



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:27 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 full wwPDB validation 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/ValidationPDFNotes.html>

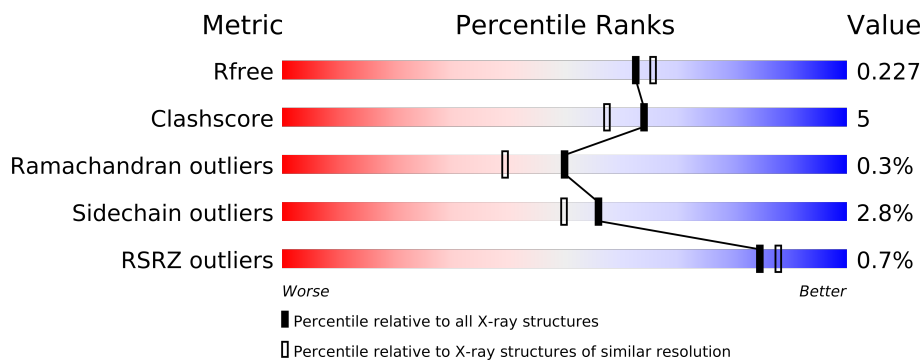
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	1224 (2.08-2.04)
Clashscore	79885	1390 (2.08-2.04)
Ramachandran outliers	78287	1381 (2.08-2.04)
Sidechain outliers	78261	1381 (2.08-2.04)
RSRZ outliers	66119	1225 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	337	
1	B	337	
1	C	337	
1	D	337	

2 Entry composition i

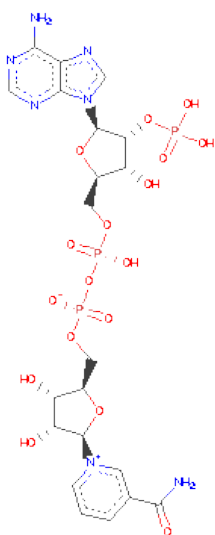
There are 4 unique types of molecules in this entry. The entry contains 11125 atoms, of which 0 are hydrogen and 0 are deuterium.

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-DINUCLEOTIDEPHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



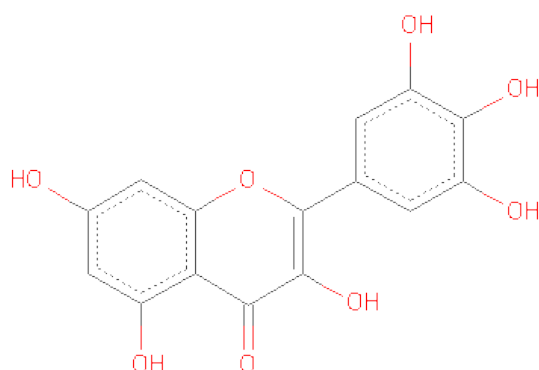
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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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.

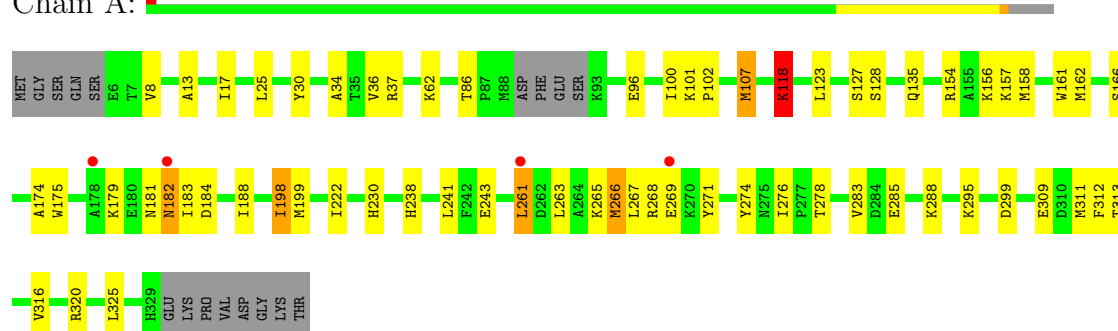
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total 151	O 151	0	0
4	B	174	Total 174	O 174	0	0
4	C	201	Total 201	O 201	0	0
4	D	242	Total 242	O 242	0	0

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 errors 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.

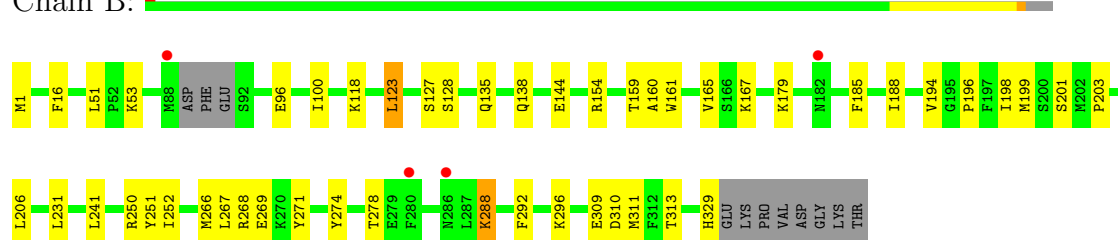
• Molecule 1: Dihydroflavonol 4-reductase

Chain A:



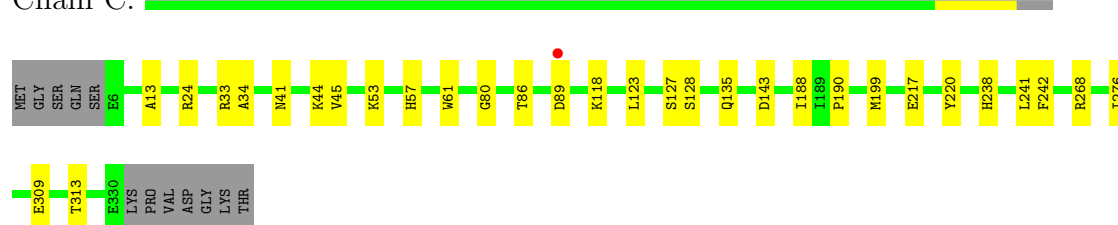
• Molecule 1: Dihydroflavonol 4-reductase

Chain B:



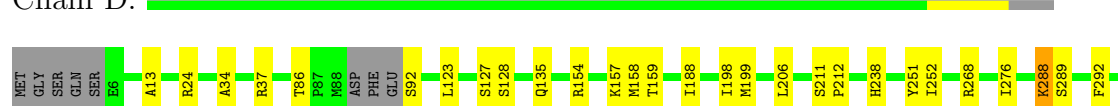
• Molecule 1: Dihydroflavonol 4-reductase

Chain C:



• Molecule 1: Dihydroflavonol 4-reductase

Chain D:



L300		E309		T313	G314	A315		H329	GLU	LYS	PRO	VAL	ASP	GLY	LYS	THR
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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 , 0.227	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)	0.36 , 54.3	EDS
Estimated twinning fraction	0.170 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 89895 reflections	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.

5 Model quality

5.1 Standard geometry

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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
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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (109) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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
1:D:309:GLU:O	1:D:313[A]:THR:HG23	2.01	0.60
1:B:16:PHE:CE1	1:B:231:LEU:HD22	2.37	0.60
1:A:175:TRP:O	1:A:179:LYS:HD3	2.02	0.59
1:B:309:GLU:O	1:B:313[A]:THR:HG23	2.04	0.58
1:A:8:VAL:HG21	1:A:25:LEU:HD13	1.86	0.58
1:A:182:ASN:HD21	1:D:159:THR:H	1.52	0.57
1:B:161:TRP:O	1:B:165:VAL:HG23	2.05	0.56
1:C:199:MET:HE1	4:C:3439:HOH:O	2.07	0.55
1:A:128:SER:HG	3:A:1342:MYC:HO3	1.54	0.55
1:B:96:GLU:OE2	1:B:154:ARG:NH1	2.39	0.55
1:B:128:SER:HG	3:B:2342:MYC:HO3	1.55	0.54
1:B:196:PRO:O	1:B:231:LEU:HD23	2.08	0.54
1:A:285:GLU:CB	4:A:1477:HOH:O	2.54	0.54
1:A:96:GLU:OE2	1:A:154:ARG:NH1	2.41	0.53
1:A:128:SER:OG	3:A:1342:MYC:O23	2.26	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:265:LYS:O	1:A:269:GLU:OE1	2.26	0.53
1:C:199:MET:HE3	4:C:3390:HOH:O	2.09	0.53
1:A:271:TYR:CE2	1:A:316:VAL:HG21	2.44	0.52
1:A:316:VAL:HG13	1:A:325:LEU:CD1	2.40	0.52
1:D:37:ARG:NE	2:D:4340:NAP:O3X	2.40	0.52
1:C:128:SER:OG	3:C:3342:MYC:O23	2.28	0.51
1:D:188:ILE:CD1	1:D:238:HIS:HA	2.39	0.51
1:D:268:ARG:HG2	1:D:276:ILE:HB	1.93	0.51
1:A:188:ILE:CD1	1:A:241:LEU:HD12	2.41	0.51
1:C:190:PRO:HG2	2:C:3340:NAP:C6N	2.40	0.51
1:A:157:LYS:HE3	1:A:161:TRP:CZ2	2.46	0.51
1:B:96:GLU:HA	1:B:100:ILE:HD12	1.94	0.50
1:A:261:LEU:HD13	1:A:283:VAL:HG11	1.94	0.50
1:B:267:LEU:O	1:B:271:TYR:N	2.39	0.50
1:D:13:ALA:CB	1:D:34:ALA:HB1	2.42	0.49
1:C:309:GLU:O	1:C:313[B]:THR:HG22	2.12	0.49
1:A:8:VAL:CG2	1:A:25:LEU:HD13	2.42	0.49
1:A:309:GLU:O	1:A:313[A]:THR:HG23	2.13	0.49
1:B:138:GLN:O	1:B:288:LYS:NZ	2.43	0.49
1:A:127:SER:O	2:A:1340:NAP:H6N	2.12	0.49
1:A:13:ALA:CB	1:A:34:ALA:HB1	2.43	0.49
1:C:53:LYS:HE2	1:C:57:HIS:CD2	2.48	0.48
1:B:144:GLU:HG2	1:B:250:ARG:O	2.13	0.48
1:B:53:LYS:HD2	4:B:2493:HOH:O	2.12	0.48
1:A:188:ILE:CD1	1:A:238:HIS:HA	2.44	0.48
1:C:309:GLU:O	1:C:313[B]:THR:CG2	2.61	0.47
1:A:184:ASP:OD1	1:A:184:ASP:C	2.50	0.47
1:A:316:VAL:HG13	1:A:325:LEU:HD12	1.95	0.47
3:C:3342:MYC:O23	4:C:3519:HOH:O	2.21	0.47
1:A:268:ARG:HA	1:A:276:ILE:HD12	1.97	0.47
1:C:190:PRO:HG2	2:C:3340:NAP:C5N	2.46	0.46
1:A:30:TYR:OH	1:A:243:GLU:OE2	2.21	0.46
1:C:188:ILE:HD13	1:C:241:LEU:HD12	1.97	0.46
1:C:217:GLU:HG2	1:C:220:TYR:CE2	2.50	0.46
1:B:123:LEU:HD13	1:B:185:PHE:CD1	2.50	0.46
1:C:44:LYS:NZ	2:C:3340:NAP:O1X	2.37	0.46
1:B:188:ILE:HG12	1:B:241:LEU:HD12	1.97	0.46
1:A:188:ILE:HD11	1:A:241:LEU:HD12	1.96	0.46
1:B:266:MET:CE	1:B:267:LEU:HD23	2.46	0.46
1:D:251:TYR:OH	1:D:300:LEU:HD11	2.15	0.46
1:C:13:ALA:CB	1:C:34:ALA:HB1	2.46	0.46
1:C:41:ASN:O	1:C:45:VAL:HG22	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:266:MET:HE3	1:A:267:LEU:HG	1.98	0.45
1:A:107:MET:HG2	1:A:174:ALA:HB2	1.98	0.45
1:A:230:HIS:HD2	1:A:311:MET:HA	1.82	0.45
1:A:157:LYS:HE3	1:A:161:TRP:CE2	2.52	0.45
1:B:251:TYR:CZ	1:B:296:LYS:HE2	2.51	0.45
1:B:199:MET:HE2	1:B:201:SER:O	2.17	0.45
1:C:188:ILE:CD1	1:C:241:LEU:HD12	2.46	0.45
1:B:252:ILE:HG21	1:B:292:PHE:HB3	1.99	0.44
1:D:252:ILE:HG21	1:D:292:PHE:HB3	1.99	0.44
1:B:199:MET:CE	1:B:201:SER:O	2.65	0.44
1:D:154:ARG:O	1:D:157:LYS:HE3	2.16	0.44
1:A:162:MET:O	1:A:166:SER:HB3	2.17	0.44
1:B:199:MET:HE1	1:B:203:PRO:HA	2.00	0.44
1:B:167:LYS:HG3	3:B:2342:MYC:O24	2.18	0.43
1:B:268:ARG:CZ	1:B:278:THR:HA	2.49	0.43
1:A:36:VAL:O	1:A:62:LYS:HA	2.19	0.43
1:B:266:MET:HE1	1:B:267:LEU:HD23	2.01	0.43
1:B:271:TYR:OH	1:B:313[A]:THR:HA	2.19	0.43
1:C:268:ARG:HG2	1:C:276:ILE:HB	2.00	0.43
1:A:295:LYS:NZ	1:A:299:ASP:OD2	2.51	0.43
1:B:194:VAL:HG13	1:B:206:LEU:CD2	2.48	0.43
1:C:188:ILE:CD1	1:C:238:HIS:HA	2.49	0.42
1:D:288:LYS:HG2	1:D:289:SER:O	2.19	0.42
1:B:51:LEU:HD21	1:B:198:ILE:CD1	2.48	0.42
1:B:271:TYR:OH	1:B:313[B]:THR:HA	2.19	0.42
1:B:310:ASP:O	1:B:311:MET:C	2.57	0.42
1:B:274:TYR:HD1	1:B:329:HIS:ND1	2.16	0.42
1:A:118:LYS:NZ	4:A:1358:HOH:O	2.53	0.42
1:B:159:THR:O	1:B:160:ALA:HB3	2.20	0.41
1:D:206:LEU:HD13	1:D:315:ALA:HB1	2.00	0.41
1:A:101:LYS:HB3	1:A:102:PRO:HD3	2.02	0.41
1:A:230:HIS:CD2	1:A:311:MET:HA	2.56	0.41
1:A:179:LYS:HE2	4:A:1493:HOH:O	2.20	0.41
1:A:181:ASN:O	1:A:183:ILE:N	2.54	0.41
3:B:2342:MYC:O27	3:B:2342:MYC:H15	2.21	0.41
1:D:127:SER:O	2:D:4340:NAP:H6N	2.21	0.41
1:B:127:SER:O	2:B:2340:NAP:H6N	2.20	0.41
1:B:160:ALA:HB2	3:B:2342:MYC:C4	2.50	0.41
1:A:96:GLU:HA	1:A:100:ILE:HD12	2.03	0.41
1:A:274:TYR:OH	1:A:320:ARG:NE	2.47	0.41
1:D:211:SER:N	1:D:212:PRO:CD	2.84	0.41
1:C:80:GLY:HA3	1:C:242:PHE:CE1	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:198:ILE:HG21	1:A:198:ILE:HD13	1.82	0.40
1:A:268:ARG:HG2	1:A:276:ILE:HB	2.02	0.40
1:D:128:SER:OG	3:D:4342:MYC:O25	2.36	0.40
1:C:127:SER:O	2:C:3340:NAP:H6N	2.20	0.40
1:C:33:ARG:HD3	1:C:61:TRP:CZ2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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%)	33	20
1	B	324/337 (96%)	308 (95%)	15 (5%)	1 (0%)	50	39
1	C	324/337 (96%)	316 (98%)	7 (2%)	1 (0%)	50	39
1	D	318/337 (94%)	307 (96%)	11 (4%)	0	100	100
All	All	1284/1348 (95%)	1233 (96%)	47 (4%)	4 (0%)	50	39

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%)	35	24
1	B	269/293 (92%)	263 (98%)	6 (2%)	64	60
1	C	269/293 (92%)	265 (98%)	4 (2%)	76	76
1	D	268/293 (92%)	261 (97%)	7 (3%)	59	54
All	All	1073/1172 (92%)	1043 (97%)	30 (3%)	56	50

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	THR
1	A	118	LYS
1	A	123	LEU
1	A	135	GLN
1	A	156	LYS
1	A	158	MET
1	A	198	ILE
1	A	199	MET
1	A	222	ILE
1	A	261	LEU
1	A	266	MET
1	A	278	THR
1	A	288	LYS
1	B	1	MET
1	B	123	LEU
1	B	135	GLN
1	B	179	LYS
1	B	269	GLU
1	B	288	LYS
1	C	86	THR
1	C	89	ASP
1	C	123	LEU
1	C	135	GLN
1	D	86	THR
1	D	92	SER
1	D	123	LEU
1	D	135	GLN
1	D	158	MET
1	D	198	ILE
1	D	288	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	HIS
1	A	133	ASN
1	A	182	ASN
1	A	230	HIS
1	A	236	ASN
1	A	275	ASN
1	B	57	HIS
1	B	236	ASN
1	C	57	HIS
1	C	236	ASN
1	C	275	ASN
1	D	133	ASN
1	D	138	GLN
1	D	181	ASN
1	D	236	ASN
1	D	275	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	-	52,52,52	1.42	6 (11%)	80,80,80	1.93	15 (18%)
3	MYC	A	1341	-	24,25,25	1.58	3 (12%)	35,38,38	1.54	6 (17%)
3	MYC	A	1342	-	24,25,25	1.78	5 (20%)	35,38,38	2.27	10 (28%)
2	NAP	B	2340	-	52,52,52	1.44	4 (7%)	80,80,80	2.14	19 (23%)
3	MYC	B	2341	-	24,25,25	1.70	3 (12%)	35,38,38	1.72	7 (20%)
3	MYC	B	2342	-	24,25,25	1.70	4 (16%)	35,38,38	1.84	9 (25%)
2	NAP	C	3340	-	52,52,52	1.31	2 (3%)	80,80,80	1.94	9 (11%)
3	MYC	C	3341	-	24,25,25	1.81	5 (20%)	35,38,38	1.86	9 (25%)
3	MYC	C	3342	-	24,25,25	1.52	4 (16%)	35,38,38	2.38	10 (28%)
2	NAP	D	4340	-	52,52,52	1.37	5 (9%)	80,80,80	2.36	20 (25%)
3	MYC	D	4341	-	24,25,25	1.73	3 (12%)	35,38,38	1.67	10 (28%)
3	MYC	D	4342	-	24,25,25	1.50	5 (20%)	35,38,38	2.25	11 (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	-	-	0/35/67/67	0/3/5/5
3	MYC	A	1341	-	-	0/4/4/4	0/1/3/3
3	MYC	A	1342	-	-	0/4/4/4	0/1/3/3
2	NAP	B	2340	-	-	0/35/67/67	0/3/5/5
3	MYC	B	2341	-	-	0/4/4/4	0/1/3/3
3	MYC	B	2342	-	-	0/4/4/4	0/1/3/3
2	NAP	C	3340	-	-	0/35/67/67	0/3/5/5
3	MYC	C	3341	-	-	0/4/4/4	0/1/3/3
3	MYC	C	3342	-	-	0/4/4/4	0/1/3/3
2	NAP	D	4340	-	-	0/35/67/67	0/3/5/5
3	MYC	D	4341	-	-	0/4/4/4	0/1/3/3
3	MYC	D	4342	-	-	0/4/4/4	0/1/3/3

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3340	NAP	O7N-C7N	6.98	1.40	1.24
2	A	1340	NAP	O7N-C7N	6.77	1.40	1.24
2	B	2340	NAP	O7N-C7N	6.63	1.39	1.24
3	B	2341	MYC	C9-C3	6.55	1.50	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	4341	MYC	C9-C3	6.46	1.50	1.40
3	A	1341	MYC	C9-C3	6.16	1.49	1.40
3	C	3341	MYC	C9-C3	6.05	1.49	1.40
3	A	1342	MYC	C9-C3	6.04	1.49	1.40
2	D	4340	NAP	O7N-C7N	5.97	1.38	1.24
3	B	2342	MYC	C9-C3	5.50	1.49	1.40
3	D	4342	MYC	C9-C3	4.22	1.47	1.40
3	B	2342	MYC	O12-C11	4.05	1.39	1.35
3	C	3342	MYC	O12-C11	3.73	1.38	1.35
3	C	3341	MYC	O12-C11	3.63	1.38	1.35
3	C	3342	MYC	C18-C17	-3.61	1.35	1.39
3	C	3342	MYC	C9-C3	3.36	1.45	1.40
2	B	2340	NAP	C2A-N3A	3.10	1.38	1.32
2	D	4340	NAP	C2N-N1N	3.05	1.39	1.35
3	A	1342	MYC	C14-C11	2.99	1.50	1.46
2	A	1340	NAP	O4D-C4D	-2.94	1.38	1.45
3	D	4342	MYC	C14-C11	2.87	1.50	1.46
3	A	1342	MYC	O12-C11	2.76	1.37	1.35
2	A	1340	NAP	C2A-N3A	2.74	1.37	1.32
3	B	2342	MYC	C14-C11	2.71	1.50	1.46
2	D	4340	NAP	C2A-N3A	2.70	1.37	1.32
3	C	3341	MYC	O13-C9	2.66	1.27	1.23
2	B	2340	NAP	PA-O3	2.63	1.64	1.59
3	C	3342	MYC	C14-C11	2.61	1.49	1.46
3	D	4342	MYC	C16-C17	-2.60	1.36	1.39
3	C	3341	MYC	C14-C11	2.47	1.49	1.46
3	D	4342	MYC	C18-C17	-2.46	1.36	1.39
3	D	4341	MYC	O12-C11	2.44	1.37	1.35
3	A	1342	MYC	C18-C17	-2.37	1.37	1.39
2	D	4340	NAP	PA-O3	2.35	1.64	1.59
3	B	2341	MYC	C14-C11	2.33	1.49	1.46
2	C	3340	NAP	C2A-N3A	2.32	1.36	1.32
3	A	1341	MYC	O12-C11	2.29	1.37	1.35
3	B	2341	MYC	O13-C9	2.25	1.26	1.23
3	B	2342	MYC	C18-C17	-2.22	1.37	1.39
3	D	4341	MYC	O13-C9	2.21	1.26	1.23
2	A	1340	NAP	C2A-N1A	2.18	1.38	1.33
2	A	1340	NAP	C2N-N1N	2.18	1.38	1.35
2	A	1340	NAP	PA-O3	2.15	1.63	1.59
3	C	3341	MYC	C2-C3	-2.14	1.39	1.43
2	D	4340	NAP	C3N-C7N	-2.13	1.46	1.50
3	A	1341	MYC	C14-C11	2.12	1.49	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2340	NAP	C4A-N9A	-2.10	1.34	1.37
3	A	1342	MYC	O13-C9	2.08	1.26	1.23
3	D	4342	MYC	C2-C3	-2.05	1.39	1.43

All (135) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4340	NAP	N3A-C2A-N1A	-13.11	117.75	128.71
2	C	3340	NAP	N3A-C2A-N1A	-12.25	118.47	128.71
2	B	2340	NAP	N3A-C2A-N1A	-10.37	120.04	128.71
2	A	1340	NAP	N3A-C2A-N1A	-8.66	121.47	128.71
3	A	1342	MYC	O12-C11-C10	-8.32	117.86	121.54
3	C	3342	MYC	C14-C19-C18	-6.60	118.14	121.03
3	B	2342	MYC	O12-C11-C10	-5.83	118.96	121.54
3	D	4342	MYC	C14-C15-C16	-5.46	118.64	121.03
3	B	2341	MYC	C14-C15-C16	-5.18	118.76	121.03
2	B	2340	NAP	C3N-C7N-N7N	5.14	123.62	117.77
2	B	2340	NAP	O3X-P2B-O2X	5.04	127.22	107.61
2	D	4340	NAP	O2X-P2B-O1X	5.02	126.84	110.44
2	B	2340	NAP	O7N-C7N-C3N	-4.98	113.97	119.58
2	D	4340	NAP	C4B-O4B-C1B	-4.96	104.36	109.75
3	D	4342	MYC	O12-C11-C10	-4.93	119.36	121.54
3	D	4342	MYC	C14-C11-C10	4.75	129.40	120.38
2	A	1340	NAP	C4B-O4B-C1B	-4.74	104.60	109.75
3	C	3342	MYC	C18-C17-C16	4.74	122.06	119.56
2	D	4340	NAP	O7N-C7N-C3N	-4.60	114.40	119.58
2	C	3340	NAP	C4B-O4B-C1B	-4.53	104.83	109.75
3	C	3342	MYC	C14-C15-C16	-4.46	119.08	121.03
2	A	1340	NAP	O7N-C7N-C3N	-4.46	114.55	119.58
2	A	1340	NAP	O4B-C1B-N9A	4.30	112.44	108.44
3	C	3341	MYC	C14-C19-C18	-4.29	119.15	121.03
3	A	1342	MYC	C14-C11-C10	4.27	128.49	120.38
3	A	1342	MYC	C14-C15-C16	-4.24	119.17	121.03
2	B	2340	NAP	C1B-N9A-C4A	-4.22	119.34	126.64
2	B	2340	NAP	O3X-P2B-O1X	-4.09	97.07	110.44
3	D	4341	MYC	O12-C11-C10	-4.09	119.73	121.54
3	A	1341	MYC	C14-C15-C16	-3.97	119.29	121.03
2	D	4340	NAP	C2D-C1D-N1N	3.95	120.54	113.86
3	D	4341	MYC	O12-C11-C14	3.92	118.99	113.25
3	C	3341	MYC	C10-C9-C3	-3.92	117.12	121.41
2	D	4340	NAP	C1B-N9A-C4A	-3.91	119.88	126.64
3	D	4342	MYC	O12-C4-C5	3.90	120.96	116.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3342	MYC	O24-C17-C18	-3.85	109.78	119.48
2	D	4340	NAP	C8A-N9A-C4A	3.83	109.82	106.90
3	C	3342	MYC	O23-C18-C19	3.83	129.55	119.42
2	A	1340	NAP	N3A-C4A-N9A	3.76	132.22	125.43
2	D	4340	NAP	O3X-P2B-O2B	3.76	117.91	107.09
2	A	1340	NAP	O2X-P2B-O1X	3.75	122.68	110.44
2	B	2340	NAP	O2X-P2B-O2B	-3.74	96.32	107.09
2	A	1340	NAP	C3N-C7N-N7N	3.62	121.89	117.77
3	D	4342	MYC	C11-O12-C4	3.60	125.24	121.27
2	C	3340	NAP	C1B-N9A-C4A	-3.59	120.43	126.64
3	B	2341	MYC	C19-C14-C11	3.53	124.45	120.20
2	C	3340	NAP	O2X-P2B-O1X	3.50	121.88	110.44
3	B	2341	MYC	C15-C14-C11	-3.48	116.01	120.20
3	C	3341	MYC	C5-C4-C3	-3.47	118.86	123.10
3	C	3342	MYC	O24-C17-C16	3.43	128.12	119.48
2	C	3340	NAP	C8A-N9A-C1B	3.41	133.09	126.38
3	D	4342	MYC	O25-C16-C15	3.30	128.14	119.42
2	D	4340	NAP	N3A-C4A-N9A	3.25	131.30	125.43
3	C	3342	MYC	O23-C18-C17	-3.24	109.69	118.06
3	B	2342	MYC	C18-C17-C16	3.21	121.25	119.56
3	C	3341	MYC	C18-C17-C16	3.17	121.23	119.56
2	D	4340	NAP	C2N-C3N-C4N	3.16	121.89	118.31
3	A	1342	MYC	C18-C17-C16	3.15	121.22	119.56
3	C	3342	MYC	C14-C11-C10	3.14	126.35	120.38
2	B	2340	NAP	C2N-C3N-C4N	3.14	121.86	118.31
3	C	3341	MYC	O12-C4-C5	3.07	119.91	116.02
3	C	3341	MYC	C15-C14-C11	-3.02	116.57	120.20
3	A	1342	MYC	O23-C18-C19	3.01	127.37	119.42
3	D	4342	MYC	O25-C16-C17	-2.99	110.32	118.06
3	D	4341	MYC	C19-C14-C11	2.99	123.80	120.20
3	C	3342	MYC	C5-C4-C3	-2.99	119.44	123.10
2	A	1340	NAP	O3-PN-O1N	-2.99	101.69	108.83
3	A	1341	MYC	C10-C9-C3	-2.97	118.16	121.41
3	B	2341	MYC	C10-C9-C3	-2.95	118.17	121.41
2	B	2340	NAP	C4A-C5A-N7A	-2.92	107.02	109.52
3	C	3342	MYC	C2-C3-C4	2.90	121.35	117.77
3	A	1341	MYC	C6-C5-C4	-2.90	117.62	120.31
3	D	4342	MYC	O24-C17-C18	2.85	126.66	119.48
2	A	1340	NAP	O4D-C1D-N1N	-2.83	105.05	107.95
2	D	4340	NAP	C6N-N1N-C2N	-2.82	118.85	122.04
2	B	2340	NAP	O2N-PN-O5D	2.81	119.80	108.19
2	D	4340	NAP	O4B-C1B-C2B	2.78	109.55	106.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1342	MYC	C19-C18-C17	-2.78	118.63	120.43
3	C	3341	MYC	C19-C14-C11	2.77	123.53	120.20
2	D	4340	NAP	N7A-C8A-N9A	-2.74	106.60	114.36
3	D	4342	MYC	O12-C4-C3	-2.73	118.50	121.29
2	B	2340	NAP	C8A-N9A-C1B	2.72	131.73	126.38
2	B	2340	NAP	O2X-P2B-O1X	2.70	119.28	110.44
3	C	3341	MYC	O12-C11-C10	2.69	122.73	121.54
3	B	2342	MYC	O12-C4-C5	2.69	119.43	116.02
2	B	2340	NAP	N7A-C8A-N9A	-2.65	106.85	114.36
2	C	3340	NAP	C2A-N1A-C6A	2.65	123.56	118.77
2	D	4340	NAP	P2B-O2B-C2B	2.62	127.48	121.96
3	A	1342	MYC	C5-C4-C3	-2.62	119.90	123.10
2	C	3340	NAP	O3X-P2B-O2X	-2.61	97.46	107.61
3	A	1341	MYC	C14-C19-C18	-2.58	119.90	121.03
3	B	2342	MYC	C14-C11-C10	2.58	125.28	120.38
3	D	4341	MYC	C14-C19-C18	-2.57	119.91	121.03
3	A	1341	MYC	O12-C11-C10	-2.56	120.41	121.54
3	D	4342	MYC	O24-C17-C16	-2.55	113.06	119.48
2	D	4340	NAP	C3N-C7N-N7N	2.49	120.60	117.77
3	A	1342	MYC	C9-C3-C4	-2.47	115.78	119.42
2	C	3340	NAP	O4B-C1B-N9A	2.46	110.73	108.44
3	D	4341	MYC	O12-C4-C5	2.45	119.13	116.02
3	B	2342	MYC	C5-C4-C3	-2.45	120.11	123.10
2	D	4340	NAP	O5B-PA-O1A	2.41	118.81	109.37
2	A	1340	NAP	C4D-O4D-C1D	2.39	112.34	109.75
2	B	2340	NAP	C4B-O4B-C1B	-2.37	107.18	109.75
3	B	2341	MYC	O12-C4-C5	2.35	119.00	116.02
3	D	4341	MYC	C15-C14-C11	-2.35	117.37	120.20
3	D	4341	MYC	C5-C4-C3	-2.35	120.23	123.10
2	B	2340	NAP	C8A-N9A-C4A	2.33	108.67	106.90
2	D	4340	NAP	C5N-C4N-C3N	-2.32	117.31	120.32
2	B	2340	NAP	C2D-C3D-C4D	2.32	107.27	102.65
3	D	4341	MYC	O29-C6-C5	-2.32	114.23	121.07
2	A	1340	NAP	O4B-C1B-C2B	-2.30	104.80	106.95
3	A	1342	MYC	C11-O12-C4	2.20	123.69	121.27
3	B	2342	MYC	C2-C3-C4	2.19	120.48	117.77
2	D	4340	NAP	C2A-N3A-C4A	2.17	120.18	114.01
3	B	2342	MYC	O23-C18-C19	2.17	125.15	119.42
2	A	1340	NAP	O2A-PA-O1A	2.15	124.23	112.21
2	A	1340	NAP	C6A-C5A-C4A	2.14	121.17	117.25
3	B	2342	MYC	C14-C15-C16	-2.13	120.10	121.03
2	A	1340	NAP	C5A-C4A-N3A	-2.12	121.08	125.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4341	MYC	C10-C9-C3	-2.11	119.10	121.41
2	B	2340	NAP	O4D-C1D-C2D	2.11	110.00	106.77
3	D	4342	MYC	C5-C4-C3	-2.09	120.54	123.10
3	B	2341	MYC	C15-C16-C17	2.06	121.77	120.43
2	D	4340	NAP	O2X-P2B-O2B	-2.06	101.17	107.09
3	D	4341	MYC	C2-C3-C4	2.05	120.30	117.77
2	B	2340	NAP	O3-PA-O5B	-2.04	94.27	103.41
3	A	1341	MYC	C1-C2-C3	-2.04	118.11	120.62
3	B	2342	MYC	C19-C18-C17	-2.03	119.11	120.43
3	B	2341	MYC	C14-C11-C10	2.03	124.23	120.38
2	B	2340	NAP	C3N-C2N-N1N	-2.02	116.95	120.36
2	A	1340	NAP	P2B-O2B-C2B	2.02	126.22	121.96
3	C	3341	MYC	C2-C3-C4	2.02	120.27	117.77
2	C	3340	NAP	P2B-O2B-C2B	2.01	126.18	121.96
3	A	1342	MYC	O12-C4-C5	2.01	118.56	116.02
2	D	4340	NAP	O4B-C1B-N9A	2.00	110.30	108.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	320/337 (94%)	0.08	4 (1%) 74 77	29, 45, 64, 79	0
1	B	326/337 (96%)	-0.02	4 (1%) 75 78	29, 44, 65, 88	0
1	C	325/337 (96%)	-0.11	1 (0%) 91 94	27, 42, 62, 80	0
1	D	321/337 (95%)	-0.12	0 100 100	27, 41, 60, 80	0
All	All	1292/1348 (95%)	-0.04	9 (0%) 84 88	27, 43, 63, 88	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	88	MET	3.2
1	A	182	ASN	2.9
1	B	280	PHE	2.9
1	A	178	ALA	2.7
1	B	182	ASN	2.5
1	B	286	ASN	2.5
1	A	269	GLU	2.5
1	C	89	ASP	2.3
1	A	261	LEU	2.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MYC	B	2342	23/23	0.20	1.22	44,55,56,57	0
3	MYC	A	1342	23/23	0.17	1.17	34,50,52,53	0
3	MYC	A	1341	23/23	0.13	1.03	36,40,41,42	0
2	NAP	C	3340	48/48	0.11	0.02	24,32,46,51	0
2	NAP	B	2340	48/48	0.10	-0.18	29,35,51,55	0
3	MYC	B	2341	23/23	0.10	-0.19	36,41,42,43	0
3	MYC	D	4342	23/23	0.11	-0.36	28,31,33,34	0
2	NAP	D	4340	48/48	0.10	-0.47	22,31,48,53	0
3	MYC	D	4341	23/23	0.10	-0.47	28,31,32,33	0
2	NAP	A	1340	48/48	0.10	-0.58	30,35,53,59	0
3	MYC	C	3341	23/23	0.09	-0.77	29,31,32,34	0
3	MYC	C	3342	23/23	0.09	-0.91	26,30,33,33	0

6.5 Other polymers ⓘ

There are no such residues in this entry.