Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 05:23 PM EDT

PDB ID	:	1QRQ
Title	:	STRUCTURE OF A VOLTAGE-DEPENDENT K+ CHANNEL BETA SUBUNIT
Authors	:	Gulbis, J.M.; Mann, S.; MacKinnon, R.
Deposited on	:	1999-06-15
Resolution	:	2.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

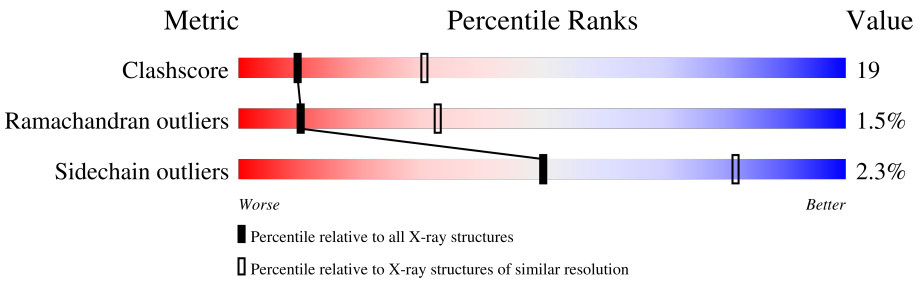
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	325	66% 32% •
1	B	325	65% 34% •
1	C	325	66% 32% •
1	D	325	66% 32% •

2 Entry composition (i)

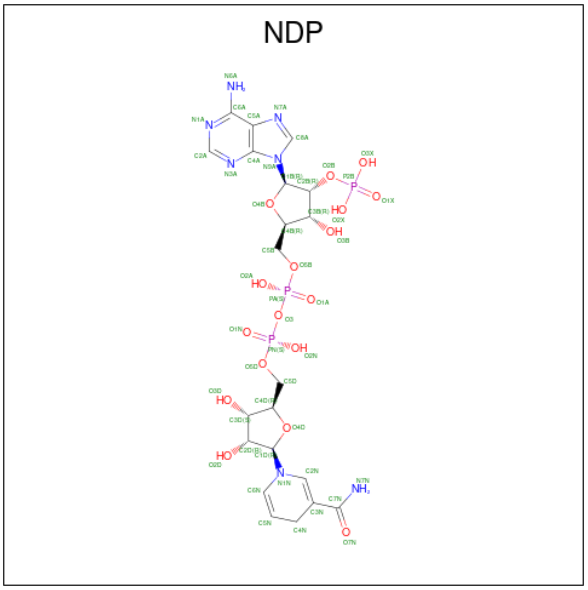
There are 3 unique types of molecules in this entry. The entry contains 10348 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (KV BETA2 PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	325	2501	1591	436	458	16	0	0	0
1	B	325	2501	1591	436	458	16	0	0	0
1	C	325	2501	1591	436	458	16	0	0	0
1	D	325	2501	1591	436	458	16	0	0	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	48	21	7	17	3	0	0
			Total	C	N	O	P		
2	D	1	48	21	7	17	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	38	38	38	0	0
			Total	O		
3	B	38	38	38	0	0
			Total	O		
3	C	38	38	38	0	0
			Total	O		
3	D	38	38	38	0	0

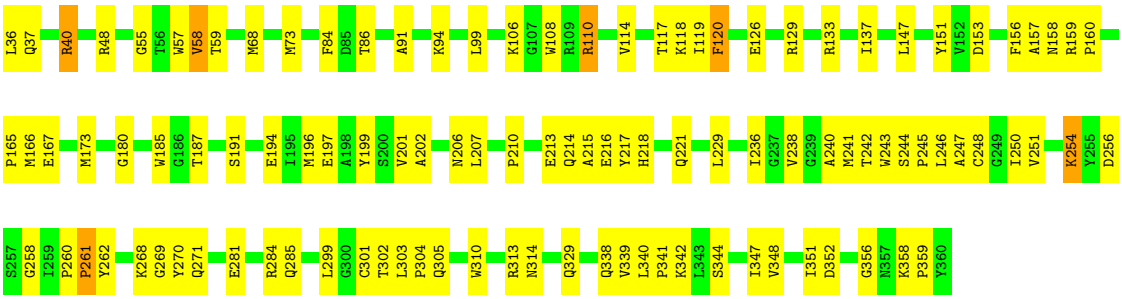
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

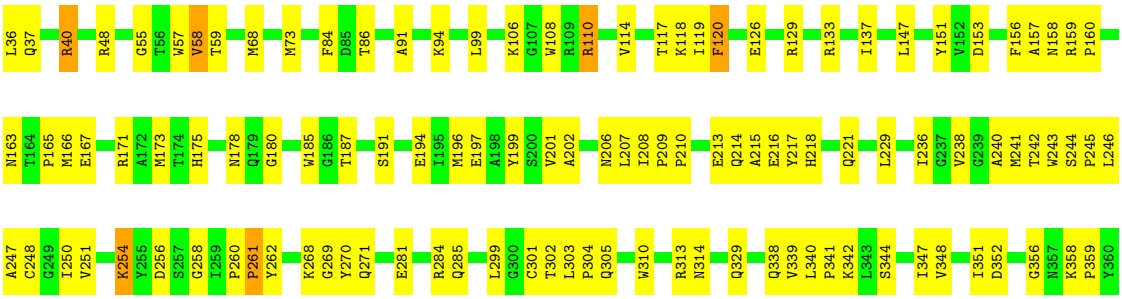
• Molecule 1: PROTEIN (KV BETA2 PROTEIN)

Chain A:



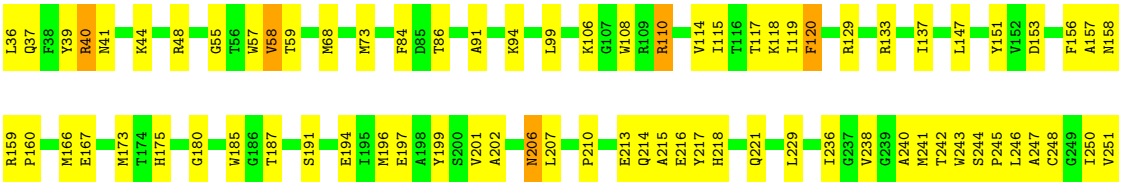
• Molecule 1: PROTEIN (KV BETA2 PROTEIN)

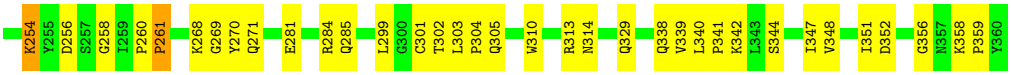
Chain B:



• Molecule 1: PROTEIN (KV BETA2 PROTEIN)

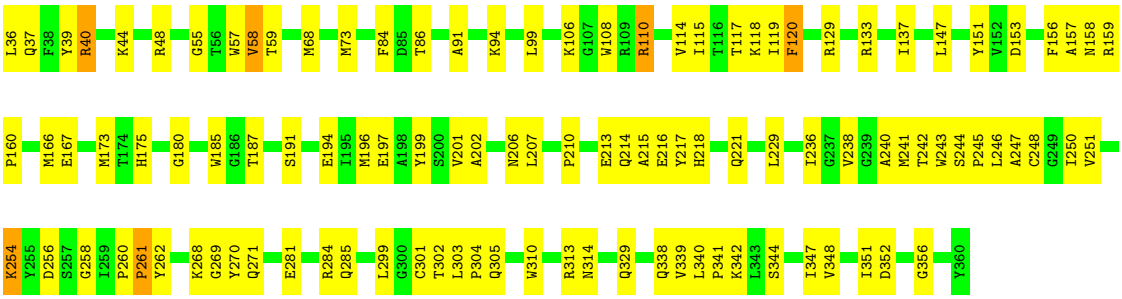
Chain C:





- Molecule 1: PROTEIN (KV BETA2 PROTEIN)

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	156.75Å 114.35Å 93.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.80	Depositor
% Data completeness (in resolution range)	97.7 (40.00-2.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.242	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10348	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.36	0/2550	0.63	2/3451 (0.1%)
1	B	0.36	0/2550	0.63	2/3451 (0.1%)
1	C	0.36	0/2550	0.63	2/3451 (0.1%)
1	D	0.36	0/2550	0.63	2/3451 (0.1%)
All	All	0.36	0/10200	0.63	8/13804 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	157	ALA	N-CA-C	-5.39	96.46	111.00
1	C	157	ALA	N-CA-C	-5.38	96.48	111.00
1	A	157	ALA	N-CA-C	-5.38	96.48	111.00
1	B	157	ALA	N-CA-C	-5.38	96.48	111.00
1	B	260	PRO	N-CA-CB	5.26	109.61	103.30
1	D	260	PRO	N-CA-CB	5.25	109.60	103.30
1	A	260	PRO	N-CA-CB	5.24	109.59	103.30
1	C	260	PRO	N-CA-CB	5.24	109.59	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2501	0	2477	93	0
1	B	2501	0	2477	98	0
1	C	2501	0	2477	97	0
1	D	2501	0	2477	96	0
2	A	48	0	26	9	0
2	B	48	0	26	9	0
2	C	48	0	26	10	0
2	D	48	0	26	10	0
3	A	38	0	0	0	0
3	B	38	0	0	0	0
3	C	38	0	0	0	0
3	D	38	0	0	0	0
All	All	10348	0	10012	390	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (390) 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:A:254:LYS:HA	1:A:258:GLY:HA3	1.40	1.04
1:B:254:LYS:HA	1:B:258:GLY:HA3	1.40	1.03
1:C:254:LYS:HA	1:C:258:GLY:HA3	1.40	1.01
1:D:254:LYS:HA	1:D:258:GLY:HA3	1.40	1.00
2:B:1001:NDP:H6N	2:B:1001:NDP:H52N	1.53	0.90
2:A:1000:NDP:H52N	2:A:1000:NDP:H6N	1.53	0.90
2:C:1002:NDP:H52N	2:C:1002:NDP:H6N	1.53	0.90
2:D:1003:NDP:H52N	2:D:1003:NDP:H6N	1.53	0.89
1:C:310:TRP:O	1:C:313:ARG:HG2	1.76	0.86
1:A:310:TRP:O	1:A:313:ARG:HG2	1.76	0.86
1:B:310:TRP:O	1:B:313:ARG:HG2	1.76	0.86
1:B:55:GLY:HA3	2:B:1001:NDP:O3D	1.77	0.85
1:D:310:TRP:O	1:D:313:ARG:HG2	1.76	0.85
1:A:55:GLY:HA3	2:A:1000:NDP:O3D	1.77	0.84
1:C:55:GLY:HA3	2:C:1002:NDP:O3D	1.77	0.84
1:D:55:GLY:HA3	2:D:1003:NDP:O3D	1.77	0.84
1:A:118:LYS:HG3	1:A:156:PHE:HB2	1.60	0.83
1:D:118:LYS:HG3	1:D:156:PHE:HB2	1.60	0.82
1:C:118:LYS:HG3	1:C:156:PHE:HB2	1.60	0.82
1:B:118:LYS:HG3	1:B:156:PHE:HB2	1.60	0.81
1:D:254:LYS:CA	1:D:258:GLY:HA3	2.13	0.78
1:C:254:LYS:CA	1:C:258:GLY:HA3	2.13	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:LYS:CA	1:A:258:GLY:HA3	2.13	0.77
1:B:254:LYS:CA	1:B:258:GLY:HA3	2.13	0.76
1:A:185:TRP:CZ2	1:A:210:PRO:HG3	2.27	0.70
1:B:73:MET:HE1	1:B:99:LEU:HD12	1.74	0.70
1:B:302:THR:H	1:B:305:GLN:NE2	1.90	0.69
1:C:185:TRP:CZ2	1:C:210:PRO:HG3	2.27	0.69
1:B:185:TRP:CZ2	1:B:210:PRO:HG3	2.27	0.69
1:A:73:MET:HE1	1:A:99:LEU:HD12	1.72	0.69
1:D:185:TRP:CZ2	1:D:210:PRO:HG3	2.27	0.69
1:A:229:LEU:HD23	1:A:240:ALA:HB2	1.75	0.69
1:A:302:THR:H	1:A:305:GLN:NE2	1.90	0.69
1:D:302:THR:H	1:D:305:GLN:NE2	1.90	0.69
1:C:302:THR:H	1:C:305:GLN:NE2	1.90	0.68
1:C:229:LEU:HD23	1:C:240:ALA:HB2	1.75	0.68
1:B:229:LEU:HD23	1:B:240:ALA:HB2	1.75	0.67
1:D:229:LEU:HD23	1:D:240:ALA:HB2	1.75	0.67
1:D:236:ILE:HG13	1:D:238:VAL:HG23	1.77	0.66
1:B:236:ILE:HG13	1:B:238:VAL:HG23	1.77	0.66
1:A:236:ILE:HG13	1:A:238:VAL:HG23	1.77	0.66
1:A:250:ILE:HG21	1:A:285:GLN:NE2	2.12	0.65
1:C:250:ILE:HG21	1:C:285:GLN:NE2	2.12	0.65
1:A:347:ILE:O	1:A:351:ILE:HG12	1.97	0.65
1:D:250:ILE:HG21	1:D:285:GLN:NE2	2.12	0.65
1:D:347:ILE:O	1:D:351:ILE:HG12	1.97	0.65
1:B:250:ILE:HG21	1:B:285:GLN:NE2	2.12	0.65
1:A:166:MET:HG2	1:A:197:GLU:HG2	1.79	0.64
1:C:236:ILE:HG13	1:C:238:VAL:HG23	1.77	0.64
1:B:299:LEU:O	1:B:342:LYS:NZ	2.31	0.64
1:B:347:ILE:O	1:B:351:ILE:HG12	1.97	0.64
1:D:299:LEU:O	1:D:342:LYS:NZ	2.31	0.64
1:C:299:LEU:O	1:C:342:LYS:NZ	2.31	0.64
1:B:110:ARG:NH2	1:B:153:ASP:OD2	2.31	0.64
1:C:110:ARG:NH2	1:C:153:ASP:OD2	2.31	0.64
1:C:347:ILE:O	1:C:351:ILE:HG12	1.97	0.64
1:A:299:LEU:O	1:A:342:LYS:NZ	2.31	0.63
1:B:166:MET:HG2	1:B:197:GLU:HG2	1.79	0.63
1:A:110:ARG:NH2	1:A:153:ASP:OD2	2.31	0.63
1:C:166:MET:HG2	1:C:197:GLU:HG2	1.79	0.63
1:D:166:MET:HG2	1:D:197:GLU:HG2	1.79	0.63
1:D:110:ARG:NH2	1:D:153:ASP:OD2	2.31	0.63
1:A:229:LEU:HD23	1:A:240:ALA:CB	2.30	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:MET:HE1	1:D:99:LEU:HD12	1.82	0.62
1:C:229:LEU:HD23	1:C:240:ALA:CB	2.30	0.62
1:D:261:PRO:CB	1:D:329:GLN:HE21	2.13	0.62
1:D:229:LEU:HD23	1:D:240:ALA:CB	2.30	0.62
1:B:229:LEU:HD23	1:B:240:ALA:CB	2.30	0.61
1:A:261:PRO:CB	1:A:329:GLN:HE21	2.13	0.61
1:B:261:PRO:CB	1:B:329:GLN:HE21	2.13	0.61
1:C:114:VAL:HA	1:C:153:ASP:OD2	2.00	0.61
1:C:196:MET:HE3	1:C:236:ILE:HD13	1.83	0.61
1:B:114:VAL:HA	1:B:153:ASP:OD2	2.00	0.61
1:C:261:PRO:CB	1:C:329:GLN:HE21	2.13	0.61
1:D:114:VAL:HA	1:D:153:ASP:OD2	2.00	0.61
1:A:114:VAL:HA	1:A:153:ASP:OD2	2.00	0.60
1:D:329:GLN:HE22	2:D:1003:NDP:H2B	1.68	0.59
1:C:281:GLU:HA	1:C:284:ARG:HD2	1.84	0.59
1:A:281:GLU:HA	1:A:284:ARG:HD2	1.84	0.59
1:D:281:GLU:HA	1:D:284:ARG:HD2	1.84	0.59
1:A:329:GLN:HE22	2:A:1000:NDP:H2B	1.68	0.59
1:B:329:GLN:HE22	2:B:1001:NDP:H2B	1.68	0.58
1:C:329:GLN:HE22	2:C:1002:NDP:H2B	1.68	0.58
1:D:313:ARG:HG3	1:D:314:ASN:N	2.19	0.58
1:A:313:ARG:HG3	1:A:314:ASN:N	2.19	0.57
1:B:313:ARG:HG3	1:B:314:ASN:N	2.19	0.57
1:A:58:VAL:HG22	1:A:270:TYR:OH	2.05	0.57
1:B:281:GLU:HA	1:B:284:ARG:HD2	1.84	0.57
1:C:313:ARG:HG3	1:C:314:ASN:N	2.19	0.57
1:B:58:VAL:HG22	1:B:270:TYR:OH	2.05	0.57
1:B:36:LEU:HD22	1:B:340:LEU:HD23	1.87	0.57
1:D:58:VAL:HG22	1:D:270:TYR:OH	2.05	0.57
1:B:352:ASP:O	1:B:356:GLY:N	2.33	0.56
1:C:58:VAL:HG22	1:C:270:TYR:OH	2.05	0.56
1:C:344:SER:O	1:C:348:VAL:HG23	2.05	0.56
1:D:301:CYS:HB2	1:D:305:GLN:HE21	1.70	0.56
1:B:245:PRO:HD2	2:B:1001:NDP:O1A	2.06	0.56
1:C:36:LEU:HD22	1:C:340:LEU:HD23	1.87	0.56
1:D:344:SER:O	1:D:348:VAL:HG23	2.05	0.56
1:D:36:LEU:HD22	1:D:340:LEU:HD23	1.87	0.56
1:D:196:MET:HE3	1:D:236:ILE:HD13	1.88	0.56
1:C:73:MET:HG3	1:C:84:PHE:CE2	2.41	0.56
1:A:73:MET:HG3	1:A:84:PHE:CE2	2.41	0.56
1:A:301:CYS:HB2	1:A:305:GLN:NE2	2.21	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ASP:O	1:A:356:GLY:N	2.33	0.56
1:D:245:PRO:HD2	2:D:1003:NDP:O1A	2.06	0.56
1:A:245:PRO:HD2	2:A:1000:NDP:O1A	2.06	0.56
1:B:301:CYS:HB2	1:B:305:GLN:NE2	2.21	0.56
1:C:245:PRO:HD2	2:C:1002:NDP:O1A	2.06	0.56
1:A:301:CYS:HB2	1:A:305:GLN:HE21	1.70	0.56
1:C:73:MET:HE1	1:C:99:LEU:HD12	1.87	0.56
1:C:301:CYS:HB2	1:C:305:GLN:NE2	2.21	0.56
1:D:301:CYS:HB2	1:D:305:GLN:NE2	2.21	0.56
1:A:344:SER:O	1:A:348:VAL:HG23	2.05	0.55
1:B:344:SER:O	1:B:348:VAL:HG23	2.05	0.55
1:A:185:TRP:CH2	1:A:210:PRO:HG3	2.41	0.55
1:C:352:ASP:O	1:C:356:GLY:N	2.33	0.55
1:B:301:CYS:HB2	1:B:305:GLN:HE21	1.70	0.55
1:C:185:TRP:CH2	1:C:210:PRO:HG3	2.41	0.55
1:D:352:ASP:O	1:D:356:GLY:N	2.33	0.55
1:A:196:MET:HE3	1:A:196:MET:HA	1.87	0.55
1:B:73:MET:HG3	1:B:84:PHE:CE2	2.41	0.55
1:B:244:SER:N	1:B:245:PRO:HD3	2.22	0.55
1:B:185:TRP:CH2	1:B:210:PRO:HG3	2.41	0.55
1:C:301:CYS:HB2	1:C:305:GLN:HE21	1.70	0.55
1:D:185:TRP:CH2	1:D:210:PRO:HG3	2.41	0.55
1:A:36:LEU:HD22	1:A:340:LEU:HD23	1.87	0.55
1:D:73:MET:HG3	1:D:84:PHE:CE2	2.41	0.55
1:B:196:MET:HE3	1:B:236:ILE:HD13	1.88	0.55
1:A:244:SER:N	1:A:245:PRO:HD3	2.22	0.54
1:C:244:SER:N	1:C:245:PRO:HD3	2.22	0.54
1:B:40:ARG:HD2	1:B:40:ARG:N	2.23	0.54
1:C:55:GLY:HA3	2:C:1002:NDP:HO3N	1.73	0.54
1:D:40:ARG:N	1:D:40:ARG:HD2	2.23	0.54
1:A:40:ARG:HD2	1:A:40:ARG:N	2.23	0.54
1:D:244:SER:N	1:D:245:PRO:HD3	2.22	0.53
2:D:1003:NDP:H6N	2:D:1003:NDP:C5D	2.35	0.53
1:B:57:TRP:HB3	2:B:1001:NDP:H3D	1.92	0.52
1:C:40:ARG:HD2	1:C:40:ARG:N	2.23	0.52
1:B:165:PRO:CG	1:C:44:LYS:O	2.57	0.52
1:B:261:PRO:CB	1:B:329:GLN:NE2	2.73	0.52
1:C:261:PRO:CB	1:C:329:GLN:NE2	2.73	0.52
1:A:57:TRP:HB3	2:A:1000:NDP:H3D	1.92	0.52
1:A:261:PRO:CB	1:A:329:GLN:NE2	2.73	0.52
1:A:120:PHE:O	1:A:129:ARG:HA	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1000:NDP:H6N	2:A:1000:NDP:C5D	2.35	0.51
1:C:55:GLY:CA	2:C:1002:NDP:O3D	2.56	0.51
1:D:57:TRP:HB3	2:D:1003:NDP:H3D	1.92	0.51
1:C:57:TRP:HB3	2:C:1002:NDP:H3D	1.92	0.51
1:C:120:PHE:O	1:C:129:ARG:HA	2.10	0.51
1:D:120:PHE:O	1:D:129:ARG:HA	2.10	0.51
1:D:261:PRO:CB	1:D:329:GLN:NE2	2.73	0.51
1:A:196:MET:HE3	1:A:236:ILE:HD13	1.93	0.51
1:B:120:PHE:O	1:B:129:ARG:HA	2.10	0.51
1:A:133:ARG:O	1:A:137:ILE:HG12	2.11	0.51
1:A:338:GLN:O	1:A:341:PRO:HD2	2.11	0.51
1:C:338:GLN:O	1:C:341:PRO:HD2	2.10	0.51
1:B:133:ARG:O	1:B:137:ILE:HG12	2.11	0.50
2:C:1002:NDP:H6N	2:C:1002:NDP:C5D	2.35	0.50
1:B:57:TRP:CD2	1:B:58:VAL:HG23	2.47	0.50
1:C:106:LYS:HG3	1:C:108:TRP:CH2	2.47	0.50
1:B:338:GLN:O	1:B:341:PRO:HD2	2.11	0.50
1:D:214:GLN:HA	1:D:241:MET:O	2.12	0.50
1:D:338:GLN:O	1:D:341:PRO:HD2	2.11	0.50
1:C:57:TRP:CD2	1:C:58:VAL:HG23	2.47	0.50
1:D:55:GLY:CA	2:D:1003:NDP:O3D	2.56	0.50
1:D:106:LYS:HG3	1:D:108:TRP:CH2	2.47	0.50
1:A:214:GLN:HA	1:A:241:MET:O	2.12	0.50
1:D:57:TRP:CD2	1:D:58:VAL:HG23	2.47	0.50
1:D:133:ARG:O	1:D:137:ILE:HG12	2.11	0.50
1:C:133:ARG:O	1:C:137:ILE:HG12	2.11	0.50
1:C:281:GLU:HA	1:C:284:ARG:CD	2.42	0.50
1:A:106:LYS:HG3	1:A:108:TRP:CH2	2.47	0.49
1:A:57:TRP:CD2	1:A:58:VAL:HG23	2.47	0.49
1:A:281:GLU:HA	1:A:284:ARG:CD	2.42	0.49
1:B:196:MET:CE	1:B:199:TYR:HB3	2.42	0.49
1:D:196:MET:HE3	1:D:196:MET:HA	1.94	0.49
1:B:281:GLU:HA	1:B:284:ARG:CD	2.42	0.49
1:C:214:GLN:HA	1:C:241:MET:O	2.12	0.49
2:C:1002:NDP:H8A	2:C:1002:NDP:H52A	1.95	0.49
1:A:216:GLU:HB2	1:A:243:TRP:CH2	2.48	0.49
1:B:217:TYR:HB3	1:B:242:THR:HB	1.95	0.49
1:B:251:VAL:HG12	1:B:251:VAL:O	2.13	0.49
1:D:217:TYR:HB3	1:D:242:THR:HB	1.95	0.49
1:A:196:MET:CE	1:A:199:TYR:HB3	2.42	0.49
1:A:217:TYR:HB3	1:A:242:THR:HB	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:VAL:O	1:A:251:VAL:HG12	2.13	0.49
1:B:106:LYS:HG3	1:B:108:TRP:CH2	2.47	0.49
1:C:196:MET:CE	1:C:199:TYR:HB3	2.42	0.49
1:B:250:ILE:HG21	1:B:285:GLN:HE21	1.78	0.49
1:C:302:THR:H	1:C:305:GLN:HE21	1.61	0.49
1:D:250:ILE:HG21	1:D:285:GLN:HE21	1.77	0.49
1:B:214:GLN:HA	1:B:241:MET:O	2.12	0.49
1:D:251:VAL:HG12	1:D:251:VAL:O	2.13	0.49
1:D:216:GLU:HB2	1:D:243:TRP:CH2	2.48	0.49
1:B:55:GLY:CA	2:B:1001:NDP:O3D	2.56	0.48
1:B:216:GLU:HB2	1:B:243:TRP:CH2	2.48	0.48
1:D:196:MET:CE	1:D:199:TYR:HB3	2.42	0.48
1:A:250:ILE:HG21	1:A:285:GLN:HE21	1.78	0.48
1:C:216:GLU:HB2	1:C:243:TRP:CH2	2.48	0.48
1:D:302:THR:H	1:D:305:GLN:HE21	1.61	0.48
1:A:166:MET:CE	1:A:166:MET:HA	2.43	0.48
1:C:166:MET:HA	1:C:166:MET:CE	2.43	0.48
2:D:1003:NDP:H52A	2:D:1003:NDP:H8A	1.95	0.48
1:B:166:MET:HA	1:B:166:MET:CE	2.43	0.48
1:A:302:THR:H	1:A:305:GLN:HE21	1.61	0.48
2:A:1000:NDP:H8A	2:A:1000:NDP:H52A	1.95	0.48
1:B:173:MET:HG3	1:B:185:TRP:CE3	2.49	0.48
2:B:1001:NDP:H8A	2:B:1001:NDP:H52A	1.95	0.48
1:C:36:LEU:HD12	1:C:37:GLN:H	1.79	0.48
1:C:217:TYR:HB3	1:C:242:THR:HB	1.95	0.48
1:D:36:LEU:HD12	1:D:37:GLN:H	1.79	0.48
1:D:173:MET:HG3	1:D:185:TRP:CE3	2.49	0.48
1:A:173:MET:HG3	1:A:185:TRP:CE3	2.49	0.47
1:B:36:LEU:HD12	1:B:37:GLN:H	1.79	0.47
1:C:251:VAL:HG12	1:C:251:VAL:O	2.13	0.47
1:B:196:MET:HE3	1:B:196:MET:HA	1.94	0.47
1:A:110:ARG:NH1	1:A:151:TYR:O	2.48	0.47
1:D:166:MET:HA	1:D:166:MET:CE	2.43	0.47
1:C:173:MET:HG3	1:C:185:TRP:CE3	2.49	0.47
1:D:281:GLU:HA	1:D:284:ARG:CD	2.42	0.47
1:D:166:MET:HA	1:D:166:MET:HE2	1.96	0.47
1:C:73:MET:CE	1:C:99:LEU:HD12	2.45	0.47
1:A:303:LEU:N	1:A:304:PRO:CD	2.78	0.47
1:B:110:ARG:NH1	1:B:151:TYR:O	2.48	0.47
1:C:250:ILE:HG21	1:C:285:GLN:HE21	1.77	0.47
1:A:36:LEU:HD12	1:A:37:GLN:H	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:340:LEU:HB3	1:C:341:PRO:HD3	1.97	0.47
1:A:254:LYS:HB2	1:A:254:LYS:HE3	1.71	0.47
1:D:110:ARG:NH1	1:D:151:TYR:O	2.48	0.47
1:D:340:LEU:HB3	1:D:341:PRO:HD3	1.97	0.47
1:B:68:MET:HA	1:B:68:MET:CE	2.46	0.46
1:B:191:SER:OG	1:B:194:GLU:HG3	2.16	0.46
1:D:73:MET:CE	1:D:99:LEU:HD12	2.45	0.46
1:C:68:MET:CE	1:C:68:MET:HA	2.45	0.46
1:C:218:HIS:CE1	1:C:221:GLN:HB2	2.50	0.46
1:C:303:LEU:N	1:C:304:PRO:CD	2.78	0.46
1:D:218:HIS:CE1	1:D:221:GLN:HB2	2.50	0.46
1:A:191:SER:OG	1:A:194:GLU:HG3	2.16	0.46
1:D:68:MET:HA	1:D:68:MET:CE	2.46	0.46
1:B:303:LEU:N	1:B:304:PRO:CD	2.78	0.46
1:D:303:LEU:N	1:D:304:PRO:CD	2.78	0.46
1:A:68:MET:CE	1:A:68:MET:HA	2.46	0.46
1:A:218:HIS:CE1	1:A:221:GLN:HB2	2.50	0.46
1:B:57:TRP:CG	1:B:58:VAL:HG23	2.51	0.46
1:C:57:TRP:CG	1:C:58:VAL:HG23	2.51	0.46
1:D:254:LYS:HA	1:D:258:GLY:CA	2.29	0.46
1:D:57:TRP:CG	1:D:58:VAL:HG23	2.51	0.46
1:A:57:TRP:CG	1:A:58:VAL:HG23	2.51	0.45
1:A:215:ALA:O	1:A:242:THR:HA	2.16	0.45
1:B:302:THR:H	1:B:305:GLN:HE21	1.61	0.45
1:D:191:SER:OG	1:D:194:GLU:HG3	2.16	0.45
1:D:196:MET:HA	1:D:196:MET:CE	2.47	0.45
1:B:196:MET:CE	1:B:196:MET:HA	2.47	0.45
1:B:340:LEU:HB3	1:B:341:PRO:HD3	1.97	0.45
1:B:215:ALA:O	1:B:242:THR:HA	2.16	0.45
1:C:254:LYS:HB2	1:C:254:LYS:HE3	1.72	0.45
1:B:218:HIS:CE1	1:B:221:GLN:HB2	2.50	0.45
1:A:340:LEU:HB3	1:A:341:PRO:HD3	1.97	0.45
1:B:165:PRO:HG2	1:C:44:LYS:O	2.15	0.45
1:A:302:THR:CB	1:A:304:PRO:HD2	2.47	0.45
1:B:167:GLU:HA	1:B:201:VAL:HG11	1.99	0.45
1:C:167:GLU:HA	1:C:201:VAL:HG11	1.99	0.45
1:C:191:SER:OG	1:C:194:GLU:HG3	2.16	0.45
1:D:254:LYS:NZ	1:D:262:TYR:O	2.49	0.45
1:D:302:THR:CB	1:D:304:PRO:HD2	2.47	0.45
1:B:36:LEU:HD13	1:B:340:LEU:CD2	2.47	0.45
1:C:215:ALA:O	1:C:242:THR:HA	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:36:LEU:HD13	1:D:340:LEU:CD2	2.47	0.45
1:C:302:THR:CB	1:C:304:PRO:HD2	2.47	0.45
1:A:36:LEU:HD13	1:A:340:LEU:CD2	2.47	0.44
1:B:269:GLY:HA2	1:B:271:GLN:HE22	1.82	0.44
1:C:196:MET:CE	1:C:196:MET:HA	2.47	0.44
1:C:339:VAL:HG12	1:C:339:VAL:O	2.17	0.44
1:C:166:MET:HA	1:C:166:MET:HE2	2.00	0.44
1:D:215:ALA:O	1:D:242:THR:HA	2.16	0.44
1:D:221:GLN:OE1	1:D:221:GLN:HA	2.17	0.44
1:A:196:MET:HA	1:A:196:MET:CE	2.47	0.44
1:B:221:GLN:HA	1:B:221:GLN:OE1	2.17	0.44
1:C:36:LEU:HD13	1:C:340:LEU:CD2	2.47	0.44
1:A:305:GLN:HB3	1:A:339:VAL:HG21	2.00	0.44
1:A:339:VAL:HG12	1:A:339:VAL:O	2.17	0.44
1:C:110:ARG:NH1	1:C:151:TYR:O	2.48	0.44
1:C:221:GLN:OE1	1:C:221:GLN:HA	2.17	0.44
1:D:167:GLU:HA	1:D:201:VAL:HG11	1.99	0.44
1:A:55:GLY:CA	2:A:1000:NDP:O3D	2.56	0.44
1:C:73:MET:HE3	1:C:73:MET:HB2	1.79	0.44
1:A:254:LYS:HA	1:A:258:GLY:CA	2.29	0.44
1:B:305:GLN:HB3	1:B:339:VAL:HG21	2.00	0.44
1:D:339:VAL:HG12	1:D:339:VAL:O	2.17	0.44
1:A:269:GLY:HA2	1:A:271:GLN:HE22	1.82	0.44
1:B:302:THR:CB	1:B:304:PRO:HD2	2.47	0.44
1:B:73:MET:CE	1:B:99:LEU:HD12	2.45	0.44
2:B:1001:NDP:H6N	2:B:1001:NDP:C5D	2.35	0.44
1:D:73:MET:HB2	1:D:73:MET:HE3	1.82	0.44
1:A:119:ILE:O	1:A:120:PHE:HB2	2.19	0.43
1:B:254:LYS:HA	1:B:258:GLY:CA	2.29	0.43
1:B:302:THR:HB	1:B:304:PRO:HD2	2.00	0.43
1:B:339:VAL:HG12	1:B:339:VAL:O	2.17	0.43
1:A:165:PRO:HG2	1:D:44:LYS:O	2.18	0.43
1:A:221:GLN:OE1	1:A:221:GLN:HA	2.17	0.43
1:C:269:GLY:HA2	1:C:271:GLN:HE22	1.82	0.43
1:A:99:LEU:HD23	1:A:147:LEU:HD21	2.00	0.43
1:B:358:LYS:HA	1:B:359:PRO:HD3	1.85	0.43
1:D:99:LEU:HD23	1:D:147:LEU:HD21	2.00	0.43
1:B:99:LEU:HD23	1:B:147:LEU:HD21	2.00	0.43
1:C:202:ALA:HA	1:C:207:LEU:HB2	2.01	0.43
1:D:151:TYR:HB3	1:D:180:GLY:O	2.18	0.43
1:A:73:MET:CE	1:A:99:LEU:HD12	2.45	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:THR:HB	1:C:304:PRO:HD2	2.01	0.43
1:A:151:TYR:HB3	1:A:180:GLY:O	2.18	0.43
1:A:302:THR:HB	1:A:304:PRO:HD2	2.01	0.43
1:D:305:GLN:HB3	1:D:339:VAL:HG21	2.00	0.43
1:A:167:GLU:HA	1:A:201:VAL:HG11	1.99	0.43
1:C:151:TYR:HB3	1:C:180:GLY:O	2.18	0.43
1:C:305:GLN:HB3	1:C:339:VAL:HG21	2.00	0.43
1:D:269:GLY:HA2	1:D:271:GLN:HE22	1.82	0.43
1:B:202:ALA:HA	1:B:207:LEU:HB2	2.01	0.43
1:B:208:ILE:HA	1:B:209:PRO:HD3	1.85	0.43
1:A:358:LYS:HA	1:A:359:PRO:HD3	1.84	0.42
1:C:99:LEU:HD23	1:C:147:LEU:HD21	2.00	0.42
1:B:151:TYR:HB3	1:B:180:GLY:O	2.18	0.42
1:C:91:ALA:HB1	1:C:94:LYS:HE3	2.02	0.42
1:A:254:LYS:N	1:A:258:GLY:HA3	2.35	0.42
1:D:246:LEU:HA	1:D:251:VAL:HB	2.02	0.42
1:A:254:LYS:NZ	1:A:262:TYR:O	2.49	0.42
1:D:302:THR:HB	1:D:304:PRO:HD2	2.01	0.42
1:B:119:ILE:O	1:B:120:PHE:HB2	2.19	0.42
1:C:246:LEU:HA	1:C:251:VAL:HB	2.02	0.42
1:D:202:ALA:HA	1:D:207:LEU:HB2	2.01	0.42
1:A:126:GLU:HG2	1:D:39:TYR:CG	2.55	0.42
2:B:1001:NDP:H52N	2:B:1001:NDP:C6N	2.38	0.42
1:C:57:TRP:C	1:C:59:THR:H	2.23	0.42
1:A:187:THR:O	1:A:213:GLU:HA	2.20	0.42
1:B:91:ALA:HB1	1:B:94:LYS:HE3	2.01	0.42
1:D:119:ILE:O	1:D:120:PHE:HB2	2.19	0.42
1:B:57:TRP:C	1:B:59:THR:H	2.23	0.42
1:B:126:GLU:HG2	1:C:39:TYR:CD2	2.55	0.42
1:B:247:ALA:O	1:B:248:CYS:HB2	2.20	0.42
1:B:254:LYS:HB2	1:B:254:LYS:HE3	1.71	0.42
1:D:120:PHE:CD1	1:D:159:ARG:HG3	2.55	0.42
1:B:178:ASN:O	1:D:175:HIS:HE1	2.02	0.41
1:C:187:THR:O	1:C:213:GLU:HA	2.20	0.41
1:D:91:ALA:HB1	1:D:94:LYS:HE3	2.02	0.41
1:D:254:LYS:N	1:D:258:GLY:HA3	2.35	0.41
1:C:119:ILE:O	1:C:120:PHE:HB2	2.19	0.41
1:B:159:ARG:HB2	1:B:160:PRO:CD	2.51	0.41
1:B:163:ASN:HB3	1:C:41:ASN:HD21	1.83	0.41
1:D:57:TRP:C	1:D:59:THR:H	2.23	0.41
1:A:159:ARG:HB2	1:A:160:PRO:CD	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:ARG:HB2	1:D:160:PRO:CD	2.51	0.41
1:D:187:THR:O	1:D:213:GLU:HA	2.20	0.41
2:D:1003:NDP:H52N	2:D:1003:NDP:C6N	2.38	0.41
1:A:57:TRP:C	1:A:59:THR:H	2.23	0.41
1:A:202:ALA:HA	1:A:207:LEU:HB2	2.01	0.41
1:C:247:ALA:O	1:C:248:CYS:HB2	2.20	0.41
1:A:86:THR:O	1:A:117:THR:HA	2.21	0.41
1:A:247:ALA:O	1:A:248:CYS:HB2	2.20	0.41
1:B:120:PHE:CD1	1:B:159:ARG:HG3	2.55	0.41
1:D:86:THR:O	1:D:117:THR:HA	2.21	0.41
1:D:247:ALA:O	1:D:248:CYS:HB2	2.20	0.41
1:C:196:MET:HE3	1:C:196:MET:HA	2.03	0.41
1:C:254:LYS:N	1:C:258:GLY:HA3	2.35	0.41
1:C:358:LYS:HA	1:C:359:PRO:HD3	1.85	0.41
1:C:115:ILE:N	1:C:153:ASP:OD2	2.52	0.41
1:D:254:LYS:HE3	1:D:254:LYS:HB2	1.72	0.41
1:A:120:PHE:CD1	1:A:159:ARG:HG3	2.55	0.41
1:A:126:GLU:HG2	1:D:39:TYR:CD2	2.55	0.41
1:A:246:LEU:HA	1:A:251:VAL:HB	2.02	0.41
2:A:1000:NDP:H52N	2:A:1000:NDP:C6N	2.38	0.41
1:B:187:THR:O	1:B:213:GLU:HA	2.20	0.41
1:B:246:LEU:HA	1:B:251:VAL:HB	2.02	0.41
1:B:254:LYS:NZ	1:B:262:TYR:O	2.49	0.41
1:C:86:THR:O	1:C:117:THR:HA	2.21	0.41
1:C:159:ARG:HB2	1:C:160:PRO:CD	2.51	0.41
1:A:302:THR:OG1	1:A:304:PRO:HD2	2.21	0.41
1:B:68:MET:O	1:B:68:MET:HE2	2.21	0.41
1:C:120:PHE:CD1	1:C:159:ARG:HG3	2.55	0.41
1:B:137:ILE:CD1	1:B:175:HIS:HD2	2.34	0.40
1:C:137:ILE:CD1	1:C:175:HIS:HD2	2.34	0.40
1:D:118:LYS:HE3	2:D:1003:NDP:N7N	2.37	0.40
1:A:91:ALA:HB1	1:A:94:LYS:HE3	2.02	0.40
1:B:171:ARG:HH22	1:C:206:ASN:ND2	2.19	0.40
1:C:118:LYS:HE3	2:C:1002:NDP:N7N	2.37	0.40
1:D:115:ILE:N	1:D:153:ASP:OD2	2.53	0.40
1:A:166:MET:HA	1:A:166:MET:HE2	2.03	0.40
1:B:302:THR:OG1	1:B:304:PRO:HD2	2.21	0.40
1:D:302:THR:OG1	1:D:304:PRO:HD2	2.21	0.40
1:B:86:THR:O	1:B:117:THR:HA	2.21	0.40
1:B:254:LYS:N	1:B:258:GLY:HA3	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	323/325 (99%)	312 (97%)	6 (2%)	5 (2%)	10	33
1	B	323/325 (99%)	312 (97%)	6 (2%)	5 (2%)	10	33
1	C	323/325 (99%)	312 (97%)	6 (2%)	5 (2%)	10	33
1	D	323/325 (99%)	312 (97%)	6 (2%)	5 (2%)	10	33
All	All	1292/1300 (99%)	1248 (97%)	24 (2%)	20 (2%)	10	33

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	261	PRO
1	B	261	PRO
1	C	261	PRO
1	D	261	PRO
1	A	58	VAL
1	A	120	PHE
1	A	256	ASP
1	B	58	VAL
1	B	120	PHE
1	B	256	ASP
1	C	58	VAL
1	C	120	PHE
1	C	256	ASP
1	D	58	VAL
1	D	120	PHE
1	D	256	ASP
1	A	254	LYS
1	B	254	LYS
1	C	254	LYS
1	D	254	LYS

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	257/272 (94%)	251 (98%)	6 (2%)	50	82
1	B	257/272 (94%)	251 (98%)	6 (2%)	50	82
1	C	257/272 (94%)	251 (98%)	6 (2%)	50	82
1	D	257/272 (94%)	251 (98%)	6 (2%)	50	82
All	All	1028/1088 (94%)	1004 (98%)	24 (2%)	50	82

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	48	ARG
1	A	110	ARG
1	A	158	ASN
1	A	206	ASN
1	A	268	LYS
1	B	40	ARG
1	B	48	ARG
1	B	110	ARG
1	B	158	ASN
1	B	206	ASN
1	B	268	LYS
1	C	40	ARG
1	C	48	ARG
1	C	110	ARG
1	C	158	ASN
1	C	206	ASN
1	C	268	LYS
1	D	40	ARG
1	D	48	ARG
1	D	110	ARG
1	D	158	ASN
1	D	206	ASN
1	D	268	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	101	ASN
1	A	148	GLN
1	A	158	ASN
1	A	175	HIS
1	A	206	ASN
1	A	271	GLN
1	A	285	GLN
1	A	305	GLN
1	B	71	HIS
1	B	101	ASN
1	B	148	GLN
1	B	158	ASN
1	B	175	HIS
1	B	206	ASN
1	B	271	GLN
1	B	285	GLN
1	B	305	GLN
1	C	71	HIS
1	C	101	ASN
1	C	148	GLN
1	C	158	ASN
1	C	175	HIS
1	C	206	ASN
1	C	271	GLN
1	C	285	GLN
1	C	305	GLN
1	D	71	HIS
1	D	101	ASN
1	D	148	GLN
1	D	158	ASN
1	D	175	HIS
1	D	206	ASN
1	D	271	GLN
1	D	285	GLN
1	D	305	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NDP	B	1001	-	47,52,52	2.26	14 (29%)	61,80,80	1.98	15 (24%)
2	NDP	D	1003	-	47,52,52	2.26	14 (29%)	61,80,80	1.98	15 (24%)
2	NDP	C	1002	-	47,52,52	2.27	14 (29%)	61,80,80	1.98	15 (24%)
2	NDP	A	1000	-	47,52,52	2.27	14 (29%)	61,80,80	1.98	15 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDP	B	1001	-	-	4/30/77/77	0/5/5/5
2	NDP	D	1003	-	-	4/30/77/77	0/5/5/5
2	NDP	C	1002	-	-	4/30/77/77	0/5/5/5
2	NDP	A	1000	-	-	4/30/77/77	0/5/5/5

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1002	NDP	PA-O3	-8.81	1.50	1.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	NDP	PA-O3	-8.76	1.50	1.59
2	B	1001	NDP	PA-O3	-8.76	1.50	1.59
2	D	1003	NDP	PA-O3	-8.72	1.50	1.59
2	C	1002	NDP	P2B-O2B	6.14	1.70	1.59
2	B	1001	NDP	P2B-O2B	6.10	1.70	1.59
2	A	1000	NDP	P2B-O2B	6.10	1.70	1.59
2	D	1003	NDP	P2B-O2B	6.09	1.70	1.59
2	D	1003	NDP	C7N-C3N	4.47	1.58	1.48
2	C	1002	NDP	C7N-C3N	4.46	1.58	1.48
2	A	1000	NDP	C7N-C3N	4.45	1.58	1.48
2	B	1001	NDP	C7N-C3N	4.45	1.58	1.48
2	C	1002	NDP	C2A-N1A	3.50	1.40	1.33
2	D	1003	NDP	C2A-N1A	3.50	1.40	1.33
2	A	1000	NDP	C2A-N1A	3.49	1.40	1.33
2	B	1001	NDP	C2A-N1A	3.44	1.40	1.33
2	C	1002	NDP	P2B-O3X	-2.95	1.43	1.54
2	A	1000	NDP	P2B-O3X	-2.95	1.43	1.54
2	B	1001	NDP	P2B-O3X	-2.95	1.43	1.54
2	D	1003	NDP	P2B-O3X	-2.93	1.43	1.54
2	D	1003	NDP	C1D-N1N	2.93	1.54	1.46
2	C	1002	NDP	C3B-C2B	2.93	1.59	1.53
2	A	1000	NDP	C1D-N1N	2.93	1.54	1.46
2	B	1001	NDP	C1D-N1N	2.92	1.54	1.46
2	C	1002	NDP	C1D-N1N	2.92	1.54	1.46
2	D	1003	NDP	C3B-C2B	2.91	1.59	1.53
2	A	1000	NDP	C3B-C2B	2.89	1.59	1.53
2	B	1001	NDP	C3B-C2B	2.88	1.59	1.53
2	C	1002	NDP	O4D-C1D	2.63	1.48	1.42
2	B	1001	NDP	O4D-C1D	2.62	1.48	1.42
2	A	1000	NDP	O4D-C1D	2.60	1.48	1.42
2	D	1003	NDP	O4D-C1D	2.58	1.48	1.42
2	C	1002	NDP	C2N-C3N	2.55	1.42	1.35
2	A	1000	NDP	C2N-C3N	2.55	1.42	1.35
2	B	1001	NDP	C2N-C3N	2.55	1.42	1.35
2	D	1003	NDP	C2N-C3N	2.55	1.42	1.35
2	C	1002	NDP	PN-O3	-2.28	1.57	1.59
2	D	1003	NDP	PN-O3	-2.28	1.57	1.59
2	A	1000	NDP	PN-O3	-2.27	1.57	1.59
2	A	1000	NDP	C8A-N7A	-2.27	1.30	1.34
2	B	1001	NDP	PN-O3	-2.26	1.57	1.59
2	B	1001	NDP	C4N-C3N	-2.26	1.45	1.50
2	C	1002	NDP	C4N-C3N	-2.26	1.45	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	NDP	C4N-C3N	-2.25	1.45	1.50
2	D	1003	NDP	C8A-N7A	-2.25	1.30	1.34
2	B	1001	NDP	C8A-N7A	-2.25	1.30	1.34
2	D	1003	NDP	C4N-C3N	-2.25	1.45	1.50
2	C	1002	NDP	C8A-N7A	-2.24	1.30	1.34
2	D	1003	NDP	C6N-N1N	2.19	1.42	1.37
2	B	1001	NDP	C6N-N1N	2.16	1.42	1.37
2	A	1000	NDP	C6N-N1N	2.16	1.42	1.37
2	C	1002	NDP	C6N-N1N	2.15	1.42	1.37
2	A	1000	NDP	C4A-N3A	2.05	1.38	1.35
2	B	1001	NDP	C4A-N3A	2.05	1.38	1.35
2	C	1002	NDP	C4A-N3A	2.04	1.38	1.35
2	D	1003	NDP	C4A-N3A	2.04	1.38	1.35

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1001	NDP	O2N-PN-O5D	-5.22	83.92	107.57
2	D	1003	NDP	O2N-PN-O5D	-5.21	83.94	107.57
2	A	1000	NDP	O2N-PN-O5D	-5.21	83.95	107.57
2	C	1002	NDP	O2N-PN-O5D	-5.21	83.96	107.57
2	C	1002	NDP	O2N-PN-O3	5.15	121.18	107.27
2	A	1000	NDP	O2N-PN-O3	5.14	121.16	107.27
2	D	1003	NDP	O2N-PN-O3	5.13	121.15	107.27
2	B	1001	NDP	O2N-PN-O3	5.13	121.14	107.27
2	D	1003	NDP	C3N-C2N-N1N	-4.76	116.22	123.20
2	A	1000	NDP	C3N-C2N-N1N	-4.74	116.24	123.20
2	C	1002	NDP	C3N-C2N-N1N	-4.73	116.25	123.20
2	B	1001	NDP	C3N-C2N-N1N	-4.73	116.26	123.20
2	C	1002	NDP	O2B-P2B-O1X	-4.31	93.98	109.33
2	D	1003	NDP	O2B-P2B-O1X	-4.30	94.02	109.33
2	A	1000	NDP	O2B-P2B-O1X	-4.29	94.03	109.33
2	B	1001	NDP	O2B-P2B-O1X	-4.29	94.06	109.33
2	C	1002	NDP	C1D-N1N-C2N	-3.96	114.61	121.14
2	A	1000	NDP	C1D-N1N-C2N	-3.95	114.63	121.14
2	B	1001	NDP	C1D-N1N-C2N	-3.95	114.64	121.14
2	D	1003	NDP	C1D-N1N-C2N	-3.95	114.64	121.14
2	D	1003	NDP	O4D-C1D-N1N	3.79	115.32	108.08
2	A	1000	NDP	O4D-C1D-N1N	3.79	115.31	108.08
2	B	1001	NDP	O4D-C1D-N1N	3.78	115.29	108.08
2	C	1002	NDP	O4D-C1D-N1N	3.77	115.28	108.08
2	C	1002	NDP	C4A-C5A-N7A	3.32	112.84	109.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1003	NDP	C4A-C5A-N7A	3.29	112.81	109.34
2	A	1000	NDP	C4A-C5A-N7A	3.27	112.79	109.34
2	B	1001	NDP	C4A-C5A-N7A	3.25	112.77	109.34
2	D	1003	NDP	PN-O5D-C5D	-3.05	103.88	121.35
2	A	1000	NDP	PN-O5D-C5D	-3.04	103.91	121.35
2	C	1002	NDP	PN-O5D-C5D	-3.04	103.93	121.35
2	B	1001	NDP	PN-O5D-C5D	-3.04	103.95	121.35
2	D	1003	NDP	O3B-C3B-C2B	2.81	119.06	111.19
2	A	1000	NDP	O3B-C3B-C2B	2.80	119.03	111.19
2	C	1002	NDP	O3B-C3B-C2B	2.80	119.02	111.19
2	B	1001	NDP	O3B-C3B-C2B	2.79	119.00	111.19
2	B	1001	NDP	O5D-C5D-C4D	2.47	117.40	108.99
2	C	1002	NDP	O5D-C5D-C4D	2.47	117.40	108.99
2	A	1000	NDP	O5D-C5D-C4D	2.46	117.37	108.99
2	D	1003	NDP	O5D-C5D-C4D	2.45	117.34	108.99
2	B	1001	NDP	N6A-C6A-N1A	2.43	123.53	118.33
2	D	1003	NDP	N6A-C6A-N1A	2.42	123.52	118.33
2	A	1000	NDP	N6A-C6A-N1A	2.42	123.51	118.33
2	C	1002	NDP	N6A-C6A-N1A	2.40	123.47	118.33
2	B	1001	NDP	C3D-C2D-C1D	2.30	105.81	101.46
2	C	1002	NDP	C3D-C2D-C1D	2.29	105.80	101.46
2	A	1000	NDP	C3D-C2D-C1D	2.28	105.78	101.46
2	D	1003	NDP	C3D-C2D-C1D	2.27	105.76	101.46
2	A	1000	NDP	C6N-N1N-C2N	2.17	121.64	119.32
2	D	1003	NDP	C6N-N1N-C2N	2.17	121.64	119.32
2	C	1002	NDP	C6N-N1N-C2N	2.16	121.63	119.32
2	B	1001	NDP	C6N-N1N-C2N	2.15	121.62	119.32
2	D	1003	NDP	C2B-C1B-N9A	2.12	117.26	112.56
2	B	1001	NDP	C2B-C1B-N9A	2.11	117.25	112.56
2	A	1000	NDP	C2B-C1B-N9A	2.10	117.23	112.56
2	D	1003	NDP	C5D-C4D-C3D	-2.10	107.64	115.21
2	C	1002	NDP	C2B-C1B-N9A	2.10	117.23	112.56
2	A	1000	NDP	C5D-C4D-C3D	-2.10	107.66	115.21
2	C	1002	NDP	C5D-C4D-C3D	-2.10	107.66	115.21
2	B	1001	NDP	C5D-C4D-C3D	-2.09	107.67	115.21

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	NDP	O4D-C1D-N1N-C2N
2	B	1001	NDP	O4D-C1D-N1N-C2N

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	C	1002	NDP	O4D-C1D-N1N-C2N
2	D	1003	NDP	O4D-C1D-N1N-C2N
2	A	1000	NDP	C3D-C4D-C5D-O5D
2	B	1001	NDP	C3D-C4D-C5D-O5D
2	C	1002	NDP	C3D-C4D-C5D-O5D
2	D	1003	NDP	C3D-C4D-C5D-O5D
2	A	1000	NDP	O4D-C4D-C5D-O5D
2	B	1001	NDP	O4D-C4D-C5D-O5D
2	C	1002	NDP	O4D-C4D-C5D-O5D
2	D	1003	NDP	O4D-C4D-C5D-O5D
2	A	1000	NDP	PA-O3-PN-O5D
2	B	1001	NDP	PA-O3-PN-O5D
2	C	1002	NDP	PA-O3-PN-O5D
2	D	1003	NDP	PA-O3-PN-O5D

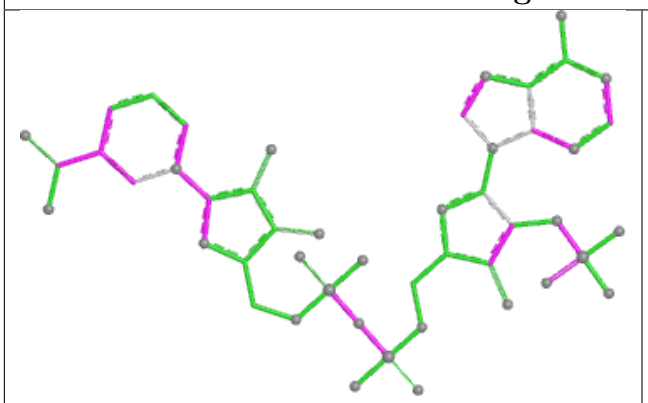
There are no ring outliers.

4 monomers are involved in 38 short contacts:

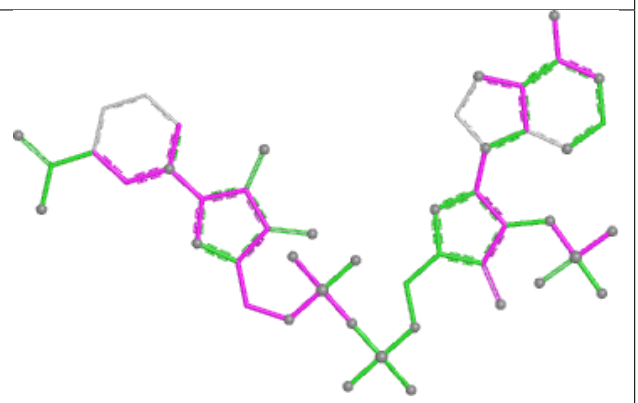
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	NDP	9	0
2	D	1003	NDP	10	0
2	C	1002	NDP	10	0
2	A	1000	NDP	9	0

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

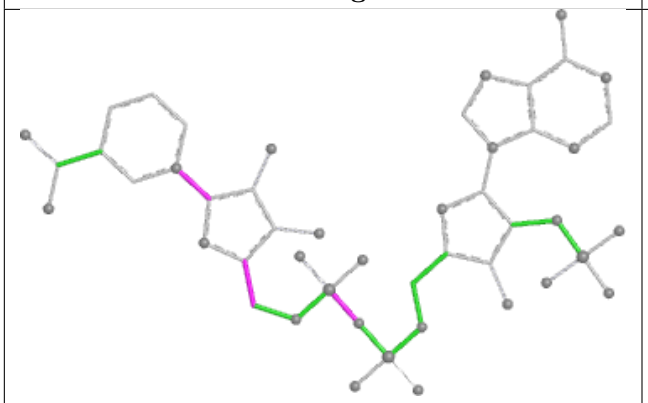
Ligand NDP B 1001



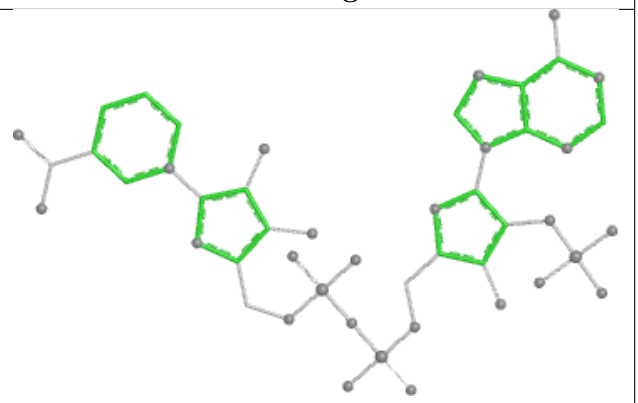
Bond lengths



Bond angles

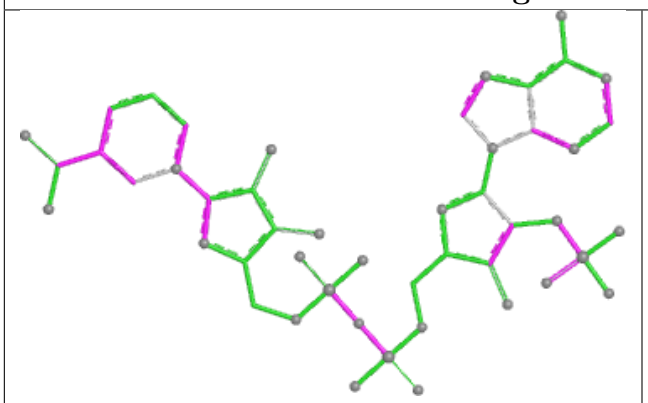


Torsions

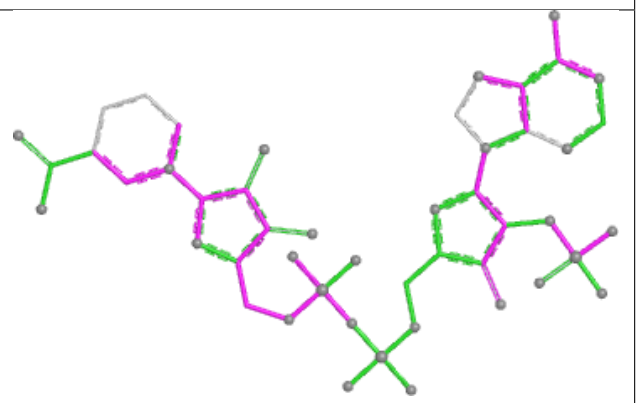


Rings

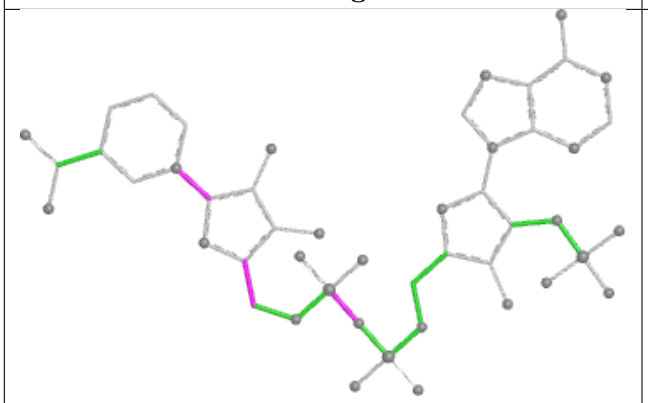
Ligand NDP D 1003



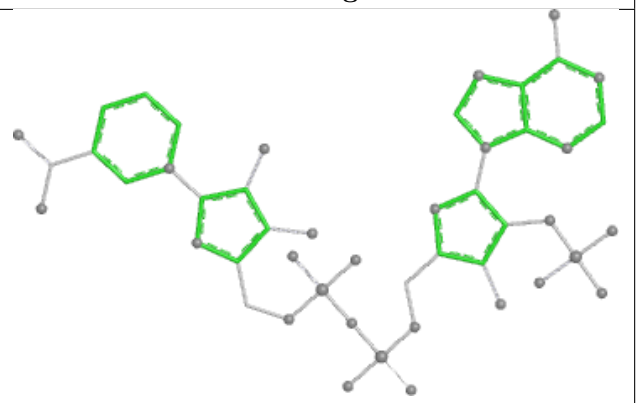
Bond lengths



Bond angles

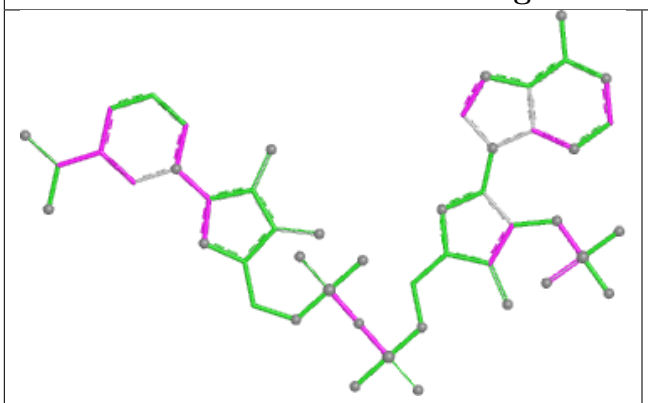


Torsions

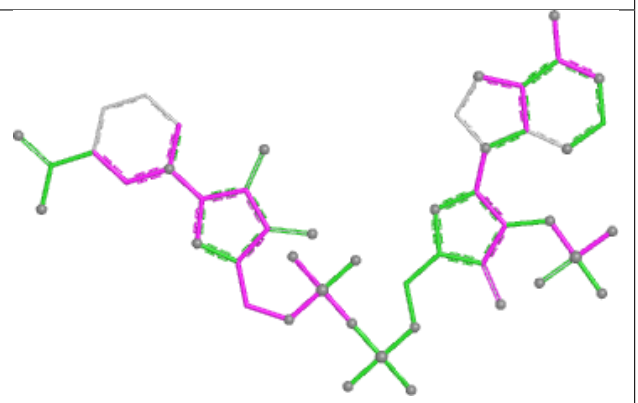


Rings

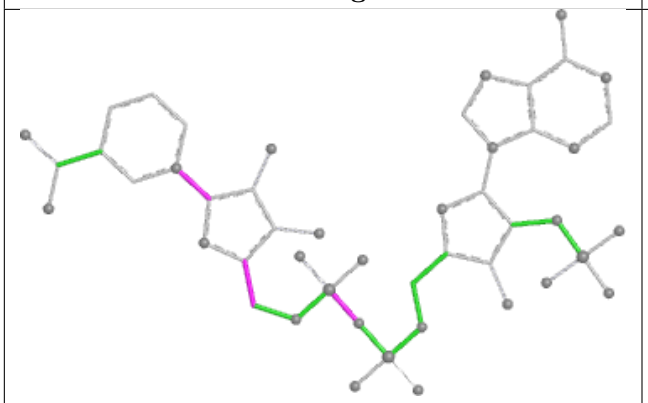
Ligand NDP C 1002



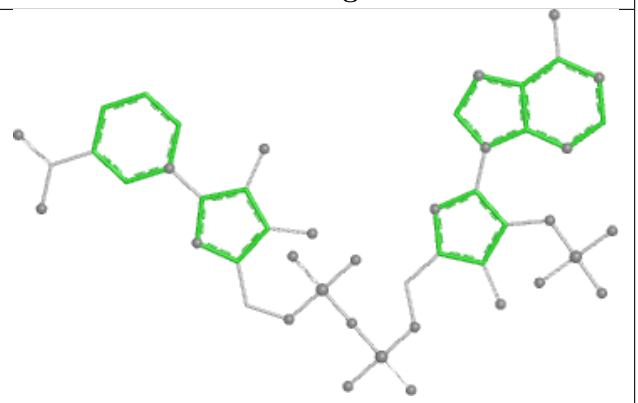
Bond lengths



Bond angles

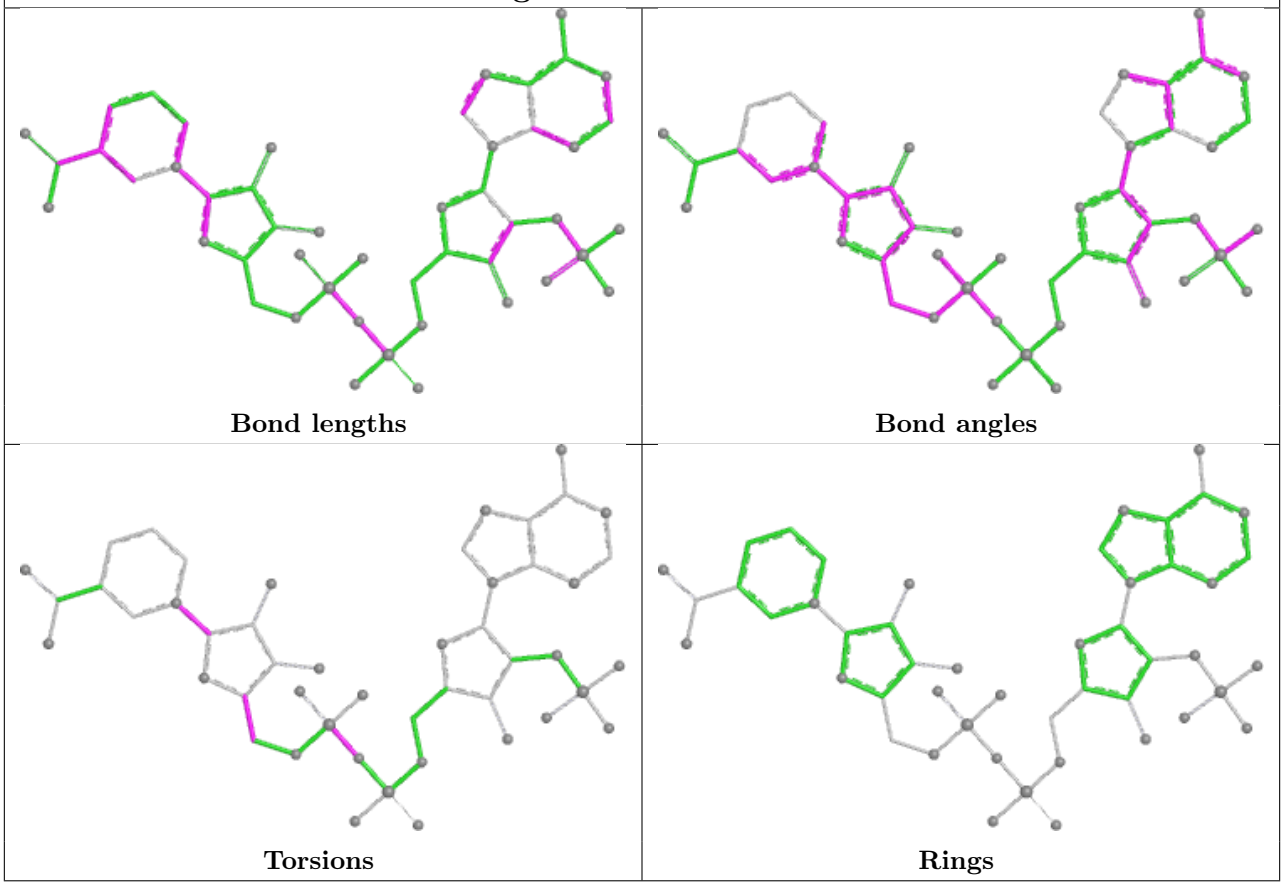


Torsions



Rings

Ligand NDP A 1000



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.