	1 (20%)
1	HZP	E	16[C]	1	6,8,9	0.52	0	5,10,12	5.16	3 (60%)
1	HYP	A	20[G]	1	6,8,9	0.64	0	5,10,12	1.30	1 (20%)
1	HZP	D	16[E]	1	6,8,9	1.20	0	5,10,12	3.37	1 (20%)
1	HYP	C	23[F]	1	6,8,9	0.52	0	5,10,12	0.79	0
1	HYP	I	29[D]	1	6,8,9	0.50	0	5,10,12	1.19	0
1	HYP	E	23[F]	1	6,8,9	0.61	0	5,10,12	1.24	0
1	HYP	F	29[D]	1	6,8,9	0.69	0	5,10,12	1.34	1 (20%)
1	HZP	H	16[D]	1	6,8,9	0.60	0	5,10,12	5.41	3 (60%)
1	HZP	F	13[A]	1	6,8,9	0.56	0	5,10,12	5.17	3 (60%)
1	HZP	F	16[F]	1	6,8,9	0.57	0	5,10,12	5.56	3 (60%)
1	HYP	D	23[D]	1	6,8,9	0.66	0	5,10,12	1.70	1 (20%)
1	HYP	D	8[C]	1	6,8,9	0.67	0	5,10,12	1.32	0
1	HYP	A	26[D]	1	6,8,9	0.65	0	5,10,12	1.22	0
1	HYP	D	8[A]	1	6,8,9	0.66	0	5,10,12	1.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	G	29[C]	1	6,8,9	0.59	0	5,10,12	1.32	0
1	HYP	D	8[G]	1	6,8,9	0.67	0	5,10,12	0.99	0
1	HYP	H	8[A]	1	6,8,9	0.71	0	5,10,12	0.74	0
1	HYP	I	2[E]	1	6,8,9	0.60	0	5,10,12	1.67	1 (20%)
1	HYP	D	8[E]	1	6,8,9	0.66	0	5,10,12	1.00	0
1	HYP	G	8[F]	1	6,8,9	0.58	0	5,10,12	1.53	1 (20%)
1	HYP	G	29[G]	1	6,8,9	0.64	0	5,10,12	1.97	2 (40%)
1	HYP	D	20[C]	1	6,8,9	0.66	0	5,10,12	1.78	1 (20%)
1	HYP	F	26[D]	1	6,8,9	0.73	0	5,10,12	0.79	0
1	HYP	I	26[B]	1	6,8,9	0.65	0	5,10,12	0.93	0
1	HYP	B	26[B]	1	6,8,9	0.73	0	5,10,12	0.86	0
1	HYP	A	23[F]	1	6,8,9	0.59	0	5,10,12	1.00	0
1	HYP	C	8[D]	1	6,8,9	0.58	0	5,10,12	1.46	1 (20%)
1	HYP	G	23[C]	1	6,8,9	0.68	0	5,10,12	0.69	0
1	HZP	E	16[B]	1	6,8,9	0.57	0	5,10,12	5.68	3 (60%)
1	HZP	H	13[A]	1	6,8,9	0.64	0	5,10,12	5.59	3 (60%)
1	HYP	B	26[F]	1	6,8,9	0.55	0	5,10,12	2.79	3 (60%)
1	HYP	I	8[F]	1	6,8,9	0.47	0	5,10,12	1.76	2 (40%)
1	HYP	I	11[F]	1	6,8,9	0.70	0	5,10,12	1.42	0
1	HYP	B	29[A]	1	6,8,9	0.52	0	5,10,12	1.90	2 (40%)
1	HYP	I	8[D]	1	6,8,9	0.65	0	5,10,12	0.89	0
1	HYP	B	29[C]	1	6,8,9	0.72	0	5,10,12	0.86	0
1	HYP	D	20[A]	1	6,8,9	0.66	0	5,10,12	1.76	1 (20%)
1	HYP	C	29[G]	1	6,8,9	0.62	0	5,10,12	1.53	1 (20%)
1	HYP	D	29[E]	1	6,8,9	0.72	0	5,10,12	2.15	3 (60%)
1	HYP	C	2[G]	1	6,8,9	0.58	0	5,10,12	1.50	1 (20%)
1	HZP	C	13[C]	1	6,8,9	0.55	0	5,10,12	5.44	3 (60%)
1	HYP	C	29[C]	1	6,8,9	0.63	0	5,10,12	1.92	3 (60%)
1	HYP	I	26[G]	1	6,8,9	0.57	0	5,10,12	2.15	2 (40%)
1	HZP	I	16[B]	1	6,8,9	0.56	0	5,10,12	5.42	3 (60%)
1	HZP	C	13[F]	1	6,8,9	0.63	0	5,10,12	3.26	3 (60%)
1	HZP	I	16[F]	1	6,8,9	0.58	0	5,10,12	4.65	3 (60%)
1	HYP	D	20[G]	1	6,8,9	0.53	0	5,10,12	0.71	0
1	HYP	G	2[F]	1	6,8,9	0.64	0	5,10,12	1.40	1 (20%)
1	HYP	D	11[D]	1	6,8,9	0.66	0	5,10,12	1.32	0
1	HYP	F	11[D]	1	6,8,9	0.67	0	5,10,12	0.94	0
1	HYP	H	5[D]	1	6,8,9	0.88	0	5,10,12	1.76	2 (40%)
1	HYP	H	8[G]	1	6,8,9	0.77	0	5,10,12	1.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	H	5[C]	1	6,8,9	0.87	0	5,10,12	1.76	2 (40%)
1	HYP	D	20[E]	1	6,8,9	0.54	0	5,10,12	0.70	0
1	HYP	B	2[E]	1	6,8,9	0.71	0	5,10,12	1.52	1 (20%)
1	HYP	A	11[G]	1	6,8,9	0.47	0	5,10,12	1.33	1 (20%)
1	HYP	F	2[B]	1	6,8,9	0.59	0	5,10,12	2.19	2 (40%)
1	HYP	A	11[E]	1	6,8,9	0.48	0	5,10,12	1.33	1 (20%)
1	HYP	A	11[C]	1	6,8,9	0.51	0	5,10,12	0.81	0
1	HYP	A	11[A]	1	6,8,9	0.51	0	5,10,12	0.80	0
1	HYP	C	5[E]	1	6,8,9	0.58	0	5,10,12	1.43	1 (20%)
1	HYP	I	20[B]	1	6,8,9	0.66	0	5,10,12	1.37	1 (20%)
1	HYP	H	5[A]	1	6,8,9	0.72	0	5,10,12	1.38	1 (20%)
1	HYP	C	5[G]	1	6,8,9	0.62	0	5,10,12	1.12	0
1	HYP	H	26[A]	1	6,8,9	0.63	0	5,10,12	1.49	1 (20%)
1	HYP	G	26[C]	1	6,8,9	0.63	0	5,10,12	1.42	1 (20%)
1	HYP	H	26[C]	1	6,8,9	0.51	0	5,10,12	1.48	1 (20%)
1	HYP	F	5[D]	1	6,8,9	0.61	0	5,10,12	1.48	1 (20%)
1	HYP	G	26[A]	1	6,8,9	0.63	0	5,10,12	1.42	1 (20%)
1	HYP	H	26[E]	1	6,8,9	0.63	0	5,10,12	1.44	1 (20%)
1	HYP	H	26[G]	1	6,8,9	0.71	0	5,10,12	1.35	0
1	HYP	A	26[G]	1	6,8,9	0.67	0	5,10,12	1.56	1 (20%)
1	HZP	E	16[G]	1	6,8,9	0.47	0	5,10,12	5.89	3 (60%)
1	HYP	D	26[G]	1	6,8,9	0.57	0	5,10,12	2.11	1 (20%)
1	HYP	G	5[A]	1	6,8,9	0.56	0	5,10,12	1.75	2 (40%)
1	HZP	A	16[B]	1	6,8,9	0.60	0	5,10,12	4.25	3 (60%)
1	HYP	G	5[C]	1	6,8,9	0.55	0	5,10,12	1.75	2 (40%)
1	HZP	A	16[F]	1	6,8,9	0.67	0	5,10,12	6.73	3 (60%)
1	HZP	H	13[D]	1	6,8,9	0.57	0	5,10,12	5.10	3 (60%)
1	HYP	I	29[C]	1	6,8,9	0.50	0	5,10,12	1.18	0
1	HZP	H	16[C]	1	6,8,9	0.61	0	5,10,12	5.42	3 (60%)
1	HZP	H	16[A]	1	6,8,9	0.61	0	5,10,12	3.59	3 (60%)
1	HZP	G	13[F]	1	6,8,9	0.72	0	5,10,12	5.23	3 (60%)
1	HZP	H	16[F]	1	6,8,9	0.66	0	5,10,12	5.77	3 (60%)
1	HYP	C	20[F]	1	6,8,9	0.59	0	5,10,12	1.10	0
1	HZP	G	13[B]	1	6,8,9	0.48	0	5,10,12	5.46	3 (60%)
1	HZP	E	13[C]	1	6,8,9	0.46	0	5,10,12	6.69	3 (60%)
1	HYP	I	5[D]	1	6,8,9	0.66	0	5,10,12	2.22	2 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	A	23[D]	1	6,8,9	0.65	0	5,10,12	1.47	1 (20%)
1	HYP	A	2[E]	1	6,8,9	0.60	0	5,10,12	1.62	2 (40%)
1	HYP	G	8[E]	1	6,8,9	0.57	0	5,10,12	1.53	1 (20%)
1	HYP	B	5[D]	1	6,8,9	1.02	0	5,10,12	1.46	0
1	HYP	A	2[G]	1	6,8,9	0.59	0	5,10,12	1.64	2 (40%)
1	HZP	E	13[G]	1	6,8,9	0.50	0	5,10,12	4.57	3 (60%)
1	HYP	G	8[G]	1	6,8,9	0.57	0	5,10,12	1.53	1 (20%)
1	HYP	H	2[E]	1	6,8,9	0.66	0	5,10,12	1.86	2 (40%)
1	HYP	G	8[A]	1	6,8,9	0.61	0	5,10,12	1.00	0
1	HYP	A	26[C]	1	6,8,9	0.60	0	5,10,12	1.00	0
1	HYP	H	2[F]	1	6,8,9	0.71	0	5,10,12	1.36	1 (20%)
1	HYP	I	26[A]	1	6,8,9	0.60	0	5,10,12	1.26	0
1	HYP	F	23[E]	1	6,8,9	0.73	0	5,10,12	0.83	0
1	HYP	G	8[C]	1	6,8,9	0.62	0	5,10,12	1.01	0
1	HYP	I	26[C]	1	6,8,9	0.66	0	5,10,12	0.93	0
1	HYP	H	2[A]	1	6,8,9	0.66	0	5,10,12	1.86	2 (40%)
1	HYP	H	29[B]	1	6,8,9	0.65	0	5,10,12	1.58	2 (40%)
1	HYP	H	2[B]	1	6,8,9	0.66	0	5,10,12	1.86	2 (40%)
1	HYP	A	8[C]	1	6,8,9	0.62	0	5,10,12	1.15	0
1	HZP	B	13[A]	1	6,8,9	0.70	0	5,10,12	7.42	3 (60%)
1	HYP	B	5[F]	1	6,8,9	0.68	0	5,10,12	1.41	0
1	HYP	A	8[A]	1	6,8,9	0.62	0	5,10,12	1.16	0
1	HZP	B	13[E]	1	6,8,9	0.71	0	5,10,12	7.40	3 (60%)
1	HYP	I	11[G]	1	6,8,9	0.68	0	5,10,12	2.37	2 (40%)
1	HZP	G	16[B]	1	6,8,9	0.36	0	5,10,12	5.09	3 (60%)
1	HYP	A	8[F]	1	6,8,9	0.50	0	5,10,12	0.82	0
1	HYP	D	29[F]	1	6,8,9	0.71	0	5,10,12	2.16	3 (60%)
1	HYP	F	29[E]	1	6,8,9	0.69	0	5,10,12	1.81	1 (20%)
1	HZP	G	16[D]	1	6,8,9	0.47	0	5,10,12	5.42	3 (60%)
1	HYP	A	8[D]	1	6,8,9	0.60	0	5,10,12	1.70	1 (20%)
1	HYP	C	29[F]	1	6,8,9	0.62	0	5,10,12	2.08	1 (20%)
1	HZP	G	16[F]	1	6,8,9	0.56	0	5,10,12	5.73	3 (60%)
1	HZP	B	13[F]	1	6,8,9	0.63	0	5,10,12	5.14	3 (60%)
1	HZP	I	13[D]	1	6,8,9	0.71	0	5,10,12	5.94	3 (60%)
1	HZP	I	13[C]	1	6,8,9	0.73	0	5,10,12	5.91	3 (60%)
1	HYP	C	29[B]	1	6,8,9	0.63	0	5,10,12	1.92	2 (40%)
1	HZP	I	13[B]	1	6,8,9	0.70	0	5,10,12	5.92	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HZP	I	13[A]	1	6,8,9	0.47	0	5,10,12	5.02	3 (60%)
1	HYP	D	2[C]	1	6,8,9	0.61	0	5,10,12	1.16	0
1	HYP	B	23[E]	1	6,8,9	0.64	0	5,10,12	1.27	0
1	HYP	D	2[D]	1	6,8,9	0.65	0	5,10,12	1.55	1 (20%)
1	HYP	F	8[B]	1	6,8,9	0.60	0	5,10,12	0.92	0
1	HYP	I	23[G]	1	6,8,9	0.56	0	5,10,12	1.04	0
1	HYP	F	8[D]	1	6,8,9	0.59	0	5,10,12	0.91	0
1	HYP	D	11[A]	1	6,8,9	0.69	0	5,10,12	0.91	0
1	HZP	I	13[F]	1	6,8,9	0.46	0	5,10,12	5.03	3 (60%)
1	HYP	D	5[B]	1	6,8,9	0.60	0	5,10,12	1.71	1 (20%)
1	HYP	E	5[F]	1	6,8,9	0.61	0	5,10,12	0.77	0
1	HYP	E	5[B]	1	6,8,9	0.54	0	5,10,12	1.44	1 (20%)
1	HYP	E	29[F]	1	6,8,9	0.63	0	5,10,12	1.96	2 (40%)
1	HYP	F	20[A]	1	6,8,9	0.62	0	5,10,12	1.41	1 (20%)
1	HZP	D	13[D]	1	6,8,9	0.64	0	5,10,12	5.55	4 (80%)
1	HYP	A	20[B]	1	6,8,9	0.65	0	5,10,12	1.44	1 (20%)
1	HYP	F	20[E]	1	6,8,9	0.60	0	5,10,12	1.41	1 (20%)
1	HYP	F	2[G]	1	6,8,9	0.57	0	5,10,12	1.22	0
1	HZP	B	16[F]	1	6,8,9	0.76	0	5,10,12	7.70	3 (60%)
1	HZP	F	16[E]	1	6,8,9	0.53	0	5,10,12	5.58	3 (60%)
1	HYP	H	5[B]	1	6,8,9	0.73	0	5,10,12	1.39	1 (20%)
1	HYP	E	8[D]	1	6,8,9	0.54	0	5,10,12	1.17	0
1	HYP	E	8[C]	1	6,8,9	0.55	0	5,10,12	1.16	0
1	HZP	B	16[B]	1	6,8,9	0.68	0	5,10,12	4.71	3 (60%)
1	HYP	E	8[B]	1	6,8,9	0.60	0	5,10,12	0.77	0
1	HYP	E	8[A]	1	6,8,9	0.58	0	5,10,12	0.77	0
1	HYP	G	26[F]	1	6,8,9	0.56	0	5,10,12	1.22	0
1	HYP	G	26[D]	1	6,8,9	0.70	0	5,10,12	0.70	0
1	HYP	E	11[C]	1	6,8,9	0.58	0	5,10,12	0.81	0
1	HYP	C	26[E]	1	6,8,9	0.65	0	5,10,12	2.38	2 (40%)
1	HZP	A	13[C]	1	6,8,9	0.60	0	5,10,12	5.60	3 (60%)
1	HZP	A	13[B]	1	6,8,9	0.62	0	5,10,12	5.61	3 (60%)
1	HYP	E	23[A]	1	6,8,9	0.60	0	5,10,12	1.06	0
1	HZP	A	13[A]	1	6,8,9	0.59	0	5,10,12	5.58	3 (60%)
1	HYP	B	8[F]	1	6,8,9	0.56	0	5,10,12	1.56	1 (20%)
1	HYP	E	23[D]	1	6,8,9	0.68	0	5,10,12	1.54	0
1	HYP	I	5[G]	1	6,8,9	0.47	0	5,10,12	1.74	2 (40%)
1	HYP	B	8[B]	1	6,8,9	0.69	0	5,10,12	1.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	G	29[A]	1	6,8,9	0.61	0	5,10,12	1.32	0
1	HYP	A	5[C]	1	6,8,9	0.65	0	5,10,12	1.28	1 (20%)
1	HYP	C	11[D]	1	6,8,9	0.61	0	5,10,12	1.35	1 (20%)
1	HYP	A	5[A]	1	6,8,9	0.64	0	5,10,12	1.28	1 (20%)
1	HYP	A	5[G]	1	6,8,9	0.58	0	5,10,12	1.14	0
1	HYP	I	5[A]	1	6,8,9	0.66	0	5,10,12	0.87	0
1	HYP	A	5[E]	1	6,8,9	0.59	0	5,10,12	1.15	0
1	HYP	B	11[D]	1	6,8,9	0.68	0	5,10,12	1.09	0
1	HYP	I	5[E]	1	6,8,9	0.65	0	5,10,12	0.88	0
1	HYP	C	2[C]	1	6,8,9	0.65	0	5,10,12	1.98	2 (40%)
1	HYP	D	8[D]	1	6,8,9	0.60	0	5,10,12	1.62	1 (20%)
1	HYP	I	2[C]	1	6,8,9	0.52	0	5,10,12	1.74	1 (20%)
1	HYP	A	23[A]	1	6,8,9	0.66	0	5,10,12	1.23	0
1	HYP	A	23[C]	1	6,8,9	0.66	0	5,10,12	1.22	0
1	HYP	F	5[G]	1	6,8,9	0.64	0	5,10,12	0.92	0
1	HZP	E	13[D]	1	6,8,9	0.47	0	5,10,12	6.69	3 (60%)
1	HYP	F	26[E]	1	6,8,9	0.59	0	5,10,12	1.83	1 (20%)
1	HYP	A	29[F]	1	6,8,9	0.65	0	5,10,12	1.31	0
1	HYP	D	20[D]	1	6,8,9	0.45	0	5,10,12	2.32	2 (40%)
1	HYP	E	26[E]	1	6,8,9	0.60	0	5,10,12	1.26	0
1	HYP	F	26[A]	1	6,8,9	0.59	0	5,10,12	1.85	2 (40%)
1	HYP	E	26[G]	1	6,8,9	0.47	0	5,10,12	1.18	0
1	HYP	C	2[A]	1	6,8,9	0.63	0	5,10,12	0.99	0
1	HYP	G	29[E]	1	6,8,9	0.64	0	5,10,12	1.96	2 (40%)
1	HYP	G	23[E]	1	6,8,9	0.63	0	5,10,12	1.45	1 (20%)
1	HZP	G	16[A]	1	6,8,9	0.38	0	5,10,12	5.08	3 (60%)
1	HYP	C	29[E]	1	6,8,9	0.61	0	5,10,12	2.07	1 (20%)
1	HZP	G	16[C]	1	6,8,9	0.38	0	5,10,12	5.06	3 (60%)
1	HYP	D	29[G]	1	6,8,9	0.70	0	5,10,12	2.16	3 (60%)
1	HZP	G	16[E]	1	6,8,9	0.57	0	5,10,12	5.71	3 (60%)
1	HZP	C	13[A]	1	6,8,9	0.63	0	5,10,12	3.26	3 (60%)
1	HYP	C	29[A]	1	6,8,9	0.61	0	5,10,12	2.10	1 (20%)
1	HZP	G	16[G]	1	6,8,9	0.59	0	5,10,12	5.70	3 (60%)
1	HYP	F	26[G]	1	6,8,9	0.50	0	5,10,12	2.38	1 (20%)
1	HZP	C	13[D]	1	6,8,9	0.53	0	5,10,12	5.45	3 (60%)
1	HYP	I	2[G]	1	6,8,9	0.65	0	5,10,12	0.91	0
1	HZP	I	16[A]	1	6,8,9	0.56	0	5,10,12	4.63	3 (60%)
1	HYP	F	8[A]	1	6,8,9	0.64	0	5,10,12	0.95	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HZP	I	16[E]	1	6,8,9	0.56	0	5,10,12	4.64	3 (60%)
1	HZP	E	16[F]	1	6,8,9	0.47	0	5,10,12	5.88	3 (60%)
1	HYP	F	11[E]	1	6,8,9	0.53	0	5,10,12	2.09	2 (40%)
1	HYP	F	8[C]	1	6,8,9	0.61	0	5,10,12	0.93	0
1	HYP	F	11[G]	1	6,8,9	0.60	0	5,10,12	2.14	2 (40%)
1	HYP	F	8[E]	1	6,8,9	0.65	0	5,10,12	0.95	0
1	HYP	H	23[A]	1	6,8,9	0.50	0	5,10,12	1.54	1 (20%)
1	HYP	F	11[A]	1	6,8,9	0.53	0	5,10,12	2.11	2 (40%)
1	HYP	F	8[G]	1	6,8,9	0.51	0	5,10,12	2.19	2 (40%)
1	HYP	H	23[B]	1	6,8,9	0.52	0	5,10,12	1.52	1 (20%)
1	HYP	H	29[G]	1	6,8,9	0.72	0	5,10,12	2.15	3 (60%)
1	HYP	H	23[C]	1	6,8,9	0.44	0	5,10,12	1.36	1 (20%)
1	HYP	F	11[C]	1	6,8,9	0.67	0	5,10,12	0.92	0
1	HYP	H	23[D]	1	6,8,9	0.44	0	5,10,12	1.36	1 (20%)
1	HYP	B	2[G]	1	6,8,9	0.68	0	5,10,12	0.80	0
1	HYP	A	11[F]	1	6,8,9	0.49	0	5,10,12	1.35	1 (20%)
1	HYP	B	2[B]	1	6,8,9	0.67	0	5,10,12	1.52	1 (20%)
1	HYP	A	11[D]	1	6,8,9	0.57	0	5,10,12	1.43	1 (20%)
1	HYP	F	26[C]	1	6,8,9	0.75	0	5,10,12	0.76	0
1	HYP	F	8[F]	1	6,8,9	0.64	0	5,10,12	0.95	0
1	HYP	A	11[B]	1	6,8,9	0.50	0	5,10,12	0.81	0
1	HYP	G	8[B]	1	6,8,9	0.63	0	5,10,12	1.01	0
1	HYP	G	20[F]	1	6,8,9	0.73	0	5,10,12	0.69	0
1	HYP	F	20[D]	1	6,8,9	0.47	0	5,10,12	1.53	1 (20%)
1	HYP	G	20[B]	1	6,8,9	0.72	0	5,10,12	1.86	2 (40%)
1	HYP	H	8[C]	1	6,8,9	0.73	0	5,10,12	1.37	1 (20%)
1	HYP	F	5[C]	1	6,8,9	0.59	0	5,10,12	1.47	1 (20%)
1	HYP	F	5[B]	1	6,8,9	0.60	0	5,10,12	1.49	1 (20%)
1	HYP	I	20[G]	1	6,8,9	0.66	0	5,10,12	0.99	0
1	HYP	A	29[G]	1	6,8,9	0.64	0	5,10,12	1.27	0
1	HYP	E	26[F]	1	6,8,9	0.47	0	5,10,12	1.18	0
1	HYP	C	2[B]	1	6,8,9	0.67	0	5,10,12	1.98	2 (40%)
1	HYP	H	20[C]	1	6,8,9	0.59	0	5,10,12	1.63	1 (20%)
1	HYP	I	20[E]	1	6,8,9	0.42	0	5,10,12	1.65	2 (40%)
1	HYP	A	29[E]	1	6,8,9	0.62	0	5,10,12	1.30	0
1	HYP	D	26[E]	1	6,8,9	0.57	0	5,10,12	2.11	1 (20%)
1	HYP	H	20[A]	1	6,8,9	0.44	0	5,10,12	1.34	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HYP	A	29[C]	1	6,8,9	0.80	0	5,10,12	1.59	1 (20%)
1	HYP	C	2[F]	1	6,8,9	0.63	0	5,10,12	0.99	0
1	HYP	H	8[F]	1	6,8,9	0.78	0	5,10,12	1.19	0
1	HYP	A	29[A]	1	6,8,9	0.80	0	5,10,12	1.59	1 (20%)
1	HYP	G	5[F]	1	6,8,9	0.58	0	5,10,12	1.05	0
1	HYP	E	29[B]	1	6,8,9	0.65	0	5,10,12	1.37	1 (20%)
1	HYP	H	8[B]	1	6,8,9	0.71	0	5,10,12	0.74	0
1	HZP	A	16[A]	1	6,8,9	0.58	0	5,10,12	4.27	3 (60%)

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
1	HYP	G	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[F]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	F	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	16[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	13[E]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	H	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[D]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	D	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	13[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[F]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	G	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[D]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	D	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	13[B]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HZP	H	13[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	16[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[C]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HZP	C	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	2[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[D]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	B	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	11[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[E]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	F	20[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	16[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	13[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[G]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	D	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[A]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	C	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	5[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	5[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	16[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	29[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	H	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	20[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	13[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	2[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[B]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	H	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	11[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	29[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	13[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[D]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[B]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	23[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	2[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	23[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	11[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	13[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	D	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	2[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[F]	1	-	0/0/11/13	0/1/1/1
1	HZP	F	16[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[D]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	E	8[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	B	16[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	8[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	26[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	26[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[C]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	A	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	5[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	8[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	26[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	23[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[A]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	C	29[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	29[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	29[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	G	16[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	C	13[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	2[G]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[A]	1	-	0/0/11/13	0/1/1/1
1	HZP	I	16[E]	1	-	0/0/11/13	0/1/1/1
1	HZP	E	16[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	29[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	11[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	23[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	B	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	26[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	11[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	20[D]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	20[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	F	5[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[G]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[G]	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	E	26[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	I	20[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	D	26[E]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	20[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[C]	1	-	0/0/11/13	0/1/1/1
1	HYP	C	2[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	29[A]	1	-	0/0/11/13	0/1/1/1
1	HYP	G	5[F]	1	-	0/0/11/13	0/1/1/1
1	HYP	E	29[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	H	8[B]	1	-	0/0/11/13	0/1/1/1
1	HYP	A	16[A]	1	-	0/0/11/13	0/1/1/1

There are no bond length outliers.

The worst 5 of 788 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	13[B]	HZP	OD1-CG-CB	-11.41	81.81	110.03
1	B	13[A]	HZP	OD1-CG-CB	-11.40	81.85	110.03
1	B	13[E]	HZP	OD1-CG-CB	-11.38	81.88	110.03
1	B	16[F]	HZP	OD1-CG-CD	-10.92	86.47	110.35
1	B	16[G]	HZP	OD1-CG-CD	-10.92	86.47	110.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

158 monomers are involved in 281 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	16[E]	HZP	1	0
1	F	13[B]	HZP	1	0
1	B	11[C]	HYP	1	0
1	C	11[G]	HYP	2	0
1	I	5[F]	HYP	1	0
1	F	23[G]	HYP	1	0
1	H	29[E]	HYP	5	0
1	I	29[E]	HYP	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	2[C]	HYP	2	0
1	D	5[D]	HYP	4	0
1	G	2[A]	HYP	12	0
1	B	29[D]	HYP	1	0
1	D	16[A]	HZP	1	0
1	D	2[A]	HYP	1	0
1	D	2[B]	HYP	1	0
1	D	16[B]	HZP	1	0
1	G	11[E]	HYP	1	0
1	G	11[G]	HYP	1	0
1	B	16[D]	HZP	1	0
1	F	16[C]	HZP	1	0
1	C	16[D]	HZP	1	0
1	H	13[E]	HZP	2	0
1	H	26[B]	HYP	1	0
1	H	5[G]	HYP	1	0
1	H	26[F]	HYP	1	0
1	H	5[E]	HYP	1	0
1	E	11[D]	HYP	1	0
1	F	29[F]	HYP	3	0
1	I	2[D]	HYP	3	0
1	E	2[C]	HYP	2	0
1	E	13[F]	HZP	1	0
1	I	2[B]	HYP	3	0
1	H	29[A]	HYP	5	0
1	D	16[F]	HZP	2	0
1	E	11[B]	HYP	1	0
1	B	29[G]	HYP	6	0
1	B	20[G]	HYP	1	0
1	A	13[D]	HZP	1	0
1	E	29[A]	HYP	17	0
1	E	29[E]	HYP	1	0
1	E	11[G]	HYP	2	0
1	B	2[A]	HYP	1	0
1	F	5[A]	HYP	1	0
1	F	20[F]	HYP	1	0
1	F	5[E]	HYP	1	0
1	G	5[D]	HYP	2	0
1	D	11[F]	HYP	1	0
1	A	16[G]	HZP	2	0
1	D	5[A]	HYP	1	0
1	B	5[G]	HYP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	H	29[D]	HYP	1	0
1	B	26[G]	HYP	1	0
1	D	16[G]	HZP	2	0
1	G	2[B]	HYP	12	0
1	G	23[D]	HYP	1	0
1	D	16[C]	HZP	1	0
1	I	29[A]	HYP	1	0
1	D	11[E]	HYP	1	0
1	F	5[F]	HYP	1	0
1	D	13[F]	HZP	1	0
1	E	8[G]	HYP	4	0
1	G	20[C]	HYP	1	0
1	E	8[E]	HYP	1	0
1	H	13[B]	HZP	1	0
1	A	13[G]	HZP	2	0
1	E	11[F]	HYP	2	0
1	F	13[C]	HZP	2	0
1	D	20[F]	HYP	1	0
1	H	29[C]	HYP	1	0
1	I	11[D]	HYP	1	0
1	C	13[E]	HZP	1	0
1	H	23[G]	HYP	4	0
1	H	20[G]	HYP	1	0
1	C	2[D]	HYP	1	0
1	B	8[E]	HYP	1	0
1	B	8[A]	HYP	1	0
1	G	13[G]	HZP	1	0
1	E	2[D]	HYP	2	0
1	F	13[D]	HZP	2	0
1	A	5[D]	HYP	1	0
1	D	13[A]	HZP	1	0
1	I	29[F]	HYP	4	0
1	G	2[D]	HYP	6	0
1	I	29[B]	HYP	1	0
1	B	13[G]	HZP	1	0
1	E	5[G]	HYP	1	0
1	D	11[G]	HYP	1	0
1	D	2[E]	HYP	1	0
1	D	13[G]	HZP	1	0
1	G	11[F]	HYP	1	0
1	B	16[E]	HZP	2	0
1	C	5[D]	HYP	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	16[A]	HZP	1	0
1	G	13[D]	HZP	1	0
1	F	16[G]	HZP	1	0
1	H	20[D]	HYP	1	0
1	D	16[E]	HZP	2	0
1	F	13[A]	HZP	1	0
1	C	8[D]	HYP	5	0
1	H	13[A]	HZP	2	0
1	B	26[F]	HYP	1	0
1	B	29[C]	HYP	1	0
1	C	29[C]	HYP	4	0
1	C	13[F]	HZP	1	0
1	D	20[G]	HYP	1	0
1	H	5[D]	HYP	7	0
1	H	5[C]	HYP	4	0
1	B	2[E]	HYP	1	0
1	H	5[A]	HYP	1	0
1	A	16[F]	HZP	1	0
1	I	29[C]	HYP	1	0
1	E	13[G]	HZP	1	0
1	H	2[F]	HYP	1	0
1	I	26[A]	HYP	4	0
1	B	5[F]	HYP	1	0
1	I	11[G]	HYP	1	0
1	D	29[F]	HYP	0	1
1	F	29[E]	HYP	2	0
1	G	16[D]	HZP	2	0
1	C	29[F]	HYP	2	0
1	G	16[F]	HZP	1	0
1	B	13[F]	HZP	1	0
1	I	13[D]	HZP	2	0
1	I	13[C]	HZP	2	0
1	C	29[B]	HYP	4	0
1	I	13[B]	HZP	1	0
1	D	2[C]	HYP	1	0
1	D	2[D]	HYP	5	0
1	I	23[G]	HYP	1	0
1	D	5[B]	HYP	1	0
1	E	5[F]	HYP	1	0
1	F	20[E]	HYP	1	0
1	F	2[G]	HYP	1	0
1	E	8[B]	HYP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	8[A]	HYP	1	0
1	E	11[C]	HYP	1	0
1	B	8[B]	HYP	1	0
1	C	11[D]	HYP	1	0
1	I	5[A]	HYP	1	0
1	B	11[D]	HYP	1	0
1	I	5[E]	HYP	1	0
1	C	2[C]	HYP	5	0
1	I	2[C]	HYP	3	0
1	A	29[F]	HYP	3	0
1	E	26[G]	HYP	4	0
1	C	29[E]	HYP	2	0
1	D	29[G]	HYP	0	1
1	G	16[E]	HZP	1	0
1	G	16[G]	HZP	1	0
1	I	2[G]	HYP	1	0
1	F	11[A]	HYP	1	0
1	A	11[B]	HYP	1	0
1	F	5[C]	HYP	1	0
1	F	5[B]	HYP	1	0
1	A	29[G]	HYP	3	0
1	E	26[F]	HYP	1	0
1	C	2[B]	HYP	5	0
1	H	20[C]	HYP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	20/30 (66%)	0.20	1 (5%) 28 32	4, 5, 15, 16	0
1	B	20/30 (66%)	0.13	0 100 100	3, 5, 14, 15	0
1	C	20/30 (66%)	0.10	0 100 100	3, 5, 16, 17	0
1	D	20/30 (66%)	0.20	2 (10%) 7 9	3, 5, 15, 16	0
1	E	20/30 (66%)	0.18	1 (5%) 28 32	4, 5, 15, 17	0
1	F	20/30 (66%)	0.12	1 (5%) 28 32	4, 5, 16, 19	0
1	G	20/30 (66%)	0.44	3 (15%) 2 2	4, 5, 16, 16	0
1	H	20/30 (66%)	0.14	0 100 100	3, 5, 15, 16	0
1	I	20/30 (66%)	0.07	0 100 100	3, 5, 17, 18	0
All	All	180/270 (66%)	0.18	8 (4%) 34 39	3, 5, 16, 19	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	1[A]	PRO	3.3
1	E	1[A]	PRO	2.6
1	F	28[A]	PRO	2.5
1	G	4[A]	PRO	2.4
1	A	1[A]	PRO	2.3

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	D	29[A]	8/9	0.88	0.18	14,15,16,17	8
1	HYP	D	29[B]	8/9	0.88	0.18	14,15,16,17	8
1	HYP	D	29[D]	8/9	0.88	0.18	5,6,7,10	8
1	HYP	D	29[G]	8/9	0.88	0.18	20,21,22,23	8
1	HYP	D	29[C]	8/9	0.88	0.18	14,15,16,17	8
1	HYP	D	29[F]	8/9	0.88	0.18	20,21,22,23	8
1	HYP	D	29[E]	8/9	0.88	0.18	20,21,22,23	8
1	HYP	G	2[D]	8/9	0.90	0.22	14,15,16,17	8
1	HYP	G	2[A]	8/9	0.90	0.22	21,22,23,24	8
1	HYP	G	2[G]	8/9	0.90	0.22	8,9,11,12	8
1	HYP	G	2[E]	8/9	0.90	0.22	8,9,11,12	8
1	HYP	G	2[B]	8/9	0.90	0.22	21,22,23,24	8
1	HYP	G	2[C]	8/9	0.90	0.22	21,22,23,24	8
1	HYP	G	2[F]	8/9	0.90	0.22	8,9,11,12	8
1	HYP	E	29[E]	8/9	0.91	0.16	20,21,22,22	8
1	HYP	E	29[C]	8/9	0.91	0.16	7,8,9,10	8
1	HYP	C	29[D]	8/9	0.91	0.17	11,12,14,16	8
1	HYP	E	29[A]	8/9	0.91	0.16	20,21,22,22	8
1	HYP	C	29[G]	8/9	0.91	0.17	12,14,14,16	8
1	HYP	E	29[D]	8/9	0.91	0.16	7,8,9,10	8
1	HYP	C	29[C]	8/9	0.91	0.17	11,12,14,16	8
1	HYP	E	29[G]	8/9	0.91	0.16	15,16,17,18	8
1	HYP	C	29[F]	8/9	0.91	0.17	19,20,20,20	8
1	HYP	C	29[B]	8/9	0.91	0.17	11,12,14,16	8
1	HYP	E	29[F]	8/9	0.91	0.16	15,16,17,18	8
1	HYP	C	29[E]	8/9	0.91	0.17	19,20,20,20	8
1	HYP	C	29[A]	8/9	0.91	0.17	19,20,20,20	8
1	HYP	E	29[B]	8/9	0.91	0.16	20,21,22,22	8
1	HYP	G	29[A]	8/9	0.92	0.12	12,13,14,16	8
1	HYP	F	29[D]	8/9	0.92	0.16	10,12,12,13	8
1	HYP	G	29[C]	8/9	0.92	0.12	12,13,14,16	8
1	HYP	F	29[G]	8/9	0.92	0.16	13,15,16,18	8
1	HYP	G	29[G]	8/9	0.92	0.12	25,26,29,51	8
1	HYP	F	29[A]	8/9	0.92	0.16	24,24,25,27	8
1	HYP	F	29[B]	8/9	0.92	0.16	10,12,12,13	8
1	HYP	F	29[C]	8/9	0.92	0.16	10,12,12,13	8
1	HYP	H	2[D]	8/9	0.92	0.14	18,20,22,22	8
1	HYP	H	2[E]	8/9	0.92	0.14	15,16,17,17	8
1	HYP	H	2[F]	8/9	0.92	0.14	6,7,7,9	8
1	HYP	H	2[A]	8/9	0.92	0.14	15,16,17,17	8
1	HYP	H	2[B]	8/9	0.92	0.14	15,16,17,17	8
1	HYP	F	29[E]	8/9	0.92	0.16	24,24,25,27	8
1	HYP	H	2[G]	8/9	0.92	0.14	6,7,7,9	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	H	2[C]	8/9	0.92	0.14	18,20,22,22	8
1	HYP	G	29[D]	8/9	0.92	0.12	6,7,8,11	8
1	HYP	G	29[E]	8/9	0.92	0.12	25,26,29,51	8
1	HYP	G	29[F]	8/9	0.92	0.12	25,26,29,51	8
1	HYP	G	29[B]	8/9	0.92	0.12	12,13,14,16	8
1	HYP	F	29[F]	8/9	0.92	0.16	24,24,25,27	8
1	HYP	I	29[C]	8/9	0.93	0.11	10,10,11,14	8
1	HYP	F	2[E]	8/9	0.93	0.13	12,14,15,18	8
1	HYP	F	2[D]	8/9	0.93	0.13	19,20,20,22	8
1	HYP	I	29[D]	8/9	0.93	0.11	10,10,11,14	8
1	HYP	I	29[E]	8/9	0.93	0.11	20,22,23,24	8
1	HYP	I	29[A]	8/9	0.93	0.11	20,22,23,24	8
1	HYP	I	29[F]	8/9	0.93	0.11	20,22,23,24	8
1	HYP	F	2[F]	8/9	0.93	0.13	12,14,15,18	8
1	HYP	I	29[B]	8/9	0.93	0.11	10,10,11,14	8
1	HYP	F	2[G]	8/9	0.93	0.13	5,5,7,8	8
1	HYP	F	2[A]	8/9	0.93	0.13	12,14,15,18	8
1	HYP	F	2[C]	8/9	0.93	0.13	19,20,20,22	8
1	HYP	I	29[G]	8/9	0.93	0.11	11,12,13,15	8
1	HYP	F	2[B]	8/9	0.93	0.13	19,20,20,22	8
1	HYP	G	5[A]	8/9	0.94	0.13	8,9,11,13	8
1	HYP	B	29[E]	8/9	0.94	0.12	18,19,19,19	8
1	HYP	H	29[E]	8/9	0.94	0.10	14,15,17,17	8
1	HYP	D	2[G]	8/9	0.94	0.14	7,8,9,11	8
1	HYP	B	29[G]	8/9	0.94	0.12	16,17,18,18	8
1	HYP	B	29[B]	8/9	0.94	0.12	18,19,19,19	8
1	HYP	B	29[A]	8/9	0.94	0.12	18,19,19,19	8
1	HYP	B	29[C]	8/9	0.94	0.12	6,7,8,10	8
1	HYP	H	29[C]	8/9	0.94	0.10	8,9,9,12	8
1	HYP	G	5[B]	8/9	0.94	0.13	8,9,11,13	8
1	HYP	A	2[F]	8/9	0.94	0.10	6,7,8,10	8
1	HYP	A	2[B]	8/9	0.94	0.10	18,20,20,21	8
1	HYP	A	2[D]	8/9	0.94	0.10	14,15,17,17	8
1	HYP	G	5[C]	8/9	0.94	0.13	8,9,11,13	8
1	HYP	B	29[D]	8/9	0.94	0.12	6,7,8,10	8
1	HYP	A	2[E]	8/9	0.94	0.10	6,7,8,10	8
1	HYP	A	2[G]	8/9	0.94	0.10	6,7,8,10	8
1	HYP	D	2[A]	8/9	0.94	0.14	16,17,18,18	8
1	HYP	G	5[G]	8/9	0.94	0.13	3,4,5,6	8
1	HYP	G	5[D]	8/9	0.94	0.13	21,22,23,24	8
1	HYP	H	29[B]	8/9	0.94	0.10	14,15,17,17	8
1	HYP	A	2[A]	8/9	0.94	0.10	18,20,20,21	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	D	2[B]	8/9	0.94	0.14	16,17,18,18	8
1	HYP	B	29[F]	8/9	0.94	0.12	16,17,18,18	8
1	HYP	A	2[C]	8/9	0.94	0.10	18,20,20,21	8
1	HYP	D	2[C]	8/9	0.94	0.14	16,17,18,18	8
1	HYP	D	2[D]	8/9	0.94	0.14	14,14,14,15	8
1	HYP	D	2[E]	8/9	0.94	0.14	7,8,9,11	8
1	HYP	D	2[F]	8/9	0.94	0.14	7,8,9,11	8
1	HYP	G	5[E]	8/9	0.94	0.13	3,4,5,6	8
1	HYP	H	29[D]	8/9	0.94	0.10	8,9,9,12	8
1	HYP	H	29[F]	8/9	0.94	0.10	16,17,19,21	8
1	HYP	H	29[G]	8/9	0.94	0.10	16,17,19,21	8
1	HYP	G	5[F]	8/9	0.94	0.13	3,4,5,6	8
1	HYP	H	29[A]	8/9	0.94	0.10	14,15,17,17	8
1	HYP	B	2[C]	8/9	0.95	0.09	19,20,21,21	8
1	HYP	C	26[B]	8/9	0.95	0.11	5,5,6,8	8
1	HYP	E	26[F]	8/9	0.95	0.10	20,21,22,22	8
1	HYP	A	29[D]	8/9	0.95	0.12	5,5,6,7	8
1	HYP	A	29[B]	8/9	0.95	0.12	15,17,19,20	8
1	HYP	C	2[G]	8/9	0.95	0.10	4,4,5,5	8
1	HYP	C	2[D]	8/9	0.95	0.10	25,26,29,51	8
1	HYP	E	2[D]	8/9	0.95	0.13	18,19,21,21	8
1	HYP	B	2[E]	8/9	0.95	0.09	11,12,13,14	8
1	HYP	B	2[A]	8/9	0.95	0.09	11,12,13,14	8
1	HYP	A	26[G]	8/9	0.95	0.09	14,14,14,15	8
1	HYP	A	26[A]	8/9	0.95	0.09	5,5,6,7	8
1	HYP	E	2[G]	8/9	0.95	0.13	6,6,7,9	8
1	HYP	E	2[C]	8/9	0.95	0.13	18,19,21,21	8
1	HYP	A	26[E]	8/9	0.95	0.09	14,14,14,15	8
1	HYP	E	2[F]	8/9	0.95	0.13	6,6,7,9	8
1	HYP	A	26[C]	8/9	0.95	0.09	5,5,6,7	8
1	HYP	C	26[G]	8/9	0.95	0.11	20,20,21,22	8
1	HYP	C	26[D]	8/9	0.95	0.11	5,5,6,8	8
1	HYP	C	26[A]	8/9	0.95	0.11	11,12,14,14	8
1	HYP	E	2[E]	8/9	0.95	0.13	14,15,16,16	8
1	HYP	E	2[A]	8/9	0.95	0.13	14,15,16,16	8
1	HYP	A	26[F]	8/9	0.95	0.09	14,14,14,15	8
1	HYP	A	26[B]	8/9	0.95	0.09	5,5,6,7	8
1	HYP	E	26[A]	8/9	0.95	0.10	7,8,9,10	8
1	HYP	E	26[B]	8/9	0.95	0.10	7,8,9,10	8
1	HYP	E	26[C]	8/9	0.95	0.10	3,3,4,5	8
1	HYP	C	26[F]	8/9	0.95	0.11	11,12,14,14	8
1	HYP	C	26[E]	8/9	0.95	0.11	11,12,14,14	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	A	26[D]	8/9	0.95	0.09	4,5,6,9	8
1	HYP	C	2[C]	8/9	0.95	0.10	25,26,29,51	8
1	HYP	A	29[F]	8/9	0.95	0.12	16,18,19,21	8
1	HYP	E	26[E]	8/9	0.95	0.10	7,8,9,10	8
1	HYP	E	26[G]	8/9	0.95	0.10	20,21,22,22	8
1	HYP	C	2[A]	8/9	0.95	0.10	7,8,10,13	8
1	HYP	C	26[C]	8/9	0.95	0.11	5,5,6,8	8
1	HYP	E	26[D]	8/9	0.95	0.10	3,3,4,5	8
1	HYP	B	2[D]	8/9	0.95	0.09	19,20,21,21	8
1	HYP	C	2[E]	8/9	0.95	0.10	7,8,10,13	8
1	HYP	B	2[G]	8/9	0.95	0.09	5,6,7,8	8
1	HYP	B	2[B]	8/9	0.95	0.09	11,12,13,14	8
1	HYP	A	29[G]	8/9	0.95	0.12	16,18,19,21	8
1	HYP	C	2[B]	8/9	0.95	0.10	25,26,29,51	8
1	HYP	A	29[E]	8/9	0.95	0.12	16,18,19,21	8
1	HYP	A	29[C]	8/9	0.95	0.12	15,17,19,20	8
1	HYP	C	2[F]	8/9	0.95	0.10	7,8,10,13	8
1	HYP	A	29[A]	8/9	0.95	0.12	15,17,19,20	8
1	HYP	E	2[B]	8/9	0.95	0.13	14,15,16,16	8
1	HYP	B	2[F]	8/9	0.95	0.09	5,6,7,8	8
1	HYP	F	5[A]	8/9	0.96	0.08	5,5,7,8	8
1	HYP	F	5[E]	8/9	0.96	0.08	5,5,7,8	8
1	HYP	H	5[F]	8/9	0.96	0.08	3,3,5,6	8
1	HYP	D	26[D]	8/9	0.96	0.08	3,3,4,6	8
1	HYP	I	5[B]	8/9	0.96	0.08	14,16,16,18	8
1	HYP	E	5[F]	8/9	0.96	0.09	2,3,5,6	8
1	HYP	D	26[A]	8/9	0.96	0.08	5,6,7,10	8
1	HYP	D	26[C]	8/9	0.96	0.08	5,6,7,10	8
1	HYP	I	2[A]	8/9	0.96	0.11	13,15,16,19	8
1	HYP	E	5[G]	8/9	0.96	0.09	2,3,5,6	8
1	HYP	D	26[B]	8/9	0.96	0.08	5,6,7,10	8
1	HYP	E	5[B]	8/9	0.96	0.09	6,6,7,9	8
1	HYP	I	2[E]	8/9	0.96	0.11	13,15,16,19	8
1	HYP	A	5[D]	8/9	0.96	0.08	18,20,20,21	8
1	HYP	H	5[B]	8/9	0.96	0.08	6,7,7,9	8
1	HYP	A	5[F]	8/9	0.96	0.08	3,3,4,6	8
1	HYP	I	5[G]	8/9	0.96	0.08	3,3,4,6	8
1	HYP	E	5[A]	8/9	0.96	0.09	6,6,7,9	8
1	HYP	A	5[C]	8/9	0.96	0.08	6,7,8,9	8
1	HYP	A	5[A]	8/9	0.96	0.08	6,7,8,9	8
1	HYP	A	5[G]	8/9	0.96	0.08	3,3,4,6	8
1	HYP	I	5[A]	8/9	0.96	0.08	3,4,6,7	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	A	5[E]	8/9	0.96	0.08	3,3,4,6	8
1	HYP	I	5[E]	8/9	0.96	0.08	3,4,6,7	8
1	HYP	I	5[C]	8/9	0.96	0.08	14,16,16,18	8
1	HYP	I	2[C]	8/9	0.96	0.11	20,22,22,22	8
1	HYP	I	2[F]	8/9	0.96	0.11	13,15,16,19	8
1	HYP	H	5[G]	8/9	0.96	0.08	3,3,5,6	8
1	HYP	I	5[F]	8/9	0.96	0.08	3,4,6,7	8
1	HYP	I	2[D]	8/9	0.96	0.11	20,22,22,22	8
1	HYP	H	5[D]	8/9	0.96	0.08	16,17,18,20	8
1	HYP	H	5[C]	8/9	0.96	0.08	16,17,18,20	8
1	HYP	H	5[E]	8/9	0.96	0.08	6,7,7,9	8
1	HYP	I	2[G]	8/9	0.96	0.11	3,4,6,7	8
1	HYP	A	5[B]	8/9	0.96	0.08	6,7,8,9	8
1	HYP	H	5[A]	8/9	0.96	0.08	6,7,7,9	8
1	HYP	F	5[D]	8/9	0.96	0.08	12,13,14,16	8
1	HYP	F	5[C]	8/9	0.96	0.08	12,13,14,16	8
1	HYP	F	5[B]	8/9	0.96	0.08	12,13,14,16	8
1	HYP	E	5[C]	8/9	0.96	0.09	15,15,16,16	8
1	HYP	F	5[G]	8/9	0.96	0.08	2,3,4,6	8
1	HYP	D	26[G]	8/9	0.96	0.08	14,15,16,16	8
1	HYP	D	26[F]	8/9	0.96	0.08	14,15,16,16	8
1	HYP	D	26[E]	8/9	0.96	0.08	14,15,16,16	8
1	HYP	I	2[B]	8/9	0.96	0.11	20,22,22,22	8
1	HYP	I	5[D]	8/9	0.96	0.08	14,16,16,18	8
1	HYP	E	5[D]	8/9	0.96	0.09	15,15,16,16	8
1	HYP	E	5[E]	8/9	0.96	0.09	6,6,7,9	8
1	HYP	F	5[F]	8/9	0.96	0.08	5,5,7,8	8
1	HYP	E	23[E]	8/9	0.97	0.06	3,3,4,5	8
1	HYP	G	8[E]	8/9	0.97	0.07	2,3,4,5	8
1	HYP	B	26[E]	8/9	0.97	0.07	6,7,8,10	8
1	HYP	G	8[G]	8/9	0.97	0.07	2,3,4,5	8
1	HYP	H	26[B]	8/9	0.97	0.06	8,9,9,12	8
1	HYP	G	8[A]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	B	5[E]	8/9	0.97	0.06	5,6,7,8	8
1	HYP	D	5[A]	8/9	0.97	0.08	7,8,9,11	8
1	HYP	I	26[A]	8/9	0.97	0.08	10,11,11,13	8
1	HYP	F	23[E]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	G	8[C]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	I	26[C]	8/9	0.97	0.08	3,5,6,6	8
1	HYP	B	5[G]	8/9	0.97	0.06	3,4,6,7	8
1	HYP	B	5[A]	8/9	0.97	0.06	5,6,7,8	8
1	HYP	B	5[C]	8/9	0.97	0.06	11,12,13,14	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	B	5[F]	8/9	0.97	0.06	3,4,6,7	8
1	HZP	G	16[B]	8/9	0.97	0.07	4,5,7,12	8
1	HYP	B	5[B]	8/9	0.97	0.06	5,6,7,8	8
1	HYP	F	26[B]	8/9	0.97	0.09	3,4,5,6	8
1	HZP	G	16[D]	8/9	0.97	0.07	4,5,7,11	8
1	HYP	B	5[D]	8/9	0.97	0.06	11,12,13,14	8
1	HZP	G	16[F]	8/9	0.97	0.07	3,4,6,6	8
1	HYP	B	26[D]	8/9	0.97	0.07	4,5,5,7	8
1	HYP	E	23[C]	8/9	0.97	0.06	3,4,6,7	8
1	HYP	F	23[B]	8/9	0.97	0.07	3,4,5,5	8
1	HYP	D	5[B]	8/9	0.97	0.08	7,8,9,11	8
1	HYP	H	26[D]	8/9	0.97	0.06	3,4,4,6	8
1	HYP	E	23[F]	8/9	0.97	0.06	7,8,9,10	8
1	HYP	F	26[F]	8/9	0.97	0.09	10,12,13,13	8
1	HYP	D	5[G]	8/9	0.97	0.08	4,4,5,6	8
1	HYP	G	26[F]	8/9	0.97	0.07	12,13,14,15	8
1	HYP	G	26[D]	8/9	0.97	0.07	3,3,4,6	8
1	HYP	D	5[C]	8/9	0.97	0.08	7,8,9,11	8
1	HYP	E	23[A]	8/9	0.97	0.06	3,3,4,5	8
1	HYP	E	23[D]	8/9	0.97	0.06	3,4,6,7	8
1	HYP	I	26[E]	8/9	0.97	0.08	10,11,11,13	8
1	HYP	B	26[A]	8/9	0.97	0.07	6,7,8,10	8
1	HYP	G	8[F]	8/9	0.97	0.07	2,3,4,5	8
1	HYP	F	23[D]	8/9	0.97	0.07	3,4,5,5	8
1	HYP	F	26[D]	8/9	0.97	0.09	3,4,5,6	8
1	HYP	I	26[B]	8/9	0.97	0.08	3,5,6,6	8
1	HYP	B	26[B]	8/9	0.97	0.07	6,7,8,10	8
1	HYP	B	26[F]	8/9	0.97	0.07	18,19,20,20	8
1	HYP	B	26[C]	8/9	0.97	0.07	4,5,5,7	8
1	HYP	D	5[E]	8/9	0.97	0.08	4,4,5,6	8
1	HYP	F	26[E]	8/9	0.97	0.09	10,12,13,13	8
1	HYP	B	26[G]	8/9	0.97	0.07	18,19,20,20	8
1	HYP	F	23[A]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	F	26[A]	8/9	0.97	0.09	10,12,13,13	8
1	HYP	D	5[D]	8/9	0.97	0.08	16,17,18,18	8
1	HYP	H	26[F]	8/9	0.97	0.06	14,15,16,16	8
1	HYP	I	26[G]	8/9	0.97	0.08	10,18,20,20	8
1	HZP	G	16[A]	8/9	0.97	0.07	4,5,7,12	8
1	HYP	F	23[G]	8/9	0.97	0.07	10,10,12,12	8
1	HZP	G	16[C]	8/9	0.97	0.07	4,5,7,12	8
1	HZP	G	16[E]	8/9	0.97	0.07	3,4,6,6	8
1	HYP	D	5[F]	8/9	0.97	0.08	4,4,5,6	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HZP	G	16[G]	8/9	0.97	0.07	3,4,6,6	8
1	HYP	F	26[G]	8/9	0.97	0.09	21,22,22,22	8
1	HYP	E	23[B]	8/9	0.97	0.06	3,3,4,5	8
1	HYP	I	26[D]	8/9	0.97	0.08	3,5,6,6	8
1	HYP	G	8[D]	8/9	0.97	0.07	8,9,10,10	8
1	HYP	F	23[F]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	F	26[C]	8/9	0.97	0.09	3,4,5,6	8
1	HYP	G	8[B]	8/9	0.97	0.07	3,4,5,6	8
1	HYP	H	26[A]	8/9	0.97	0.06	8,9,9,12	8
1	HYP	G	26[C]	8/9	0.97	0.07	6,7,8,11	8
1	HYP	H	26[C]	8/9	0.97	0.06	3,4,4,6	8
1	HYP	I	26[F]	8/9	0.97	0.08	10,11,11,13	8
1	HYP	G	26[A]	8/9	0.97	0.07	6,7,8,11	8
1	HYP	H	26[E]	8/9	0.97	0.06	8,9,9,12	8
1	HYP	H	26[G]	8/9	0.97	0.06	14,15,16,16	8
1	HYP	F	23[C]	8/9	0.97	0.07	3,4,5,5	8
1	HYP	G	26[G]	8/9	0.97	0.07	12,13,14,15	8
1	HYP	G	26[B]	8/9	0.97	0.07	6,7,8,11	8
1	HYP	G	26[E]	8/9	0.97	0.07	12,13,14,15	8
1	HYP	E	23[G]	8/9	0.97	0.06	7,8,9,10	8
1	HYP	C	23[D]	8/9	0.98	0.06	3,3,4,5	8
1	HZP	E	13[E]	8/9	0.98	0.06	4,5,7,9	8
1	HZP	A	16[G]	8/9	0.98	0.06	3,4,5,9	8
1	HZP	D	13[A]	8/9	0.98	0.05	2,3,4,7	8
1	HYP	A	20[D]	8/9	0.98	0.07	3,3,4,4	8
1	HYP	G	23[B]	8/9	0.98	0.06	3,3,4,6	8
1	HYP	B	8[G]	8/9	0.98	0.05	2,3,4,5	8
1	HZP	H	16[B]	8/9	0.98	0.06	4,4,6,9	8
1	HZP	D	16[A]	8/9	0.98	0.07	5,6,7,13	8
1	HYP	I	8[G]	8/9	0.98	0.05	4,4,5,6	8
1	HYP	C	23[B]	8/9	0.98	0.06	3,3,4,5	8
1	HYP	I	8[E]	8/9	0.98	0.05	3,3,4,6	8
1	HYP	I	11[A]	8/9	0.98	0.07	4,4,5,5	8
1	HYP	I	11[E]	8/9	0.98	0.07	4,4,5,5	8
1	HZP	B	13[G]	8/9	0.98	0.06	3,4,7,12	8
1	HYP	B	8[C]	8/9	0.98	0.05	5,6,7,8	8
1	HYP	B	23[A]	8/9	0.98	0.06	4,5,5,7	8
1	HYP	B	20[F]	8/9	0.98	0.06	4,5,5,7	8
1	HYP	B	20[D]	8/9	0.98	0.06	2,2,2,3	8
1	HZP	H	16[G]	8/9	0.98	0.06	2,4,6,10	8
1	HZP	H	16[E]	8/9	0.98	0.06	4,4,6,9	8
1	HYP	C	5[B]	8/9	0.98	0.05	7,8,10,12	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	C	23[G]	8/9	0.98	0.06	11,12,14,16	8
1	HZP	D	13[C]	8/9	0.98	0.05	2,3,4,7	8
1	HYP	A	20[C]	8/9	0.98	0.07	2,3,3,4	8
1	HZP	D	13[G]	8/9	0.98	0.05	4,5,5,8	8
1	HYP	B	20[B]	8/9	0.98	0.06	3,3,4,4	8
1	HYP	B	23[D]	8/9	0.98	0.06	3,3,4,4	8
1	HZP	D	13[E]	8/9	0.98	0.05	4,5,5,8	8
1	HYP	F	20[C]	8/9	0.98	0.06	2,3,3,4	8
1	HZP	B	16[E]	8/9	0.98	0.06	3,5,7,12	8
1	HYP	C	5[D]	8/9	0.98	0.05	7,8,10,12	8
1	HZP	F	16[B]	8/9	0.98	0.06	5,6,8,12	8
1	HYP	F	20[G]	8/9	0.98	0.06	3,3,4,6	8
1	HZP	B	16[A]	8/9	0.98	0.06	3,5,7,12	8
1	HYP	I	8[C]	8/9	0.98	0.05	3,4,6,7	8
1	HZP	G	13[D]	8/9	0.98	0.07	2,3,3,4	8
1	HZP	F	16[G]	8/9	0.98	0.06	2,3,4,4	8
1	HZP	D	16[B]	8/9	0.98	0.07	5,6,7,13	8
1	HZP	C	16[A]	8/9	0.98	0.06	3,4,6,11	8
1	HYP	C	11[C]	8/9	0.98	0.06	3,4,5,7	8
1	HYP	I	8[A]	8/9	0.98	0.05	3,3,4,6	8
1	HYP	B	23[B]	8/9	0.98	0.06	4,5,5,7	8
1	HZP	C	16[F]	8/9	0.98	0.06	3,4,6,11	8
1	HZP	B	13[C]	8/9	0.98	0.06	2,3,3,4	8
1	HYP	I	23[F]	8/9	0.98	0.06	3,5,6,6	8
1	HYP	A	20[G]	8/9	0.98	0.07	4,5,7,9	8
1	HZP	D	16[E]	8/9	0.98	0.07	2,3,5,8	8
1	HZP	F	13[E]	8/9	0.98	0.06	5,6,8,12	8
1	HZP	B	16[D]	8/9	0.98	0.06	3,4,5,11	8
1	HYP	A	23[B]	8/9	0.98	0.06	4,5,6,9	8
1	HZP	E	13[B]	8/9	0.98	0.06	4,5,7,9	8
1	HZP	H	16[D]	8/9	0.98	0.06	4,5,7,12	8
1	HZP	F	13[A]	8/9	0.98	0.06	5,6,8,12	8
1	HZP	F	16[F]	8/9	0.98	0.06	4,5,6,13	8
1	HYP	D	8[C]	8/9	0.98	0.06	4,4,5,6	8
1	HZP	F	16[C]	8/9	0.98	0.06	5,6,8,12	8
1	HYP	D	8[A]	8/9	0.98	0.06	4,4,5,6	8
1	HYP	I	23[B]	8/9	0.98	0.06	2,3,4,5	8
1	HYP	D	8[G]	8/9	0.98	0.06	2,3,4,5	8
1	HZP	B	13[D]	8/9	0.98	0.06	2,3,3,4	8
1	HYP	A	20[A]	8/9	0.98	0.07	2,3,3,4	8
1	HYP	D	8[E]	8/9	0.98	0.06	2,3,4,5	8
1	HYP	C	5[F]	8/9	0.98	0.05	4,4,4,5	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	HZP	C	16[E]	8/9	0.98	0.06	3,4,6,11	8
1	HZP	E	13[F]	8/9	0.98	0.06	4,5,5,9	8
1	HZP	B	13[B]	8/9	0.98	0.06	3,4,6,9	8
1	HZP	D	16[G]	8/9	0.98	0.07	2,3,5,8	8
1	HYP	A	23[F]	8/9	0.98	0.06	5,5,6,7	8
1	HYP	G	23[C]	8/9	0.98	0.06	3,3,4,6	8
1	HZP	E	16[B]	8/9	0.98	0.06	5,5,7,11	8
1	HZP	H	13[A]	8/9	0.98	0.06	4,4,6,12	8
1	HYP	I	23[C]	8/9	0.98	0.06	2,3,4,5	8
1	HYP	I	8[F]	8/9	0.98	0.05	3,3,4,6	8
1	HYP	I	11[F]	8/9	0.98	0.07	4,4,5,5	8
1	HYP	G	23[D]	8/9	0.98	0.06	3,3,5,5	8
1	HYP	I	8[D]	8/9	0.98	0.05	3,4,6,7	8
1	HZP	D	16[C]	8/9	0.98	0.07	5,6,7,13	8
1	HYP	I	11[C]	8/9	0.98	0.07	3,4,4,6	8
1	HZP	I	13[G]	8/9	0.98	0.06	3,4,5,7	8
1	HZP	H	13[F]	8/9	0.98	0.06	4,5,7,11	8
1	HZP	C	13[C]	8/9	0.98	0.06	3,3,4,7	8
1	HYP	I	8[B]	8/9	0.98	0.05	3,4,6,7	8
1	HZP	I	13[E]	8/9	0.98	0.06	5,5,6,8	8
1	HZP	I	16[B]	8/9	0.98	0.06	5,5,7,12	8
1	HZP	C	13[F]	8/9	0.98	0.06	3,4,5,9	8
1	HZP	I	16[F]	8/9	0.98	0.06	3,4,5,7	8
1	HYP	E	20[F]	8/9	0.98	0.07	3,3,4,5	8
1	HYP	G	23[G]	8/9	0.98	0.06	6,7,8,11	8
1	HZP	E	16[G]	8/9	0.98	0.06	3,4,4,7	8
1	HZP	D	16[F]	8/9	0.98	0.07	2,3,5,8	8
1	HYP	C	5[C]	8/9	0.98	0.05	7,8,10,12	8
1	HZP	D	13[B]	8/9	0.98	0.05	2,3,4,7	8
1	HYP	C	5[E]	8/9	0.98	0.05	4,4,4,5	8
1	HYP	I	20[B]	8/9	0.98	0.05	4,5,7,8	8
1	HYP	A	23[G]	8/9	0.98	0.06	5,5,6,7	8
1	HYP	C	5[G]	8/9	0.98	0.05	3,4,5,6	8
1	HZP	D	13[F]	8/9	0.98	0.05	4,5,5,8	8
1	HZP	A	13[G]	8/9	0.98	0.07	4,4,7,10	8
1	HYP	I	11[B]	8/9	0.98	0.07	3,4,4,6	8
1	HZP	F	16[A]	8/9	0.98	0.06	4,5,6,13	8
1	HZP	B	16[G]	8/9	0.98	0.06	3,3,5,8	8
1	HZP	C	16[D]	8/9	0.98	0.06	3,4,5,9	8
1	HZP	H	13[G]	8/9	0.98	0.06	4,5,7,11	8
1	HYP	E	8[E]	8/9	0.98	0.06	2,3,5,6	8
1	HZP	F	16[D]	8/9	0.98	0.06	5,6,8,12	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HZP	E	16[C]	8/9	0.98	0.06	4,4,7,9	8
1	HZP	A	16[B]	8/9	0.98	0.06	3,4,7,10	8
1	HZP	H	13[E]	8/9	0.98	0.06	4,4,6,12	8
1	HZP	A	16[F]	8/9	0.98	0.06	3,4,5,9	8
1	HZP	H	13[D]	8/9	0.98	0.06	2,2,3,6	8
1	HZP	B	16[C]	8/9	0.98	0.06	3,4,5,11	8
1	HZP	H	16[C]	8/9	0.98	0.06	4,5,7,12	8
1	HZP	H	16[A]	8/9	0.98	0.06	4,4,6,9	8
1	HZP	G	13[F]	8/9	0.98	0.07	4,5,5,8	8
1	HZP	H	16[F]	8/9	0.98	0.06	2,4,6,10	8
1	HZP	G	13[B]	8/9	0.98	0.07	4,5,7,11	8
1	HZP	E	13[C]	8/9	0.98	0.06	2,3,6,10	8
1	HZP	H	13[B]	8/9	0.98	0.06	4,4,6,12	8
1	HYP	A	23[D]	8/9	0.98	0.06	2,3,3,4	8
1	HZP	H	13[C]	8/9	0.98	0.06	2,2,3,6	8
1	HZP	C	16[C]	8/9	0.98	0.06	3,4,5,9	8
1	HYP	C	23[F]	8/9	0.98	0.06	5,5,6,8	8
1	HZP	A	13[F]	8/9	0.98	0.07	4,4,7,10	8
1	HZP	E	13[G]	8/9	0.98	0.06	4,5,5,9	8
1	HYP	A	20[E]	8/9	0.98	0.07	4,5,7,9	8
1	HZP	E	16[E]	8/9	0.98	0.06	5,5,7,11	8
1	HYP	E	20[D]	8/9	0.98	0.07	2,3,4,4	8
1	HYP	B	20[E]	8/9	0.98	0.06	3,3,4,4	8
1	HZP	E	16[A]	8/9	0.98	0.06	5,5,7,11	8
1	HZP	F	13[G]	8/9	0.98	0.06	4,4,5,5	8
1	HZP	F	13[C]	8/9	0.98	0.06	3,3,4,6	8
1	HYP	I	20[F]	8/9	0.98	0.05	3,3,4,5	8
1	HZP	C	13[B]	8/9	0.98	0.06	3,3,4,7	8
1	HYP	C	11[F]	8/9	0.98	0.06	3,3,5,7	8
1	HYP	D	8[B]	8/9	0.98	0.06	4,4,5,6	8
1	HZP	F	13[B]	8/9	0.98	0.06	3,3,4,6	8
1	HZP	B	13[A]	8/9	0.98	0.06	3,4,6,9	8
1	HYP	A	23[E]	8/9	0.98	0.06	5,5,6,7	8
1	HZP	B	13[E]	8/9	0.98	0.06	3,4,6,9	8
1	HYP	I	11[G]	8/9	0.98	0.07	2,3,4,4	8
1	HYP	C	11[B]	8/9	0.98	0.06	3,4,5,7	8
1	HYP	D	8[F]	8/9	0.98	0.06	2,3,4,5	8
1	HYP	B	20[G]	8/9	0.98	0.06	4,5,5,7	8
1	HYP	I	23[E]	8/9	0.98	0.06	3,5,6,6	8
1	HZP	C	13[G]	8/9	0.98	0.06	3,3,4,7	8
1	HZP	I	16[C]	8/9	0.98	0.06	5,5,7,12	8
1	HZP	B	13[F]	8/9	0.98	0.06	3,4,7,12	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HZP	I	13[D]	8/9	0.98	0.06	4,5,6,9	8
1	HZP	I	13[C]	8/9	0.98	0.06	4,5,6,9	8
1	HYP	I	23[A]	8/9	0.98	0.06	3,5,6,6	8
1	HZP	I	13[B]	8/9	0.98	0.06	4,5,6,9	8
1	HZP	I	13[A]	8/9	0.98	0.06	5,5,6,8	8
1	HYP	B	20[A]	8/9	0.98	0.06	3,3,4,4	8
1	HYP	B	23[E]	8/9	0.98	0.06	4,5,5,7	8
1	HYP	B	20[C]	8/9	0.98	0.06	2,2,2,3	8
1	HZP	I	13[F]	8/9	0.98	0.06	5,5,6,8	8
1	HZP	A	13[E]	8/9	0.98	0.07	4,4,7,10	8
1	HZP	I	16[G]	8/9	0.98	0.06	3,3,4,4	8
1	HZP	C	16[B]	8/9	0.98	0.06	3,4,5,9	8
1	HYP	F	20[A]	8/9	0.98	0.06	3,4,5,5	8
1	HZP	D	13[D]	8/9	0.98	0.05	2,2,3,4	8
1	HYP	A	20[B]	8/9	0.98	0.07	2,3,3,4	8
1	HYP	F	20[E]	8/9	0.98	0.06	3,4,5,5	8
1	HYP	G	23[A]	8/9	0.98	0.06	3,3,4,6	8
1	HZP	B	16[F]	8/9	0.98	0.06	3,3,5,8	8
1	HZP	F	16[E]	8/9	0.98	0.06	4,5,6,13	8
1	HZP	A	13[D]	8/9	0.98	0.07	3,3,5,6	8
1	HYP	E	8[D]	8/9	0.98	0.06	6,6,7,9	8
1	HYP	E	8[C]	8/9	0.98	0.06	6,6,7,9	8
1	HZP	B	16[B]	8/9	0.98	0.06	3,5,7,12	8
1	HYP	E	8[B]	8/9	0.98	0.06	2,3,5,6	8
1	HYP	E	8[A]	8/9	0.98	0.06	2,3,5,6	8
1	HYP	I	11[D]	8/9	0.98	0.07	3,4,4,6	8
1	HYP	E	20[B]	8/9	0.98	0.07	3,4,6,7	8
1	HZP	D	16[D]	8/9	0.98	0.07	2,3,4,7	8
1	HZP	A	13[C]	8/9	0.98	0.07	3,3,7,11	8
1	HZP	A	13[B]	8/9	0.98	0.07	3,3,7,11	8
1	HYP	B	23[F]	8/9	0.98	0.06	6,7,8,10	8
1	HZP	A	13[A]	8/9	0.98	0.07	3,3,7,11	8
1	HYP	B	8[F]	8/9	0.98	0.05	2,3,4,5	8
1	HZP	C	13[E]	8/9	0.98	0.06	3,4,5,9	8
1	HYP	E	8[G]	8/9	0.98	0.06	3,3,5,8	8
1	HYP	B	8[B]	8/9	0.98	0.05	3,4,6,7	8
1	HYP	B	23[G]	8/9	0.98	0.06	6,7,8,10	8
1	HZP	I	16[D]	8/9	0.98	0.06	5,5,7,12	8
1	HYP	C	11[D]	8/9	0.98	0.06	3,4,5,7	8
1	HYP	G	23[F]	8/9	0.98	0.06	6,7,8,11	8
1	HYP	E	8[F]	8/9	0.98	0.06	3,3,5,8	8
1	HYP	H	23[E]	8/9	0.98	0.05	3,4,4,6	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	C	5[A]	8/9	0.98	0.05	4,4,4,5	8
1	HYP	H	23[F]	8/9	0.98	0.05	8,9,9,12	8
1	HYP	H	23[G]	8/9	0.98	0.05	8,9,9,12	8
1	HYP	D	8[D]	8/9	0.98	0.06	7,8,9,11	8
1	HZP	E	16[D]	8/9	0.98	0.06	4,4,7,9	8
1	HYP	A	23[A]	8/9	0.98	0.06	4,5,6,9	8
1	HYP	A	23[C]	8/9	0.98	0.06	4,5,6,9	8
1	HZP	E	13[D]	8/9	0.98	0.06	2,3,6,10	8
1	HYP	C	11[E]	8/9	0.98	0.06	3,3,5,7	8
1	HYP	F	20[B]	8/9	0.98	0.06	2,3,3,4	8
1	HYP	I	20[C]	8/9	0.98	0.05	4,5,7,8	8
1	HYP	I	20[A]	8/9	0.98	0.05	3,3,4,5	8
1	HYP	E	20[G]	8/9	0.98	0.07	3,3,4,5	8
1	HYP	E	20[E]	8/9	0.98	0.07	3,4,6,7	8
1	HZP	A	16[E]	8/9	0.98	0.06	3,4,5,9	8
1	HYP	G	23[E]	8/9	0.98	0.06	6,7,8,11	8
1	HYP	E	20[C]	8/9	0.98	0.07	2,3,4,4	8
1	HYP	C	11[G]	8/9	0.98	0.06	3,3,5,6	8
1	HYP	A	20[F]	8/9	0.98	0.07	4,5,7,9	8
1	HYP	I	23[G]	8/9	0.98	0.06	10,11,11,13	8
1	HYP	E	20[A]	8/9	0.98	0.07	3,4,6,7	8
1	HZP	C	13[A]	8/9	0.98	0.06	3,4,5,9	8
1	HYP	F	20[F]	8/9	0.98	0.06	3,4,5,5	8
1	HYP	C	23[E]	8/9	0.98	0.06	5,5,6,8	8
1	HYP	I	20[D]	8/9	0.98	0.05	4,5,7,8	8
1	HZP	C	13[D]	8/9	0.98	0.06	3,3,4,7	8
1	HYP	B	8[E]	8/9	0.98	0.05	3,4,6,7	8
1	HZP	I	16[A]	8/9	0.98	0.06	3,4,5,7	8
1	HZP	I	16[E]	8/9	0.98	0.06	3,4,5,7	8
1	HZP	E	16[F]	8/9	0.98	0.06	3,4,4,7	8
1	HYP	H	23[A]	8/9	0.98	0.05	3,4,4,6	8
1	HYP	H	23[B]	8/9	0.98	0.05	3,4,4,6	8
1	HZP	A	16[D]	8/9	0.98	0.06	3,3,5,6	8
1	HYP	H	23[C]	8/9	0.98	0.05	3,3,4,5	8
1	HYP	H	23[D]	8/9	0.98	0.05	3,3,4,5	8
1	HYP	B	8[A]	8/9	0.98	0.05	3,4,6,7	8
1	HZP	G	13[E]	8/9	0.98	0.07	4,5,5,8	8
1	HYP	B	8[D]	8/9	0.98	0.05	5,6,7,8	8
1	HYP	B	23[C]	8/9	0.98	0.06	3,3,4,4	8
1	HYP	F	20[D]	8/9	0.98	0.06	2,3,3,4	8
1	HYP	C	23[C]	8/9	0.98	0.06	3,3,4,5	8
1	HZP	G	13[G]	8/9	0.98	0.07	4,5,5,8	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	I	20[G]	8/9	0.98	0.05	4,5,6,6	8
1	HYP	C	23[A]	8/9	0.98	0.06	5,5,6,8	8
1	HZP	G	13[A]	8/9	0.98	0.07	4,5,7,11	8
1	HZP	G	13[C]	8/9	0.98	0.07	4,5,7,11	8
1	HYP	I	20[E]	8/9	0.98	0.05	3,3,4,5	8
1	HZP	F	13[F]	8/9	0.98	0.06	5,6,8,12	8
1	HZP	F	13[D]	8/9	0.98	0.06	3,3,4,6	8
1	HYP	C	11[A]	8/9	0.98	0.06	3,3,5,7	8
1	HZP	C	16[G]	8/9	0.98	0.06	2,2,3,3	8
1	HZP	E	13[A]	8/9	0.98	0.06	4,5,7,9	8
1	HZP	A	16[C]	8/9	0.98	0.06	3,4,7,10	8
1	HYP	I	23[D]	8/9	0.98	0.06	2,3,4,5	8
1	HZP	A	16[A]	8/9	0.98	0.06	3,4,7,10	8
1	HYP	H	20[E]	8/9	0.99	0.05	3,3,4,5	8
1	HYP	C	8[F]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	G	11[D]	8/9	0.99	0.06	3,3,4,5	8
1	HYP	F	11[B]	8/9	0.99	0.06	2,3,3,5	8
1	HYP	D	20[G]	8/9	0.99	0.06	3,3,4,6	8
1	HYP	A	8[G]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	D	11[D]	8/9	0.99	0.05	4,4,5,6	8
1	HYP	F	11[D]	8/9	0.99	0.06	2,3,3,5	8
1	HYP	G	11[F]	8/9	0.99	0.06	2,3,4,4	8
1	HYP	H	8[E]	8/9	0.99	0.04	3,3,5,6	8
1	HYP	A	8[E]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	D	20[E]	8/9	0.99	0.06	3,3,4,6	8
1	HYP	C	20[A]	8/9	0.99	0.05	3,3,4,5	8
1	HYP	A	11[G]	8/9	0.99	0.05	4,4,6,11	8
1	HYP	G	11[E]	8/9	0.99	0.06	2,3,4,4	8
1	HYP	A	11[E]	8/9	0.99	0.05	4,4,6,11	8
1	HYP	A	11[C]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	A	11[A]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	E	11[D]	8/9	0.99	0.06	2,3,5,6	8
1	HYP	E	11[C]	8/9	0.99	0.06	2,3,5,6	8
1	HYP	G	20[A]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	G	11[G]	8/9	0.99	0.06	2,3,4,4	8
1	HYP	C	8[G]	8/9	0.99	0.05	2,3,5,7	8
1	HYP	C	20[G]	8/9	0.99	0.05	5,5,6,8	8
1	HYP	G	20[D]	8/9	0.99	0.06	2,3,4,4	8
1	HYP	H	11[B]	8/9	0.99	0.05	4,4,5,7	8
1	HYP	H	11[A]	8/9	0.99	0.05	4,4,5,7	8
1	HYP	B	11[F]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	C	20[E]	8/9	0.99	0.05	3,3,4,5	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	HYP	H	11[F]	8/9	0.99	0.05	3,3,4,4	8
1	HYP	H	20[D]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	H	20[B]	8/9	0.99	0.05	3,3,4,5	8
1	HYP	D	20[B]	8/9	0.99	0.06	3,4,4,5	8
1	HYP	H	11[E]	8/9	0.99	0.05	4,4,5,7	8
1	HYP	E	11[A]	8/9	0.99	0.06	3,4,5,8	8
1	HYP	H	8[G]	8/9	0.99	0.04	3,4,5,7	8
1	HYP	D	11[E]	8/9	0.99	0.05	4,4,6,10	8
1	HYP	B	11[D]	8/9	0.99	0.05	3,4,6,6	8
1	HYP	E	11[G]	8/9	0.99	0.06	3,3,4,6	8
1	HYP	E	11[E]	8/9	0.99	0.06	3,4,5,8	8
1	HYP	D	23[E]	8/9	0.99	0.04	5,6,7,10	8
1	HYP	D	20[F]	8/9	0.99	0.06	3,3,4,6	8
1	HYP	D	23[F]	8/9	0.99	0.04	5,6,7,10	8
1	HYP	B	11[C]	8/9	0.99	0.05	3,4,6,6	8
1	HYP	C	20[F]	8/9	0.99	0.05	3,3,4,5	8
1	HYP	B	11[E]	8/9	0.99	0.05	2,3,4,5	8
1	HYP	D	23[G]	8/9	0.99	0.04	5,6,7,10	8
1	HYP	D	20[D]	8/9	0.99	0.06	3,3,4,4	8
1	HYP	B	11[G]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	H	11[D]	8/9	0.99	0.05	3,3,5,5	8
1	HYP	C	20[B]	8/9	0.99	0.05	2,3,4,4	8
1	HYP	D	11[C]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	D	23[A]	8/9	0.99	0.04	3,3,4,6	8
1	HYP	D	23[D]	8/9	0.99	0.04	3,4,4,5	8
1	HYP	G	20[G]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	C	20[C]	8/9	0.99	0.05	2,3,4,4	8
1	HYP	D	23[B]	8/9	0.99	0.04	3,3,4,6	8
1	HYP	C	20[D]	8/9	0.99	0.05	2,3,4,4	8
1	HYP	G	20[C]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	H	8[A]	8/9	0.99	0.04	3,3,5,6	8
1	HYP	D	23[C]	8/9	0.99	0.04	3,3,4,6	8
1	HYP	H	8[D]	8/9	0.99	0.04	6,7,7,9	8
1	HYP	C	8[C]	8/9	0.99	0.05	4,4,4,5	8
1	HYP	G	11[A]	8/9	0.99	0.06	2,3,4,5	8
1	HYP	B	11[A]	8/9	0.99	0.05	2,3,4,5	8
1	HYP	D	20[C]	8/9	0.99	0.06	3,4,4,5	8
1	HYP	F	8[A]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	D	11[B]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	A	8[C]	8/9	0.99	0.05	3,3,4,6	8
1	HYP	F	11[E]	8/9	0.99	0.06	3,4,5,6	8
1	HYP	F	8[C]	8/9	0.99	0.05	5,5,7,8	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	F	11[G]	8/9	0.99	0.06	3,3,3,4	8
1	HYP	F	8[E]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	C	8[B]	8/9	0.99	0.05	4,4,4,5	8
1	HYP	F	11[A]	8/9	0.99	0.06	3,4,5,6	8
1	HYP	F	8[G]	8/9	0.99	0.05	3,4,4,6	8
1	HYP	C	8[A]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	A	8[A]	8/9	0.99	0.05	3,3,4,6	8
1	HYP	D	11[F]	8/9	0.99	0.05	4,4,6,10	8
1	HYP	F	11[C]	8/9	0.99	0.06	2,3,3,5	8
1	HYP	C	8[D]	8/9	0.99	0.05	4,4,4,5	8
1	HYP	G	11[C]	8/9	0.99	0.06	2,3,4,5	8
1	HYP	A	11[F]	8/9	0.99	0.05	4,4,6,11	8
1	HYP	A	8[F]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	A	11[D]	8/9	0.99	0.05	3,3,4,6	8
1	HYP	E	11[B]	8/9	0.99	0.06	3,4,5,8	8
1	HYP	F	8[F]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	A	11[B]	8/9	0.99	0.05	2,3,4,6	8
1	HYP	A	8[B]	8/9	0.99	0.05	3,3,4,6	8
1	HYP	G	20[F]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	B	11[B]	8/9	0.99	0.05	2,3,4,5	8
1	HYP	G	20[B]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	H	8[C]	8/9	0.99	0.04	6,7,7,9	8
1	HYP	A	8[D]	8/9	0.99	0.05	6,7,9,10	8
1	HYP	H	11[C]	8/9	0.99	0.05	3,3,5,5	8
1	HYP	G	20[E]	8/9	0.99	0.06	3,3,5,5	8
1	HYP	H	11[G]	8/9	0.99	0.05	3,3,4,4	8
1	HYP	D	11[G]	8/9	0.99	0.05	4,4,6,10	8
1	HYP	C	8[E]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	H	20[C]	8/9	0.99	0.05	3,4,5,6	8
1	HYP	D	20[A]	8/9	0.99	0.06	3,4,4,5	8
1	HYP	E	11[F]	8/9	0.99	0.06	3,3,4,6	8
1	HYP	H	20[G]	8/9	0.99	0.05	3,4,4,6	8
1	HYP	H	20[A]	8/9	0.99	0.05	3,3,4,5	8
1	HYP	F	11[F]	8/9	0.99	0.06	3,4,5,6	8
1	HYP	H	20[F]	8/9	0.99	0.05	3,4,4,6	8
1	HYP	H	8[F]	8/9	0.99	0.04	3,4,5,7	8
1	HYP	G	11[B]	8/9	0.99	0.06	2,3,4,5	8
1	HYP	F	8[B]	8/9	0.99	0.05	5,5,7,8	8
1	HYP	F	8[D]	8/9	0.99	0.05	5,5,7,8	8
1	HYP	H	8[B]	8/9	0.99	0.04	3,3,5,6	8
1	HYP	D	11[A]	8/9	0.99	0.05	2,3,4,6	8

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.