



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2017 – 05:38 PM EDT

PDB ID : 1CRU
Title : SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE FROM
ACINETOBACTER CALCOACETICUS IN COMPLEX WITH PQQ AND
METHYLHYDRAZINE
Authors : Oubrie, A.; Rozeboom, H.J.; Dijkstra, B.W.
Deposited on : unknown
Resolution : 1.50 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

<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 : rb-20030345
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) : rb-20030345

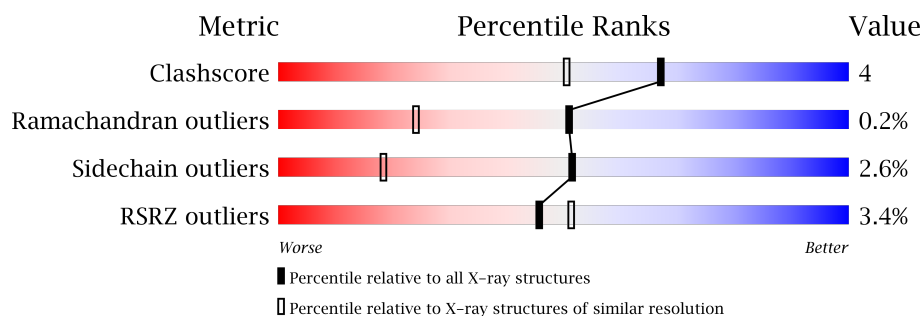
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	112137	2503 (1.50-1.50)
Ramachandran outliers	110173	2445 (1.50-1.50)
Sidechain outliers	110143	2443 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)

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	454	<div> <div>4%</div> <div>89%</div> <div>9%</div> <div>..</div> </div>
1	B	454	<div> <div>3%</div> <div>90%</div> <div>9%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	A	501	-	-	-	X
4	HDN	A	505[C]	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	HDN	B	3001	-	-	-	X
5	GOL	A	506	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8003 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.

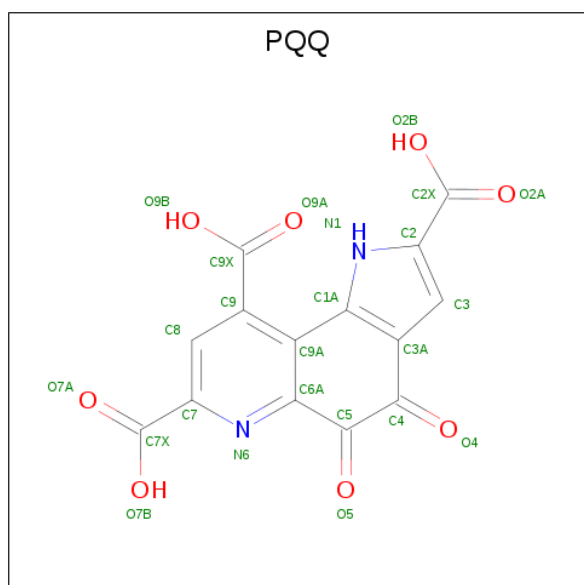
- Molecule 1 is a protein called PROTEIN (SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3502	2226	595	676	5			
1	B	452	Total	C	N	O	S	0	0	0
			3538	2249	600	684	5			

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

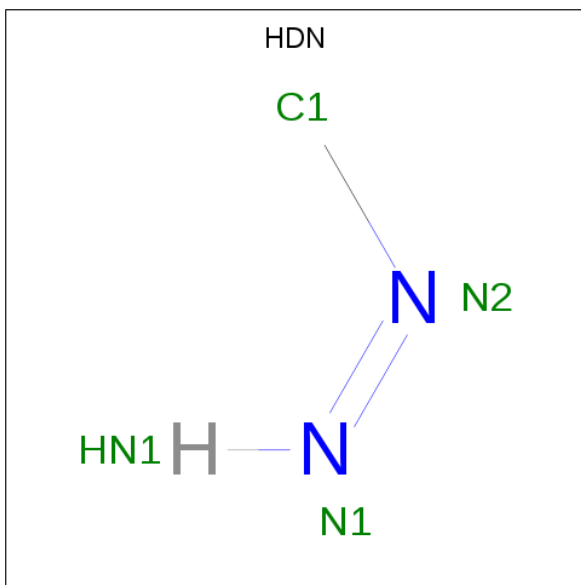
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Ca	0	0
			3	3		
2	A	3	Total	Ca	0	0
			3	3		

- Molecule 3 is PYRROLOQUINOLINE QUINONE (three-letter code: PQQ) (formula: C₁₄H₆N₂O₈).



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

- Molecule 4 is METHYLHYDRAZINE (three-letter code: HDN) (formula: CH_4N_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	1
			9	3	6		
4	B	1	Total	C	N	0	0
			3	1	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

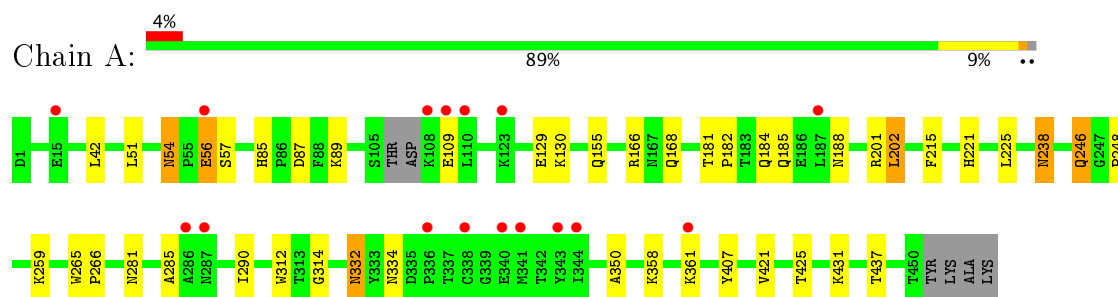
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	432	Total	O	0	0
			432	432		
6	B	459	Total	O	0	0
			459	459		

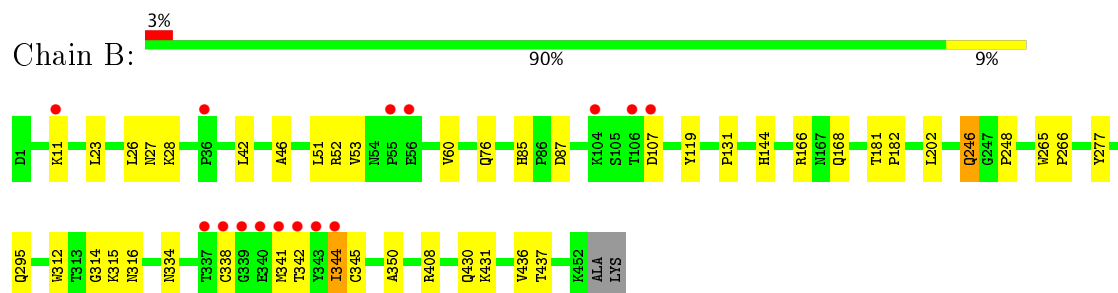
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: PROTEIN (SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE)



- Molecule 1: PROTEIN (SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.58Å 92.66Å 85.73Å 90.00° 105.37° 90.00°	Depositor
Resolution (Å)	20.00 – 1.50 82.66 – 1.50	Depositor EDS
% Data completeness (in resolution range)	95.4 (20.00-1.50) 95.5 (82.66-1.50)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 1.50Å)	Xtriage
Refinement program	REFMAC, X-PLOR	Depositor
R, R_{free}	0.174 , 0.195 0.167 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8003	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HDN, 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	0.37	0/3590	0.85	2/4890 (0.0%)
1	B	0.37	0/3628	0.89	4/4943 (0.1%)
All	All	0.37	0/7218	0.87	6/9833 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	408	ARG	NE-CZ-NH2	-7.36	116.62	120.30
1	A	166	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	B	52	ARG	NE-CZ-NH2	-5.73	117.44	120.30
1	B	166	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	B	277	TYR	CB-CG-CD2	5.50	124.30	121.00
1	A	166	ARG	NE-CZ-NH2	-5.39	117.61	120.30

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	3502	0	3444	27	0
1	B	3538	0	3478	27	0
2	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3	0	0	0	0
3	A	24	0	3	1	0
3	B	24	0	3	1	0
4	A	9	0	11	5	0
4	B	3	0	3	1	0
5	A	6	0	8	0	0
6	A	432	0	0	7	0
6	B	459	0	0	4	0
All	All	8003	0	6950	62	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 4.

All (62) 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)
4:A:505[A]:HDN:N2	4:A:505[A]:HDN:N1	1.61	1.46
4:A:505[B]:HDN:N2	4:A:505[B]:HDN:N1	1.61	1.46
1:A:85:HIS:HD2	1:A:87:ASP:H	1.31	0.76
1:A:285:ALA:HB1	1:A:290:ILE:HD12	1.71	0.73
1:A:202:LEU:HD12	1:A:221:HIS:CD2	2.29	0.67
1:B:53:VAL:HG22	1:B:60:VAL:HG13	1.75	0.67
1:B:85:HIS:HD2	1:B:87:ASP:H	1.44	0.66
1:B:23:LEU:HD11	1:B:60:VAL:HG21	1.77	0.65
1:B:338:CYS:SG	1:B:344:ILE:HG13	2.36	0.64
4:B:3001:HDN:H13	6:B:3167:HOH:O	2.00	0.60
1:A:265:TRP:CD2	1:A:266:PRO:HA	2.37	0.60
1:B:265:TRP:CD2	1:B:266:PRO:HA	2.37	0.59
1:B:344:ILE:HG12	1:B:436:VAL:HG22	1.84	0.59
1:B:344:ILE:HD13	1:B:430:GLN:HB2	1.85	0.58
1:A:129:GLU:HG3	1:A:130:LYS:HG3	1.85	0.57
1:B:334:ASN:HA	1:B:342:THR:HG21	1.87	0.57
4:A:505[C]:HDN:N2	6:A:675:HOH:O	2.31	0.56
1:A:54:ASN:ND2	1:A:57:SER:H	2.03	0.56
1:A:312:TRP:CZ2	1:A:314:GLY:HA3	2.42	0.55
3:A:504:PQQ:N1	3:A:504:PQQ:O9B	2.37	0.55
1:B:315:LYS:NZ	1:B:316:ASN:HD21	2.03	0.55
1:B:315:LYS:HZ3	1:B:316:ASN:HD21	1.53	0.55
1:A:202:LEU:HD12	1:A:221:HIS:HD2	1.73	0.54
4:A:505[C]:HDN:H12	6:A:1008:HOH:O	2.07	0.54
1:B:85:HIS:CD2	1:B:87:ASP:H	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:505[C]:HDN:C1	6:A:675:HOH:O	2.56	0.53
1:B:344:ILE:CG1	1:B:436:VAL:HG22	2.40	0.52
1:A:85:HIS:CD2	1:A:87:ASP:H	2.21	0.52
1:A:168:GLN:HG3	6:A:709:HOH:O	2.09	0.52
1:B:334:ASN:HA	1:B:342:THR:CG2	2.40	0.51
1:A:238:ASN:H	1:A:238:ASN:HD22	1.58	0.51
1:B:23:LEU:HD13	1:B:26:LEU:HD21	1.92	0.51
1:B:23:LEU:HD11	1:B:60:VAL:CG2	2.41	0.50
1:A:246:GLN:NE2	1:A:350:ALA:HA	2.27	0.50
3:B:3005:PQQ:N1	3:B:3005:PQQ:O9B	2.45	0.49
1:A:431:LYS:HD2	1:A:437:THR:HB	1.94	0.49
1:B:76:GLN:NE2	1:B:144:HIS:H	2.10	0.49
1:A:201:ARG:C	1:A:202:LEU:HD13	2.33	0.48
1:B:28:LYS:HD2	1:B:46:ALA:HB2	1.95	0.48
1:A:407:TYR:CD2	1:A:421:VAL:HG11	2.49	0.47
1:A:184:GLN:HE21	1:A:188:ASN:HD21	1.62	0.47
1:A:259:LYS:HE2	6:A:910:HOH:O	2.13	0.47
1:A:332:ASN:ND2	1:A:334:ASN:H	2.12	0.47
1:A:181:THR:HG21	1:A:215:PHE:HB3	1.97	0.46
1:A:54:ASN:HD22	1:A:57:SER:H	1.62	0.46
1:A:358:LYS:HE3	6:A:854:HOH:O	2.16	0.46
1:B:246:GLN:NE2	1:B:350:ALA:HA	2.31	0.45
1:A:425:THR:HG23	6:A:1015:HOH:O	2.14	0.45
1:B:312:TRP:CZ2	1:B:314:GLY:HA3	2.52	0.45
1:A:54:ASN:ND2	1:A:56:GLU:H	2.15	0.45
1:B:431:LYS:HD2	1:B:437:THR:HB	1.99	0.45
1:B:42:LEU:HD11	1:B:51:LEU:HD12	1.99	0.44
1:A:312:TRP:CE2	1:A:314:GLY:HA3	2.52	0.44
1:A:181:THR:HB	1:A:182:PRO:HD2	1.99	0.43
1:B:168:GLN:HG3	6:B:3336:HOH:O	2.20	0.42
1:B:312:TRP:CE2	1:B:314:GLY:HA3	2.55	0.42
1:A:42:LEU:HD11	1:A:51:LEU:HD12	2.02	0.41
1:A:225:LEU:HD12	1:A:225:LEU:C	2.40	0.41
1:B:181:THR:HB	1:B:182:PRO:HD2	2.01	0.41
1:B:28:LYS:HE3	6:B:3500:HOH:O	2.20	0.41
1:B:295:GLN:NE2	6:B:3296:HOH:O	2.55	0.40
1:B:119:TYR:CE2	1:B:131:PRO:HB3	2.57	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	444/454 (98%)	427 (96%)	16 (4%)	1 (0%)	51	24
1	B	450/454 (99%)	436 (97%)	13 (3%)	1 (0%)	51	24
All	All	894/908 (98%)	863 (96%)	29 (3%)	2 (0%)	51	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	PRO
1	B	248	PRO

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	386/391 (99%)	374 (97%)	12 (3%)	45	13
1	B	390/391 (100%)	382 (98%)	8 (2%)	59	26
All	All	776/782 (99%)	756 (97%)	20 (3%)	51	18

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	56	GLU
1	A	89	LYS
1	A	109	GLU

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Mol	Chain	Res	Type
1	A	155	GLN
1	A	185	GLN
1	A	202	LEU
1	A	238	ASN
1	A	246	GLN
1	A	281	ASN
1	A	332	ASN
1	A	361	LYS
1	B	11	LYS
1	B	27	ASN
1	B	107	ASP
1	B	202	LEU
1	B	246	GLN
1	B	341	MET
1	B	344	ILE
1	B	345	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	85	HIS
1	A	180	HIS
1	A	188	ASN
1	A	216	ASN
1	A	229	ASN
1	A	238	ASN
1	A	246	GLN
1	A	281	ASN
1	A	332	ASN
1	B	27	ASN
1	B	76	GLN
1	B	85	HIS
1	B	168	GLN
1	B	231	GLN
1	B	246	GLN
1	B	295	GLN
1	B	316	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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	$\# Z > 2$
3	PQQ	A	504	2	17,26,26	3.27	5 (29%)	15,40,40	3.19	6 (40%)
4	HDN	A	505[A]	-	0,2,2	0.00	-	0,1,1	0.00	-
4	HDN	A	505[B]	-	0,2,2	0.00	-	0,1,1	0.00	-
4	HDN	A	505[C]	-	0,2,2	0.00	-	0,1,1	0.00	-
5	GOL	A	506	-	5,5,5	0.85	0	5,5,5	0.51	0
4	HDN	B	3001	3	0,2,2	0.00	-	0,1,1	0.00	-
3	PQQ	B	3005	2,4	17,26,26	3.29	6 (35%)	15,40,40	3.18	5 (33%)

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
3	PQQ	A	504	2	-	0/0/28/28	0/3/3/3
4	HDN	A	505[A]	-	-	0/0/0/0	0/0/0/0
4	HDN	A	505[B]	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HDN	A	505[C]	-	-	0/0/0/0	0/0/0/0
5	GOL	A	506	-	-	0/4/4/4	0/0/0/0
4	HDN	B	3001	3	-	0/0/0/0	0/0/0/0
3	PQQ	B	3005	2,4	-	0/0/28/28	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	504	PQQ	C9A-C1A	-6.19	1.43	1.48
3	B	3005	PQQ	C9A-C1A	-5.65	1.44	1.48
3	A	504	PQQ	C3A-C4	-4.86	1.38	1.48
3	B	3005	PQQ	C3A-C4	-4.46	1.39	1.48
3	B	3005	PQQ	C3A-C1A	-2.47	1.37	1.40
3	A	504	PQQ	C3A-C1A	-2.22	1.37	1.40
3	B	3005	PQQ	C7-N6	-2.17	1.31	1.34
3	B	3005	PQQ	O4-C4	6.68	1.37	1.23
3	A	504	PQQ	O4-C4	6.86	1.38	1.23
3	A	504	PQQ	O5-C5	6.88	1.38	1.23
3	B	3005	PQQ	O5-C5	7.68	1.39	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	3005	PQQ	O5-C5-C6A	-9.45	111.27	122.03
3	A	504	PQQ	O5-C5-C6A	-8.95	111.84	122.03
3	A	504	PQQ	C5-C6A-N6	-5.02	108.68	115.82
3	B	3005	PQQ	C5-C6A-N6	-4.83	108.96	115.82
3	B	3005	PQQ	O5-C5-C4	-3.84	112.43	119.33
3	A	504	PQQ	O5-C5-C4	-3.83	112.44	119.33
3	A	504	PQQ	O4-C4-C5	-2.75	114.39	119.33
3	B	3005	PQQ	C3A-C4-C5	2.35	121.37	118.10
3	A	504	PQQ	C3A-C4-C5	2.42	121.47	118.10
3	B	3005	PQQ	C9A-C6A-N6	3.07	127.45	123.40
3	A	504	PQQ	C9A-C6A-N6	3.46	127.96	123.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504	PQQ	1	0
4	A	505[A]	HDN	1	0
4	A	505[B]	HDN	1	0
4	A	505[C]	HDN	3	0
4	B	3001	HDN	1	0
3	B	3005	PQQ	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

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	448/454 (98%)	-0.17	16 (3%) 43 49	8, 14, 32, 45	0
1	B	452/454 (99%)	-0.16	15 (3%) 47 52	7, 14, 30, 50	0
All	All	900/908 (99%)	-0.17	31 (3%) 46 51	7, 14, 31, 50	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	338	CYS	8.4
1	B	106	THR	8.2
1	B	56	GLU	5.9
1	B	344	ILE	5.7
1	B	340	GLU	5.1
1	A	338	CYS	4.2
1	B	36	PRO	4.0
1	A	287	ASN	3.6
1	A	340	GLU	3.5
1	B	107	ASP	3.4
1	B	337	THR	3.1
1	B	343	TYR	3.1
1	A	343	TYR	3.0
1	A	56	GLU	3.0
1	A	110	LEU	2.8
1	A	187	LEU	2.8
1	A	108	LYS	2.6
1	B	55	PRO	2.6
1	A	286	ALA	2.6
1	B	104	LYS	2.4
1	A	336	PRO	2.4
1	A	341	MET	2.4
1	B	342	THR	2.3
1	B	11	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	344	ILE	2.2
1	B	339	GLY	2.2
1	B	341	MET	2.2
1	A	123	LYS	2.1
1	A	15	GLU	2.1
1	A	361	LYS	2.0
1	A	109	GLU	2.0

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(Å ²)	Q<0.9
4	HDN	B	3001	3/3	0.50	0.26	15.11	19,19,22,23	3
5	GOL	A	506	6/6	0.77	0.13	2.15	27,29,30,32	0
2	CA	A	501	1/1	1.00	0.08	2.00	8,8,8,8	0
2	CA	B	3002	1/1	1.00	0.08	0.99	7,7,7,7	0
2	CA	B	3003	1/1	1.00	0.07	0.65	8,8,8,8	0
3	PQQ	A	504	24/24	0.93	0.10	0.50	8,9,13,14	0
2	CA	A	503	1/1	0.99	0.07	0.11	10,10,10,10	0
2	CA	A	502	1/1	1.00	0.07	-0.34	8,8,8,8	0
3	PQQ	B	3005	24/24	0.97	0.06	-0.44	10,11,16,19	0
2	CA	B	3004	1/1	1.00	0.06	-1.09	10,10,10,10	0
4	HDN	A	505[C]	3/3	0.78	0.24	-	19,19,22,23	3
4	HDN	A	505[B]	3/3	0.78	0.24	-	30,30,31,31	3
4	HDN	A	505[A]	3/3	0.78	0.24	-	31,31,31,31	3

6.5 Other polymers

There are no such residues in this entry.