



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 11:21 pm GMT

PDB ID : 2IOD
Title : Binding of two substrate analogue molecules to dihydroflavonol-4-reductase alters the functional geometry of the catalytic site
Authors : Petit, P.; Langlois d'Estaintot, B.; Granier, T.; Gallois, B.
Deposited on : 2006-10-10
Resolution : 2.06 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28683
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

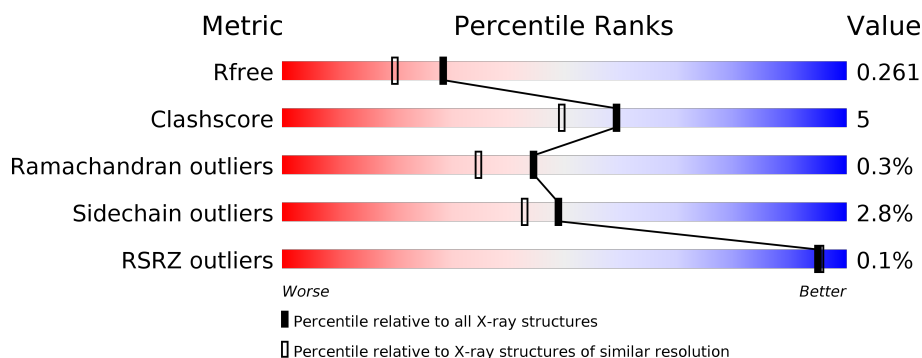
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.06 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}	100719	2028 (2.08-2.04)
Clashscore	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)
RSRZ outliers	101464	2035 (2.08-2.04)

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. 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	337	 76% 18% 5%
1	B	337	 82% 14% . .
1	C	337	 87% 9% .
1	D	337	 86% 9% 5%

2 Entry composition [i](#)

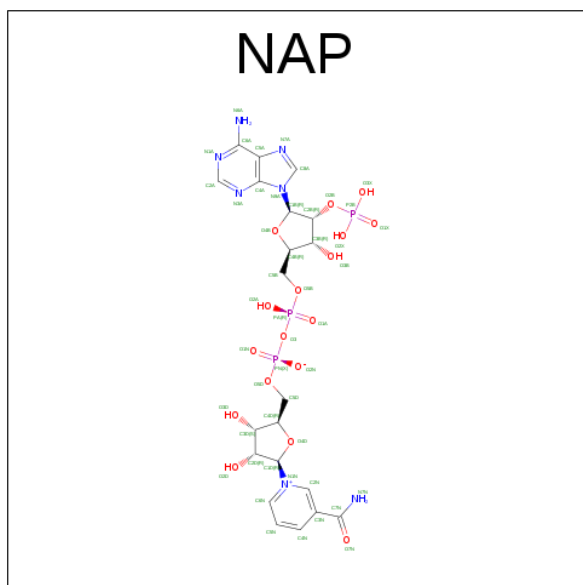
There are 4 unique types of molecules in this entry. The entry contains 11125 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dihydroflavonol 4-reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	2	0
			2477	1588	412	457	20			
1	B	326	Total	C	N	O	S	0	2	0
			2511	1608	415	466	22			
1	C	325	Total	C	N	O	S	0	1	0
			2509	1606	413	469	21			
1	D	321	Total	C	N	O	S	0	1	0
			2484	1590	410	463	21			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



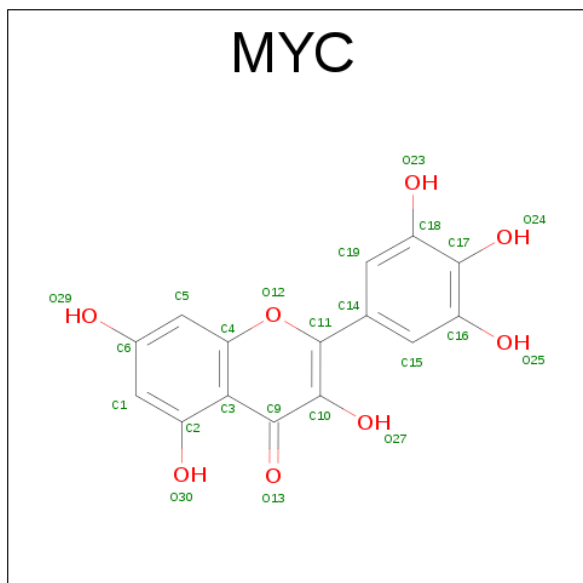
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

Continued on next page...

Continued from previous page...

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

- Molecule 3 is 3,5,7-TRIHYDROXY-2-(3,4,5-TRIHYDROXYPHENYL)-4H-CHROMEN-4-ONE (three-letter code: MYC) (formula: C₁₅H₁₀O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			23	15	8		
3	A	1	Total	C	O	0	0
			23	15	8		
3	B	1	Total	C	O	0	0
			23	15	8		
3	B	1	Total	C	O	0	0
			23	15	8		
3	C	1	Total	C	O	0	0
			23	15	8		
3	C	1	Total	C	O	0	0
			23	15	8		
3	D	1	Total	C	O	0	0
			23	15	8		
3	D	1	Total	C	O	0	0
			23	15	8		

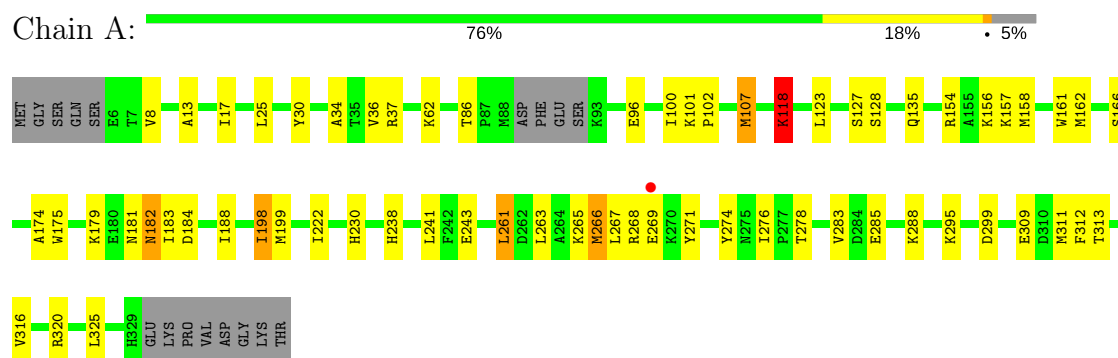
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total 151	O 151	0	0
4	B	174	Total 174	O 174	0	0
4	C	201	Total 201	O 201	0	0
4	D	242	Total 242	O 242	0	0

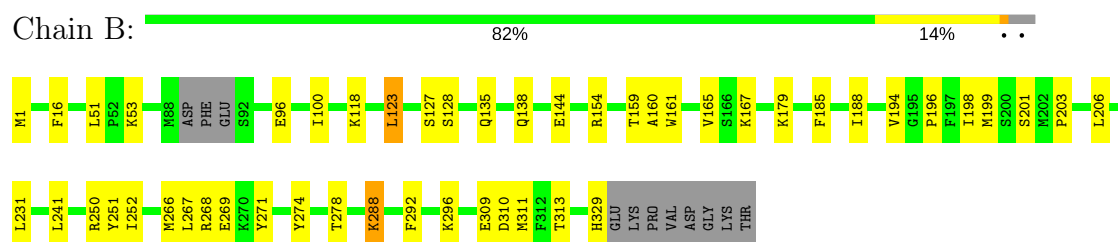
3 Residue-property plots

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.

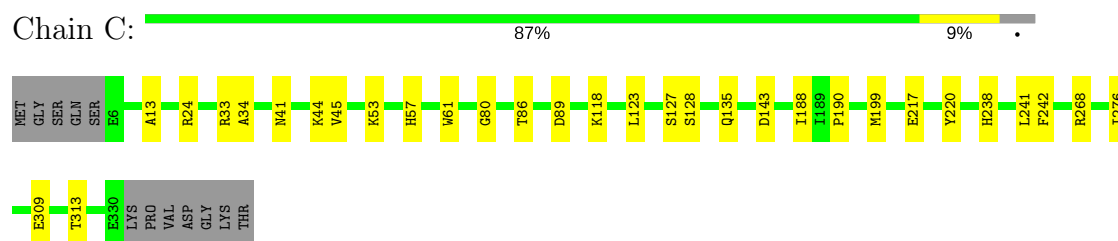
- Molecule 1: Dihydroflavonol 4-reductase



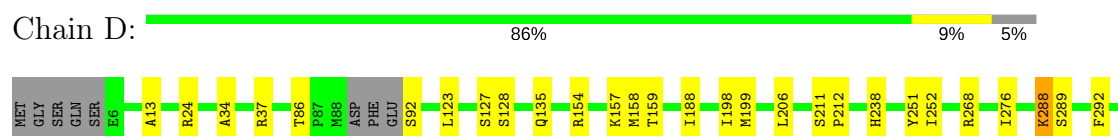
- Molecule 1: Dihydroflavonol 4-reductase



- Molecule 1: Dihydroflavonol 4-reductase



- Molecule 1: Dihydroflavonol 4-reductase



L300	
E309	
T313	
G314	
A315	
H329	
GLU	
LYS	
PRO	
VAL	
ASP	
GLY	
LYS	
THR	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.23Å 177.96Å 92.60Å 90.00° 104.77° 90.00°	Depositor
Resolution (Å)	89.44 – 2.06 89.54 – 2.06	Depositor EDS
% Data completeness (in resolution range)	98.9 (89.44-2.06) 98.9 (89.54-2.06)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.07Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.257 0.195 , 0.261	Depositor DCC
R_{free} test set	4501 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.170 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11125	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.66	0/2539	0.89	2/3450 (0.1%)
1	B	0.64	0/2573	0.87	0/3494
1	C	0.65	0/2568	0.85	2/3490 (0.1%)
1	D	0.69	0/2542	0.90	1/3453 (0.0%)
All	All	0.66	0/10222	0.88	5/13887 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	D	24	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	C	143	ASP	CB-CG-OD1	5.76	123.48	118.30
1	A	107	MET	CG-SD-CE	5.36	108.78	100.20
1	C	24	ARG	NE-CZ-NH1	5.05	122.83	120.30

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	2477	0	2431	42	0
1	B	2511	0	2457	31	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2509	0	2447	19	0
1	D	2484	0	2432	16	0
2	A	48	0	25	2	0
2	B	48	0	25	1	0
2	C	48	0	25	4	0
2	D	48	0	25	2	0
3	A	46	0	11	2	0
3	B	46	0	11	4	0
3	C	46	0	15	2	0
3	D	46	0	10	1	0
4	A	151	0	0	3	0
4	B	174	0	0	1	0
4	C	201	0	0	3	0
4	D	242	0	0	1	0
All	All	11125	0	9914	109	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 5.

The worst 5 of 109 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:D:309:GLU:O	1:D:313[B]:THR:HG22	1.65	0.95
1:A:312:PHE:O	1:A:316:VAL:HG23	1.81	0.80
1:D:199:MET:HE3	4:D:4522:HOH:O	1.92	0.69
1:A:17:ILE:HD12	2:A:1340:NAP:H51N	1.82	0.61
1:A:263:LEU:HD12	1:A:266:MET:HE2	1.82	0.61

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	318/337 (94%)	302 (95%)	14 (4%)	2 (1%)	28	17
1	B	324/337 (96%)	308 (95%)	15 (5%)	1 (0%)	44	35
1	C	324/337 (96%)	316 (98%)	7 (2%)	1 (0%)	44	35
1	D	318/337 (94%)	307 (96%)	11 (4%)	0	100	100
All	All	1284/1348 (95%)	1233 (96%)	47 (4%)	4 (0%)	44	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	118	LYS
1	B	118	LYS
1	C	118	LYS

5.3.2 Protein sidechains ⓘ

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	267/293 (91%)	254 (95%)	13 (5%)	29	20
1	B	269/293 (92%)	263 (98%)	6 (2%)	57	52
1	C	269/293 (92%)	265 (98%)	4 (2%)	70	67
1	D	268/293 (92%)	261 (97%)	7 (3%)	51	46
All	All	1073/1172 (92%)	1043 (97%)	30 (3%)	49	43

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1	MET
1	B	179	LYS
1	D	158	MET
1	B	135	GLN
1	B	269	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	236	ASN
1	C	57	HIS
1	D	138	GLN
1	B	57	HIS
1	D	181	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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	NAP	A	1340	-	44,52,52	1.56	4 (9%)	51,80,80	1.98	8 (15%)
3	MYC	A	1341	-	23,25,25	1.48	1 (4%)	29,38,38	1.20	3 (10%)
3	MYC	A	1342	-	23,25,25	1.67	3 (13%)	29,38,38	1.81	7 (24%)
2	NAP	B	2340	-	44,52,52	1.58	2 (4%)	51,80,80	2.41	14 (27%)
3	MYC	B	2341	-	23,25,25	1.66	1 (4%)	29,38,38	1.30	4 (13%)
3	MYC	B	2342	-	23,25,25	1.47	3 (13%)	29,38,38	1.52	6 (20%)
2	NAP	C	3340	-	44,52,52	1.54	2 (4%)	51,80,80	2.20	6 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MYC	C	3341	-	23,25,25	1.64	3 (13%)	29,38,38	1.55	5 (17%)
3	MYC	C	3342	-	23,25,25	1.31	3 (13%)	29,38,38	2.16	10 (34%)
2	NAP	D	4340	-	44,52,52	1.48	4 (9%)	51,80,80	2.51	10 (19%)
3	MYC	D	4341	-	23,25,25	1.66	1 (4%)	29,38,38	1.28	4 (13%)
3	MYC	D	4342	-	23,25,25	1.49	5 (21%)	29,38,38	1.95	9 (31%)

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	NAP	A	1340	-	-	0/27/67/67	0/5/5/5
3	MYC	A	1341	-	-	0/4/4/4	0/3/3/3
3	MYC	A	1342	-	-	0/4/4/4	0/3/3/3
2	NAP	B	2340	-	-	0/27/67/67	0/5/5/5
3	MYC	B	2341	-	-	0/4/4/4	0/3/3/3
3	MYC	B	2342	-	-	0/4/4/4	0/3/3/3
2	NAP	C	3340	-	-	0/27/67/67	0/5/5/5
3	MYC	C	3341	-	-	0/4/4/4	0/3/3/3
3	MYC	C	3342	-	-	0/4/4/4	0/3/3/3
2	NAP	D	4340	-	-	0/27/67/67	0/5/5/5
3	MYC	D	4341	-	-	0/4/4/4	0/3/3/3
3	MYC	D	4342	-	-	0/4/4/4	0/3/3/3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3342	MYC	C18-C17	-3.82	1.35	1.39
2	A	1340	NAP	O4D-C4D	-3.03	1.38	1.45
3	D	4342	MYC	C16-C17	-2.75	1.36	1.39
3	D	4342	MYC	C18-C17	-2.60	1.36	1.39
3	A	1342	MYC	C18-C17	-2.50	1.37	1.39

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4340	NAP	N3A-C2A-N1A	-12.75	117.75	128.86
2	C	3340	NAP	N3A-C2A-N1A	-11.93	118.47	128.86
2	B	2340	NAP	N3A-C2A-N1A	-10.13	120.04	128.86
2	A	1340	NAP	N3A-C2A-N1A	-8.49	121.47	128.86

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4340	NAP	C4B-O4B-C1B	-5.08	104.36	109.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1340	NAP	2	0
3	A	1342	MYC	2	0
2	B	2340	NAP	1	0
3	B	2342	MYC	4	0
2	C	3340	NAP	4	0
3	C	3342	MYC	2	0
2	D	4340	NAP	2	0
3	D	4342	MYC	1	0

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	320/337 (94%)	-0.21	1 (0%) 93 94	29, 45, 64, 79	0
1	B	326/337 (96%)	-0.29	0 100 100	29, 44, 65, 88	0
1	C	325/337 (96%)	-0.37	0 100 100	27, 42, 62, 80	0
1	D	321/337 (95%)	-0.38	0 100 100	27, 41, 60, 80	0
All	All	1292/1348 (95%)	-0.31	1 (0%) 95 95	27, 43, 63, 88	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	269	GLU	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	MYC	B	2342	23/23	0.92	0.17	1.44	44,55,56,57	0
3	MYC	A	1342	23/23	0.94	0.13	0.61	34,50,52,53	0
2	NAP	C	3340	48/48	0.98	0.10	0.09	24,32,46,51	0
3	MYC	A	1341	23/23	0.96	0.10	-0.10	36,40,41,42	0
2	NAP	B	2340	48/48	0.98	0.10	-0.18	29,35,51,55	0
3	MYC	B	2341	23/23	0.95	0.09	-0.26	36,41,42,43	0
2	NAP	A	1340	48/48	0.98	0.09	-0.32	30,35,53,59	0
2	NAP	D	4340	48/48	0.98	0.09	-0.36	22,31,48,53	0
3	MYC	C	3342	23/23	0.97	0.09	-0.50	26,30,33,33	0
3	MYC	D	4341	23/23	0.98	0.08	-0.68	28,31,32,33	0
3	MYC	D	4342	23/23	0.97	0.09	-0.97	28,31,33,34	0
3	MYC	C	3341	23/23	0.97	0.08	-1.22	29,31,32,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.