Full wwPDB X-ray Structure Validation Report (i)

May 29, 2020 – 02:15 am BST

PDB ID	:	1C9U
Title	:	CRYSTAL STRUCTURE OF THE SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE IN COMPLEX WITH PQQ
Authors	:	Oubrie, A.; Rozeboom, H.J.; Dijkstra, B.W.
Deposited on	:	1999-08-03
Resolution	:	2.20 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 following versions of software and data (see references (i)) were used in the production of this report:

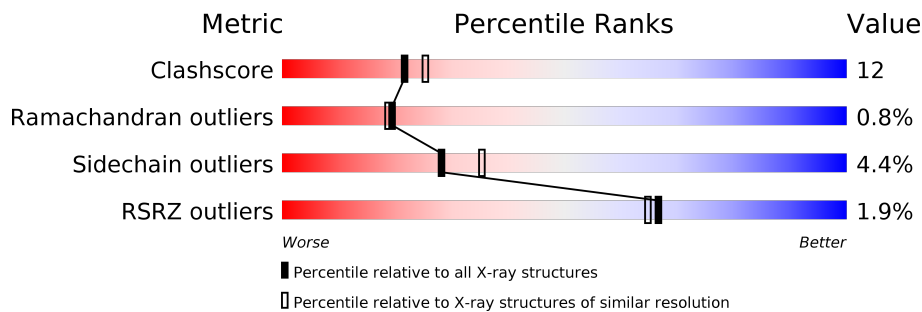|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 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	Percentile Ranks	Value
Clashscore		12
Ramachandran outliers		0.8%
Sidechain outliers		4.4%
RSRZ outliers		1.9%

Worse — *Better*

▌ Percentile relative to all X-ray structures

▐ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	454	2% — 67% — 28% — · ·
1	B	454	2% — 76% — 20% — ·

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7634 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.
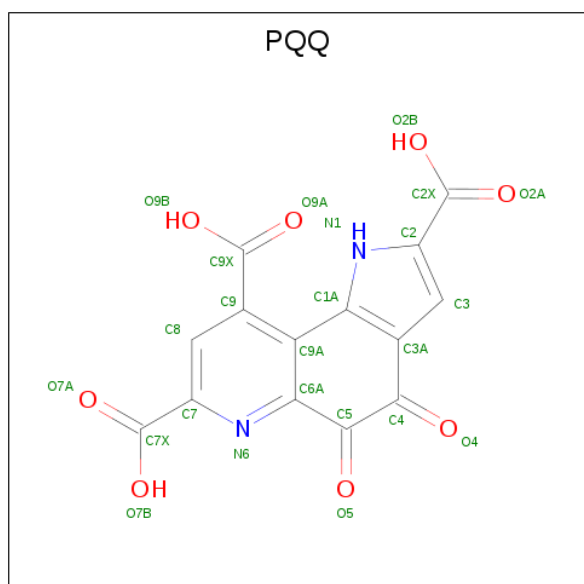
- Molecule 1 is a protein called SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGE-NASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total 3470	C 2206	N 590	O 669	S 5	0	0	0
1	B	452	Total 3538	C 2249	N 600	O 684	S 5	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total 3	Ca 3	0	0
2	A	3	Total 3	Ca 3	0	0

- Molecule 3 is PYRROLOQUINOLINE QUINONE (three-letter code: PQQ) (formula: $C_{14}H_6N_2O_8$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 24	C 14	N 2	O 8	0	0
3	B	1	Total 24	C 14	N 2	O 8	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 6	C 3	O 3	0	0
4	A	1	Total 6	C 3	O 3	0	0
4	A	1	Total 6	C 3	O 3	0	0
4	B	1	Total 6	C 3	O 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	255	Total 255	O 255	0	0
5	B	293	Total 293	O 293	0	0

3 Residue-property plots ⓘ

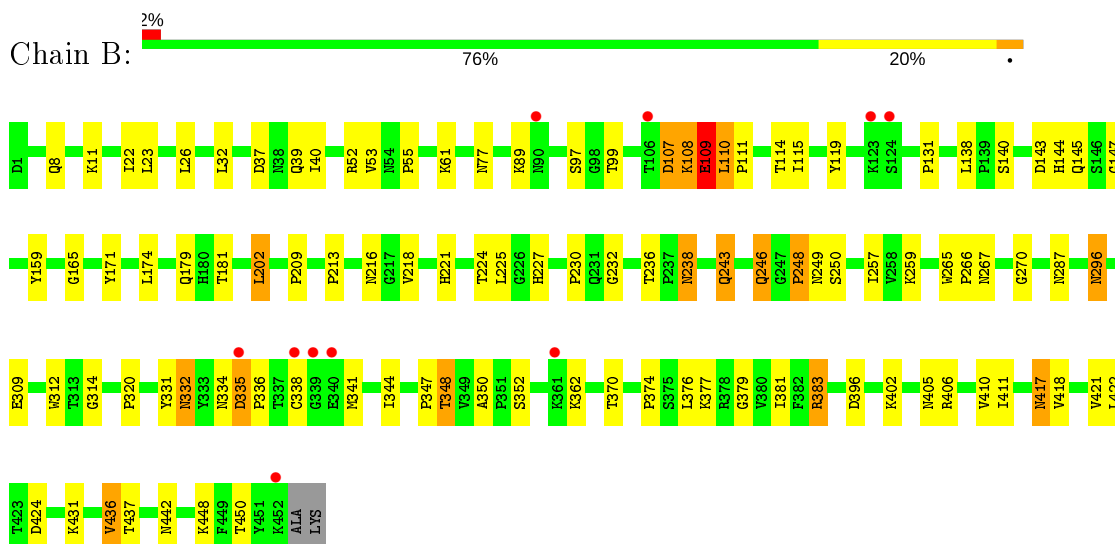These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	60.59Å 158.72Å 221.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 39.85 – 2.13	Depositor EDS
% Data completeness (in resolution range)	76.1 (20.00-2.20) 80.4 (39.85-2.13)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 2.12Å)	Xtriage
Refinement program	X-PLOR, REFMAC	Depositor
R, R_{free}	0.223 , 0.286 0.219 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å²)	23.8	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.35 , 54.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7634	wwPDB-VP
Average B, all atoms (Å²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.
[2] Theoretical values of $< \|L\| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CA, PQQ

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	0.30	0/3558	0.71	1/4847 (0.0%)
1	B	0.30	0/3628	0.71	1/4943 (0.0%)
All	All	0.30	0/7186	0.71	2/9790 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	378	ARG	NE-CZ-NH2	-8.13	116.24	120.30
1	B	109	GLU	N-CA-CB	7.34	123.81	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3470	0	3408	84	0
1	B	3538	0	3476	81	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	24	0	3	1	0
3	B	24	0	3	1	0
4	A	18	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
5	A	255	0	0	7	0
5	B	293	0	0	2	0
All	All	7634	0	6922	167	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 12.

All (167) 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:B:109:GLU:C	1:B:111:PRO:HD3	1.81	1.01
1:A:405:ASN:HD21	1:A:442:ASN:H	1.11	0.95
1:B:405:ASN:HD21	1:B:442:ASN:H	1.22	0.85
1:B:110:LEU:N	1:B:111:PRO:HD3	1.99	0.75
1:B:110:LEU:N	1:B:111:PRO:CD	2.52	0.72
1:A:431:LYS:HD2	1:A:437:THR:HB	1.72	0.72
1:A:23:LEU:HD11	1:A:60:VAL:HG21	1.71	0.71
1:B:22:ILE:HD11	1:B:448:LYS:HB3	1.72	0.71
1:A:268:VAL:HG22	1:A:309:GLU:HB3	1.72	0.70
3:A:1004:PQQ:N1	3:A:1004:PQQ:O9B	2.26	0.68
1:A:160:THR:HG23	1:A:233:LEU:HD22	1.75	0.67
1:A:405:ASN:HD21	1:A:442:ASN:N	1.89	0.67
1:A:66:VAL:HB	1:A:69:ILE:HD13	1.77	0.67
1:B:171:TYR:HB3	1:B:174:LEU:HD12	1.76	0.66
3:B:1004:PQQ:N1	3:B:1004:PQQ:O9B	2.27	0.65
1:B:227:HIS:HB3	1:B:230:PRO:HG3	1.79	0.64
1:A:447:ILE:HD11	1:A:449:PHE:CZ	2.33	0.64
1:A:420:TYR:HB3	1:A:446:LEU:HD21	1.79	0.63
1:B:109:GLU:CA	1:B:111:PRO:HD3	2.29	0.63
1:A:19:LYS:HG3	1:A:447:ILE:HD12	1.82	0.62
1:B:181:THR:HG21	1:B:216:ASN:HD22	1.63	0.62
1:A:140:SER:HA	1:A:145:GLN:HE22	1.64	0.61
1:B:250:SER:HA	1:B:348:THR:HG23	1.82	0.61
1:A:89:LYS:HD2	1:A:89:LYS:H	1.66	0.61
1:A:40:ILE:HG13	1:A:55:PRO:HG3	1.83	0.60
1:A:248:PRO:HB2	1:A:296:ASN:HD21	1.66	0.60
1:A:32:LEU:HD22	1:A:422:LEU:HD13	1.83	0.60
1:A:295:GLN:HE21	1:A:299:LYS:HE2	1.67	0.60
1:A:418:VAL:HG12	1:A:450:THR:HG23	1.85	0.59
1:B:431:LYS:HD3	1:B:437:THR:HG21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:THR:HG21	1:B:383:ARG:HD3	1.85	0.58
1:A:52:ARG:NH2	1:A:61:LYS:HD3	2.17	0.58
1:B:265:TRP:CD2	1:B:266:PRO:HA	2.38	0.58
1:B:39:GLN:NE2	1:B:55:PRO:HD2	2.19	0.57
1:B:89:LYS:HD2	1:B:89:LYS:H	1.68	0.57
1:A:405:ASN:ND2	1:A:442:ASN:H	1.92	0.56
1:A:246:GLN:NE2	1:A:350:ALA:HA	2.19	0.56
1:B:179:GLN:HA	1:B:225:LEU:HD13	1.87	0.56
1:B:332:ASN:HD22	1:B:334:ASN:H	1.53	0.56
1:B:32:LEU:HB3	1:B:422:LEU:HD11	1.86	0.56
1:B:109:GLU:OE1	1:B:110:LEU:N	2.37	0.56
1:A:53:VAL:HG22	1:A:60:VAL:HG22	1.87	0.56
1:B:344:ILE:HD13	1:B:436:VAL:HG11	1.87	0.56
1:A:42:LEU:HD11	1:A:51:LEU:HD12	1.87	0.55
1:A:410:VAL:HG23	1:A:421:VAL:HG12	1.89	0.55
1:A:265:TRP:CD2	1:A:266:PRO:HA	2.41	0.55
1:A:5:THR:HB	1:A:6:PRO:HD2	1.90	0.54
1:B:417:ASN:H	1:B:417:ASN:HD22	1.55	0.54
1:B:246:GLN:NE2	1:B:350:ALA:HA	2.23	0.54
1:B:109:GLU:C	1:B:111:PRO:CD	2.65	0.54
1:B:410:VAL:HG23	1:B:421:VAL:HG12	1.90	0.53
1:B:8:GLN:HA	1:B:11:LYS:HE2	1.90	0.53
1:A:406:ARG:HB2	1:A:424:ASP:HB2	1.90	0.53
1:A:183:THR:H	1:A:186:GLU:HG3	1.73	0.53
1:B:383:ARG:NH1	1:B:383:ARG:HB3	2.24	0.53
1:A:160:THR:HG22	1:A:199:VAL:HG22	1.90	0.53
1:A:425:THR:HA	1:A:444:GLY:H	1.74	0.52
1:A:186:GLU:HB3	1:A:191:ASP:HB3	1.92	0.52
1:A:346:TRP:C	5:A:1102:HOH:O	2.48	0.52
1:B:352:SER:HB3	1:B:376:LEU:HG	1.92	0.52
1:A:301:ALA:O	1:A:304:VAL:HG12	2.09	0.51
1:A:28:LYS:HD2	1:A:46:ALA:HB2	1.93	0.51
1:A:121:TYR:HE2	1:A:123:LYS:HG2	1.74	0.51
1:A:341:MET:HB3	1:A:344:ILE:CD1	2.40	0.51
1:A:23:LEU:HD21	1:A:60:VAL:HG21	1.93	0.51
1:B:352:SER:OG	1:B:374:PRO:HB2	2.11	0.51
1:A:114:THR:HB	1:A:138:LEU:HB2	1.93	0.51
1:A:352:SER:HB3	1:A:376:LEU:HG	1.93	0.51
1:A:425:THR:HA	1:A:444:GLY:N	2.26	0.51
1:B:202:LEU:HB3	1:B:221:HIS:HD2	1.76	0.50
1:B:418:VAL:HG22	1:B:450:THR:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ASN:HB2	5:B:1170:HOH:O	2.12	0.50
1:B:249:ASN:H	1:B:296:ASN:ND2	2.10	0.50
1:B:405:ASN:ND2	1:B:442:ASN:H	2.00	0.50
1:B:248:PRO:HB2	1:B:296:ASN:HD21	1.77	0.50
1:A:157:ILE:HB	1:A:202:LEU:HG	1.93	0.50
1:B:344:ILE:HA	1:B:377:LYS:HD2	1.93	0.50
1:B:381:ILE:HD11	1:B:421:VAL:HG11	1.95	0.49
1:A:249:ASN:H	1:A:296:ASN:ND2	2.10	0.49
1:A:97:SER:HA	1:A:115:ILE:O	2.13	0.48
1:B:143:ASP:HB2	1:B:165:GLY:HA3	1.95	0.48
1:B:236:THR:OG1	1:B:238:ASN:ND2	2.47	0.48
1:B:344:ILE:HD13	1:B:436:VAL:CG1	2.43	0.48
1:B:270:GLY:HA2	1:B:320:PRO:HG3	1.95	0.47
1:A:169:LEU:HD11	4:A:1005:GOL:H2	1.97	0.47
1:A:6:PRO:HG3	5:A:1122:HOH:O	2.14	0.47
1:A:5:THR:C	5:A:1250:HOH:O	2.53	0.47
1:B:40:ILE:HG13	1:B:55:PRO:HG3	1.96	0.47
1:A:341:MET:HB3	1:A:344:ILE:HD13	1.97	0.47
1:B:312:TRP:CE2	1:B:314:GLY:HA3	2.50	0.47
1:B:147:GLY:HA2	1:B:159:TYR:CZ	2.50	0.47
1:B:114:THR:HB	1:B:138:LEU:HB2	1.98	0.46
1:B:374:PRO:HG3	1:B:410:VAL:HG12	1.97	0.46
1:B:144:HIS:ND1	1:B:165:GLY:HA2	2.31	0.46
1:A:248:PRO:HB2	1:A:296:ASN:ND2	2.29	0.46
1:A:181:THR:HG23	1:A:182:PRO:HD2	1.98	0.46
1:B:338:CYS:HB3	1:B:341:MET:O	2.15	0.46
1:A:362:LYS:HD2	1:A:415:ASP:HB3	1.96	0.46
1:B:53:VAL:O	1:B:55:PRO:HD3	2.16	0.45
1:B:52:ARG:NH2	1:B:61:LYS:HD3	2.31	0.45
1:B:406:ARG:HB2	1:B:424:ASP:HB2	1.98	0.45
1:A:238:ASN:HD22	1:A:238:ASN:H	1.65	0.45
1:A:181:THR:C	1:A:194:THR:HG21	2.36	0.45
1:B:32:LEU:HD11	1:B:411:ILE:HG12	1.99	0.45
1:A:324:LEU:HD12	1:A:349:VAL:HG21	1.99	0.45
1:B:37:ASP:O	1:B:39:GLN:HG2	2.16	0.45
1:A:76:GLN:NE2	1:A:144:HIS:H	2.15	0.45
1:B:248:PRO:HB2	1:B:296:ASN:ND2	2.32	0.45
1:B:381:ILE:CD1	1:B:421:VAL:HG11	2.47	0.45
1:B:431:LYS:HD3	1:B:437:THR:CG2	2.47	0.45
1:A:347:PRO:N	5:A:1102:HOH:O	2.50	0.45
1:B:405:ASN:HD21	1:B:442:ASN:N	2.03	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:TYR:CE2	1:A:123:LYS:HG2	2.51	0.45
1:A:413:SER:HB2	1:A:414:PRO:HD2	1.99	0.45
1:A:357:TYR:OH	1:A:364:ILE:HD12	2.18	0.44
1:B:181:THR:HG21	1:B:216:ASN:ND2	2.29	0.44
1:B:23:LEU:HD13	1:B:26:LEU:HD21	1.98	0.44
1:B:97:SER:HA	1:B:115:ILE:O	2.18	0.44
1:A:166:ARG:NH1	5:A:1139:HOH:O	2.51	0.44
1:B:107:ASP:HB3	1:B:110:LEU:HB2	2.01	0.43
1:B:331:TYR:CE2	1:B:347:PRO:HD3	2.53	0.43
1:B:77:ASN:HB2	1:B:99:THR:OG1	2.18	0.43
1:A:83:ALA:HB2	1:A:149:LEU:O	2.19	0.43
1:A:300:VAL:HG21	1:A:306:VAL:HG21	2.01	0.43
1:B:108:LYS:C	1:B:109:GLU:O	2.53	0.43
1:B:362:LYS:HB3	1:B:417:ASN:HB3	2.01	0.43
1:A:168:GLN:N	1:A:172:LEU:HA	2.33	0.42
1:A:312:TRP:CZ2	1:A:314:GLY:HA3	2.54	0.42
1:A:262:ASN:O	1:A:317:PHE:HA	2.18	0.42
1:B:218:VAL:HB	5:B:1225:HOH:O	2.20	0.42
1:A:304:VAL:HA	1:A:305:PRO:HD3	1.89	0.42
1:B:267:ASN:O	1:B:309:GLU:HG2	2.20	0.42
1:A:331:TYR:CE2	1:A:347:PRO:HD3	2.55	0.42
1:B:238:ASN:HD22	1:B:238:ASN:H	1.67	0.42
1:B:246:GLN:HE21	1:B:246:GLN:HB3	1.67	0.42
1:A:381:ILE:CD1	1:A:421:VAL:HG11	2.50	0.42
1:A:440:LEU:HD13	5:A:1046:HOH:O	2.20	0.42
1:B:119:TYR:CE2	1:B:131:PRO:HB3	2.55	0.42
1:A:85:HIS:HD2	1:A:87:ASP:H	1.68	0.41
1:A:160:THR:HB	1:A:230:PRO:HG2	2.00	0.41
1:A:387:ASP:HB2	1:A:388:PRO:HD2	2.01	0.41
1:A:69:ILE:HD12	1:A:100:PHE:CE2	2.55	0.41
1:A:225:LEU:HD23	1:A:262:ASN:HA	2.02	0.41
1:A:74:ASP:OD1	1:A:142:LYS:HD3	2.20	0.41
1:A:215:PHE:CE2	1:A:225:LEU:HD22	2.55	0.41
1:B:352:SER:HG	1:B:374:PRO:HB2	1.86	0.41
1:A:146:SER:OG	1:A:230:PRO:HD2	2.19	0.41
1:B:140:SER:HA	1:B:145:GLN:HE22	1.85	0.41
1:A:443:PRO:O	1:A:444:GLY:C	2.57	0.41
1:A:177:GLN:HA	1:A:180:HIS:CD2	2.55	0.41
1:A:232:GLY:O	1:A:243:GLN:HG2	2.20	0.41
1:A:33:LEU:HD11	1:A:82:PHE:O	2.21	0.41
1:B:379:GLY:HA2	1:B:405:ASN:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ASN:ND2	1:A:289:SER:OG	2.53	0.41
1:A:379:GLY:O	1:A:402:LYS:HA	2.21	0.41
1:A:344:ILE:HD13	1:A:436:VAL:HG11	2.03	0.41
1:B:108:LYS:HB3	1:B:108:LYS:NZ	2.36	0.41
1:B:334:ASN:O	1:B:336:PRO:HD3	2.21	0.41
1:B:224:THR:HG21	1:B:257:ILE:HG23	2.02	0.40
1:B:232:GLY:O	1:B:243:GLN:HG2	2.21	0.40
1:B:341:MET:HB2	1:B:436:VAL:HG21	2.03	0.40
1:A:252:ASP:OD2	1:A:348:THR:HB	2.22	0.40
1:B:202:LEU:HA	1:B:209:PRO:HD3	2.03	0.40
1:B:335:ASP:HA	1:B:336:PRO:HD3	1.82	0.40
1:A:286:ALA:HB1	5:A:1204:HOH:O	2.22	0.40
1:B:213:PRO:HD3	1:B:259:LYS:HE3	2.04	0.40
1:B:379:GLY:O	1:B:402:LYS:HA	2.21	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	440/454 (97%)	400 (91%)	35 (8%)	5 (1%)	14	12
1	B	450/454 (99%)	418 (93%)	30 (7%)	2 (0%)	34	37
All	All	890/908 (98%)	818 (92%)	65 (7%)	7 (1%)	19	19

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	PRO
1	B	248	PRO
1	A	286	ALA
1	B	110	LEU

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Mol	Chain	Res	Type
1	A	146	SER
1	A	170	ALA
1	A	339	GLY

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	382/391 (98%)	363 (95%)	19 (5%)	24	30
1	B	390/391 (100%)	375 (96%)	15 (4%)	33	42
All	All	772/782 (99%)	738 (96%)	34 (4%)	28	35

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	15	GLU
1	A	39	GLN
1	A	68	GLU
1	A	101	LYS
1	A	156	LYS
1	A	181	THR
1	A	186	GLU
1	A	202	LEU
1	A	238	ASN
1	A	243	GLN
1	A	246	GLN
1	A	296	ASN
1	A	315	LYS
1	A	377	LYS
1	A	417	ASN
1	A	433	ASP
1	A	446	LEU
1	A	447	ILE
1	B	107	ASP

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Mol	Chain	Res	Type
1	B	108	LYS
1	B	109	GLU
1	B	202	LEU
1	B	238	ASN
1	B	243	GLN
1	B	246	GLN
1	B	296	ASN
1	B	332	ASN
1	B	335	ASP
1	B	348	THR
1	B	383	ARG
1	B	396	ASP
1	B	417	ASN
1	B	436	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	85	HIS
1	A	145	GLN
1	A	216	ASN
1	A	238	ASN
1	A	246	GLN
1	A	287	ASN
1	A	295	GLN
1	A	296	ASN
1	A	332	ASN
1	A	404	ASN
1	A	405	ASN
1	A	417	ASN
1	A	428	ASN
1	B	71	ASN
1	B	91	ASN
1	B	145	GLN
1	B	180	HIS
1	B	184	GLN
1	B	193	HIS
1	B	216	ASN
1	B	238	ASN
1	B	246	GLN
1	B	296	ASN

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Mol	Chain	Res	Type
1	B	332	ASN
1	B	334	ASN
1	B	404	ASN
1	B	405	ASN
1	B	417	ASN
1	B	428	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)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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	$\#|Z| > 2$
4	GOL	A	1006	-	5,5,5	0.75	0	5,5,5	0.41	0
3	PQQ	B	1004	2	18,26,26	3.59	9 (50%)	14,40,40	1.51	4 (28%)
4	GOL	B	1005	-	5,5,5	0.74	0	5,5,5	0.31	0
4	GOL	A	1007	-	5,5,5	0.74	0	5,5,5	0.52	0
4	GOL	A	1005	-	5,5,5	0.76	0	5,5,5	0.37	0
3	PQQ	A	1004	2	18,26,26	3.59	9 (50%)	14,40,40	1.55	4 (28%)

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
4	GOL	A	1006	-	-	2/4/4/4	-
3	PQQ	B	1004	2	-	0/0/28/28	0/3/3/3
4	GOL	B	1005	-	-	1/4/4/4	-
4	GOL	A	1007	-	-	2/4/4/4	-
4	GOL	A	1005	-	-	2/4/4/4	-
3	PQQ	A	1004	2	-	0/0/28/28	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1004	PQQ	O4-C4	7.46	1.39	1.23
3	A	1004	PQQ	O4-C4	7.34	1.38	1.23
3	B	1004	PQQ	O5-C5	6.28	1.36	1.23
3	A	1004	PQQ	O5-C5	6.26	1.36	1.23
3	A	1004	PQQ	C6A-C5	-6.08	1.42	1.50
3	B	1004	PQQ	C6A-C5	-6.01	1.42	1.50
3	B	1004	PQQ	C9-C9X	-5.03	1.42	1.47
3	A	1004	PQQ	C9-C9X	-5.01	1.42	1.47
3	A	1004	PQQ	C5-C4	-4.82	1.37	1.53
3	B	1004	PQQ	C5-C4	-4.80	1.37	1.53
3	A	1004	PQQ	C3A-C4	-4.40	1.39	1.48
3	B	1004	PQQ	C3A-C4	-4.40	1.39	1.48
3	A	1004	PQQ	C9A-C1A	-4.07	1.41	1.48
3	B	1004	PQQ	C9A-C1A	-4.03	1.41	1.48
3	A	1004	PQQ	C3A-C1A	-2.20	1.37	1.40
3	B	1004	PQQ	C3-C3A	-2.14	1.35	1.40
3	A	1004	PQQ	C3-C3A	-2.10	1.36	1.40
3	B	1004	PQQ	C3A-C1A	-2.03	1.37	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1004	PQQ	C9A-C1A-N1	2.71	129.90	124.25
3	A	1004	PQQ	C9A-C1A-N1	2.49	129.46	124.25
3	A	1004	PQQ	C6A-N6-C7	-2.48	114.49	118.19
3	A	1004	PQQ	C5-C6A-N6	-2.37	110.94	114.96
3	B	1004	PQQ	C9-C9A-C1A	2.27	127.91	122.86
3	B	1004	PQQ	C6A-N6-C7	-2.26	114.81	118.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1004	PQQ	C9-C9A-C1A	2.23	127.83	122.86
3	B	1004	PQQ	C5-C6A-N6	-2.08	111.43	114.96

There are no chirality outliers.
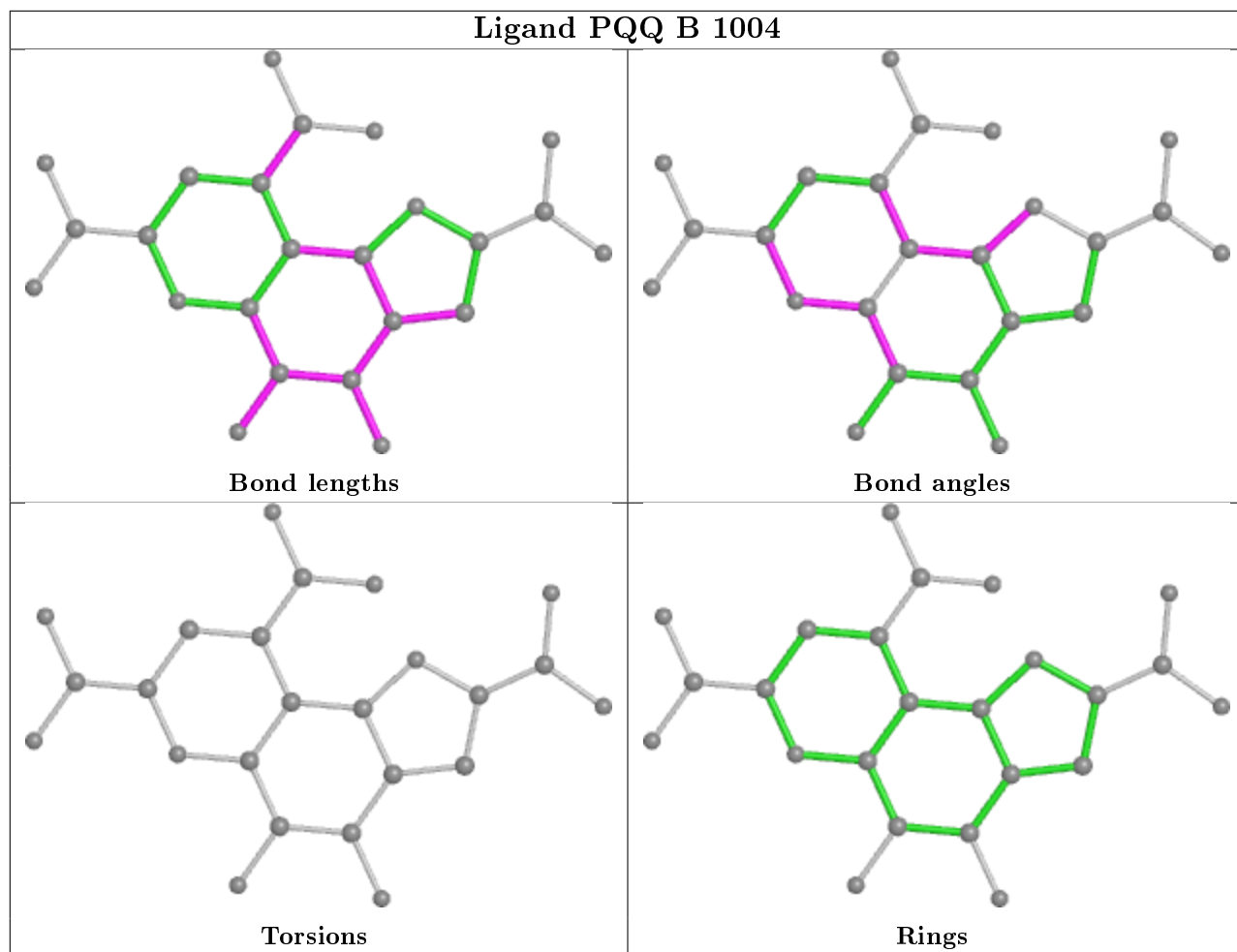
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1006	GOL	O1-C1-C2-O2
4	A	1006	GOL	O1-C1-C2-C3
4	A	1007	GOL	O1-C1-C2-C3
4	A	1005	GOL	O1-C1-C2-C3
4	A	1007	GOL	O1-C1-C2-O2
4	A	1005	GOL	O1-C1-C2-O2
4	B	1005	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1004	PQQ	1	0
4	A	1005	GOL	1	0
3	A	1004	PQQ	1	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 PQQ B 1004

Bond lengths

Bond angles

Torsions

Rings

Ligand PQQ A 1004

Bond lengths

Bond angles

Torsions

Rings

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(Å²)	Q<0.9
1	A	444/454 (97%)	-0.09	7 (1%) 72	70	11, 30, 52, 66	0
1	B	452/454 (99%)	-0.19	10 (2%) 62	59	12, 25, 52, 69	0
All	All	896/908 (98%)	-0.14	17 (1%) 66	65	11, 27, 52, 69	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	ASN	7.6
1	B	338	CYS	4.3
1	B	340	GLU	4.1
1	B	339	GLY	3.2
1	B	124	SER	3.1
1	B	335	ASP	2.9
1	A	103	PRO	2.7
1	A	15	GLU	2.6
1	B	106	THR	2.5
1	B	123	LYS	2.4
1	A	289	SER	2.3
1	A	363	ALA	2.3
1	B	361	LYS	2.2
1	A	185	GLN	2.2
1	A	124	SER	2.1
1	B	90	ASN	2.1
1	B	452	LYS	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)

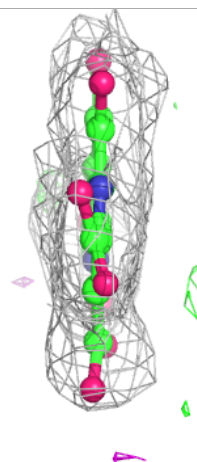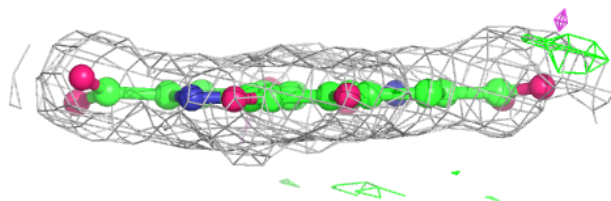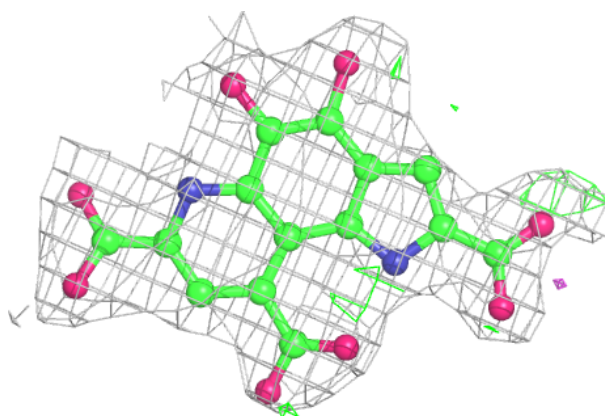There are no carbohydrates in this entry.

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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.
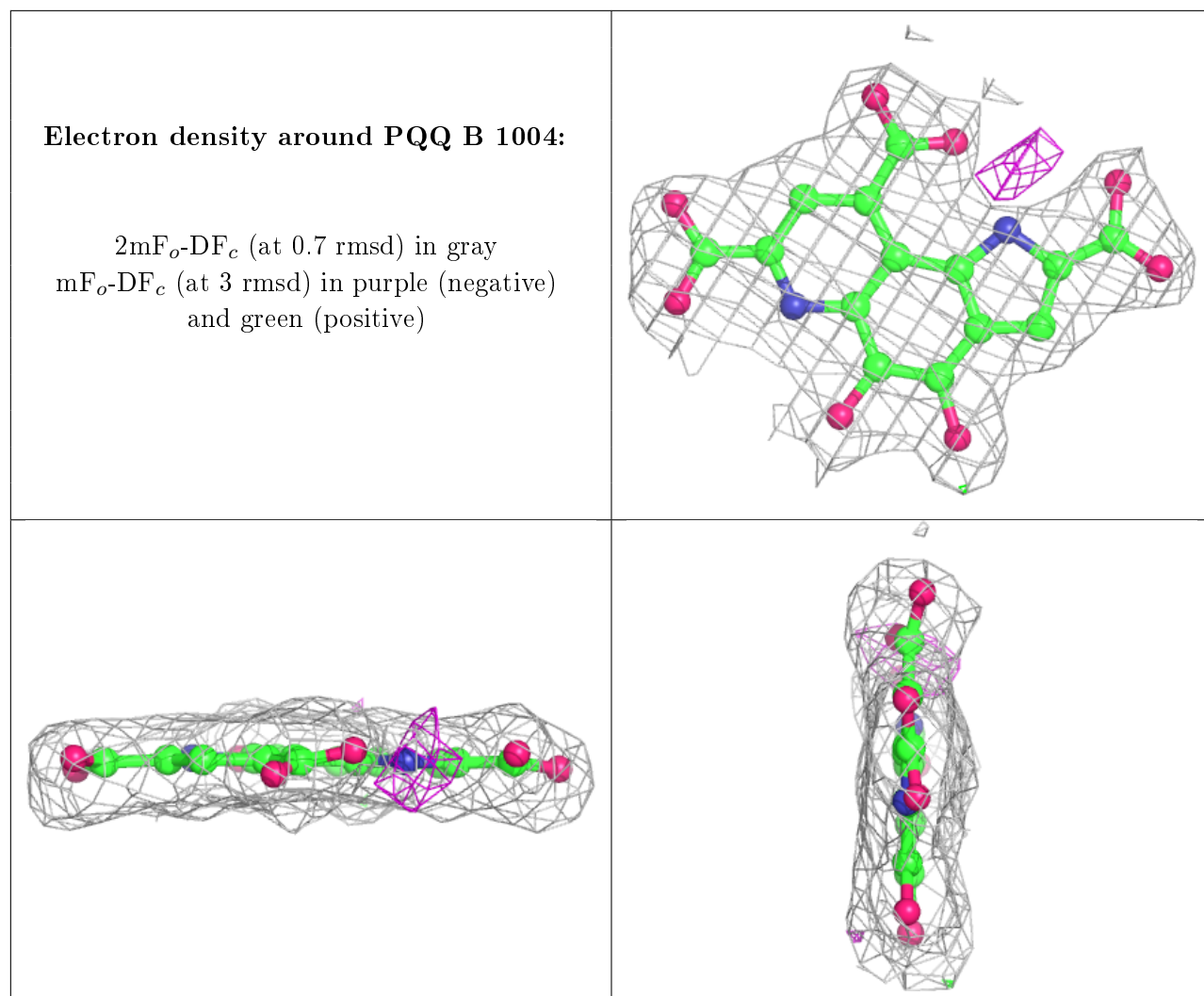
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	A	1006	6/6	0.70	0.18	48,52,54,55	0
4	GOL	B	1005	6/6	0.71	0.18	43,50,51,51	0
4	GOL	A	1007	6/6	0.80	0.26	42,47,52,52	0
4	GOL	A	1005	6/6	0.87	0.17	41,43,45,46	0
3	PQQ	A	1004	24/24	0.90	0.13	29,35,44,47	0
3	PQQ	B	1004	24/24	0.91	0.12	22,32,36,37	0
2	CA	B	1002	1/1	0.98	0.17	21,21,21,21	0
2	CA	A	1003	1/1	0.99	0.04	19,19,19,19	0
2	CA	A	1001	1/1	0.99	0.16	23,23,23,23	0
2	CA	A	1002	1/1	0.99	0.12	15,15,15,15	0
2	CA	B	1001	1/1	0.99	0.06	12,12,12,12	0
2	CA	B	1003	1/1	0.99	0.07	23,23,23,23	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PQQ A 1004:

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

Electron density around PQQ B 1004:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.